(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 October 2001 (11.10.2001)

PCT

(10) International Publication Number
WO 01/75067 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number: PCT/US01/08631

(22) International Filing Date: 30 March 2001 (30.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/540,217	31 March 2000 (31.03.2000)	US
09/649,167	23 August 2000 (23.08.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/540,217 (CIP)
Filed on	31 March 2000 (31.03.2000)
US	09/649,167 (CIP)
Filed on	23 August 2000 (23.08.2000)

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/75067 A2

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-30368. The polypeptides sequences are designated SEQ ID NO: 30369-60736. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-30368 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-30368. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-30368 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-30368.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-30368; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-30368. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (*e.g.*, SEQ ID NO: 30369-60736); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-30368; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-30368.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-30368. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-30368; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 30369-60736; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 30369-60736. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-30368; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 30369-60736. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-30368 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-30368 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-30368 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-30368, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-30368, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-30368 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-30368 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-30368, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-30368, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 30369-60736 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-30368 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-30368), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -uni ts, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-30368). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-30368 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, Proc. *Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′ flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.,* inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 30369-60736 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-30368 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 30369-60736.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: *A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 30369-60736.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.,* cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (*e.g.*, adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (*e.g.*, liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (*e.g.*, a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (*e.g.* proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

(ii) increased sprouting of neurons in culture or in vivo;

(iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

(iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01μg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1μg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.,* amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 30369), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention that is located on the

surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™ as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-30368 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-30368 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-30368, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-30368. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO: 1-30368 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm$_7$), is then added to a final concentration of 10 mM 1-MeIm$_7$. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm$_7$, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed.

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-30368 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-30368) of the present invention are incorporated in the attached Sequence Listing. A subset the predicted polypeptide sequences contain an unknown amino acid, a stop codon, a possible nucleotide deletion or a possible nucleotide insertion. These sequences have been shown in their entirety with the special characters in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-30368. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by

reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-30368 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 121 and Geneseq release 200103 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-30368. The nearest neighbor results for SEQ ID NO: 1-30368 are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provodes the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by PFAM analysis for each peptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-30368. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/540,217

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

21 The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 October 2001 (11.10.2001)

PCT

(10) International Publication Number
WO 01/75067 A3

(51) International Patent Classification[7]: C12N 15/00, 15/12

(21) International Application Number: PCT/US01/08631

(22) International Filing Date: 30 March 2001 (30.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/540,217	31 March 2000 (31.03.2000)	US
09/649,167	23 August 2000 (23.08.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/540,217 (CIP)
Filed on	31 March 2000 (31.03.2000)
US	09/649,167 (CIP)
Filed on	23 August 2000 (23.08.2000)

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report:
4 April 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/75067 A3

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/08631

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/00, 15/12
US CL : 536/23.1, 23.5; 435/6, 320.1, 325

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.1, 23.5; 435/6, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
NONE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- A	Database Genbank, Accession No. AL135937, 15 March 2001 (15.03.2001), particularly nucleotides 29925 through 30325.	1-8 --- 9, 19
X --- A	Database Genbank, Accession No. AA004350, HILLIER et al., Generation and analyhsis of 280.000 Human Expressed Sequence Tags. Genome Res. 07 May 1997 (07.05.1997), Vol. 6, No. 9, pages 807-828.	1-8 --- 9, 19

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search 23 October 2001 (23.10.2001)	Date of mailing of the international search report 02 JAN 2002
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Marianne P. Allen Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/08631

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.
The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I-III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct invention.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 October 2001 (11.10.2001)

PCT

(10) International Publication Number
WO 01/075067 A3

(51) International Patent Classification[7]: C12N 15/00, 15/12

(21) International Application Number: PCT/US01/08631

(22) International Filing Date: 30 March 2001 (30.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/540,217	31 March 2000 (31.03.2000)	US
09/649,167	23 August 2000 (23.08.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/540,217 (CIP)
Filed on	31 March 2000 (31.03.2000)
US	09/649,167 (CIP)
Filed on	23 August 2000 (23.08.2000)

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report:
4 April 2002

(48) Date of publication of this corrected version:
31 October 2002

(15) Information about Correction:
see PCT Gazette No. 44/2002 of 31 October 2002, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/075067 A3

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-30368. The polypeptides sequences are designated SEQ ID NO: 30369-60736. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-30368 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-30368. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-30368 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-30368.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-30368; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-30368. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (*e.g.*, SEQ ID NO: 30369-60736); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-30368; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-30368.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-30368. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-30368; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 30369-60736; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 30369-60736. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-30368; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 30369-60736. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-30368 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-30368 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-30368 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-30368, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-30368, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-30368 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-30368 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-30368, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-30368, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 30369-60736 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-30368 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-30368), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -uni ts, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-30368). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-30368 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, Proc. *Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′ flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 30369-60736 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-30368 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 30369-60736.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: *A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 30369-60736.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (*e.g.*, adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (*e.g.*, liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (*e.g.*, a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (*e.g.* proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

(ii) increased sprouting of neurons in culture or in vivo;

(iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

(iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01μg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1μg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 30369), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention that is located on the

surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™ as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-30368 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-30368 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-30368, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-30368. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO: 1-30368 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-$MeIm_7$), is then added to a final concentration of 10 mM 1-$MeIm_7$. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-$MeIm_7$, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed.

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-30368 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-30368) of the present invention are incorporated in the attached Sequence Listing. A subset the predicted polypeptide sequences contain an unknown amino acid, a stop codon, a possible nucleotide deletion or a possible nucleotide insertion. These sequences have been shown in their entirety with the special characters in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-30368. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by

reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-30368 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 121 and Geneseq release 200103 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-30368. The nearest neighbor results for SEQ ID NO: 1-30368 are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provodes the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by PFAM analysis for each peptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-30368. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/540,217

Table 1

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	39-41 192 197-200 315-316 540-542 576-580 608-622 635 1004 1185-1187 1273-1279 1431 1474 1721-1722 2036 2136-2137 2457 2471-2474 2513 2599-2603 2988-2989 3105-3106 3212 3276-3277 3306-3308 3352 3365 3374-3376 3433 3448-3450 3555-3558 3693 3949-3953 4067-4072 4160-4162 4558-4560 4581-4582 4612-4614 4837-4840 5483-5484 5603-5606 5700 5802 5980-5984 6135-6136 6403-6404 6452-6453 7209-7212 7447-7449 7452-7460 7536-7541 7554-7555 7622-7623 7630-7636 7660-7665 7701-7703 7771 7778-7783 7798-7801 7921-7923 7994 8010-8012 8025-8026 8145-8151 8227-8229 8415 8497-8499 8936-8938 8986-8991 9002-9004 9013-9017 9337-9338 9366-9368 9375-9376 9391-9392 9395-9396 9431-9436 9443 9475-9476 9517-9518 9522-9525 9586-9589 9603-9604 9851-9852 9854-9855 9874-9895 9905-9908 9947-9952 9969-9980 9986-9992 10025-10026 10033-10037 10167-10172 10277 10480-10482 10488-10489 10498-10503 10520-10522 10537-10538 10592-10594 10628-10630 11226-11227 11339-11344 11406-11407 11431-11432 11731-11734 12150-12151 12239 12241-12244 12555-12559 12615-12618 12785-12787 12978-12981 12984-12985 12997-12999 13567-13568 13592-13595 13606-13608 13873-13875 13999-14004 14360-14369 14650-14651 14684-14685 15013-15018 15096 15174-15181 15209-15210 15250-15251 15257 15323-15324 15548-15552 15568-15572 15576-15577 15588-15589 15699-15700 15881-15883 16438-16439 16473-16478 16496-16497 16609-16611 16686-16693 16700-16701 16727-16729 16836-16842 16934-16937 16949-16953 17455-17456 17857-17861 17958-17963 18029-18030 18136-18138 18423-18425 18516-18518 18535-18537 18624-18626 18668-18672 18719-18722 18750-18756 18790-18793 18802-18804 18836-18838 18899-18903 18919-18921 18943-18945 18947-18950 18964-18969 18989-18990 19013-19017 19045-19048 19057-19065 19142-19147 19154-19155 19224 19316-19317 19345-19349 19355-19360 19362 19370 19385-19389 19415-19417 19422-19431 19442-19444 19503 19560-19562 19566 19604-19607 19693 19709-19710 19727-19732 19736-19742 19772 19804-19808 19921-19929 19933-19938 19943-19946 19969-19981 20015-20017 20029-20043 20087-20094 20099-20102 20111-20112 20122-20127 20161-20164 20167-20171 20180-20181 20189-20194 20198-20199 20215-20218 20281-20282 20289 20321-20324 20349-20354 20361 20393-20400 20415-20417 20437-20440 20524-20535 20542-20545 20554-20558 20607-20612 20614-20615 20646-20652 20698-20707 20718-20725 20727-20732 20789-20791 20806-20812 20844-20849 20888-20889 20926 20938-20942 20999-21004 21027-21031 21062-21066 21072-21075 21137-21140 21145-21148 21153-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			21154 21272-21274 21277-21283 21410-21414 21434-21439 21485-21491 21495-21500 21647-21655 21729-21733 21929-21935 21958-21961 21973-21974 21978 22000-22006 22026-22029 22040-22041 22087-22088 22101-22107 22141-22143 22160 22250-22252 22284-22289 22309 22314-22317 22336-22342 22347-22348 22358-22359 22372 22405-22408 22495 22534-22539 22634-22643 22653-22654 22661-22662 22665-22667 22671-22674 22700-22701 22794-22796 22805-22809 22887-22891 22899-22900 22948-22950 22952-22953 22982-22986 22991-22994 23059-23060 23071 23141 23249 23251 23329-23337 23412-23414 23489-23490 23492-23493 23508-23509 23543-23544 23704 23834-23835 23890-23892 23959 24014-24018 25289-25290 25319-25321 25374-25375 25966-25968 26205-26206 26258-26259 26303 26316-26321 26327 26337 26373-26374 26596-26601 26788-26789 26843 26850-26852 26897 27067-27070 27100-27102 27150-27151 27247-27251 27304-27305 27439-27440 27493-27495 27636-27639 27750-27754 27814-27818 27861-27864 27890-27892 27989-27990 28099-28100 28311-28313 28424 28426-28428 29278-29283 29409-29416 29444 29718-29721 30141-30142
adult brain	GIBCO	ABD003	30 51-52 144-145 170-171 180-181 202-203 255-256 302 315-316 319-323 326-327 395 406-407 412-413 464-465 540-542 549 553-554 576-578 626-637 652-653 656 697-699 716-717 721-725 785-786 825 847-855 952 967 969-971 1001-1004 1047 1067-1071 1092-1094 1097-1098 1123-1127 1169-1179 1259-1262 1269-1279 1307 1431 1453-1454 1471-1477 1483 1490-1492 1602-1603 1644-1645 1667-1668 1840 1860 1887-1889 1931 1967 1986-1987 2058 2275-2276 2383-2388 2455-2457 2469 2471-2474 2513 2540-2541 2577-2584 2591 2599-2603 2663-2665 2692-2694 2710 2814-2815 2926 2937-2938 2975-2977 3001 3006-3008 3090 3151-3154 3205-3207 3366 3433 3451 3472-3473 3531-3534 3555-3558 3590 3624 3635 3671-3672 3685 3705-3706 3735-3736 3949-3953 4053-4054 4080-4082 4124-4126 4406-4407 4489-4493 4517-4522 4562-4573 4623-4639 4785-4789 4845-4851 4857-4861 4874-4889 4897-4898 4971-4974 5092-5094 5267-5268 5291-5294 5335-5336 5480-5482 5608-5609 5700 5762 5802 5808-5812 5919-5921 5956-5957 5980-5984 5986-5988 6011-6021 6140-6143 6293-6296 6400 6403-6404 6406-6410 6651-6653 6662-6664 6791-6794 6877-6878 6932-6938 7214-7215 7245-7248 7447-7449 7536-7541 7611-7612 7624-7629 7640-7642 7668-7670 7695-7696 7757-7759 7771 7778-7786 7789-7793 7798-7801 7890 7898-7900 7976 7986-7987 7995-7998 8002 8017-8019 8049-8056 8069 8117-8121 8152-8156 8162 8174-8177 8182-8183 8242-8246 8250 8301-8306 8343-8344 8351-8360 8363-8366 8368-8370 8409-8414 8497-8499 8512-8513 8543-8550 8607-8609 8612-8616 8754-8759 8762-8766 8768-8770 8777-8779 8917-8918 9013-9017 9031-9035 9038-9045 9063-9067 9072-9074 9306-9313 9321-9323 9375-9376 9391-9392 9406-9407 9437-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			9440 9444-9445 9454-9455 9517-9518 9531 9561-9562 9603-9604 9729-9731 9733-9738 9757-9758 9763-9767 9826 9828-9832 9851-9852 9854-9855 9864-9866 9874-9897 9923-9924 9947-9953 9956-9957 9969-9980 10011 10015-10016 10033-10040 10167-10172 10265-10272 10277 10306 10449-10450 10470-10473 10498-10503 10537-10542 10592-10594 10607-10608 10612-10614 10624-10626 10628-10630 10638-10639 10870-10875 10881-10883 10886-10889 10891-10893 10895-10898 10904-10905 10913-10914 10980-10985 11035-11037 11066-11068 11081 11123-11124 11274-11275 11295-11299 11339-11350 11419-11422 11465-11466 11582-11583 11586-11602 11607-11608 11679 11693-11695 11731-11734 11749-11750 11775-11776 11780-11782 11803-11804 11835-11836 11840 11842-11855 11901-11905 11937-11938 12042-12044 12121-12126 12131-12132 12150-12151 12186-12189 12194-12196 12206-12208 12283-12284 12361 12555-12559 12573-12574 12581-12582 12615-12618 12637 12653-12654 12673-12675 12723 12760-12762 12785-12787 12796-12798 12805-12806 13077-13079 13083-13086 13576-13579 13592-13595 13603-13612 13638-13641 13664 13865-13866 13885-13887 13903-13905 13994-13997 14008-14020 14023-14026 14044-14045 14130-14131 14141-14142 14187-14195 14264-14265 14268-14269 14299-14301 14313-14317 14346 14360-14369 14604 14607-14609 14640-14642 14650-14651 14684-14685 14789-14791 15019-15024 15093-15095 15182-15183 15218-15219 15257-15259 15290-15291 15406-15407 15486-15489 15532-15535 15543-15546 15553-15556 15576-15577 15588-15589 15631-15632 15699-15700 15988-15990 16006-16015 16044-16046 16075-16079 16086-16088 16107-16109 16172 16397-16398 16422-16429 16451-16452 16470-16478 16498-16500 16609-16611 16636-16637 16642 16652 16698-16705 16836-16842 16934-16939 17010-17014 17284-17285 17330-17332 17963 18015-18016 18029-18030 18136-18138 18400-18402 18419-18420 18423-18425 18492-18494 18516-18518 18527 18533-18537 18617 18625-18626 18633-18637 18671-18672 18689-18692 18717-18722 18750-18756 18759-18761 18771-18772 18778-18793 18796 18802-18804 18811-18813 18822-18824 18856-18880 18882-18888 18899-18903 18919-18921 18934-18939 18941 18947-18951 18955-18959 18975-18977 18989-18990 18993-18996 19005-19009 19013-19018 19045-19048 19057-19058 19062-19065 19074-19080 19102-19105 19142-19147 19154-19155 19159 19209-19210 19213-19220 19251-19252 19257 19260-19262 19266-19267 19306-19309 19316-19317 19355-19360 19362-19364 19370 19373-19374 19380-19384 19387-19389 19395-19400 19415-19417 19422-19434 19442-19444 19446-19448 19461 19487 19526-19529 19536 19560-19562 19566 19604-19607 19626 19656-19657 19667-19668 19693 19698 19709-19710 19727-19742 19759-19763 19800-19808 19813-19815 19921-19929 19933-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			19946 19953-19957 19962-19963 19972-19981 20029-20043 20072-20079 20099-20102 20106-20112 20114-20120 20130 20146-20148 20151-20154 20161-20164 20167-20171 20180-20194 20198-20207 20222-20225 20235-20240 20257-20262 20265-20278 20289 20316 20321-20324 20328-20330 20345-20354 20360 20393-20400 20415-20420 20425-20431 20441-20446 20469-20474 20476-20479 20485-20490 20502-20503 20505-20510 20514-20520 20542-20545 20548-20557 20559-20562 20568 20607-20612 20614-20619 20644-20645 20649-20671 20681 20683-20685 20689-20692 20698-20707 20712-20713 20718-20725 20753 20758-20767 20789-20797 20806-20812 20824-20849 20863 20897-20900 20927-20928 20938-20942 20952-20954 20999-21004 21027-21045 21062-21066 21069-21075 21105-21111 21141-21142 21153-21154 21171-21174 21197-21198 21202-21207 21225-21226 21229-21235 21237-21247 21256-21262 21272-21274 21277-21280 21297-21298 21301-21303 21351-21352 21434-21439 21446-21450 21467-21469 21485-21491 21647-21655 21712-21717 21729-21733 21881-21885 21899-21902 21905-21910 21917-21921 21924 21929-21938 21948-21950 21955-21957 21971-21972 21978-21982 22000-22015 22020-22029 22042-22046 22080-22088 22090-22094 22101-22107 22117-22119 22141-22151 22160 22169-22170 22187-22192 22208-22226 22230 22251-22252 22261-22264 22277-22289 22300-22302 22318 22329-22332 22343-22350 22358-22359 22365-22371 22373 22381-22388 22399-22404 22409-22410 22434-22435 22440-22448 22495 22559 22571-22581 22607-22609 22644-22651 22653-22654 22661-22662 22665-22667 22671-22674 22703-22706 22760-22762 22794-22796 22823-22829 22857-22858 22870-22874 22881-22893 22923-22924 22948-22954 22973 22982-22986 23007-23021 23047-23052 23070 23080-23083 23112-23116 23212-23215 23229-23233 23237-23239 23249 23251 23329-23337 23343-23344 23382-23390 23399 23412-23421 23486-23487 23489-23490 23492-23493 23495-23496 23508-23509 23704 23718-23721 23726-23730 23761-23763 23771-23780 23800 23802-23809 23816-23819 23827-23833 23836-23837 23843-23844 23878-23880 23890-23892 23941-23956 23959 24005-24011 24014-24018 24021-24024 24772-24774 25085-25090 25279-25290 25307-25308 25319-25322 25373-25375 25403-25407 25598-25603 26196-26199 26209-26213 26217-26218 26221-26223 26237-26239 26258-26259 26266 26304 26327 26337 26347-26348 26350-26352 26359-26365 26373-26374 26376-26377 26395 26423 26469-26470 26596-26601 26665-26666 26681-26683 26691-26694 26736 26755-26756 26788-26789 26844-26845 26876-26879 27044-27047 27053-27057 27067-27070 27100-27102 27105 27133-27134 27193-27200 27206 27209-27213 27218 27254-27260 27269-27270 27281-27282 27299-27301 27304-27305 27334 27340-27342 27493-27495 27501-27503 27544-27545 27574-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			27577 27600-27606 27700-27701 27814-27815 27823-27824 27861-27864 27890-27892 27940-27942 27970 28040-28041 28099-28100 28142-28145 28186 28263-28268 28286 28311-28313 28324-28345 28361-28362 28424 29301-29303 29328-29337 29339-29340 29343-29345 29409-29416 29594-29604 29718-29721 29940-29949 29960-29961 30141-30142 30150-30156 30218-30220 30233-30235 30240-30242
adult brain	Clontech	ABR001	15 227-230 329-330 414-418 716-717 934-935 1136-1139 1436-1437 1472-1473 1505-1506 1593-1594 2058 2132-2137 2139-2142 2378-2381 2407 2550-2552 2577-2584 2587-2588 3094-3096 3221-3222 3377 3414-3417 3526-3529 3861 3949-3953 4340-4341 4515-4516 4574-4576 4857-4861 4986-4987 5092-5094 5654 5700 5864-5866 5992 6140-6143 6540-6541 6570-6571 6814-6831 7668-7670 7802-7804 7994 8008-8009 8017-8019 8111 8129-8131 8160 8162 8242-8246 8368-8369 8453-8454 8512-8513 8762-8766 8982-8983 9339 9391-9392 9510-9516 9531 9666 9682-9683 9828 10167-10172 10312 10520-10522 10913-10914 10959-10962 11064 11071-11075 11345-11350 11805-11808 11835-11836 11900 11937-11938 12050-12056 12194-12197 12796-12798 13925-13926 14604 14714-14717 14785-14786 15182-15183 15400-15403 15462-15463 15545-15546 15563-15564 16123-16128 16174-16176 16570-16573 16601 16623 16642 16851-16853 16924 16934-16937 17963 18015-18016 18046-18048 18500-18501 18516-18518 18535 18655-18658 18671-18672 18762-18766 18955-18959 19018 19045-19048 19207-19208 19257 19350 19380-19384 19447-19449 19484-19486 19526-19529 19659-19661 19670-19671 19706-19710 19764-19767 19804-19808 19924-19925 19962-19963 19965-19967 20120 20189-20194 20231-20234 20271-20273 20412-20413 20441-20446 20456-20468 20485-20494 20521-20523 20676-20680 20710-20711 20718-20725 20733-20734 20747-20751 20824-20826 20836-20843 20926 21060-21061 21069-21075 21105-21111 21153-21154 21353-21354 21410-21414 21454-21457 21554-21556 21647-21655 21924 21929-21935 22003-22015 22040-22041 22045-22046 22077-22083 22108-22116 22165-22168 22246-22249 22284-22289 22373-22374 22411-22432 22625-22628 22637-22643 22671-22674 23080-23083 23112-23119 23141 23201-23202 23358-23360 23412-23418 23526-23531 23761 23793-23797 23802-23805 23878-23880 24014-24018 24105-24113 24116 25403-25407 26232-26233 26270-26272 26285-26290 26685-26686 27012-27014 27028-27029 27098-27099 27377-27378 27493-27495 27544-27545 27623 27640-27641 27729-27739 27840-27844 27970 28361-28362 28424 29427-29438 30233-30235
adult brain	Clontech	ABR006	21 360-361 510-511 546-547 579-580 792-795 969-971 1165-1168 1228-1231 1252-1256 1453-1454 1472-1473 1681-1687 1975-1977 2044-2045 2214-2219 2231-2232 2270-2271 2306 2396-2400 2458 2826-2827 2951-2955 3158 3274-3275 3313-3314 3326-3331 3483-3484 3686

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3856-3857 3939-3941 4080-4082 4091-4095 4173 4441-4443 4484-4485 4765-4773 4785-4789 4795-4809 4988 4992 5364 5930-5931 5971-5972 6155-6159 6450-6451 7353-7367 7374 7580-7597 7701-7703 7784-7786 7972-7975 8020 8101-8104 8106 8152-8156 8162 8184-8185 8342 8370 8489 8758-8759 8936-8938 8978-8981 9009-9017 9029-9030 9063-9067 9069-9078 9306-9311 9339 9479-9485 9517-9518 9828 9874-9895 9909-9912 10033-10037 10254-10261 10498-10503 10523-10532 10624-10639 10923-10926 10936-10937 11328-11331 11708-11710 12573-12574 12743-12750 12785-12787 13556-13559 13660-13675 13847-13849 14054-14056 14170-14172 14347-14348 14390 14604 14666-14668 14996 15097 15257 15283-15286 15336-15340 15397-15398 15576-15577 15886-15887 15896-15905 16022-16023 16237 16461-16464 16496-16497 16623 16643-16648 16652 16752-16753 17238-17241 17369-17370 17937-17939 17956-17957 18029-18030 18044-18045 18049-18064 18393-18394 18411-18418 18423-18425 18527 18536-18537 18719-18722 18762-18766 18778-18780 18829-18834 18899-18903 18934-18935 19001-19004 19159 19207-19208 19211-19212 19221-19222 19273 19350 19484-19486 19670-19671 19698 19727-19732 19736-19742 19800-19808 19814-19815 19855-19856 19939 19943-19946 19951-19952 19972-19980 20069-20071 20087-20094 20099-20102 20122-20127 20157-20181 20200-20207 20274-20278 20316 20321-20324 20414 20441-20446 20456-20468 20491-20494 20524-20535 20542-20545 20547 20554-20557 20607-20612 20676-20680 20718-20725 20747-20751 20897-20900 21005-21008 21069-21071 21088-21096 21145-21148 21157-21169 21171-21174 21176-21180 21213-21215 21241-21247 21263-21266 21272-21274 21277-21280 21343-21350 21377-21397 21463-21465 21554-21556 21911-21912 21929-21935 21955-21957 21973-21974 21978 22007-22015 22019 22045-22046 22070-22076 22080-22088 22090-22091 22108-22114 22120-22127 22135-22138 22144-22151 22158-22159 22246-22249 22284-22289 22347-22348 22375-22382 22389-22432 22625-22628 22653-22654 22671-22674 22833-22834 22881-22886 22916-22922 23007-23021 23071 23080-23083 23223-23225 23229-23233 23358-23360 23379-23381 23412-23414 23434-23438 23486 23506-23507 23543-23544 23555-23565 23771-23780 23827-23833 23841-23844 23941-23956 24035-24040 25213-25219 25279-25290 25315 25383-25415 26235-26236 26280 26310-26314 26337 26361-26365 26409-26410 26425-26427 26603 26687 26860-26862 27067-27070 27100-27102 27105 27193-27200 27209-27213 27441-27443 27562-27563 27589-27592 27821-27822 27825-27838 28146-28147 28296 28464 29328-29331 29343-29345 29409-29416 29439-29445 29940-29949 30205 30221-30223
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult lung	GIBCO	ALG001	112 156 197-200 227-230 273-278 310-314 332 373-374 419-420 459-460 505 524-525 532-533 549 576-578 635 669 692-693 716-717 845-848 891 919-922 945-946 1028 1064-1066 1071 1136-1139 1158-1161 1235-1237 1307 1411-1413 1431-1435 1705-1714 1721-1722 1792-1794 1879-1880 1986-1987 2072 2202-2203 2299 2306 2599-2603 2886-2887 2975-2977 3195-3197 3273-3275 3281-3282 3433 3487-3503 3550-3554 3686 3731-3732 3820-3821 3840-3852 4489-4493 4612-4614 4720-4725 5057-5059 5335-5336 5557-5560 5801-5804 5846 5919-5921 6170 6400 6405 6791-6794 7056-7057 7209-7212 7536-7541 7654-7655 7660-7665 7693-7694 7742-7743 7747-7751 7806-7808 7812-7818 7988 8079 8263-8265 8339-8341 8349-8360 8368-8369 8430-8433 8466-8476 8497-8499 8510-8511 8688 8917-8918 9072-9074 9306-9311 9340-9342 9408-9414 9456-9458 9531 9615-9616 9815-9820 9835-9840 9851-9852 9874-9895 9899-9901 9989-9992 10017-10019 10038-10040 10277 10306 10498-10503 10520-10522 10550 10592-10594 10603-10606 10759-10764 10873-10875 10895-10898 10980-10985 11123-11124 11212-11216 11339-11344 11359-11369 11372-11396 11399-11402 11423-11426 11431-11432 11473-11474 11476-11478 11495 11578 11609 11658-11659 11669-11671 11711-11712 11731-11734 11809 12140 12150-12151 12186-12189 12241-12244 12258 12374-12377 12470-12471 12519-12540 12555-12559

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lymph node	Clontech	ALN001	167 170-171 180-181 302 332 395 425-427 505 635 670-671 849-851 919-922 973-987 998-1000 1028 1047 1086-1087 1232-1234 1259-1262 1273-1279 1307 1456-1460 1499 1569-1570 1667-1668 1705-1714 1879-1880 1943 2063-2065 2126-2129 2272-2274 2404-2406 2409 2471-2474 2533 3151-3154 3322-3323 3377 3461-3463 3512-3514 3737 3822 3834-3835 3879-3880 4255 4555-4556 4562-4568 5335-5336 5572-5573 5580 5650-5651 5802 5805-5807 5910-5911 6403-6404 6832-6850 7216-7219 7447-7449 7643-7647 7654-7655 7697 7744-7746 7757-7759 7763-7770 7890 7972-7975 7978-7985 8010-8012 8342 8698-8700 9043-9045 9306-9311 9475-9476 9487-9488 9531 9615-9616 9780-9781 9916-9920 10273-10274 10306 11123-11124 11295-11296 11339-11344 11431-11432 11476-11478 11538-11540 11607-11608 11696 11780-11782 11835-11836 12140 12150-12151 12374-12377 12545-12546 12615-12618 12642-12644 12723 12760-12762 12782-12784 12796-12798 12872-12881 13077-13082 13592-13595 13906 14304-14305 14546-14549 15182-15183 15190-15191 15290-15291 15545-15546 15548-15550 15576-15577 15699-15700 16044-16046 16110-16112 16284-16289 16370-16374 16536-16538 16545 16609-16611 16628-16631 16636-16637 16642 16652 16954-16961 17046-17057 17131-17132 17330-17332 17454-17456 17958-17962 18015-18016 18029-18030 18405-18406 18411 18533-18534 18579-18581 18617 18719-18726 18750-18758 18771-18772 18778-18780 18789 18805 18811-18813 18822-18824 18836-18838 18846-18853 18899-18903 18975 18996 19018 19062-19065 19090 19122-19131 19138-19140 19154-19155 19211-19212 19274 19283-19294 19370 19380-19384 19390-19394 19401-19402 19415-19417 19442-19444 19503 19526-19529 19688 19693 19706-19708 19743-19751 19813-19815 19915-19918 19921-19923 19948-19949 19972-19980 20048-20052 20066-20068 20106-20110 20161-20164 20172-20179 20182-20188 20235-20240 20257-20262 20437-20440 20558 20563-20567 20767 20924-20925 20938-20942 21027-21031 21233-21235 21277-21280 21377-21402 21480-21482 21495-21500 21529-21530 21587-21646 21978-21982 22115-22116 22141-22143 22160 22277-22283 22312-22313 22336-22342 22358-22359 22373 22455-22465 22644-22651 22668 22690 22700-22701 22732-22735 22737-22739 22823-22827 22838-22842 23046 23070 23074-23076 23098-23101 23237-23239 23379-23381 23433 23448-23450 23473-23474 23486 23492-23493 23495-23496 23508-23509 23526-23531 23761 23802-23805 23999-24001 24014-24018 24772-

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young liver	GIBCO	ALV001	10-14 165-166 170-171 202-203 218-219 324-325 332 461-463 534-535 582-584 674-676 847-848 900-904 1035-1037 1058-1060 1123-1127 1346-1347 1431 1470 1478 1527-1528 1705-1714 1778-1779 1908-1909 1967 1980-1982 2015-2018 2284-2298 2570-2574 2599-2603 3255-3259 3276-3277 3374-3376 3507 3512-3514 3518-3520 4091-4095 4160-4162 4273-4274 4343-4346 4370-4371 4515-4516 4562-4568 4600-4601 4640-4643 4857-4861 5152-5153 5335-5336 5370 5512-5516 5519-5521 5572-5573 5899-5902 5997-6000 6011-6021 6400 6572-6574 6585-6592 6791-6794 7209-7212 7214-7215 7258-7263 7426-7442 7536-7541 7630-7636 7648-7653 7671-7673 7681-7687 7701-7703 7742-7743 7778-7783 7798-7805 7815-7818 7930-7932 7947-7948 7995-7997 8017-8019 8079 8113-8114 8145-8151 8157-8159 8187-8200 8242-8246 8250 8342 8349-8350 8377-8379 8434-8452 8461-8464 8497-8499 8502-8503 8512-8513 8543-8550 8554-8555 8607-8609 8689-8690 8758-8759 8762-8766 9317-9318 9391-9392 9395-9396 9460 9475-9476 9478 9522-9525 9531 9558 9561-9562 9585-9589 9617-9626 9719-9722 9829-9832 9848-9850 9854-9855 9874-9895 9902-9904 9929-9935 9965-9968 9984-9985 10167-10172 10265-10267 10277 10484-10487 10520-10522 10588-10591 10907-10912 10936-10937 10966 11314-11315 11406-11407 11431-11432 11468-11472 11495 11741-11742 11803-11804 11840 11890-11891 12140 12173 12177-12181 12637 12723 12829-12830 12948-12962 13077-13079 13638-13641 13865-13866 13873-13875 13999-14003 14054-14056 14692-14693 14784 14789-14791 15011-15012 15019-15024 15096 15182-15183 15218-15219 15243-15248 15250-15251 15290-15291 15381-15385 15406-15407 15412-15414 15530-15531 15548-15550 15576-15577 15588-15589 15591-15592 15863-15866 16168-16171 16177-16181 16365-16366 16484-16486 16545 16550-16552 16601 16636-16637 16642-16648 16652 16702-16703 16710-16712 16752-16753 16851-16853 16878-16881 16894-16896 16913-16915 16934-16937 17026-17028 17284-17285 17330-17332 17857-17861 17955 18001-18003 18029-18030 18069-18072 18207-18210 18421-18422 18500-18501 18527 18536-18537 18642-18643 18668-18677 18719-18722 18730-18732 18745-18758 18761 18773-18777 18789 18796 18829-18834 18857-18880 18906-18907 18925-18933 18942 18955-18959 18976-18977 19029-19035 19221-19222 19224-19225 19228-19229

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC002	4007 4037-4042 4177-4190 4193-4199 4905-4907 5030 5036-5046 5326-5330 7036-7037 7043-7055 7089-7091 7094-7099 7175-7177 7374 7392-7395 7407-7414 7421-7442 7444-7446 8466-8476 8710-8715 8802-8806 8839-8841 8855-8859 8866-8868 9150-9151 9182-9193 9201-9208 9213-9229 9231-9234 9258-9259 9277-9286 9291-9296 9300 9312-9313 10324-10325 10330-10331 10349-10350 10443-10444 10704-10718 10723-10724 10726-10750 10755-10769 10773-10777 10835-10839 10842-10867 10879-10880 11890-11891 13176 13184-13188 13324-13325 13701 13706-13736 13751 13815-13818 13823 13825-13831 13854-13860 14962 14981-14983 15110-15114 15718-15725 15838-15841 15847-15854 15910-15911 15939-15943 15951-15960 15964-15982 15991-16000 16016-16018 16024-16027 17275-17277 17409-17430 17637-17641 17688-17696 17699-17700 17748-17751 17771-17776 17783-17786 17805-17806 17813-17817 17819-17824 17828-17829 17837-17841 17843-17847 17871-17873 17876-17879 17888-17890

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC003	1578-1585 4052 4205 4899-4903 4908-4910 5031-5032 5042 5334 6796-6800 7061-7064 7067-7087 7091 7094-7099 7374 7392-7395 7426-7442 7467-7476 8839-8841 8859 8862 8899-8902 9145-9149 9152-9181 9259 9269-9304 10443-10444 10759-10764 10819-10868 11076-11077 13130-13132 13183 13751 13815-13832 15112 15120-15123 15718-15725 15847-15854 15944-15945 15966-15968 15991-16018 16021 17609 17653-17667 17683-17684 17734-17736 17771-17776 17783-17786 17791-17799 17805-17806 17827 17837-17841 17843-17847 17862-17868 18010-18012 18075-18080 18152-18154 18175-18183 18211-18214 18216-18218 18230-18239 18255-18258 18275-18370 21304-21325 21501-21515 21728 21788-21799 22498-22522 22525-22530 22582-22598 22603-22606 22610-22617 22702 23029-

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	1604-1607 4008-4036 4049-4051 4180-4190 4923-4928 5242 5326-5330 7067-7087 7093 7175-7177 7426-7442 7475 8807-8813 8822-8835 8839-8846 8850-8853 8855-8858 8862 8870-8873 8876 8892-8898 9088-9099 9152-9181 9205-9208 9226-9229 9239-9257 9259 9294-9296 9301-9304 10343 10347-10350 10443-10444 10726-10727 10759-10764 10775-10777 10842-10867 13000-13004 13307-13308 13341 13422-13423 13425-13495 13730-13735 13737-13750 13823 14981-14983 15110-15111 15120-15123 15718-15725 15815-15817 15827-15833 15939-15943 15966-15968 15991-15996 16016-16018 17606-17608 17701 17836 17857-17874 17876-17887 17891-17894 18097-18134 18145-18151 18155-18156 18184 18255-18263 18291-18292 18335-18340 18354 21549-21553 21573-21586 21660-21711 21728 21788-21799 21863-21876 22525-22530 22596-22598 22605-22606 22658-22660 24187-24193 24227 24358-24369 24436-24438 24473-24480 24607-24609 24722-24726 24749-24771 24795-24816 24869-24870 24908-24923 24963 25017-25048 25052-25060 25078-25084 25091-25100 25114-25139 25147-25170 25187-25192 25247-25248 25359-25363 25461-25470 25489-25494 25515-25521 25539-25550 25572-25593 25623 25633-25650 25676-25679 25728-25732 25741-25782 25883-25889 25901-25902 25906-25911 25957-25959 25969-26016 26059-26067 26136-26138 26150-26152 26157-26164 26629-26653 27943-27947 28522-28524 28533-28539 28571 28607-28614 28646-28650 28709-28719 28748 28754-28760 28768-28781 28809-28814 28822-28824 28882-28887 28914-28916 28933-28935 29012 29031-29038 29071-29082 29087-29095 29104-29107 29116-29141 29154-29158 29327 29446-29450 29492-29494 29590-29605 29614-29620 29630 29645-29654 29663-29678 29686-29703 29741-29742 29763-29836 29842-29869 29879 29902-29911 29964-29968 30002-30003 30048-30052 30084-30093 30118-30134 30145-30149 30167-30177 30179-30182 30201-30204 30236-30239 30254-30255 30275-30281 30343-30347
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fetal brain	Clontech	FBR001	202-203 847-848 1097-1098 1259-1262 1721-1722 2404-2406 2951-2955 5276-5278 5802 7902-7903 8377-8379 9196-9200 9443 9828 9969-9980 10273-10274 10326-10328 10876 10976-10978 11024-11025 11476-11478 11731-11734 11803-11804 12127-12128 12150-12151 13107-13117 13581-13583 14604 17366-17368 17455-17456 18627-18628 18964-18969 19018 19211-19212 19362 19387-19389 19401-19402 20328-20330 20345-20348 20554-20557 21256-21266 21377-21397 21434-21439 21978 22141-22143 22200-22203 22637-22643 22899-22900 23222 23709 23893-23902 25416-25417 26307-26309 26329 26831 27113 27245-27246 27386-27389 27976-27982 28186 30141-30142
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fetal brain	Clontech	FBR006	3-4 168 192 197-200 240-250 324-325 329-330 362 373-374 464-465 532-535 553-554 576-578 613-614 713-715 847-848 912 927 934-935 949-950 1044-1045 1071 1097-1098 1203-1204 1235-1237 1273-1279 1304 1411-1413 1488-1489 1569-1570 1591-1592 1678-1687 1705-1714 1923-1924 1977 2023-2029 2145 2228 2231-2253 2259-2264 2356 2375 2396-2400 2404-2406 2431 2437-2439 2475 2525-2528 2599-2603 2656-2658 2663-2665 2707-2716 2720-2732 2734-2745 2770-2772 2808-2811 2871-2873 2889-2891 2931-2935 2951-2955 3001 3039 3080-3081 3105-3106 3205-3207 3213 3261-3263 3377 3477-3478 3507 3512-3514 3555-3558 3596 3671-3673 3683 3687-3691 3693 3708 3711-3712 3729-3730 3781-3784 3809 3939-3941 3949-3953 4055-4061 4065 4091-4100 4122-4126 4137-4139 4209-4210 4542 4562-4568 4574-4576 4667 4673 4683-4684 4720-4725 4765-4773 4795-4809 4845-4851 4854-4856 4870-4871 4948 4964-4965 4970 5136-5137 5139 5246 5251-5252 5291-5294 5392 5532-5533 5557-5560 5567-5568 5594-5602 5744-5747 6011-6021 6137 6155-6161 6209-6211 6217-6222 6378-6388 6393-6395 6406-6410 6452-6453 6488-6490 6513-6515 6542-6543 6669-6670 6674-6675 6775-6778 7194-7197 7220-7227 7236-7237 7264-7266 7350-7352 7364-7365 7426-7442 7452-7460 7482-7517 7557-7559 7580-7597 7604-7605 7630-7636 7657-7659 7695-7696 7745-7746 7778-7783 7787-7788 7898-7900 7946 7957 7986-7987 7993 8013-8016 8079 8137-8141 8152-8156 8162-8173 8187-8200 8204-8205 8211-8213 8230-8233 8247-8249 8263-8265 8301-8310 8313-8314 8320-8322 8335-8336 8347-8348 8351-8360 8371-8374 8383-8389 8420-8421 8426-8428 8457-8458 8461-8465 8497-8499 8506 8512-8513 8588-8597 8607-8609 8688 8733-8735 8758-8759 8762-8766 8919-8933 8936-8945 8974-8977 8982-8983 8998-9004 9029-9030 9043-9045 9068 9306-9311 9380-9381 9510-9518 9529-9531 9585 9603-9604 9729-9731 9763-9767 9799-9800 9808-9812 9829-9832 9929-9935 9958-9959 9969-9980 9989-9992 9997-10009 10015-10016 10033-10037 10449-10453 10477-10478 10483 10513-10518 10523-10530 10537-10538 10603-10608 10638-10639 10780-10782 10901-10902 10931-10933 10965 11026 11081 11123-11124 11317 11345-11350 11465-11472 11476-11478 11577 11672 11711-11712 11731-11734 11739-11740 11803-11804 11934 12102-12110 12117-12118 12131-12132 12202-12208 12215-12217 12226-12228 12333-12334 12374-12377

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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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induced neuron cells	Stratagene	NTD001	188-191 289-291 576-578 617-618 716-717 1030 1034 1097-1098 1646 2540-2541 2599-2603 2675-2678 2724-2726 2871-2873 2973 3326-3331 3374-3376 3649-3653 3908-3910 3930 3949-3953 4165-4170 4486-4487 4515-4516 4581-4582 4984-4985 5053-5054 5272-5275 5335-5336 5777-5778 5802 5919-5921 5980-5984 6403-6404 6787-6790 6795-6800 7170-7172 7258-7263 7325-7343 7363 7368-7369 7557-7559 7688-7689 7693-7694 7701-7703 7745-7746 7778-7783 7906-7912 7990-7992 8187-8200 8250 8497-8499 8689-8690 8758-8759 8998-9001 9029-9030 9040-9042 9047-9048 9087 9321-9323 9559-9560 9829-9832 9909-9912 9947-9952 9993-9996 10477-10478 10494 10531-10532 10592-10594 10615-10623 10842-10867 10980-10985 11045 11228-11229 11314-11315 11405 11431-11432 11541-11543 11546 11609 11700-11707 11739-11740 11803-11808 11886-11891 11941-11944 12131-12132 12241-12244 12258-12262 12898-12899 12902-12905 12997-12999 13592-13595 13609-13612 13652-13659 14304-14305 15182-15183 15190-15191 15290-15291 15588-15589 15969-15974 16028-16029 16180-16181 16545 16619-16621 16642 17292-17296 17401-17432 17435 17455-17456 18029-18030 18097-18134 18300-18307 18400-18402 18412-18418 18691-18692 18771-18772 18796-18801 18839-18841 18846-18853 18899-18903 18989-18990 19001-19004 19012 19074-19080 19106-19118 19207-19208 19256-19257 19266-19267 19306-19307 19316-19317 19343 19355-19360 19387-19389 19447-19448 19458-19460 19488-19493 19566 19598-19601 19617-19619 19659-19661 19736-19742 19804-19808 19813 19939 19972-19980 20029-20043 20099-20102 20106-20110 20114-20119 20122-20127 20182-20188 20208-20218 20485-20490 20521-20523 20607-20612 20681 20698-20707 20827-20835 20853-20854 20871 21105-21111 21248-21271 21275-21280 21284-21294 21463-21465 21495-21500 21587-21646 21929-21935 22020-22025 22045-22046 22070-22073 22141-22143 22160 22187-22192 22195-22198 22243-22245 22358-22359 22365-22371 22381-22388 22433 22653-22654 22671-22674 22690 22916-22922 22977 23201-23202 23251 23358-23360 23420-23421 23700-23701 23798-23799 23806-23809 23890-23892 24749-24754 24928-24938 24985-24988 25029-25040 25279-25288 25376-25379 26024-26028 26205-26206 26209-26213 26266 26280 26310-26314 26327 26361-26365 26678-26680 27091 27100-27102 27269-27270 27446-27449 27522-27539 27544-27545 27729-27739 27861-27864 27896-27927 27989-27990 28315-28316 28361-28364 29117-29123 29328-29337 29343-29345 29418-29419 29426-29431 29885-29891 30167-30177 30352 30361-30368

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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neuronal cells	Stratagene	NTU001	240-250 373-374 425-427 576-578 847-848 1388-1401 1432-1435 1470 1499 1778-1779 2306 2599-2603 2944 3040-3076 3107-3108 3326-3331 3421-3422 3477-3478 3483-3484 3789-3794 3912-3915 4055-4058 4171-4172 4206-4208 4515-4516 4562-4568 4581-4582 4785-4789 5186-5189 5253-5266 5272-5275 5279-5283 5525-5526 5943-5945 6135-6136 6403-6404 7264-7266 7346-7352 7784-7786 7815-7818 8203 8227-8229 8465 8497-8499 8716-8718 8998-9004 9007-9008 9038-9039 9049-9068 9472-9474 9479-9481 9535-9537 9594-9602 9735-9738 9929-9935 9969-9980 10161-10163 10167-10196 10516-10518 10615-10623 10873-10875 10915-10918 11308-11310 11334-11335 11775-11776 11840 12150-12151 12258 12590-12592 12653-12654 12716-12719 12997-12999 13552-13555 13638-13641 13847-13849 14038-14041 14044-14045 14137-14138 14277-14280 14640-14642 14814-14815 15025-15069 15100-15109 15277-15278 15408-15411 15530-15531 15563-15564 15576-15577 15588-15589 15863-15870 16141-16143 16174-16176 16182-16189 16545 16642 16652 16836-16842 16851-16853 17284-17285 17435-17440 17451-17454 17958-17962 18029-18030 18043 18097-18134 18500-18501 18562-18576 18671-18672 18796-18801 18825-18828 18857-18880 18925-18933 18975 18993-18995 19049-19053 19153 19298-19300 19306-19307 19316-19317 19351-19354 19370 19375-19379 19395-19400 19415-19417 19432-19434 19511 19515-19521 19526-19529 19564-19566 19625 19659-19661 19683-19687 19813-19815 19855-19856 19938 19940-19942 19965-19967 19972-19980 20026-20027 20099-20102 20106-20110 20161-20164 20200-20207 20241 20289 20336-20338 20406-20407 20437-20440 20485-20490 20521-20523 20537-20541 20602-20612 20631-20634 20639-20640 20646-20648 20666-20671 20792-20797 20827-20843 20871 20897-20900 20924-20925 20927-20928 20938-20942 20957-20962 21032-21045 21208-21210 21241-21247 21256-21262 21272-21283 21295-21296 21554-21556 21587-21655 21899-21904 21936-21938 21951-21954 21958-21966 22007-22015 22040-22041 22047-22049 22070-22073 22152-22156 22165-22168 22171-22175 22218-22224 22243-22245 22253-22255 22292-22299 22312-22313 22343-22346 22372-22373

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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pituitary gland	Clontech	PIT004	307-308 395 845-846 1440-1447 1451 1453-1454 2272-2274 2362-2363 3105-3106 3322-3323 3433 4080-4082 4612-4614 4714-4719 4971-4974 5284 5335-5336 5572-5573 6140-6143 6405 6488-6489 7216-7219 7611-7612 7988 8343-8344 8917-8918 9007-9008 9029-9030 9444 9759-9762 10451-10453 10640-10644 10873-10875 11649-11650 11660-11661 11731-11734 11803-11804 11835-11836 12361 12637 13077-13079 13592-13595 14261-14263 14723-14724 15093-15095 15190-15191 15392-15396 16141-16143 16422-16429 16636-16637 16642 16894-16896 18691-18692 18836-18838 18899-18903 18975 19074-19080 19260-19262 19362 19415-19417 19458-19460 19921-19923 20161-20164 20452-20455 20548-20553 20575-20578 20629-20630 20666-20671 21072-21075 21149-21151 21256-21262 21881-21885 21955-21957 22160 22187-22192 22199 22358-22359 22375-22376 22383-22388 22644-22651 22768-22770 22805-22809 22852-22853 22991-22994 23080-23083 23242-23244 23704 23720-23721 23761 26196-26199 26327 26361-26365 26431 26755-26756 27067-27070 27254-27260 27755-27756 27825-27826 27861-27864 28311-28313 29332-29337 29360-29362 29370 30085-30087 30141-30142 30150-30156
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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rectum	Invitrogen	REC001	180-181 534-535 540-542 1681-1687 1705-1714 1721-1722 1745-1746 2272-2274 2675-2678 2695-2698 2813-2846 3326-3331 3555-3558 3687-3691 3717-3720 3834-3835 3949-3953 4692-4695 4857-4861 5246 5337-5341 5572-5573 5802-5804 5919-5921 6209-6211 6400-6404 6406-6410 7209-7212 7426-7442 7609 7747-7751 7757-7759 7778-7783 8074-8078 8323-8325 8329-8334 8453-8454 8741-8750 8986-8991 9029-9030 9043-9045 9305 9375-9376 9391-9392 9456-9458 9531 9585 9828 9921-9922 9986-9988 10263-10264 10277 10306 10480-10482

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salivary gland	Clontech	SAL001	260 307-308 331 551-552 832-836 969-971 981-985 1312-1313 1721-1722 1810-1811 2072 2303 2306-2307 2599-2603 2847 2850-2860 3151-3154 3657 3723-3728 3737 3840-3852 3949-3953 4515-4516 4531-4533 4555-4556 4581-4582 4857-4861 4971-4974 5269-5271 5525-5526 5652-5653 5658 5700 6337-6338 6411-6412 6442-6449 6762-6764 7452-7460 7678-7687 7701-7703 7745-7746 7778-7783 7805 7988 8145-8151 8187-8200 8337-8342 8383-8389 8554-8555 8986-8991 9018-9020 9038-9039 9427-9428 9531 9535-9537 9782-9783 9828 9899-9901 9923-9924 9997-10009 10306 10531-10532 10607-10611 10876 11009 11123-11124 11609 11644-11648 11669-11671 11731-11734 11835-11836 12040-12041 12175-12176 12202-12205 12229-12230 12362 12434 12468-12469 12474 12565-12568 12573-12574 12642-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Salivary gland	Clontech	SALs03	981-985 8698-8700 11538-11540 14546-14549 20316 27814-27815 27989-27990 28424
skin fibroblast	ATCC	SFB001	1307 3374-3376 6285-6288 6791-6794 10306 12258 17026-17028 18029-18030 19011 19939 19972-19980 20182-20188 22141-22143 22160 22495 23415-23418 28424 30150-30156
skin fibroblast	ATCC	SFB002	2926 5805-5807 6166-6168 10306 12258 17026-17028 17038-17041 17455-17456 18029-18030 19011 19548-19553 19813 21060-21061 22141-22143 22160 22373 22495 22531-22533 26879 27636-27639 28424 30150-30156
skin fibroblast	ATCC	SFB003	5803-5804 6166-6168 12258 17335-17339 18029-18030 18778-18780 19062-19065 19548-19553 20182-20188 22007-22015 23051-23052 23419 25340-25341 27269-27270 27814-27815 28424 30150-30156
small intestine	Clontech	SIN001	83 87-94 195-200 307-308 332 373-374 557-559 674-675 783-784 852-855 901-904 1071 1240-1241 1470 1678-1680 1755-1762 1764-1766 1769-1772 2030 2048 2089-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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			27600-27601 27814-27815 27819-27820 28142-28145 28233 29367 30141-30142
uterus	Clontech	UTR001	124-125 188-191 227-230 251-252 301 329-331 738-740 919-922 1028 1047 1453-1454 1562-1564 1705-1714 1893-1901 1912-1913 2366 2374-2377 2926 2988-2989 3001 3205-3207 4557-4560 4712-4713 4971-4974 5903-5906 5919-5921 6114-6136 6235-6237 6403-6404 6533-6535 6625-6626 6932-6938 7678-7680 7728 7771 7798-7801 7921-7923 7946 8010-8012 8084-8085 8090-8093 8137-8141 8313-8314 8368-8370 8415 8420-8421 8689-8690 9072-9074 9264-9265 9517-9521 9535-9537 9577-9578 9828-9832 9848-9850 9929-9935 9953 10033-10037 10268-10272 10508-10512 10537-10538 10980-10985 11071-11075 11135 11505-11506 11546 11609 11731-11734 11803-11804 12023-12026 12046-12049 12190-12191 12378-12397 12432-12433 12894-12897 13107-13117 13592-13597 13888-13895 13954-13956 14058-14059 14261-14263 14445-14447 14604 14650-14651 14988-14992 15182-15183 15187-15189 15290-15291 15390 15576-15577 15699-15700 15855-15857 16145-16146 16174-16176 16600 16643-16648 16716-16723 16851-16853 17330-17332 17454 17958-17962 18015-18016 18527 18655-18658 18673-18677 18761 18789 18825-18834 18894-18896 18899-18903 18936-18939 19036-19039 19074-19083 19362 19370 19375-19379 19387-19389 19442-19444 19560-19562 19609-19615 19693 19727-19732 19764-19767 19816-19818 19926-19929 19933-19937 19950 19981 20029-20043 20120 20122-20127 20146-20148 20151-20154 20289-20296 20298 20328-20330 20366-20368 20401-20405 20427-20431 20469-20471 20491-20494 20554-20557 20602-20606 20629-20630 20649-20652 20689-20692 20753 20758-20767 20801-20805 20858-20862 20864 20938-20942 21005-21008 21072-21075 21213-21215 21281-21294 21377-21397 21911-21912 21955-21957 21978-21982 22019-22025 22050-22055 22090-22091 22187-22192 22218-22224 22251-22252 22261-22264 22358-22359 22362-22364 22373 22405-22408 22571-22581 22622-22624 22644-22651 22663-22664 22887-22891 22955-22957 22969-22970 23047-23050 23094-23097 23141 23425-23427 23439-23447 23543-23544 24029-24033 24130-24144 25085-25090 25340-25341 25374-25375 25416-25417 26221-26223 26270-26272 26285-26290 26327 26607-26609 26676-26677 26755-26756 26853-26854 26860-26862 27173-27174 27294 27348-27353 27493-27496 27602-27606 27636-27639 27649-27654 27729-27739 27861-27864 27896-27927 28105-28121 28133-28137 28311-28313 28424 28426-28428 29339-29340 29378-29379 29962-29963 30150-30156

*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen),

4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	30369	C	1	23	76	
2	30370	B	2	1	735	
3	30371	B	3	1	783	
4	30372	B	4	104	266	
5	30373	B	5	1	1113	
6	30374	C	6	3	164	
7	30375	B	7	112	279	
8	30376	B	8	198	405	
9	30377	B	9	1	687	
10	30378	C	10	346	598	
11	30379	B	11	1	960	
12	30380	B	12	44	350	
13	30381	B	13	264	465	
14	30382	B	14	483	1556	
15	30383	B	15	140	838	
16	30384	B	16	1	372	
17	30385	B	17	1	1404	
18	30386	B	18	25	2013	
19	30387	C	19	1	381	
20	30388	C	20	605	755	
21	30389	B	21	1	912	
22	30390	C	22	124	315	
23	30391	C	23	44	310	
24	30392	B	24	1	330	
25	30393	B	25	1	411	
26	30394	B	26	147	257	
27	30395	B	27	1	597	
28	30396	B	28	201	862	
29	30397	C	29	249	515	
30	30398	B	30	41	816	
31	30399	C	31	26	142	
32	30400	B	32	259	2328	
33	30401	B	33	1	759	
34	30402	B	34	964	2121	
35	30403	C	35	298	449	
36	30404	C	36	115	396	
37	30405	C	37	148	318	
38	30406	C	38	383	483	
39	30407	B	39	1	1125	
40	30408	B	40	1	831	
41	30409	C	41	363	602	
42	30410	B	42	1	324	
43	30411	B	43	64	199	
44	30412	B	44	1	1007	
45	30413	C	45	380	583	
46	30414	B	46	1	432	
47	30415	C	47	1	249	
48	30416	B	48	1	798	
49	30417	B	49	14	1070	
50	30418	C	50	1	225	
51	30419	B	51	1	2673	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
52	30420	B	52	1	258	
53	30421	B	54	1	624	
54	30422	C	55	166	333	
55	30423	B	56	298	380	
56	30424	C	57	139	379	
57	30425	B	58	1	157	
58	30426	B	59	1	447	
59	30427	B	60	1	579	
60	30428	B	61	1	1059	
61	30429	B	62	1	816	
62	30430	B	63	1	558	
63	30431	B	64	1	540	
64	30432	B	65	1	555	
65	30433	B	66	1	648	
66	30434	B	67	1	798	
67	30435	B	68	1	1455	
68	30436	B	69	1	1278	
69	30437	B	70	88	3012	
70	30438	B	71	1	1092	
71	30439	B	72	575	1033	
72	30440	B	73	644	926	
73	30441	B	74	1	1239	
74	30442	B	75	1	1074	
75	30443	B	76	81	467	
76	30444	C	77	44	286	
77	30445	B	78	1	297	
78	30446	B	79	1	978	
79	30447	B	80	72	715	
80	30448	B	81	1	1296	
81	30449	B	82	63	162	
82	30450	C	83	22	420	
83	30451	C	84	201	733	
84	30452	C	85	417	575	
85	30453	B	86	1	267	
86	30454	B	87	112	738	
87	30455	C	88	260	379	
88	30456	B	89	77	399	
89	30457	B	90	158	420	
90	30458	B	91	1	1437	
91	30459	C	92	22	321	
92	30460	B	93	1	843	
93	30461	B	94	142	2798	
94	30462	B	95	887	8434	
95	30463	B	96	1	1014	
96	30464	B	97	1	1197	
97	30465	B	98	16	555	
98	30466	B	99	1	423	
99	30467	B	100	1	651	
100	30468	B	101	233	556	
101	30469	B	102	192	883	
102	30470	C	103	65	274	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
103	30471	C	104	328	546	
104	30472	B	105	80	3900	
105	30473	B	106	1	951	
106	30474	C	107	1	279	
107	30475	C	108	246	368	
108	30476	B	109	1	819	
109	30477	B	110	1	634	
110	30478	B	111	1	379	
111	30479	B	112	80	2747	
112	30480	C	113	139	414	
113	30481	C	114	1	330	
114	30482	B	115	53	618	
115	30483	B	116	1	426	
116	30484	C	117	135	296	
117	30485	C	118	239	432	
118	30486	C	119	381	776	
119	30487	B	120	1	381	
120	30488	C	121	42	175	
121	30489	C	122	1	399	
122	30490	B	123	1	792	
123	30491	B	124	1	894	
124	30492	B	125	1	3498	
125	30493	B	126	8	874	
126	30494	B	127	1	2160	
127	30495	B	128	1	1776	
128	30496	B	129	1	567	
129	30497	B	130	195	728	
130	30498	B	131	1	615	
131	30499	B	132	1	420	
132	30500	B	133	661	2711	
133	30501	B	134	1	621	
134	30502	C	136	1	465	
135	30503	C	137	113	502	
136	30504	C	139	78	269	
137	30505	C	140	98	472	
138	30506	B	141	403	533	
139	30507	C	142	64	315	
140	30508	B	143	1	591	
141	30509	C	144	528	1151	
142	30510	C	145	1	414	
143	30511	B	146	1	936	
144	30512	C	147	91	195	
145	30513	C	148	562	705	
146	30514	C	149	122	313	
147	30515	B	150	566	1535	
148	30516	C	151	75	248	
149	30517	C	152	1	624	
150	30518	C	153	551	655	
151	30519	C	154	315	497	
152	30520	C	155	262	554	
153	30521	C	156	1	282	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
154	30522	B	157	1	508	
155	30523	C	158	243	545	
156	30524	B	159	8	395	
157	30525	C	160	33	194	
158	30526	B	161	50	355	
159	30527	B	162	128	1230	
160	30528	B	163	243	710	
161	30529	B	164	121	742	
162	30530	B	165	152	227	
163	30531	C	166	156	503	
164	30532	B	167	67	1280	
165	30533	B	168	1	444	
166	30534	B	169	161	206	
167	30535	B	170	189	1207	
168	30536	B	171	1	613	
169	30537	B	172	1	70	
170	30538	C	173	611	751	
171	30539	B	174	398	2472	
172	30540	B	175	87	646	
173	30541	B	176	1	1455	
174	30542	C	177	1	339	
175	30543	B	178	1	1458	
176	30544	B	179	278	766	
177	30545	B	181	85	749	
178	30546	B	182	50	498	
179	30547	C	183	1	522	
180	30548	B	184	90	482	
181	30549	B	185	86	442	
182	30550	C	187	129	308	
183	30551	C	188	1	414	
184	30552	B	190	1	378	
185	30553	C	192	252	308	
186	30554	B	193	1	576	
187	30555	C	194	1093	1311	
188	30556	B	195	45	324	
189	30557	B	196	1	249	
190	30558	C	197	309	443	
191	30559	C	198	615	866	
192	30560	B	199	86	1332	
193	30561	B	200	49	334	
194	30562	B	201	64	638	
195	30563	C	202	195	338	
196	30564	C	203	1	357	
197	30565	B	204	1	693	
198	30566	C	205	121	291	
199	30567	C	206	156	380	
200	30568	C	207	1211	1456	
201	30569	B	208	62	328	
202	30570	C	209	105	179	
203	30571	B	210	229	1483	
204	30572	B	211	1	749	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
205	30573	B	212	1	190	
206	30574	C	213	121	367	
207	30575	B	214	121	456	
208	30576	B	215	1	2631	
209	30577	B	216	63	419	
210	30578	B	217	114	485	
211	30579	B	218	628	1447	
212	30580	C	219	252	377	
213	30581	B	220	1	847	
214	30582	B	221	68	343	
215	30583	B	222	138	911	
216	30584	B	223	44	882	
217	30585	B	224	1	429	
218	30586	B	225	87	312	
219	30587	C	226	44	343	
220	30588	C	227	41	286	
221	30589	C	228	1145	1372	
222	30590	B	229	1	720	
223	30591	C	230	1	430	
224	30592	C	231	58	297	
225	30593	B	232	613	683	
226	30594	B	233	613	683	
227	30595	C	234	238	455	
228	30596	B	235	319	615	
229	30597	C	236	255	494	
230	30598	B	237	106	600	
231	30599	B	238	1	654	
232	30600	B	239	1	654	
233	30601	B	240	243	356	
234	30602	B	241	1	932	
235	30603	C	242	36	215	
236	30604	B	243	1	288	
237	30605	C	244	25	186	
238	30606	B	245	1	574	
239	30607	B	246	1	1257	
240	30608	B	247	162	263	
241	30609	C	248	79	207	
242	30610	B	249	194	276	
243	30611	B	250	1	1671	
244	30612	C	251	118	311	
245	30613	B	252	88	1485	
246	30614	B	253	339	443	
247	30615	B	254	667	1165	
248	30616	B	255	1	981	
249	30617	B	256	450	3131	
250	30618	B	257	900	1199	
251	30619	C	258	5	271	
252	30620	B	259	65	689	
253	30621	C	260	1	321	
254	30622	B	261	1	137	
255	30623	B	262	34	282	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
256	30624	B	263	46	856	
257	30625	C	264	157	468	
258	30626	B	265	148	403	
259	30627	C	266	248	481	
260	30628	B	267	171	393	
261	30629	B	268	1	1078	
262	30630	B	269	1	550	
263	30631	B	270	1	1455	
264	30632	B	271	171	602	
265	30633	B	272	1	1056	
266	30634	B	273	1	1101	
267	30635	B	274	1	2335	
268	30636	B	275	303	419	
269	30637	B	276	1	615	
270	30638	B	277	1	543	
271	30639	B	278	1	1602	
272	30640	C	279	585	1001	
273	30641	C	280	260	379	
274	30642	B	281	1	1437	
275	30643	C	282	22	321	
276	30644	B	283	1	843	
277	30645	B	284	142	2796	
278	30646	B	285	458	7217	
279	30647	B	286	84	186	
280	30648	C	287	67	229	
281	30649	C	288	15	245	
282	30650	C	289	125	232	
283	30651	B	290	1	594	
284	30652	B	291	376	670	
285	30653	C	292	82	405	
286	30654	B	293	35	651	
287	30655	B	294	56	487	
288	30656	C	295	313	498	
289	30657	C	296	118	261	
290	30658	B	297	198	1868	
291	30659	B	298	1	1665	
292	30660	C	299	73	108	
293	30661	B	300	1	408	
294	30662	B	301	1	444	
295	30663	B	302	8	311	
296	30664	C	303	144	350	
297	30665	B	304	1	669	
298	30666	C	305	416	820	
299	30667	B	306	253	837	
300	30668	B	307	44	475	
301	30669	B	308	185	885	
302	30670	C	309	206	337	
303	30671	B	310	1	393	
304	30672	B	311	1	1259	
305	30673	B	312	24	434	
306	30674	B	313	44	2687	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
307	30675	B	314	1	154	
308	30676	B	315	288	770	
309	30677	B	316	85	683	
310	30678	B	317	1	873	
311	30679	B	318	1	1737	
312	30680	C	319	1	690	
313	30681	B	320	58	1487	
314	30682	B	321	1	816	
315	30683	B	322	25	772	
316	30684	B	323	42	271	
317	30685	C	324	16	159	
318	30686	C	325	74	280	
319	30687	C	326	221	545	
320	30688	B	327	192	364	
321	30689	C	328	390	638	
322	30690	B	329	151	4215	
323	30691	B	330	1	2076	
324	30692	B	331	1	465	
325	30693	B	332	40	1350	
326	30694	B	333	1	489	
327	30695	B	334	285	744	
328	30696	C	335	96	347	
329	30697	C	336	213	326	
330	30698	B	337	776	4384	
331	30699	B	338	201	317	
332	30700	B	339	1	2713	
333	30701	B	340	1	894	
334	30702	B	341	1	3842	
335	30703	C	342	745	1131	
336	30704	B	343	82	411	
337	30705	B	344	126	2123	
338	30706	B	345	57	1641	
339	30707	C	346	211	654	
340	30708	B	347	44	266	
341	30709	B	348	1	927	
342	30710	C	349	20	124	
343	30711	C	350	9	455	
344	30712	C	351	188	304	
345	30713	C	352	1	333	
346	30714	C	353	140	298	
347	30715	B	354	73	2171	
348	30716	B	355	1	1374	
349	30717	B	356	150	398	
350	30718	B	357	1	585	
351	30719	B	358	1	1716	
352	30720	B	359	81	1912	
353	30721	B	360	249	770	
354	30722	B	361	474	2875	
355	30723	C	362	1	483	
356	30724	C	363	1	251	
357	30725	C	364	28	407	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
358	30726	C	365	88	204	
359	30727	B	366	474	684	
360	30728	C	367	41	394	
361	30729	B	368	253	1044	
362	30730	B	369	468	1111	
363	30731	B	370	1	558	
364	30732	B	371	21	345	
365	30733	B	372	1	744	
366	30734	B	373	1	795	
367	30735	B	374	1	685	
368	30736	B	375	94	414	
369	30737	C	376	86	268	
370	30738	B	377	1	1003	
371	30739	B	378	41	1385	
372	30740	B	379	1	510	
373	30741	B	380	40	746	
374	30742	B	381	100	1991	
375	30743	B	382	1	267	
376	30744	C	383	168	278	
377	30745	C	384	173	208	
378	30746	B	385	141	4538	
379	30747	B	386	1	4086	
380	30748	C	387	398	474	
381	30749	B	388	1	762	
382	30750	B	389	1	1584	
383	30751	B	390	1	2703	
384	30752	B	391	1	489	
385	30753	B	392	527	780	
386	30754	B	393	1	4050	
387	30755	B	394	859	2958	
388	30756	B	395	639	2307	
389	30757	B	396	1	642	
390	30758	B	397	1	3639	
391	30759	B	398	219	540	
392	30760	B	399	1	3225	
393	30761	B	400	1	7552	
394	30762	C	401	626	1201	
395	30763	C	402	627	827	
396	30764	C	403	1	243	
397	30765	B	404	335	538	
398	30766	B	405	41	409	
399	30767	B	406	160	540	
400	30768	B	407	1	597	
401	30769	B	408	1	1605	
402	30770	B	409	1	351	
403	30771	B	410	65	601	
404	30772	B	411	1	870	
405	30773	B	412	91	2867	
406	30774	B	413	33	410	
407	30775	B	414	298	343	
408	30776	B	415	70	310	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
409	30777	B	416	64	1929	
410	30778	B	417	1	298	
411	30779	B	418	37	2612	
412	30780	B	419	1	510	
413	30781	B	420	44	1111	
414	30782	B	421	26	175	
415	30783	C	422	7	57	
416	30784	C	423	27	230	
417	30785	C	424	7	144	
418	30786	B	425	1	1746	
419	30787	C	426	318	486	
420	30788	B	427	896	1115	
421	30789	C	428	106	309	
422	30790	C	429	52	402	
423	30791	B	430	1	309	
424	30792	B	431	167	492	
425	30793	C	432	144	296	
426	30794	B	433	1	786	
427	30795	B	434	336	1303	
428	30796	B	435	333	419	
429	30797	B	436	1	489	
430	30798	C	437	1	199	
431	30799	C	438	110	239	
432	30800	C	439	175	303	
433	30801	C	440	35	181	
434	30802	B	441	1	1896	
435	30803	C	442	1	331	
436	30804	C	443	71	344	
437	30805	C	444	25	135	
438	30806	C	445	406	595	
439	30807	C	446	148	228	
440	30808	C	447	80	106	
441	30809	C	448	7	375	
442	30810	C	449	300	437	
443	30811	C	450	1	357	
444	30812	B	451	1	729	
445	30813	B	452	58	1287	
446	30814	C	453	1	410	
447	30815	C	454	1	411	
448	30816	C	455	1	420	
449	30817	B	456	1	555	
450	30818	B	457	376	1035	
451	30819	B	458	678	807	
452	30820	B	459	88	1485	
453	30821	B	460	300	2082	
454	30822	B	461	1	819	
455	30823	B	462	780	998	
456	30824	B	463	1	1871	
457	30825	B	464	1	1703	
458	30826	B	465	1	594	
459	30827	C	466	120	245	

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460	30828	C	467	1	387	
461	30829	B	468	1	1678	
462	30830	B	469	1	533	
463	30831	B	470	347	656	
464	30832	B	471	1	1098	
465	30833	B	472	224	1518	
466	30834	C	473	44	244	
467	30835	B	474	1	1251	
468	30836	B	475	1	428	
469	30837	B	476	1	495	
470	30838	C	477	233	373	
471	30839	B	478	8	950	
472	30840	C	479	1	813	
473	30841	B	480	1	1071	
474	30842	C	481	224	418	
475	30843	B	482	39	851	
476	30844	B	483	1	2006	
477	30845	B	484	1	561	
478	30846	B	485	167	227	
479	30847	B	486	1	777	
480	30848	B	487	1	645	
481	30849	B	488	1	1749	
482	30850	C	489	26	847	
483	30851	C	490	243	392	
484	30852	C	491	303	407	
485	30853	C	492	23	300	
486	30854	B	493	131	336	
487	30855	C	494	64	156	
488	30856	B	495	180	712	
489	30857	B	496	1	1104	
490	30858	B	497	24	917	
491	30859	B	498	65	228	
492	30860	B	499	1	2172	
493	30861	B	500	1	1338	
494	30862	B	501	1	795	
495	30863	C	502	181	410	
496	30864	B	503	69	1322	
497	30865	B	504	531	1315	
498	30866	C	505	24	320	
499	30867	B	506	1	791	
500	30868	B	507	1	3256	
501	30869	C	508	361	549	
502	30870	B	509	729	3252	
503	30871	B	510	424	1710	
504	30872	C	511	247	750	
505	30873	B	512	11	124	
506	30874	B	514	116	1079	
507	30875	B	515	1	766	
508	30876	B	516	185	796	
509	30877	B	517	1	456	
510	30878	B	518	99	435	

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511	30879	B	519	1	834	
512	30880	B	520	54	246	
513	30881	B	521	1	372	
514	30882	C	522	78	305	
515	30883	C	523	329	484	
516	30884	B	524	1	459	
517	30885	B	525	630	889	
518	30886	B	526	95	343	
519	30887	B	527	353	610	
520	30888	B	528	113	529	
521	30889	B	529	362	1400	
522	30890	B	530	1	441	
523	30891	C	531	1	327	
524	30892	B	532	1	909	
525	30893	B	534	669	1268	
526	30894	B	535	293	826	
527	30895	C	536	12	155	
528	30896	C	537	1488	1706	
529	30897	C	538	26	211	
530	30898	C	539	30	185	
531	30899	B	540	1	789	
532	30900	B	541	63	358	
533	30901	B	542	1	900	
534	30902	B	543	1	728	
535	30903	B	544	112	220	
536	30904	B	545	49	386	
537	30905	B	546	1	585	
538	30906	B	547	328	531	
539	30907	B	548	10	987	
540	30908	B	549	49	248	
541	30909	B	550	131	368	
542	30910	B	551	80	1098	
543	30911	B	552	1	1364	
544	30912	B	553	1	1294	
545	30913	B	554	1	1995	
546	30914	B	555	1	279	
547	30915	B	556	175	715	
548	30916	B	557	1	636	
549	30917	B	558	1331	1600	
550	30918	B	559	32	406	
551	30919	B	560	38	206	
552	30920	B	561	1	1266	
553	30921	C	562	359	501	
554	30922	B	563	315	465	
555	30923	B	564	94	1683	
556	30924	B	565	1	1570	
557	30925	B	566	139	1734	
558	30926	B	567	1	810	
559	30927	B	568	658	1548	
560	30928	B	569	9	395	
561	30929	B	570	1	567	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
562	30930	B	571	1	567	
563	30931	B	572	1	789	
564	30932	B	573	49	3187	
565	30933	B	574	1	1824	
566	30934	B	575	49	1413	
567	30935	B	576	1	1572	
568	30936	C	577	372	468	
569	30937	C	578	58	225	
570	30938	B	579	79	299	
571	30939	B	580	1	645	
572	30940	C	581	582	749	
573	30941	B	582	170	463	
574	30942	B	583	311	520	
575	30943	B	584	1	1074	
576	30944	B	585	39	140	
577	30945	B	586	60	1685	
578	30946	B	587	106	879	
579	30947	C	588	67	362	
580	30948	B	589	45	126	
581	30949	C	590	1	390	
582	30950	C	591	49	240	
583	30951	B	592	1	496	
584	30952	B	593	94	482	
585	30953	C	594	12	341	
586	30954	B	595	1	354	
587	30955	B	596	1	711	
588	30956	B	597	123	412	
589	30957	B	598	1	1107	
590	30958	B	599	1	800	
591	30959	C	600	82	408	
592	30960	B	601	1	3174	
593	30961	B	602	1	444	
594	30962	B	603	1	1671	
595	30963	B	604	1	603	
596	30964	B	605	339	443	
597	30965	C	606	237	380	
598	30966	B	607	1	771	
599	30967	B	608	1	1767	
600	30968	C	609	1	801	
601	30969	B	610	1	1062	
602	30970	B	611	450	3131	
603	30971	C	612	178	435	
604	30972	C	613	164	319	
605	30973	C	614	1	385	
606	30974	C	615	392	853	
607	30975	C	616	24	200	
608	30976	C	617	34	327	
609	30977	B	618	1	624	
610	30978	B	619	179	1222	
611	30979	B	620	1	916	
612	30980	B	621	151	339	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
613	30981	B	622	135	218	
614	30982	B	623	126	300	
615	30983	C	624	258	467	
616	30984	B	625	58	1038	
617	30985	B	626	246	4677	
618	30986	B	627	1	583	
619	30987	C	628	65	283	
620	30988	B	629	162	909	
621	30989	B	630	1	1062	
622	30990	B	631	1	909	
623	30991	C	632	160	297	
624	30992	B	633	352	1143	
625	30993	C	634	301	459	
626	30994	B	635	1	906	
627	30995	B	636	1	654	
628	30996	B	637	1	528	
629	30997	B	638	1	1102	
630	30998	C	639	81	299	
631	30999	B	640	1	345	
632	31000	B	641	39	360	
633	31001	B	642	22	293	
634	31002	C	643	1	504	
635	31003	B	644	107	3786	
636	31004	B	645	1	576	
637	31005	B	646	66	152	
638	31006	B	647	226	522	
639	31007	B	648	1	49	
640	31008	C	649	50	172	
641	31009	C	650	1	516	
642	31010	B	651	1	615	
643	31011	B	652	1	495	
644	31012	B	653	1	663	
645	31013	B	654	1	1812	
646	31014	B	655	1	1401	
647	31015	B	656	102	1151	
648	31016	B	657	1	385	
649	31017	B	658	232	987	
650	31018	B	659	1	1221	
651	31019	B	660	296	496	
652	31020	B	661	57	285	
653	31021	C	662	203	271	
654	31022	B	663	1	711	
655	31023	C	664	351	542	
656	31024	C	665	420	695	
657	31025	B	666	1	1860	
658	31026	B	667	71	2167	
659	31027	B	668	6	344	
660	31028	B	669	217	693	
661	31029	C	670	1	417	
662	31030	B	671	1	990	
663	31031	B	672	109	1169	

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664	31032	C	673	40	117	
665	31033	C	674	301	560	
666	31034	B	675	1	396	
667	31035	B	676	483	1033	
668	31036	B	677	673	3407	
669	31037	B	678	4	672	
670	31038	C	679	39	116	
671	31039	B	680	1	459	
672	31040	B	681	19	370	
673	31041	B	682	112	704	
674	31042	C	683	387	578	
675	31043	B	684	175	254	
676	31044	B	685	1	501	
677	31045	B	686	290	389	
678	31046	B	687	1	486	
679	31047	B	688	1	651	
680	31048	B	689	181	401	
681	31049	B	690	117	406	
682	31050	B	691	1	169	
683	31051	B	692	1	1539	
684	31052	B	693	1	475	
685	31053	B	694	1	1575	
686	31054	B	695	1	507	
687	31055	B	696	1	498	
688	31056	C	697	253	492	
689	31057	B	698	1	588	
690	31058	B	699	75	291	
691	31059	B	700	1	1355	
692	31060	B	701	112	259	
693	31061	C	702	492	833	
694	31062	B	703	297	483	
695	31063	B	704	45	471	
696	31064	C	705	175	318	
697	31065	B	706	1	1074	
698	31066	B	707	94	1180	
699	31067	B	708	1	3866	
700	31068	C	709	215	424	
701	31069	B	710	1	499	
702	31070	B	711	210	325	
703	31071	B	712	1	786	
704	31072	B	713	1	777	
705	31073	B	714	174	1804	
706	31074	B	715	17	368	
707	31075	B	716	769	1831	
708	31076	B	717	76	301	
709	31077	B	718	1	825	
710	31078	C	719	1	396	
711	31079	B	720	93	2449	
712	31080	B	721	408	687	
713	31081	B	722	97	662	
714	31082	B	723	169	610	

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715	31083	B	724	1	2511	
716	31084	C	725	104	410	
717	31085	C	726	75	527	
718	31086	C	727	7	263	
719	31087	B	728	40	1725	
720	31088	B	729	290	1671	
721	31089	B	730	46	465	
722	31090	C	731	378	644	
723	31091	B	732	48	2331	
724	31092	B	733	1	738	
725	31093	B	734	1	1051	
726	31094	B	735	1	840	
727	31095	C	736	291	551	
728	31096	B	737	1	1308	
729	31097	B	738	1	291	
730	31098	C	739	1	702	
731	31099	B	740	1	379	
732	31100	B	741	80	2747	
733	31101	B	742	1	1992	
734	31102	B	743	293	1296	
735	31103	C	744	769	1017	
736	31104	C	745	166	294	
737	31105	B	746	928	1483	
738	31106	B	747	247	375	
739	31107	C	748	47	582	
740	31108	B	749	47	388	
741	31109	B	750	53	458	
742	31110	C	751	32	277	
743	31111	B	752	1	1641	
744	31112	C	753	1	483	
745	31113	B	754	1	1518	
746	31114	B	755	1	321	
747	31115	C	756	604	779	
748	31116	B	757	695	967	
749	31117	B	758	1	768	
750	31118	B	759	101	531	
751	31119	B	760	1	1014	
752	31120	C	761	424	564	
753	31121	B	762	1	333	
754	31122	B	763	15	165	
755	31123	B	764	1	555	
756	31124	B	765	344	476	
757	31125	B	766	1	648	
758	31126	B	767	1	981	
759	31127	C	768	22	162	
760	31128	B	769	1	225	
761	31129	B	770	232	1671	
762	31130	B	771	166	504	
763	31131	B	772	473	1694	
764	31132	C	773	232	414	
765	31133	C	774	374	463	

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766	31134	B	775	1	1128	
767	31135	B	776	337	1284	
768	31136	C	777	25	282	
769	31137	C	778	4	63	
770	31138	C	779	496	1041	
771	31139	C	780	234	365	
772	31140	B	781	1	669	
773	31141	B	782	228	305	
774	31142	B	783	102	755	
775	31143	B	784	1	465	
776	31144	B	785	45	336	
777	31145	C	786	220	366	
778	31146	B	787	332	456	
779	31147	B	788	169	450	
780	31148	B	789	1	1173	
781	31149	B	790	36	355	
782	31150	C	791	354	482	
783	31151	C	792	328	708	
784	31152	B	793	1	829	
785	31153	B	794	14	182	
786	31154	B	795	307	1412	
787	31155	C	796	3	332	
788	31156	B	797	57	704	
789	31157	B	798	1	2406	
790	31158	C	799	1	759	
791	31159	B	800	1	351	
792	31160	B	801	142	272	
793	31161	B	802	34	2951	
794	31162	B	803	92	994	
795	31163	B	804	115	1746	
796	31164	C	805	292	408	
797	31165	B	806	1	880	
798	31166	C	807	156	329	
799	31167	C	808	119	328	
800	31168	C	809	1	492	
801	31169	B	810	1	516	
802	31170	B	811	1	624	
803	31171	B	812	24	1868	
804	31172	C	813	164	208	
805	31173	C	814	91	249	
806	31174	B	815	1	1059	
807	31175	C	816	80	106	
808	31176	C	817	283	408	
809	31177	C	818	1	357	
810	31178	C	819	1	909	
811	31179	B	820	26	71	
812	31180	B	821	1	714	
813	31181	B	822	1	678	
814	31182	B	823	1	675	
815	31183	B	824	24	1046	
816	31184	B	825	1	933	

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817	31185	B	826	1	363	
818	31186	B	827	112	1655	
819	31187	B	828	1	417	
820	31188	B	829	88	1485	
821	31189	C	830	1	411	
822	31190	B	831	114	277	
823	31191	C	832	671	1039	
824	31192	B	833	63	342	
825	31193	B	834	3530	4798	
826	31194	B	835	1	333	
827	31195	B	836	1	831	
828	31196	B	837	1	2514	
829	31197	B	838	98	250	
830	31198	B	839	1	5247	
831	31199	B	840	1	531	
832	31200	B	841	167	466	
833	31201	B	842	160	417	
834	31202	B	843	215	380	
835	31203	B	844	706	1262	
836	31204	B	845	41	368	
837	31205	C	846	252	578	
838	31206	C	847	18	380	
839	31207	C	848	14	349	
840	31208	B	849	1	1176	
841	31209	B	850	244	1174	
842	31210	C	851	27	146	
843	31211	B	852	217	1866	
844	31212	B	853	98	242	
845	31213	B	854	52	2112	
846	31214	B	855	98	242	
847	31215	C	856	237	518	
848	31216	C	857	1	528	
849	31217	C	858	213	365	
850	31218	B	859	86	478	
851	31219	B	860	1	903	
852	31220	B	861	191	539	
853	31221	C	862	283	480	
854	31222	B	863	248	738	
855	31223	B	864	7	1602	
856	31224	B	865	113	375	
857	31225	B	866	50	435	
858	31226	B	867	50	646	
859	31227	B	868	1	2292	
860	31228	B	869	1	2385	
861	31229	B	870	184	852	
862	31230	B	871	1	408	
863	31231	B	872	218	484	
864	31232	B	873	90	588	
865	31233	B	874	445	625	
866	31234	B	875	138	618	
867	31235	B	876	1	753	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
868	31236	B	877	1	489	
869	31237	B	878	113	366	
870	31238	C	879	271	489	
871	31239	B	880	918	3257	
872	31240	B	881	185	631	
873	31241	C	882	3	194	
874	31242	B	883	80	3219	
875	31243	B	884	213	1835	
876	31244	C	885	132	224	
877	31245	B	886	1	741	
878	31246	C	887	132	224	
879	31247	B	888	1	1281	
880	31248	B	889	125	1910	
881	31249	B	890	1	1449	
882	31250	B	891	284	696	
883	31251	B	892	139	390	
884	31252	B	893	1	1308	
885	31253	B	894	1	594	
886	31254	B	895	1	678	
887	31255	B	896	19	240	
888	31256	B	897	47	330	
889	31257	B	898	1	388	
890	31258	B	899	52	564	
891	31259	C	900	310	672	
892	31260	B	901	1	1338	
893	31261	C	902	77	214	
894	31262	C	903	213	467	
895	31263	C	904	202	426	
896	31264	B	905	68	567	
897	31265	C	906	32	205	
898	31266	C	907	513	701	
899	31267	B	908	1	1083	
900	31268	B	909	787	1633	
901	31269	C	910	40	288	
902	31270	B	911	178	330	
903	31271	B	912	129	520	
904	31272	B	913	2267	2626	
905	31273	C	914	34	87	
906	31274	B	915	23	610	
907	31275	B	916	1	1011	
908	31276	B	917	1	156	
909	31277	B	918	1	754	
910	31278	B	919	1	679	
911	31279	B	920	149	761	
912	31280	B	921	38	1175	
913	31281	C	922	542	724	
914	31282	B	923	31	283	
915	31283	B	924	21	341	
916	31284	B	925	199	361	
917	31285	B	926	293	427	
918	31286	B	927	56	145	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
919	31287	B	928	21	341	
920	31288	B	929	199	361	
921	31289	B	930	293	427	
922	31290	B	931	305	465	
923	31291	B	932	280	457	
924	31292	C	933	45	562	
925	31293	B	934	130	618	
926	31294	B	935	418	1620	
927	31295	B	936	115	252	
928	31296	B	937	1	573	
929	31297	B	938	1	2661	
930	31298	B	939	1	1345	
931	31299	C	940	747	1220	
932	31300	C	941	249	429	
933	31301	B	942	1	363	
934	31302	C	943	390	589	
935	31303	B	944	437	1553	
936	31304	B	945	1	1521	
937	31305	C	946	84	347	
938	31306	B	949	80	315	
939	31307	B	950	1	537	
940	31308	C	951	181	330	
941	31309	C	952	55	123	
942	31310	C	953	52	195	
943	31311	C	954	55	123	
944	31312	B	955	336	648	
945	31313	B	956	1	894	
946	31314	B	957	239	1008	
947	31315	B	958	126	308	
948	31316	B	959	1	747	
949	31317	B	960	101	351	
950	31318	B	961	179	1161	
951	31319	B	962	1	138	
952	31320	B	963	8	791	
953	31321	C	964	218	358	
954	31322	C	965	155	454	
955	31323	C	966	124	303	
956	31324	C	967	1	246	
957	31325	B	968	208	364	
958	31326	C	969	95	256	
959	31327	C	970	312	467	
960	31328	B	971	92	424	
961	31329	B	972	88	147	
962	31330	C	973	434	775	
963	31331	B	974	26	1781	
964	31332	C	975	363	692	
965	31333	B	976	201	563	
966	31334	B	977	348	687	
967	31335	C	978	529	660	
968	31336	C	979	418	738	
969	31337	C	980	25	177	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
970	31338	B	981	308	388	
971	31339	C	982	230	580	
972	31340	B	983	101	342	
973	31341	B	984	1	2341	
974	31342	C	985	1	642	
975	31343	B	986	1	1173	
976	31344	B	987	39	6743	
977	31345	B	988	1	516	
978	31346	B	989	1	756	
979	31347	B	990	1	912	
980	31348	B	991	310	441	
981	31349	C	992	58	300	
982	31350	B	993	80	1344	
983	31351	C	994	325	414	
984	31352	B	995	80	1582	
985	31353	C	996	143	499	
986	31354	B	997	173	375	
987	31355	C	998	126	268	
988	31356	B	999	1	762	
989	31357	B	1000	1	642	
990	31358	B	1001	1	1980	
991	31359	B	1002	67	456	
992	31360	B	1003	48	335	
993	31361	B	1004	1	1251	
994	31362	B	1005	1	642	
995	31363	B	1006	1	570	
996	31364	C	1007	1	687	
997	31365	B	1008	1	5450	
998	31366	B	1009	586	852	
999	31367	B	1010	299	530	
1000	31368	B	1011	1	1659	
1001	31369	B	1012	2	550	
1002	31370	C	1013	2	97	
1003	31371	B	1014	1114	1476	
1004	31372	B	1015	22	822	
1005	31373	C	1016	646	903	
1006	31374	C	1017	1	351	
1007	31375	B	1018	226	1284	
1008	31376	B	1019	138	997	
1009	31377	B	1020	341	527	
1010	31378	B	1021	157	1415	
1011	31379	B	1022	55	211	
1012	31380	B	1023	55	211	
1013	31381	C	1024	18	197	
1014	31382	B	1025	1	876	
1015	31383	B	1026	276	487	
1016	31384	B	1027	1	294	
1017	31385	B	1028	273	377	
1018	31386	B	1029	1	936	
1019	31387	B	1030	1	1158	
1020	31388	C	1031	104	283	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1021	31389	B	1032	1	720	
1022	31390	B	1033	1	219	
1023	31391	B	1034	1	170	
1024	31392	B	1035	300	831	
1025	31393	C	1036	1	456	
1026	31394	B	1037	1	1149	
1027	31395	B	1038	1	627	
1028	31396	B	1039	161	375	
1029	31397	B	1040	1	360	
1030	31398	B	1041	1	549	
1031	31399	B	1042	1	384	
1032	31400	B	1046	1	675	
1033	31401	C	1047	379	675	
1034	31402	B	1048	166	388	
1035	31403	B	1049	26	66	
1036	31404	B	1050	1	897	
1037	31405	B	1051	30	1359	
1038	31406	B	1052	1	990	
1039	31407	B	1053	52	1507	
1040	31408	C	1054	66	290	
1041	31409	B	1055	158	2072	
1042	31410	B	1056	1	654	
1043	31411	B	1057	51	1143	
1044	31412	C	1058	66	290	
1045	31413	B	1059	547	1510	
1046	31414	B	1060	1	1499	
1047	31415	B	1061	1	3347	
1048	31416	C	1062	116	235	
1049	31417	B	1063	1	1185	
1050	31418	C	1064	221	823	
1051	31419	B	1065	235	359	
1052	31420	C	1066	1	360	
1053	31421	B	1067	49	386	
1054	31422	C	1068	63	383	
1055	31423	B	1069	60	213	
1056	31424	B	1070	1	919	
1057	31425	B	1071	294	557	
1058	31426	B	1072	1	486	
1059	31427	B	1073	1	450	
1060	31428	C	1074	28	207	
1061	31429	B	1075	1	585	
1062	31430	B	1076	60	213	
1063	31431	B	1077	18	457	
1064	31432	B	1078	112	177	
1065	31433	C	1079	1	375	
1066	31434	B	1080	39	91	
1067	31435	B	1081	91	237	
1068	31436	B	1082	255	376	
1069	31437	B	1083	18	431	
1070	31438	B	1084	98	552	
1071	31439	B	1085	1679	1964	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1072	31440	B	1086	132	1200	
1073	31441	B	1087	95	418	
1074	31442	B	1088	26	56	
1075	31443	B	1089	1	873	
1076	31444	C	1090	107	196	
1077	31445	B	1091	157	777	
1078	31446	B	1092	1	1273	
1079	31447	B	1093	1	202	
1080	31448	B	1094	1	382	
1081	31449	C	1095	189	449	
1082	31450	C	1096	325	429	
1083	31451	C	1097	3	80	
1084	31452	B	1098	50	691	
1085	31453	B	1099	1	474	
1086	31454	B	1100	3	335	
1087	31455	B	1101	137	617	
1088	31456	C	1102	69	134	
1089	31457	B	1103	369	886	
1090	31458	B	1104	1	1332	
1091	31459	B	1105	106	584	
1092	31460	C	1106	97	420	
1093	31461	C	1107	142	381	
1094	31462	B	1108	214	2544	
1095	31463	B	1109	238	1323	
1096	31464	B	1110	1	3000	
1097	31465	B	1111	203	313	
1098	31466	B	1112	288	375	
1099	31467	B	1113	1	480	
1100	31468	C	1114	286	351	
1101	31469	B	1115	59	376	
1102	31470	C	1116	287	504	
1103	31471	B	1117	878	2032	
1104	31472	B	1118	52	648	
1105	31473	B	1119	1	207	
1106	31474	C	1120	1	492	
1107	31475	B	1121	46	830	
1108	31476	B	1122	1	525	
1109	31477	B	1123	1	930	
1110	31478	C	1124	157	606	
1111	31479	C	1125	70	405	
1112	31480	C	1126	247	411	
1113	31481	C	1127	339	590	
1114	31482	B	1128	1	1881	
1115	31483	C	1129	258	452	
1116	31484	B	1130	241	733	
1117	31485	C	1131	294	530	
1118	31486	B	1132	1	439	
1119	31487	B	1133	16	612	
1120	31488	C	1134	234	377	
1121	31489	B	1135	134	763	
1122	31490	C	1136	1	228	

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1123	31491	B	1137	63	443	
1124	31492	C	1138	30	269	
1125	31493	B	1139	44	151	
1126	31494	B	1140	69	199	
1127	31495	B	1141	347	2830	
1128	31496	B	1142	1	576	
1129	31497	C	1143	49	129	
1130	31498	B	1144	1	1107	
1131	31499	B	1145	17	153	
1132	31500	B	1146	277	694	
1133	31501	B	1147	1	735	
1134	31502	B	1148	1	1110	
1135	31503	B	1149	55	552	
1136	31504	C	1150	463	591	
1137	31505	B	1151	136	266	
1138	31506	B	1152	1	795	
1139	31507	B	1153	128	880	
1140	31508	C	1154	178	366	
1141	31509	B	1155	1	654	
1142	31510	B	1156	1	3294	
1143	31511	B	1157	16	854	
1144	31512	B	1158	1093	1185	
1145	31513	B	1159	1	930	
1146	31514	B	1160	1	3969	
1147	31515	B	1161	1	4173	
1148	31516	B	1162	1	2187	
1149	31517	B	1163	47	993	
1150	31518	B	1164	1	1241	
1151	31519	B	1165	46	2170	
1152	31520	B	1166	1	1781	
1153	31521	B	1167	179	583	
1154	31522	C	1168	167	442	
1155	31523	B	1169	44	1848	
1156	31524	C	1170	1	417	
1157	31525	B	1171	1	198	
1158	31526	B	1172	231	452	
1159	31527	B	1173	219	326	
1160	31528	B	1174	212	302	
1161	31529	B	1175	748	1084	
1162	31530	B	1176	1	540	
1163	31531	C	1177	21	143	
1164	31532	B	1178	76	1300	
1165	31533	B	1179	1	1324	
1166	31534	B	1180	1	1065	
1167	31535	B	1181	1	1263	
1168	31536	B	1182	1	1809	
1169	31537	B	1183	10	406	
1170	31538	B	1184	65	287	
1171	31539	B	1185	25	337	
1172	31540	B	1186	59	698	
1173	31541	C	1187	329	527	

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1174	31542	B	1188	1	1068	
1175	31543	B	1189	72	330	
1176	31544	B	1190	14	239	
1177	31545	B	1191	1	919	
1178	31546	B	1192	462	786	
1179	31547	B	1193	1	3468	
1180	31548	B	1194	16	457	
1181	31549	B	1195	1	697	
1182	31550	C	1196	1	145	
1183	31551	B	1197	91	450	
1184	31552	B	1198	1	1050	
1185	31553	B	1199	101	428	
1186	31554	B	1200	41	205	
1187	31555	B	1201	358	1082	
1188	31556	B	1202	1	183	
1189	31557	B	1203	1	1053	
1190	31558	B	1204	73	336	
1191	31559	B	1205	553	1587	
1192	31560	C	1206	118	366	
1193	31561	B	1207	1	423	
1194	31562	B	1208	120	338	
1195	31563	B	1209	1	1665	
1196	31564	B	1210	1	639	
1197	31565	B	1211	1	660	
1198	31566	B	1212	11	434	
1199	31567	B	1213	1	567	
1200	31568	B	1214	1	801	
1201	31569	C	1215	56	177	
1202	31570	B	1216	439	678	
1203	31571	B	1217	20	201	
1204	31572	B	1218	74	267	
1205	31573	B	1219	74	325	
1206	31574	B	1220	37	340	
1207	31575	B	1221	1	588	
1208	31576	B	1222	136	294	
1209	31577	B	1223	238	392	
1210	31578	B	1224	109	1394	
1211	31579	C	1225	300	653	
1212	31580	B	1226	32	3327	
1213	31581	B	1227	497	1306	
1214	31582	C	1228	1	333	
1215	31583	C	1229	1	249	
1216	31584	C	1230	1	249	
1217	31585	B	1231	147	297	
1218	31586	B	1232	1	714	
1219	31587	B	1233	1	1587	
1220	31588	C	1234	103	243	
1221	31589	C	1235	133	509	
1222	31590	B	1236	1	1594	
1223	31591	B	1237	1	628	
1224	31592	B	1238	1	948	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1225	31593	B	1239	382	1020	
1226	31594	B	1240	163	5459	
1227	31595	B	1241	1	1386	
1228	31596	B	1242	44	344	
1229	31597	B	1243	6	398	
1230	31598	B	1244	77	468	
1231	31599	B	1245	520	2001	
1232	31600	B	1246	1	645	
1233	31601	B	1247	91	690	
1234	31602	B	1248	70	382	
1235	31603	B	1249	183	427	
1236	31604	B	1250	159	621	
1237	31605	B	1251	34	259	
1238	31606	B	1252	155	496	
1239	31607	B	1253	1	1416	
1240	31608	C	1254	18	355	
1241	31609	C	1255	665	826	
1242	31610	B	1256	1	559	
1243	31611	B	1257	343	1329	
1244	31612	B	1258	1	265	
1245	31613	B	1259	1	5081	
1246	31614	B	1260	373	1395	
1247	31615	B	1261	83	373	
1248	31616	B	1262	298	1252	
1249	31617	C	1263	142	327	
1250	31618	B	1264	1	237	
1251	31619	C	1265	1	330	
1252	31620	C	1266	20	358	
1253	31621	C	1267	347	493	
1254	31622	B	1268	220	1314	
1255	31623	B	1269	1	1244	
1256	31624	B	1270	35	368	
1257	31625	B	1271	145	444	
1258	31626	B	1272	1	657	
1259	31627	B	1273	84	273	
1260	31628	C	1274	47	148	
1261	31629	B	1275	1	528	
1262	31630	B	1276	34	1370	
1263	31631	C	1277	81	299	
1264	31632	C	1278	22	201	
1265	31633	B	1279	1	672	
1266	31634	B	1280	1	753	
1267	31635	C	1281	14	79	
1268	31636	C	1282	61	227	
1269	31637	B	1283	95	1124	
1270	31638	B	1284	1	891	
1271	31639	B	1285	1	1323	
1272	31640	B	1286	11	127	
1273	31641	B	1287	281	437	
1274	31642	C	1288	62	136	
1275	31643	B	1289	251	874	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1276	31644	C	1290	16	231	
1277	31645	C	1291	299	412	
1278	31646	B	1292	310	968	
1279	31647	B	1293	237	1802	
1280	31648	B	1294	337	1143	
1281	31649	C	1295	75	176	
1282	31650	C	1296	193	414	
1283	31651	C	1297	98	679	
1284	31652	B	1298	186	260	
1285	31653	B	1299	1	732	
1286	31654	B	1300	123	268	
1287	31655	C	1301	1	420	
1288	31656	C	1302	86	223	
1289	31657	B	1303	1	594	
1290	31658	B	1304	1	4464	
1291	31659	C	1305	1	531	
1292	31660	B	1307	1	780	
1293	31661	C	1308	1	249	
1294	31662	B	1309	1	139	
1295	31663	B	1310	1	156	
1296	31664	B	1311	38	403	
1297	31665	B	1312	128	1089	
1298	31666	C	1313	262	429	
1299	31667	C	1314	209	592	
1300	31668	B	1315	1	684	
1301	31669	C	1316	1	339	
1302	31670	C	1317	71	310	
1303	31671	B	1318	1	476	
1304	31672	B	1319	133	198	
1305	31673	B	1320	1	227	
1306	31674	C	1321	612	977	
1307	31675	C	1322	65	523	
1308	31676	C	1323	35	121	
1309	31677	B	1324	8	430	
1310	31678	C	1325	1	438	
1311	31679	B	1326	1935	3296	
1312	31680	B	1332	254	462	
1313	31681	B	1333	1006	1540	
1314	31682	B	1335	127	1799	
1315	31683	B	1336	221	402	
1316	31684	C	1337	1	567	
1317	31685	C	1338	193	342	
1318	31686	B	1339	652	775	
1319	31687	B	1340	1	552	
1320	31688	B	1341	83	318	
1321	31689	B	1342	166	352	
1322	31690	C	1343	1	228	
1323	31691	B	1344	25	244	
1324	31692	C	1345	58	285	
1325	31693	B	1346	34	822	
1326	31694	B	1347	1	1563	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1327	31695	B	1348	229	1185	
1328	31696	B	1349	59	819	
1329	31697	B	1350	1	5955	
1330	31698	B	1351	1	654	
1331	31699	B	1352	1	1299	
1332	31700	B	1353	943	1872	
1333	31701	B	1354	1	942	
1334	31702	B	1355	444	560	
1335	31703	B	1356	1	1605	
1336	31704	B	1357	1	831	
1337	31705	C	1358	48	383	
1338	31706	C	1359	1	318	
1339	31707	B	1360	186	470	
1340	31708	C	1361	1	321	
1341	31709	B	1362	1	720	
1342	31710	B	1363	1	939	
1343	31711	B	1364	1	576	
1344	31712	B	1365	1	114	
1345	31713	B	1366	129	588	
1346	31714	B	1367	24	724	
1347	31715	B	1368	1	1840	
1348	31716	B	1369	14	350	
1349	31717	B	1370	1	3187	
1350	31718	C	1371	1	261	
1351	31719	B	1372	117	890	
1352	31720	B	1373	1	438	
1353	31721	B	1374	1	217	
1354	31722	B	1375	1	160	
1355	31723	C	1376	6	191	
1356	31724	B	1377	1	759	
1357	31725	B	1378	10	251	
1358	31726	B	1379	1	719	
1359	31727	C	1380	425	886	
1360	31728	C	1381	1	216	
1361	31729	C	1382	38	229	
1362	31730	B	1383	38	672	
1363	31731	B	1384	1	1845	
1364	31732	B	1385	1	2590	
1365	31733	B	1386	32	108	
1366	31734	C	1387	215	460	
1367	31735	B	1388	1	1008	
1368	31736	B	1389	1	368	
1369	31737	B	1390	44	2402	
1370	31738	B	1391	80	1617	
1371	31739	C	1392	199	531	
1372	31740	B	1393	1	465	
1373	31741	C	1394	415	612	
1374	31742	B	1395	16	147	
1375	31743	B	1396	1	1314	
1376	31744	B	1397	1	465	
1377	31745	B	1398	1	1569	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1378	31746	B	1399	1	490	
1379	31747	B	1400	405	573	
1380	31748	B	1401	1	2106	
1381	31749	B	1402	1	1593	
1382	31750	B	1403	1	666	
1383	31751	B	1404	1	652	
1384	31752	B	1405	352	1239	
1385	31753	B	1406	1	3184	
1386	31754	B	1407	467	1433	
1387	31755	B	1408	95	428	
1388	31756	C	1409	164	208	
1389	31757	C	1410	118	511	
1390	31758	C	1411	339	431	
1391	31759	B	1412	1	396	
1392	31760	B	1413	1	663	
1393	31761	B	1414	1	864	
1394	31762	C	1415	1	471	
1395	31763	B	1416	1	642	
1396	31764	B	1417	594	1764	
1397	31765	B	1418	1	771	
1398	31766	B	1419	1	5131	
1399	31767	B	1420	60	617	
1400	31768	B	1421	587	1202	
1401	31769	C	1422	336	638	
1402	31770	C	1423	30	200	
1403	31771	B	1424	1	1363	
1404	31772	B	1425	1	1113	
1405	31773	B	1426	1	1101	
1406	31774	B	1427	575	805	
1407	31775	C	1428	1	149	
1408	31776	C	1429	1	294	
1409	31777	C	1430	228	469	
1410	31778	B	1431	182	518	
1411	31779	B	1432	239	448	
1412	31780	B	1433	1	434	
1413	31781	C	1434	24	290	
1414	31782	C	1435	334	459	
1415	31783	B	1436	69	320	
1416	31784	B	1437	1	426	
1417	31785	B	1438	605	1423	
1418	31786	C	1439	9	113	
1419	31787	B	1440	1	58	
1420	31788	B	1441	1	210	
1421	31789	B	1442	1	2985	
1422	31790	C	1443	152	292	
1423	31791	B	1444	57	849	
1424	31792	C	1445	41	142	
1425	31793	C	1446	38	341	
1426	31794	C	1447	220	450	
1427	31795	C	1448	154	469	
1428	31796	B	1449	139	1023	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1429	31797	B	1450	55	2370	
1430	31798	B	1451	1	1707	
1431	31799	B	1452	566	2356	
1432	31800	B	1453	72	255	
1433	31801	B	1454	51	182	
1434	31802	B	1455	466	600	
1435	31803	B	1456	481	1209	
1436	31804	B	1457	1	1638	
1437	31805	B	1458	8	874	
1438	31806	B	1459	1	552	
1439	31807	B	1460	1	2566	
1440	31808	B	1461	85	270	
1441	31809	B	1462	159	392	
1442	31810	B	1463	88	459	
1443	31811	B	1464	131	406	
1444	31812	B	1465	69	194	
1445	31813	B	1466	59	3134	
1446	31814	B	1467	1	3097	
1447	31815	B	1468	328	519	
1448	31816	C	1469	40	436	
1449	31817	B	1470	1	981	
1450	31818	B	1471	30	285	
1451	31819	B	1475	93	932	
1452	31820	B	1476	1	369	
1453	31821	C	1477	102	227	
1454	31822	B	1478	613	679	
1455	31823	B	1479	51	587	
1456	31824	C	1480	3	188	
1457	31825	B	1481	1	1434	
1458	31826	C	1482	27	173	
1459	31827	C	1483	294	503	
1460	31828	C	1484	506	718	
1461	31829	C	1485	97	504	
1462	31830	C	1486	27	185	
1463	31831	B	1487	50	3247	
1464	31832	B	1488	1	1032	
1465	31833	B	1489	8	95	
1466	31834	B	1490	17	303	
1467	31835	B	1491	34	81	
1468	31836	B	1492	1	1110	
1469	31837	B	1493	1	928	
1470	31838	C	1494	498	704	
1471	31839	B	1495	4	747	
1472	31840	B	1496	1	933	
1473	31841	B	1497	137	687	
1474	31842	B	1498	1524	1676	
1475	31843	B	1499	1	156	
1476	31844	B	1500	1	1126	
1477	31845	B	1501	122	765	
1478	31846	B	1503	95	304	
1479	31847	B	1504	1	156	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1480	31848	C	1505	12	173	
1481	31849	B	1506	10	252	
1482	31850	B	1507	25	301	
1483	31851	B	1508	34	267	
1484	31852	B	1509	10	366	
1485	31853	B	1510	536	2776	
1486	31854	B	1511	1	276	
1487	31855	B	1512	1	420	
1488	31856	B	1513	235	363	
1489	31857	B	1514	664	741	
1490	31858	C	1515	312	452	
1491	31859	B	1516	1	504	
1492	31860	B	1517	52	346	
1493	31861	B	1518	458	1283	
1494	31862	B	1519	324	473	
1495	31863	B	1520	137	286	
1496	31864	B	1521	1	2682	
1497	31865	B	1522	352	1132	
1498	31866	B	1523	245	397	
1499	31867	C	1524	371	661	
1500	31868	B	1525	69	325	
1501	31869	B	1526	38	997	
1502	31870	B	1527	1	1753	
1503	31871	B	1528	215	2588	
1504	31872	C	1529	38	124	
1505	31873	C	1530	33	317	
1506	31874	C	1531	224	379	
1507	31875	B	1532	1	480	
1508	31876	C	1533	145	256	
1509	31877	C	1534	64	198	
1510	31878	B	1535	1	394	
1511	31879	C	1536	1	696	
1512	31880	B	1537	67	246	
1513	31881	C	1538	95	253	
1514	31882	B	1539	145	476	
1515	31883	C	1540	1	361	
1516	31884	C	1541	1	276	
1517	31885	B	1542	1	658	
1518	31886	B	1543	1	623	
1519	31887	C	1544	187	465	
1520	31888	C	1545	1	207	
1521	31889	C	1546	24	512	
1522	31890	C	1547	20	121	
1523	31891	B	1548	1	785	
1524	31892	B	1549	1	498	
1525	31893	C	1550	17	118	
1526	31894	C	1551	1	291	
1527	31895	B	1552	1	504	
1528	31896	B	1553	62	413	
1529	31897	B	1554	1	282	
1530	31898	C	1555	236	408	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1531	31899	C	1556	220	398	
1532	31900	C	1557	1	732	
1533	31901	C	1558	1	372	
1534	31902	B	1559	1	1086	
1535	31903	C	1560	286	642	
1536	31904	B	1561	8	339	
1537	31905	B	1562	16	88	
1538	31906	C	1563	227	405	
1539	31907	B	1564	253	693	
1540	31908	C	1565	1	129	
1541	31909	B	1566	1	390	
1542	31910	B	1567	1	1377	
1543	31911	C	1568	16	264	
1544	31912	C	1569	51	269	
1545	31913	C	1570	39	266	
1546	31914	B	1571	200	260	
1547	31915	B	1572	220	372	
1548	31916	B	1573	1	377	
1549	31917	C	1574	280	441	
1550	31918	C	1575	50	131	
1551	31919	C	1576	47	265	
1552	31920	C	1577	10	291	
1553	31921	B	1578	1	522	
1554	31922	B	1579	756	1166	
1555	31923	B	1580	382	1228	
1556	31924	B	1581	63	229	
1557	31925	B	1582	1	452	
1558	31926	C	1583	299	556	
1559	31927	B	1584	1	870	
1560	31928	B	1585	1	708	
1561	31929	C	1586	1	420	
1562	31930	B	1587	1	1011	
1563	31931	C	1588	84	176	
1564	31932	C	1589	52	201	
1565	31933	C	1590	55	154	
1566	31934	C	1591	1	390	
1567	31935	C	1592	15	317	
1568	31936	B	1593	1	501	
1569	31937	B	1594	306	398	
1570	31938	B	1595	204	402	
1571	31939	C	1596	30	155	
1572	31940	B	1597	1	2274	
1573	31941	B	1598	1	486	
1574	31942	C	1599	148	504	
1575	31943	C	1600	82	282	
1576	31944	C	1601	82	282	
1577	31945	B	1602	66	395	
1578	31946	B	1603	114	237	
1579	31947	B	1604	1	1326	
1580	31948	B	1605	1	1900	
1581	31949	B	1606	1	1548	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1582	31950	B	1607	1	1440	
1583	31951	B	1608	1	1878	
1584	31952	C	1609	402	563	
1585	31953	B	1610	1	2964	
1586	31954	B	1611	1	1284	
1587	31955	C	1612	144	449	
1588	31956	B	1613	1	1050	
1589	31957	B	1614	1	561	
1590	31958	B	1615	127	330	
1591	31959	C	1616	202	443	
1592	31960	B	1617	1	924	
1593	31961	C	1618	60	419	
1594	31962	C	1619	285	602	
1595	31963	C	1620	1	93	
1596	31964	B	1621	1	480	
1597	31965	B	1622	96	416	
1598	31966	B	1623	78	1581	
1599	31967	B	1624	1	2259	
1600	31968	C	1625	180	371	
1601	31969	B	1626	1	852	
1602	31970	B	1627	1	204	
1603	31971	B	1628	37	2613	
1604	31972	B	1629	66	1505	
1605	31973	B	1630	1	1792	
1606	31974	B	1631	100	522	
1607	31975	B	1632	252	2347	
1608	31976	C	1633	294	450	
1609	31977	C	1634	118	372	
1610	31978	B	1635	1	799	
1611	31979	B	1636	1	2496	
1612	31980	B	1637	100	1188	
1613	31981	B	1638	35	1654	
1614	31982	B	1639	46	783	
1615	31983	B	1640	8	1428	
1616	31984	B	1641	1	2121	
1617	31985	B	1642	92	667	
1618	31986	B	1643	1	339	
1619	31987	C	1644	79	434	
1620	31988	C	1645	592	921	
1621	31989	C	1646	1	171	
1622	31990	C	1647	76	264	
1623	31991	B	1648	157	912	
1624	31992	B	1649	10	462	
1625	31993	C	1650	10	333	
1626	31994	C	1651	763	1001	
1627	31995	B	1652	202	701	
1628	31996	C	1653	215	572	
1629	31997	B	1654	261	399	
1630	31998	C	1655	623	749	
1631	31999	B	1656	198	1524	
1632	32000	B	1657	108	575	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1633	32001	B	1658	40	2173	
1634	32002	B	1659	1	479	
1635	32003	B	1660	1	1542	
1636	32004	B	1661	1	849	
1637	32005	B	1662	1	684	
1638	32006	B	1663	1	318	
1639	32007	B	1664	1	406	
1640	32008	B	1665	1	393	
1641	32009	B	1666	1	210	
1642	32010	B	1667	1	450	
1643	32011	B	1668	1	471	
1644	32012	B	1669	1	471	
1645	32013	B	1670	282	580	
1646	32014	B	1671	1	789	
1647	32015	B	1672	1	324	
1648	32016	B	1673	1	465	
1649	32017	B	1674	1	948	
1650	32018	C	1675	24	401	
1651	32019	B	1676	46	401	
1652	32020	B	1677	251	1041	
1653	32021	C	1678	1	177	
1654	32022	B	1679	1	189	
1655	32023	B	1680	65	769	
1656	32024	C	1681	1	564	
1657	32025	B	1682	65	769	
1658	32026	B	1683	1	1743	
1659	32027	B	1684	1	615	
1660	32028	B	1685	1	323	
1661	32029	B	1686	1	618	
1662	32030	B	1687	1	579	
1663	32031	C	1688	142	216	
1664	32032	C	1689	145	432	
1665	32033	B	1690	1	729	
1666	32034	C	1691	1	192	
1667	32035	C	1692	1	474	
1668	32036	B	1693	326	1662	
1669	32037	B	1694	50	1462	
1670	32038	C	1695	1	432	
1671	32039	B	1696	173	375	
1672	32040	B	1697	1	1917	
1673	32041	B	1698	57	365	
1674	32042	B	1699	78	1250	
1675	32043	B	1700	8	2210	
1676	32044	B	1701	1	474	
1677	32045	B	1702	47	879	
1678	32046	B	1703	1	465	
1679	32047	B	1704	65	473	
1680	32048	B	1705	89	1908	
1681	32049	C	1706	1	612	
1682	32050	C	1707	80	226	
1683	32051	B	1708	992	2023	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1684	32052	B	1709	1293	1497	
1685	32053	B	1710	29	1480	
1686	32054	C	1711	1664	2179	
1687	32055	B	1712	183	8544	
1688	32056	C	1713	60	472	
1689	32057	B	1714	202	735	
1690	32058	B	1715	532	661	
1691	32059	B	1716	1	453	
1692	32060	B	1717	24	320	
1693	32061	B	1718	59	583	
1694	32062	B	1719	1	369	
1695	32063	B	1720	51	204	
1696	32064	B	1721	318	849	
1697	32065	B	1722	1	597	
1698	32066	B	1723	1	325	
1699	32067	B	1724	1	675	
1700	32068	B	1725	1	631	
1701	32069	B	1726	1	1017	
1702	32070	B	1727	158	727	
1703	32071	B	1728	296	798	
1704	32072	B	1729	1	1128	
1705	32073	C	1730	237	356	
1706	32074	C	1731	393	519	
1707	32075	B	1732	1	6432	
1708	32076	B	1733	124	402	
1709	32077	B	1734	35	421	
1710	32078	C	1735	203	385	
1711	32079	B	1736	16	406	
1712	32080	B	1737	21	306	
1713	32081	B	1738	97	352	
1714	32082	B	1739	64	7164	
1715	32083	B	1740	553	1197	
1716	32084	B	1741	553	720	
1717	32085	B	1742	1	4029	
1718	32086	B	1743	63	422	
1719	32087	B	1744	342	451	
1720	32088	B	1745	1	1238	
1721	32089	B	1746	1	2393	
1722	32090	B	1747	1667	1833	
1723	32091	C	1748	33	287	
1724	32092	B	1749	1	469	
1725	32093	B	1750	75	166	
1726	32094	B	1751	120	756	
1727	32095	C	1752	1	1098	
1728	32096	B	1753	1	486	
1729	32097	C	1754	25	374	
1730	32098	C	1755	149	394	
1731	32099	B	1756	1	660	
1732	32100	B	1757	26	391	
1733	32101	B	1758	282	419	
1734	32102	B	1759	132	717	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1735	32103	B	1760	127	698	
1736	32104	B	1761	56	549	
1737	32105	B	1762	325	2681	
1738	32106	C	1763	465	893	
1739	32107	C	1764	123	764	
1740	32108	B	1765	206	402	
1741	32109	B	1766	393	900	
1742	32110	C	1767	1	360	
1743	32111	B	1768	285	482	
1744	32112	B	1769	1	405	
1745	32113	C	1770	304	399	
1746	32114	B	1771	1	273	
1747	32115	B	1772	67	1464	
1748	32116	B	1773	1	1122	
1749	32117	B	1774	1	1185	
1750	32118	B	1775	44	145	
1751	32119	B	1776	1	1050	
1752	32120	B	1777	250	762	
1753	32121	B	1778	1	390	
1754	32122	B	1779	172	867	
1755	32123	B	1780	327	637	
1756	32124	B	1781	1	1101	
1757	32125	C	1782	10	216	
1758	32126	B	1783	1	1449	
1759	32127	B	1784	1	402	
1760	32128	C	1785	134	418	
1761	32129	B	1786	1	417	
1762	32130	B	1787	1	384	
1763	32131	C	1788	1	738	
1764	32132	C	1789	68	280	
1765	32133	B	1790	101	327	
1766	32134	B	1791	1	1257	
1767	32135	C	1792	168	311	
1768	32136	B	1793	33	120	
1769	32137	C	1794	1	150	
1770	32138	C	1795	1	378	
1771	32139	C	1796	100	267	
1772	32140	C	1797	1	318	
1773	32141	C	1798	1	429	
1774	32142	C	1799	194	379	
1775	32143	B	1800	1	363	
1776	32144	B	1801	1	384	
1777	32145	B	1802	1	4462	
1778	32146	B	1803	235	425	
1779	32147	B	1804	8	1187	
1780	32148	B	1805	1	480	
1781	32149	B	1806	1	240	
1782	32150	B	1807	1	891	
1783	32151	C	1808	1	366	
1784	32152	B	1809	376	776	
1785	32153	B	1810	304	876	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1786	32154	B	1811	1	939	
1787	32155	B	1812	4	744	
1788	32156	B	1813	1	717	
1789	32157	C	1814	67	366	
1790	32158	B	1815	185	847	
1791	32159	C	1816	1	315	
1792	32160	B	1817	87	297	
1793	32161	B	1818	1	1190	
1794	32162	B	1819	1	848	
1795	32163	B	1820	934	1158	
1796	32164	C	1821	1	477	
1797	32165	C	1822	6	125	
1798	32166	B	1823	335	536	
1799	32167	B	1824	157	324	
1800	32168	C	1825	176	361	
1801	32169	C	1826	1	120	
1802	32170	C	1827	25	360	
1803	32171	C	1828	246	377	
1804	32172	C	1829	4782	5015	
1805	32173	B	1830	1105	3034	
1806	32174	B	1831	818	874	
1807	32175	C	1832	1	444	
1808	32176	B	1833	589	734	
1809	32177	B	1834	1	264	
1810	32178	B	1835	46	112	
1811	32179	B	1836	1	360	
1812	32180	B	1837	589	734	
1813	32181	B	1838	1	675	
1814	32182	B	1839	1	1194	
1815	32183	B	1840	121	880	
1816	32184	B	1841	35	853	
1817	32185	B	1842	1	426	
1818	32186	C	1843	1	252	
1819	32187	B	1844	1	323	
1820	32188	B	1845	1	789	
1821	32189	C	1846	337	1521	
1822	32190	C	1847	1	345	
1823	32191	B	1848	331	3385	
1824	32192	B	1849	1	1584	
1825	32193	B	1850	1	957	
1826	32194	B	1851	226	1794	
1827	32195	B	1852	52	594	
1828	32196	C	1853	1	615	
1829	32197	B	1854	1	318	
1830	32198	B	1855	297	450	
1831	32199	C	1856	87	404	
1832	32200	C	1857	1	171	
1833	32201	C	1858	1	171	
1834	32202	B	1859	34	831	
1835	32203	B	1860	1	1375	
1836	32204	B	1861	1	546	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1837	32205	C	1862	36	182	
1838	32206	B	1863	392	1043	
1839	32207	B	1864	1	1283	
1840	32208	C	1865	283	591	
1841	32209	C	1866	97	108	
1842	32210	C	1867	25	250	
1843	32211	C	1868	142	448	
1844	32212	C	1869	1	576	
1845	32213	C	1870	1	396	
1846	32214	B	1871	1	885	
1847	32215	C	1872	321	848	
1848	32216	B	1873	82	871	
1849	32217	C	1874	1	723	
1850	32218	C	1875	1	426	
1851	32219	C	1876	624	803	
1852	32220	B	1877	1	588	
1853	32221	B	1878	39	58	
1854	32222	B	1879	1	1011	
1855	32223	B	1880	1	654	
1856	32224	C	1881	1	498	
1857	32225	C	1882	1	249	
1858	32226	C	1883	507	785	
1859	32227	C	1885	310	404	
1860	32228	B	1886	448	618	
1861	32229	B	1887	1	388	
1862	32230	B	1888	106	414	
1863	32231	B	1889	82	4206	
1864	32232	B	1890	1	240	
1865	32233	B	1891	1	324	
1866	32234	C	1892	243	447	
1867	32235	C	1893	139	228	
1868	32236	C	1894	61	300	
1869	32237	C	1895	271	429	
1870	32238	B	1896	545	1054	
1871	32239	B	1897	609	706	
1872	32240	B	1898	1	2521	
1873	32241	C	1899	152	517	
1874	32242	B	1900	217	313	
1875	32243	C	1901	86	193	
1876	32244	C	1902	29	271	
1877	32245	B	1903	1	522	
1878	32246	C	1904	37	225	
1879	32247	C	1905	84	308	
1880	32248	B	1906	36	1569	
1881	32249	B	1907	1	522	
1882	32250	C	1908	1	510	
1883	32251	B	1909	1	936	
1884	32252	C	1910	1	162	
1885	32253	C	1911	155	427	
1886	32254	B	1912	1	1282	
1887	32255	B	1913	165	270	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1888	32256	B	1914	513	9470	
1889	32257	B	1915	35	871	
1890	32258	B	1916	1	690	
1891	32259	C	1917	86	271	
1892	32260	B	1918	1	690	
1893	32261	C	1919	14	301	
1894	32262	B	1920	1	936	
1895	32263	B	1921	1	1901	
1896	32264	B	1922	36	238	
1897	32265	B	1923	1	738	
1898	32266	C	1924	5	364	
1899	32267	C	1925	43	494	
1900	32268	C	1926	96	263	
1901	32269	B	1927	1	207	
1902	32270	B	1928	1	290	
1903	32271	B	1929	52	482	
1904	32272	B	1930	271	408	
1905	32273	B	1931	114	309	
1906	32274	C	1932	218	398	
1907	32275	B	1933	1	1011	
1908	32276	B	1934	1	702	
1909	32277	B	1935	1	1305	
1910	32278	C	1936	141	374	
1911	32279	B	1937	1	834	
1912	32280	B	1938	47	363	
1913	32281	B	1939	73	558	
1914	32282	B	1940	373	864	
1915	32283	B	1941	96	377	
1916	32284	B	1942	55	2711	
1917	32285	B	1945	833	1352	
1918	32286	B	1946	1	1101	
1919	32287	B	1947	865	1070	
1920	32288	C	1948	1	285	
1921	32289	B	1949	1	642	
1922	32290	B	1950	124	813	
1923	32291	B	1951	1	654	
1924	32292	B	1952	180	303	
1925	32293	C	1953	15	170	
1926	32294	B	1954	245	646	
1927	32295	B	1955	100	824	
1928	32296	C	1956	52	348	
1929	32297	B	1957	1	678	
1930	32298	B	1958	1	954	
1931	32299	B	1959	1	675	
1932	32300	C	1960	52	348	
1933	32301	B	1961	71	251	
1934	32302	B	1962	427	747	
1935	32303	B	1963	1	453	
1936	32304	B	1964	1	375	
1937	32305	B	1965	117	1109	
1938	32306	C	1966	47	133	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1939	32307	B	1967	79	1149	
1940	32308	B	1968	1	693	
1941	32309	B	1969	1	1179	
1942	32310	B	1970	1	639	
1943	32311	B	1971	502	1294	
1944	32312	C	1972	670	1185	
1945	32313	B	1973	1	1044	
1946	32314	B	1974	1	3645	
1947	32315	B	1975	1	2877	
1948	32316	B	1976	1	1579	
1949	32317	B	1977	1	750	
1950	32318	B	1978	1	438	
1951	32319	C	1979	122	307	
1952	32320	C	1980	71	271	
1953	32321	C	1981	151	363	
1954	32322	C	1982	122	307	
1955	32323	C	1983	55	282	
1956	32324	C	1984	89	385	
1957	32325	C	1985	48	275	
1958	32326	C	1986	246	557	
1959	32327	B	1987	394	2565	
1960	32328	B	1988	1	432	
1961	32329	B	1989	46	483	
1962	32330	B	1990	150	482	
1963	32331	B	1991	10	265	
1964	32332	C	1992	40	162	
1965	32333	B	1993	1	3639	
1966	32334	B	1994	83	179	
1967	32335	B	1995	39	1452	
1968	32336	B	1996	50	384	
1969	32337	B	1997	256	351	
1970	32338	B	1998	1	771	
1971	32339	B	1999	1	489	
1972	32340	B	2000	37	447	
1973	32341	B	2001	1	1272	
1974	32342	B	2002	1	2559	
1975	32343	C	2003	221	589	
1976	32344	C	2004	415	1033	
1977	32345	B	2007	318	694	
1978	32346	B	2008	31	819	
1979	32347	B	2009	1	276	
1980	32348	B	2010	1	369	
1981	32349	B	2011	85	628	
1982	32350	B	2012	19	178	
1983	32351	B	2013	217	393	
1984	32352	B	2014	1	779	
1985	32353	B	2015	107	650	
1986	32354	B	2016	313	527	
1987	32355	B	2017	32	258	
1988	32356	C	2018	51	345	
1989	32357	B	2019	1	393	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1990	32358	B	2020	647	1362	
1991	32359	C	2021	16	378	
1992	32360	B	2022	32	349	
1993	32361	C	2023	256	425	
1994	32362	C	2024	134	382	
1995	32363	B	2025	138	171	
1996	32364	B	2026	1	1626	
1997	32365	B	2027	509	810	
1998	32366	C	2028	1	513	
1999	32367	C	2029	7	375	
2000	32368	C	2030	1	410	
2001	32369	B	2031	1	864	
2002	32370	B	2032	110	928	
2003	32371	B	2033	1	1026	
2004	32372	B	2034	1	1008	
2005	32373	B	2035	1	588	
2006	32374	B	2036	1	412	
2007	32375	B	2037	1	1851	
2008	32376	B	2038	309	663	
2009	32377	B	2039	1	525	
2010	32378	B	2040	1	2214	
2011	32379	B	2041	1	486	
2012	32380	B	2042	1	774	
2013	32381	B	2043	1	596	
2014	32382	B	2044	305	395	
2015	32383	C	2045	27	185	
2016	32384	B	2046	1	1071	
2017	32385	B	2047	1	1326	
2018	32386	B	2048	1	3761	
2019	32387	C	2049	55	189	
2020	32388	B	2050	1016	1683	
2021	32389	C	2051	942	1130	
2022	32390	B	2052	1	598	
2023	32391	B	2053	1	768	
2024	32392	B	2054	1	999	
2025	32393	C	2055	1	252	
2026	32394	B	2056	154	606	
2027	32395	B	2057	1	846	
2028	32396	C	2058	334	690	
2029	32397	B	2059	268	5712	
2030	32398	C	2060	117	662	
2031	32399	B	2061	1	3504	
2032	32400	B	2062	816	927	
2033	32401	B	2063	1	342	
2034	32402	B	2064	1	1443	
2035	32403	C	2065	53	102	
2036	32404	C	2066	271	528	
2037	32405	B	2067	1	843	
2038	32406	C	2068	187	408	
2039	32407	C	2069	174	320	
2040	32408	B	2070	31	534	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2041	32409	C	2071	183	329	
2042	32410	B	2072	3	389	
2043	32411	B	2073	78	974	
2044	32412	B	2074	467	692	
2045	32413	C	2075	605	965	
2046	32414	B	2076	1	555	
2047	32415	B	2077	1	390	
2048	32416	B	2078	1	2522	
2049	32417	B	2079	24	94	
2050	32418	B	2080	78	593	
2051	32419	B	2081	1	612	
2052	32420	B	2082	42	342	
2053	32421	B	2083	1	477	
2054	32422	B	2084	57	1640	
2055	32423	C	2085	110	307	
2056	32424	B	2086	1	591	
2057	32425	C	2087	14	355	
2058	32426	B	2088	47	998	
2059	32427	B	2089	1	498	
2060	32428	C	2090	357	560	
2061	32429	B	2091	1	522	
2062	32430	C	2092	231	659	
2063	32431	C	2093	36	167	
2064	32432	B	2094	394	2695	
2065	32433	B	2096	61	2215	
2066	32434	B	2097	204	572	
2067	32435	C	2098	476	652	
2068	32436	B	2099	1	190	
2069	32437	C	2100	1	259	
2070	32438	B	2101	1	2625	
2071	32439	B	2102	1403	2950	
2072	32440	B	2103	672	1955	
2073	32441	C	2104	1	351	
2074	32442	B	2105	1	567	
2075	32443	C	2106	176	304	
2076	32444	C	2107	27	308	
2077	32445	C	2108	68	307	
2078	32446	C	2109	322	567	
2079	32447	B	2110	1	1297	
2080	32448	B	2111	281	1488	
2081	32449	B	2112	12	2497	
2082	32450	C	2113	90	284	
2083	32451	B	2114	1	2466	
2084	32452	B	2115	1	603	
2085	32453	B	2116	1	954	
2086	32454	B	2117	205	441	
2087	32455	B	2118	68	2052	
2088	32456	B	2119	271	639	
2089	32457	B	2120	1	1356	
2090	32458	B	2121	247	1326	
2091	32459	B	2122	1	1041	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2092	32460	B	2123	1	1695	
2093	32461	B	2124	1	1767	
2094	32462	B	2125	1	2286	
2095	32463	B	2126	1	1167	
2096	32464	B	2127	1	2343	
2097	32465	B	2128	1	1056	
2098	32466	B	2129	1	1379	
2099	32467	B	2130	1	1839	
2100	32468	B	2131	1	5460	
2101	32469	B	2132	133	549	
2102	32470	B	2133	1	534	
2103	32471	B	2134	1	537	
2104	32472	B	2135	1	49	
2105	32473	C	2136	1	432	
2106	32474	B	2137	1	615	
2107	32475	B	2138	146	556	
2108	32476	B	2139	133	1434	
2109	32477	B	2140	1	357	
2110	32478	C	2141	1	429	
2111	32479	B	2142	1	411	
2112	32480	B	2143	1	459	
2113	32481	C	2144	224	550	
2114	32482	B	2145	1	1035	
2115	32483	B	2146	1	342	
2116	32484	C	2147	1	321	
2117	32485	C	2148	1	317	
2118	32486	B	2149	1	495	
2119	32487	B	2150	146	556	
2120	32488	C	2151	1	390	
2121	32489	C	2152	461	643	
2122	32490	C	2153	198	416	
2123	32491	C	2154	258	500	
2124	32492	B	2155	291	1034	
2125	32493	B	2156	1	834	
2126	32494	B	2157	1	7852	
2127	32495	B	2158	1	1320	
2128	32496	B	2159	1631	1756	
2129	32497	B	2160	500	8643	
2130	32498	C	2161	193	475	
2131	32499	B	2162	1	795	
2132	32500	B	2163	1	663	
2133	32501	C	2164	1	303	
2134	32502	B	2165	266	385	
2135	32503	B	2166	1	704	
2136	32504	B	2167	1	720	
2137	32505	B	2168	364	507	
2138	32506	B	2169	44	197	
2139	32507	C	2170	72	224	
2140	32508	C	2171	228	393	
2141	32509	C	2172	241	396	
2142	32510	C	2173	415	552	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2143	32511	B	2174	64	268	
2144	32512	C	2175	1	462	
2145	32513	C	2176	1	357	
2146	32514	B	2177	1	3213	
2147	32515	B	2178	119	682	
2148	32516	B	2179	1	405	
2149	32517	B	2180	297	769	
2150	32518	B	2181	1	1314	
2151	32519	C	2182	156	287	
2152	32520	B	2183	1	756	
2153	32521	B	2184	1	645	
2154	32522	B	2185	1	948	
2155	32523	B	2186	1	660	
2156	32524	B	2187	186	518	
2157	32525	B	2188	1	3570	
2158	32526	B	2189	1	3354	
2159	32527	B	2190	1	2232	
2160	32528	B	2191	1	1356	
2161	32529	B	2192	1	1103	
2162	32530	B	2193	1	1902	
2163	32531	B	2194	1	2232	
2164	32532	B	2195	1	2991	
2165	32533	B	2196	1	2136	
2166	32534	B	2197	1	1524	
2167	32535	B	2198	1	2106	
2168	32536	B	2199	1	1224	
2169	32537	B	2200	1	1935	
2170	32538	B	2201	1	1428	
2171	32539	B	2202	1	858	
2172	32540	B	2203	1	2162	
2173	32541	B	2204	1	1374	
2174	32542	B	2205	205	3666	
2175	32543	B	2206	59	4311	
2176	32544	B	2207	1	1311	
2177	32545	B	2208	1	2742	
2178	32546	B	2209	1	1878	
2179	32547	B	2210	1	1074	
2180	32548	B	2211	1	2217	
2181	32549	B	2212	1	1945	
2182	32550	B	2213	1	1941	
2183	32551	B	2214	1	1737	
2184	32552	B	2215	1	1422	
2185	32553	B	2216	22	9087	
2186	32554	B	2217	1	4954	
2187	32555	B	2218	1	1812	
2188	32556	B	2219	1	939	
2189	32557	B	2220	1	2895	
2190	32558	B	2221	1	6223	
2191	32559	B	2222	109	4966	
2192	32560	B	2223	3807	9479	
2193	32561	B	2224	1	4903	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2194	32562	B	2225	210	516	
2195	32563	C	2226	185	292	
2196	32564	B	2227	1	657	
2197	32565	B	2228	1	1011	
2198	32566	B	2229	1	1303	
2199	32567	C	2230	69	182	
2200	32568	B	2231	1	321	
2201	32569	B	2232	88	522	
2202	32570	B	2233	527	1207	
2203	32571	B	2234	118	375	
2204	32572	B	2235	8	148	
2205	32573	B	2236	609	1121	
2206	32574	B	2237	1	1500	
2207	32575	C	2238	121	330	
2208	32576	B	2239	1	591	
2209	32577	B	2240	125	471	
2210	32578	B	2241	64	909	
2211	32579	B	2242	13	579	
2212	32580	B	2243	249	531	
2213	32581	C	2244	107	928	
2214	32582	B	2245	213	322	
2215	32583	C	2246	373	441	
2216	32584	B	2247	54	2723	
2217	32585	B	2248	94	529	
2218	32586	B	2249	57	260	
2219	32587	B	2250	674	1972	
2220	32588	B	2251	1	1053	
2221	32589	C	2252	186	347	
2222	32590	B	2253	26	193	
2223	32591	B	2254	1	5442	
2224	32592	B	2255	428	3792	
2225	32593	B	2256	9	199	
2226	32594	B	2257	421	2932	
2227	32595	B	2258	305	547	
2228	32596	B	2259	1	891	
2229	32597	B	2260	1	641	
2230	32598	B	2261	108	542	
2231	32599	B	2262	105	440	
2232	32600	B	2263	553	729	
2233	32601	B	2264	1	645	
2234	32602	B	2265	291	452	
2235	32603	B	2266	143	348	
2236	32604	C	2267	310	426	
2237	32605	B	2268	1	1344	
2238	32606	B	2269	237	2834	
2239	32607	B	2270	1	2922	
2240	32608	B	2271	109	3499	
2241	32609	B	2272	1	1611	
2242	32610	B	2273	1	1575	
2243	32611	B	2274	1	1314	
2244	32612	B	2275	1	1209	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2245	32613	B	2276	1	2022	
2246	32614	B	2277	1	1938	
2247	32615	B	2279	1	1806	
2248	32616	B	2280	1	2361	
2249	32617	B	2281	1	2732	
2250	32618	B	2282	1	3703	
2251	32619	C	2283	1	507	
2252	32620	B	2284	118	316	
2253	32621	B	2285	1	272	
2254	32622	B	2286	37	388	
2255	32623	B	2287	1	660	
2256	32624	B	2288	431	633	
2257	32625	B	2289	1	1032	
2258	32626	B	2290	1	1227	
2259	32627	C	2291	27	296	
2260	32628	B	2292	58	370	
2261	32629	B	2293	1	1275	
2262	32630	B	2294	1	1299	
2263	32631	C	2295	227	613	
2264	32632	B	2296	1	297	
2265	32633	B	2297	126	206	
2266	32634	C	2298	1	387	
2267	32635	B	2299	19	279	
2268	32636	B	2300	1	612	
2269	32637	C	2301	81	191	
2270	32638	B	2302	120	308	
2271	32639	B	2303	1	2145	
2272	32640	C	2304	270	416	
2273	32641	B	2305	31	627	
2274	32642	B	2306	128	499	
2275	32643	B	2307	61	388	
2276	32644	B	2308	744	2094	
2277	32645	B	2309	241	669	
2278	32646	B	2310	1	285	
2279	32647	B	2311	137	307	
2280	32648	C	2312	168	362	
2281	32649	C	2313	8	394	
2282	32650	B	2314	1	489	
2283	32651	C	2315	1	204	
2284	32652	B	2316	1	2361	
2285	32653	B	2317	1	2265	
2286	32654	B	2318	1	2268	
2287	32655	B	2319	1	2337	
2288	32656	B	2320	1	2196	
2289	32657	B	2321	1	2298	
2290	32658	B	2322	1	2880	
2291	32659	B	2323	1	2562	
2292	32660	B	2324	1	2835	
2293	32661	B	2325	1	2172	
2294	32662	B	2326	675	2515	
2295	32663	B	2327	1	2709	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2296	32664	B	2328	1	2478	
2297	32665	B	2329	1	2748	
2298	32666	B	2330	877	4763	
2299	32667	B	2331	1	2590	
2300	32668	B	2332	1	597	
2301	32669	C	2333	279	412	
2302	32670	C	2334	507	878	
2303	32671	C	2335	1	147	
2304	32672	B	2336	52	573	
2305	32673	C	2337	211	446	
2306	32674	B	2338	1	1669	
2307	32675	B	2339	69	418	
2308	32676	B	2340	1	2778	
2309	32677	B	2341	1	1896	
2310	32678	B	2342	1	1836	
2311	32679	B	2343	1	2463	
2312	32680	B	2344	287	1785	
2313	32681	B	2345	1	2860	
2314	32682	B	2346	1	1281	
2315	32683	B	2347	1	1176	
2316	32684	B	2348	1	1431	
2317	32685	B	2349	1	2361	
2318	32686	B	2350	592	1815	
2319	32687	B	2351	1	2764	
2320	32688	C	2352	309	581	
2321	32689	B	2353	99	5619	
2322	32690	B	2354	133	3213	
2323	32691	B	2355	1	3193	
2324	32692	B	2356	1	3291	
2325	32693	B	2357	1	4019	
2326	32694	B	2358	167	4093	
2327	32695	B	2359	1	3534	
2328	32696	B	2360	1	3405	
2329	32697	B	2361	1	3555	
2330	32698	B	2362	1	3786	
2331	32699	B	2363	1	3414	
2332	32700	B	2364	1	5130	
2333	32701	B	2365	1	8244	
2334	32702	B	2366	1	7995	
2335	32703	B	2367	1	1980	
2336	32704	B	2368	1	4269	
2337	32705	B	2369	1	169	
2338	32706	B	2370	1	573	
2339	32707	B	2371	388	1101	
2340	32708	C	2372	1	354	
2341	32709	B	2373	134	1057	
2342	32710	B	2374	91	1464	
2343	32711	B	2375	117	767	
2344	32712	B	2376	1	486	
2345	32713	C	2377	1	726	
2346	32714	C	2378	31	447	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2347	32715	B	2379	1	402	
2348	32716	B	2380	22	427	
2349	32717	B	2381	351	560	
2350	32718	B	2382	1	1122	
2351	32719	B	2383	1	1035	
2352	32720	B	2384	1	309	
2353	32721	B	2385	80	673	
2354	32722	B	2386	160	659	
2355	32723	B	2387	1	858	
2356	32724	C	2388	228	365	
2357	32725	B	2389	1	531	
2358	32726	B	2390	218	670	
2359	32727	C	2391	182	484	
2360	32728	C	2392	1	738	
2361	32729	C	2393	27	316	
2362	32730	B	2394	291	498	
2363	32731	C	2395	230	409	
2364	32732	B	2396	228	1361	
2365	32733	C	2397	210	548	
2366	32734	B	2398	309	1202	
2367	32735	C	2399	100	406	
2368	32736	B	2400	440	2579	
2369	32737	C	2401	102	359	
2370	32738	B	2402	1	414	
2371	32739	B	2403	717	976	
2372	32740	B	2404	1	777	
2373	32741	B	2405	1	208	
2374	32742	B	2406	1	570	
2375	32743	B	2407	187	525	
2376	32744	B	2408	20	499	
2377	32745	B	2409	1	210	
2378	32746	B	2410	41	166	
2379	32747	B	2411	29	348	
2380	32748	B	2412	1	564	
2381	32749	C	2413	250	366	
2382	32750	B	2414	164	430	
2383	32751	C	2415	141	340	
2384	32752	B	2416	304	422	
2385	32753	B	2417	1	2031	
2386	32754	B	2418	1	1527	
2387	32755	B	2419	1	2892	
2388	32756	B	2420	218	4186	
2389	32757	B	2421	203	655	
2390	32758	C	2422	1	346	
2391	32759	B	2423	299	433	
2392	32760	B	2424	172	525	
2393	32761	B	2425	1	3270	
2394	32762	B	2426	202	481	
2395	32763	B	2427	148	3473	
2396	32764	C	2428	182	460	
2397	32765	B	2429	116	2953	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2398	32766	B	2430	153	332	
2399	32767	B	2431	267	2752	
2400	32768	B	2432	1	848	
2401	32769	C	2433	54	350	
2402	32770	B	2434	160	531	
2403	32771	B	2435	159	184	
2404	32772	B	2436	44	293	
2405	32773	C	2437	129	438	
2406	32774	C	2438	255	469	
2407	32775	B	2439	292	456	
2408	32776	B	2440	86	225	
2409	32777	B	2441	1	603	
2410	32778	B	2442	305	402	
2411	32779	C	2443	117	332	
2412	32780	B	2444	1	642	
2413	32781	B	2445	50	238	
2414	32782	B	2446	350	1331	
2415	32783	B	2447	1	867	
2416	32784	B	2448	1	498	
2417	32785	B	2449	40	849	
2418	32786	B	2450	187	404	
2419	32787	B	2451	1	921	
2420	32788	B	2452	439	517	
2421	32789	C	2453	143	682	
2422	32790	B	2454	87	401	
2423	32791	B	2455	44	277	
2424	32792	B	2456	1	639	
2425	32793	B	2457	1	816	
2426	32794	B	2458	100	454	
2427	32795	C	2459	717	923	
2428	32796	C	2460	1	412	
2429	32797	C	2461	80	394	
2430	32798	B	2462	278	323	
2431	32799	C	2463	9	239	
2432	32800	B	2464	1	537	
2433	32801	B	2465	1	798	
2434	32802	B	2466	1	861	
2435	32803	B	2467	611	979	
2436	32804	B	2468	56	166	
2437	32805	C	2469	40	495	
2438	32806	B	2470	1	216	
2439	32807	B	2471	273	385	
2440	32808	B	2472	77	489	
2441	32809	C	2473	480	791	
2442	32810	B	2474	110	1318	
2443	32811	B	2475	114	563	
2444	32812	B	2476	813	3193	
2445	32813	C	2477	198	650	
2446	32814	B	2478	1	234	
2447	32815	B	2479	7	174	
2448	32816	B	2480	1	1035	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2449	32817	B	2481	1	564	
2450	32818	B	2482	16	894	
2451	32819	B	2483	1	207	
2452	32820	B	2484	1	2742	
2453	32821	B	2485	1	1071	
2454	32822	B	2486	58	1228	
2455	32823	C	2487	51	179	
2456	32824	B	2488	1	1119	
2457	32825	C	2489	147	398	
2458	32826	C	2490	1	504	
2459	32827	C	2491	4	240	
2460	32828	B	2492	190	388	
2461	32829	B	2493	1	594	
2462	32830	C	2494	299	477	
2463	32831	B	2495	1	2328	
2464	32832	C	2496	1	924	
2465	32833	B	2497	1	2703	
2466	32834	B	2498	504	1392	
2467	32835	C	2499	649	1239	
2468	32836	B	2500	46	842	
2469	32837	B	2501	251	555	
2470	32838	B	2502	258	326	
2471	32839	B	2503	49	386	
2472	32840	C	2504	63	383	
2473	32841	B	2505	150	585	
2474	32842	B	2506	65	678	
2475	32843	C	2507	477	634	
2476	32844	B	2508	80	337	
2477	32845	B	2509	1	1233	
2478	32846	B	2510	1	2526	
2479	32847	B	2511	192	2617	
2480	32848	B	2512	1	921	
2481	32849	B	2513	1	1650	
2482	32850	B	2514	79	1587	
2483	32851	B	2515	1	657	
2484	32852	B	2516	1	1260	
2485	32853	B	2517	1	762	
2486	32854	C	2518	1	729	
2487	32855	B	2519	1	1299	
2488	32856	B	2520	1	882	
2489	32857	C	2521	1	369	
2490	32858	B	2522	52	573	
2491	32859	B	2523	1	570	
2492	32860	B	2524	1	2376	
2493	32861	B	2525	1	786	
2494	32862	B	2526	1	760	
2495	32863	B	2527	73	714	
2496	32864	B	2528	1	2976	
2497	32865	B	2529	1	1021	
2498	32866	B	2530	1	1386	
2499	32867	B	2531	352	1239	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2500	32868	B	2532	1	1740	
2501	32869	B	2533	1	915	
2502	32870	B	2534	392	1393	
2503	32871	B	2535	1	4868	
2504	32872	B	2536	1	2667	
2505	32873	B	2537	1	825	
2506	32874	B	2538	1	735	
2507	32875	B	2539	88	469	
2508	32876	C	2540	1	390	
2509	32877	C	2541	113	328	
2510	32878	B	2542	475	848	
2511	32879	B	2543	472	1482	
2512	32880	C	2544	42	593	
2513	32881	B	2545	470	998	
2514	32882	B	2546	83	339	
2515	32883	B	2547	1	501	
2516	32884	B	2548	1198	1432	
2517	32885	B	2549	1	486	
2518	32886	B	2550	454	1626	
2519	32887	C	2551	227	388	
2520	32888	B	2552	25	687	
2521	32889	B	2553	569	753	
2522	32890	C	2554	147	384	
2523	32891	B	2555	210	419	
2524	32892	B	2556	1	1185	
2525	32893	C	2557	93	257	
2526	32894	C	2558	41	375	
2527	32895	C	2559	155	579	
2528	32896	B	2560	1	375	
2529	32897	C	2561	37	351	
2530	32898	C	2562	39	518	
2531	32899	B	2563	310	493	
2532	32900	C	2564	83	373	
2533	32901	B	2565	120	843	
2534	32902	C	2566	327	468	
2535	32903	B	2567	1	732	
2536	32904	C	2568	243	434	
2537	32905	C	2569	117	347	
2538	32906	C	2570	1	363	
2539	32907	C	2571	1	219	
2540	32908	B	2572	82	390	
2541	32909	B	2573	1152	1737	
2542	32910	C	2574	294	524	
2543	32911	B	2575	1	345	
2544	32912	B	2576	106	1073	
2545	32913	B	2577	1	313	
2546	32914	C	2578	1	594	
2547	32915	C	2579	16	102	
2548	32916	C	2580	1	441	
2549	32917	B	2581	1	462	
2550	32918	B	2582	113	1257	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2551	32919	B	2583	1	402	
2552	32920	B	2584	489	570	
2553	32921	B	2585	218	356	
2554	32922	C	2586	225	345	
2555	32923	C	2587	472	621	
2556	32924	B	2588	1	984	
2557	32925	B	2589	1	1119	
2558	32926	B	2590	1	771	
2559	32927	B	2591	97	681	
2560	32928	B	2592	112	202	
2561	32929	C	2593	1	381	
2562	32930	C	2594	115	321	
2563	32931	C	2595	3	200	
2564	32932	B	2596	212	303	
2565	32933	C	2597	236	396	
2566	32934	B	2598	119	625	
2567	32935	C	2599	68	334	
2568	32936	C	2600	85	351	
2569	32937	B	2601	1	723	
2570	32938	C	2602	235	463	
2571	32939	B	2603	1	498	
2572	32940	C	2604	179	346	
2573	32941	B	2605	21	486	
2574	32942	B	2606	20	600	
2575	32943	B	2607	172	294	
2576	32944	B	2608	130	1200	
2577	32945	B	2609	61	243	
2578	32946	B	2610	1	753	
2579	32947	B	2611	1	2274	
2580	32948	B	2612	1	1848	
2581	32949	B	2613	1	1263	
2582	32950	B	2614	412	654	
2583	32951	C	2615	176	658	
2584	32952	B	2616	310	628	
2585	32953	B	2617	1	579	
2586	32954	C	2618	145	309	
2587	32955	B	2619	298	353	
2588	32956	B	2620	163	594	
2589	32957	B	2621	1	468	
2590	32958	B	2622	1	552	
2591	32959	B	2623	1	876	
2592	32960	B	2624	140	1333	
2593	32961	C	2625	1	222	
2594	32962	B	2626	1	645	
2595	32963	C	2627	49	339	
2596	32964	B	2628	1	1944	
2597	32965	C	2629	79	189	
2598	32966	C	2630	513	767	
2599	32967	B	2631	114	230	
2600	32968	B	2632	24	629	
2601	32969	B	2633	98	230	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2602	32970	B	2634	99	462	
2603	32971	B	2635	127	1498	
2604	32972	B	2636	22	105	
2605	32973	B	2637	1	1173	
2606	32974	B	2638	403	660	
2607	32975	B	2639	58	507	
2608	32976	C	2640	103	480	
2609	32977	B	2641	1	657	
2610	32978	B	2642	1	508	
2611	32979	B	2643	1	999	
2612	32980	C	2644	1	756	
2613	32981	C	2645	1	675	
2614	32982	B	2646	1	810	
2615	32983	B	2647	1	334	
2616	32984	B	2648	1	781	
2617	32985	B	2649	76	211	
2618	32986	B	2650	1	687	
2619	32987	B	2651	1	753	
2620	32988	B	2652	37	1038	
2621	32989	B	2653	1	456	
2622	32990	B	2654	1	168	
2623	32991	B	2655	1	786	
2624	32992	C	2656	571	1278	
2625	32993	C	2657	96	548	
2626	32994	C	2658	391	504	
2627	32995	B	2659	1	183	
2628	32996	C	2660	1	381	
2629	32997	B	2661	1	642	
2630	32998	B	2662	1	1164	
2631	32999	B	2663	1	471	
2632	33000	B	2664	1	972	
2633	33001	C	2665	75	182	
2634	33002	C	2666	125	226	
2635	33003	B	2667	1	462	
2636	33004	B	2668	1	422	
2637	33005	B	2669	81	616	
2638	33006	B	2670	197	713	
2639	33007	B	2671	1	882	
2640	33008	B	2672	1	507	
2641	33009	C	2673	176	274	
2642	33010	B	2674	250	446	
2643	33011	B	2675	19	118	
2644	33012	B	2676	21	120	
2645	33013	B	2677	373	389	
2646	33014	B	2678	1	1452	
2647	33015	B	2679	70	148	
2648	33016	C	2680	7	96	
2649	33017	C	2681	360	550	
2650	33018	B	2682	55	1618	
2651	33019	B	2683	1	309	
2652	33020	B	2684	100	528	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2653	33021	B	2685	1	1191	
2654	33022	B	2686	52	834	
2655	33023	B	2687	1	933	
2656	33024	C	2688	80	322	
2657	33025	B	2689	127	415	
2658	33026	B	2690	74	190	
2659	33027	B	2691	150	380	
2660	33028	B	2692	1	1098	
2661	33029	C	2693	185	502	
2662	33030	B	2694	1	180	
2663	33031	C	2695	257	498	
2664	33032	B	2696	88	409	
2665	33033	C	2697	720	902	
2666	33034	C	2698	201	437	
2667	33035	C	2699	16	189	
2668	33036	B	2701	1	2286	
2669	33037	B	2702	1	1026	
2670	33038	B	2703	777	1035	
2671	33039	B	2704	1	1200	
2672	33040	B	2705	332	462	
2673	33041	B	2706	351	480	
2674	33042	B	2707	10	327	
2675	33043	B	2708	108	1325	
2676	33044	B	2709	36	189	
2677	33045	B	2710	54	3192	
2678	33046	B	2711	1	3423	
2679	33047	C	2712	5	280	
2680	33048	C	2713	1	88	
2681	33049	C	2714	1	153	
2682	33050	B	2715	70	231	
2683	33051	B	2716	11	427	
2684	33052	B	2717	74	943	
2685	33053	C	2718	109	315	
2686	33054	B	2719	1	335	
2687	33055	B	2720	108	506	
2688	33056	C	2721	1	486	
2689	33057	C	2722	87	441	
2690	33058	C	2723	85	276	
2691	33059	C	2724	86	280	
2692	33060	C	2725	108	254	
2693	33061	B	2726	1	930	
2694	33062	B	2727	23	847	
2695	33063	B	2728	19	182	
2696	33064	C	2729	190	300	
2697	33065	B	2730	67	650	
2698	33066	B	2731	1	1149	
2699	33067	B	2732	1	263	
2700	33068	B	2733	73	676	
2701	33069	B	2734	1	414	
2702	33070	B	2735	4	256	
2703	33071	B	2736	29	493	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2704	33072	B	2737	1	1323	
2705	33073	B	2738	1	4209	
2706	33074	B	2739	538	728	
2707	33075	B	2740	344	1447	
2708	33076	C	2741	223	477	
2709	33077	B	2742	1	1091	
2710	33078	B	2743	1	2865	
2711	33079	B	2744	1	1203	
2712	33080	C	2745	120	401	
2713	33081	B	2746	1	688	
2714	33082	B	2747	1	549	
2715	33083	B	2748	196	1647	
2716	33084	B	2749	1	378	
2717	33085	C	2750	2	166	
2718	33086	B	2751	1	807	
2719	33087	C	2752	343	532	
2720	33088	B	2753	1	885	
2721	33089	C	2754	32	247	
2722	33090	B	2755	1	1152	
2723	33091	B	2756	1	885	
2724	33092	B	2757	87	359	
2725	33093	B	2758	71	418	
2726	33094	B	2759	117	1983	
2727	33095	B	2760	176	1045	
2728	33096	B	2761	25	187	
2729	33097	B	2762	1	315	
2730	33098	B	2763	1	351	
2731	33099	B	2764	1	396	
2732	33100	B	2765	12	350	
2733	33101	B	2766	1	411	
2734	33102	B	2767	1	1020	
2735	33103	B	2768	72	359	
2736	33104	B	2769	1	526	
2737	33105	B	2770	1	1233	
2738	33106	B	2771	1	1563	
2739	33107	B	2772	1	246	
2740	33108	B	2773	1	747	
2741	33109	B	2774	1	861	
2742	33110	C	2775	1	1278	
2743	33111	B	2776	1	630	
2744	33112	C	2777	22	147	
2745	33113	B	2778	242	744	
2746	33114	B	2779	54	178	
2747	33115	B	2780	1	2277	
2748	33116	B	2781	1	204	
2749	33117	B	2782	1	447	
2750	33118	B	2783	1	819	
2751	33119	B	2784	1	720	
2752	33120	B	2785	1	444	
2753	33121	B	2786	1	519	
2754	33122	B	2787	1	864	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2755	33123	B	2788	1	654	
2756	33124	B	2789	1	772	
2757	33125	B	2790	1	930	
2758	33126	B	2791	1	3594	
2759	33127	B	2792	1	654	
2760	33128	B	2793	1	444	
2761	33129	B	2794	403	1560	
2762	33130	B	2795	1412	1495	
2763	33131	B	2796	536	2770	
2764	33132	B	2797	417	1025	
2765	33133	B	2798	108	326	
2766	33134	B	2799	1	694	
2767	33135	B	2800	380	541	
2768	33136	B	2801	1	916	
2769	33137	B	2802	509	1643	
2770	33138	C	2803	40	180	
2771	33139	B	2804	1	345	
2772	33140	C	2805	170	361	
2773	33141	C	2806	1	312	
2774	33142	C	2807	307	450	
2775	33143	B	2808	1	993	
2776	33144	B	2809	1	321	
2777	33145	B	2810	1	321	
2778	33146	C	2811	604	779	
2779	33147	B	2812	52	646	
2780	33148	C	2813	7	177	
2781	33149	C	2814	118	294	
2782	33150	B	2815	337	1512	
2783	33151	B	2816	32	335	
2784	33152	B	2817	1	1026	
2785	33153	C	2818	1	1044	
2786	33154	B	2819	1	1575	
2787	33155	B	2820	1	1356	
2788	33156	B	2821	1	3726	
2789	33157	B	2822	158	627	
2790	33158	B	2823	814	3116	
2791	33159	B	2824	1	2667	
2792	33160	B	2825	1	2778	
2793	33161	B	2826	96	662	
2794	33162	C	2827	163	245	
2795	33163	B	2828	1	381	
2796	33164	B	2829	47	378	
2797	33165	B	2830	1	614	
2798	33166	B	2831	277	528	
2799	33167	B	2832	1	1059	
2800	33168	C	2833	354	491	
2801	33169	C	2834	161	466	
2802	33170	B	2835	78	2700	
2803	33171	C	2836	37	111	
2804	33172	B	2837	1	1929	
2805	33173	B	2838	36	612	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2806	33174	B	2839	189	498	
2807	33175	C	2840	302	430	
2808	33176	C	2841	58	219	
2809	33177	C	2842	56	275	
2810	33178	C	2843	21	293	
2811	33179	C	2844	337	543	
2812	33180	B	2845	1	507	
2813	33181	C	2846	232	489	
2814	33182	C	2847	314	476	
2815	33183	C	2848	572	937	
2816	33184	C	2849	259	528	
2817	33185	B	2850	1	597	
2818	33186	B	2851	1	564	
2819	33187	B	2852	368	732	
2820	33188	C	2853	58	375	
2821	33189	B	2854	608	1222	
2822	33190	C	2855	41	358	
2823	33191	C	2856	73	177	
2824	33192	B	2857	1	582	
2825	33193	C	2858	1	543	
2826	33194	B	2859	1	1538	
2827	33195	B	2860	40	704	
2828	33196	C	2861	303	407	
2829	33197	B	2862	131	336	
2830	33198	C	2863	64	156	
2831	33199	B	2864	180	712	
2832	33200	B	2865	1	1104	
2833	33201	B	2866	65	228	
2834	33202	B	2867	1	2172	
2835	33203	B	2868	1	1338	
2836	33204	C	2869	181	410	
2837	33205	B	2870	1	1137	
2838	33206	B	2871	69	1322	
2839	33207	C	2872	24	266	
2840	33208	B	2873	1033	1089	
2841	33209	B	2874	367	463	
2842	33210	B	2875	1	3256	
2843	33211	C	2876	278	466	
2844	33212	B	2877	323	4268	
2845	33213	B	2878	424	1711	
2846	33214	B	2879	567	643	
2847	33215	B	2880	1	258	
2848	33216	B	2881	1	806	
2849	33217	B	2882	56	984	
2850	33218	B	2883	1	807	
2851	33219	B	2884	1	396	
2852	33220	C	2885	107	411	
2853	33221	B	2886	1	678	
2854	33222	B	2887	1	246	
2855	33223	C	2888	41	316	
2856	33224	B	2889	1	300	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2857	33225	C	2890	1	273	
2858	33226	B	2891	78	169	
2859	33227	B	2892	1	882	
2860	33228	C	2893	1	246	
2861	33229	B	2894	1	639	
2862	33230	B	2895	1	411	
2863	33231	C	2896	427	522	
2864	33232	B	2897	158	826	
2865	33233	B	2898	275	310	
2866	33234	B	2899	429	933	
2867	33235	B	2900	1	560	
2868	33236	B	2901	1	798	
2869	33237	B	2902	45	384	
2870	33238	B	2903	845	983	
2871	33239	C	2904	171	422	
2872	33240	C	2905	139	360	
2873	33241	C	2906	188	436	
2874	33242	C	2907	76	303	
2875	33243	C	2908	362	574	
2876	33244	C	2909	42	347	
2877	33245	B	2910	1	766	
2878	33246	B	2911	170	1381	
2879	33247	B	2912	274	543	
2880	33248	B	2913	768	2001	
2881	33249	B	2914	140	279	
2882	33250	B	2915	1	2858	
2883	33251	B	2916	1	321	
2884	33252	B	2917	1	552	
2885	33253	B	2918	1	603	
2886	33254	C	2919	122	406	
2887	33255	B	2920	508	679	
2888	33256	B	2921	1	942	
2889	33257	B	2922	1	753	
2890	33258	B	2923	136	326	
2891	33259	B	2924	445	625	
2892	33260	B	2925	1	639	
2893	33261	B	2926	1	1850	
2894	33262	B	2927	76	1341	
2895	33263	C	2928	184	495	
2896	33264	B	2929	1	226	
2897	33265	B	2930	1	972	
2898	33266	B	2931	57	1493	
2899	33267	C	2932	207	404	
2900	33268	B	2933	664	1647	
2901	33269	B	2934	1	1305	
2902	33270	B	2935	1	639	
2903	33271	B	2936	59	1108	
2904	33272	B	2937	276	1311	
2905	33273	B	2938	1	708	
2906	33274	B	2939	123	309	
2907	33275	B	2940	1	957	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2908	33276	C	2941	199	357	
2909	33277	B	2942	319	355	
2910	33278	B	2943	574	1044	
2911	33279	B	2944	1	426	
2912	33280	C	2945	1	381	
2913	33281	C	2946	145	301	
2914	33282	B	2947	1	1644	
2915	33283	B	2948	1	906	
2916	33284	B	2949	249	317	
2917	33285	B	2950	388	655	
2918	33286	C	2951	228	379	
2919	33287	C	2952	200	343	
2920	33288	B	2953	1	600	
2921	33289	B	2954	123	719	
2922	33290	B	2955	1	879	
2923	33291	B	2956	88	445	
2924	33292	B	2957	518	1508	
2925	33293	C	2958	1	414	
2926	33294	C	2959	202	408	
2927	33295	B	2960	1	351	
2928	33296	B	2961	1	378	
2929	33297	C	2962	84	194	
2930	33298	B	2963	1	306	
2931	33299	B	2964	238	354	
2932	33300	C	2965	326	331	
2933	33301	B	2966	1	1005	
2934	33302	C	2967	31	408	
2935	33303	B	2968	48	335	
2936	33304	B	2969	1	241	
2937	33305	B	2970	1	768	
2938	33306	B	2971	93	728	
2939	33307	B	2972	25	88	
2940	33308	B	2973	1	414	
2941	33309	B	2974	1	555	
2942	33310	B	2976	83	3457	
2943	33311	B	2977	59	1280	
2944	33312	B	2978	1	414	
2945	33313	B	2979	1	354	
2946	33314	B	2980	1	477	
2947	33315	B	2981	1	357	
2948	33316	B	2982	182	394	
2949	33317	B	2983	148	1104	
2950	33318	B	2984	494	641	
2951	33319	C	2985	44	310	
2952	33320	C	2986	303	395	
2953	33321	C	2987	229	407	
2954	33322	B	2988	195	707	
2955	33323	B	2989	713	1063	
2956	33324	B	2990	67	746	
2957	33325	B	2991	468	1010	
2958	33326	C	2992	1	258	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2959	33327	B	2993	1	282	
2960	33328	B	2994	139	767	
2961	33329	B	2995	1	133	
2962	33330	B	2996	136	291	
2963	33331	B	2997	172	634	
2964	33332	B	2998	1	435	
2965	33333	B	2999	503	1294	
2966	33334	B	3000	1	495	
2967	33335	B	3001	1	1416	
2968	33336	B	3002	1	321	
2969	33337	B	3003	1	378	
2970	33338	B	3004	1	337	
2971	33339	C	3005	1	474	
2972	33340	B	3006	1	633	
2973	33341	C	3007	142	423	
2974	33342	C	3008	226	360	
2975	33343	C	3009	45	281	
2976	33344	B	3010	1	369	
2977	33345	C	3011	2082	2558	
2978	33346	C	3012	99	356	
2979	33347	C	3013	312	467	
2980	33348	B	3014	89	463	
2981	33349	C	3015	16	357	
2982	33350	B	3016	239	541	
2983	33351	C	3017	176	345	
2984	33352	B	3018	1	2238	
2985	33353	C	3019	40	309	
2986	33354	B	3020	80	835	
2987	33355	B	3021	1	741	
2988	33356	B	3022	1	1005	
2989	33357	B	3023	185	3661	
2990	33358	B	3024	1	1539	
2991	33359	B	3025	1	1197	
2992	33360	C	3026	258	584	
2993	33361	B	3027	103	905	
2994	33362	B	3028	1	159	
2995	33363	B	3029	72	642	
2996	33364	C	3030	195	424	
2997	33365	C	3031	350	454	
2998	33366	B	3032	1	1494	
2999	33367	C	3033	1	336	
3000	33368	C	3034	169	423	
3001	33369	C	3035	131	307	
3002	33370	C	3036	80	423	
3003	33371	B	3037	1	663	
3004	33372	C	3039	619	1068	
3005	33373	B	3040	1	441	
3006	33374	B	3041	1	453	
3007	33375	C	3042	174	431	
3008	33376	B	3043	236	1145	
3009	33377	C	3044	99	215	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3010	33378	B	3045	1	675	
3011	33379	B	3046	1	479	
3012	33380	C	3047	18	272	
3013	33381	C	3048	800	1097	
3014	33382	C	3049	1	231	
3015	33383	C	3050	1	777	
3016	33384	B	3051	194	328	
3017	33385	B	3052	1	633	
3018	33386	C	3053	431	838	
3019	33387	B	3054	1	450	
3020	33388	B	3055	684	1367	
3021	33389	B	3056	112	423	
3022	33390	B	3057	28	420	
3023	33391	B	3058	28	280	
3024	33392	B	3059	1	1335	
3025	33393	B	3060	516	1396	
3026	33394	B	3061	1	1563	
3027	33395	B	3062	1	903	
3028	33396	B	3063	191	628	
3029	33397	B	3064	1	534	
3030	33398	B	3065	1	1134	
3031	33399	B	3066	1	1248	
3032	33400	B	3067	1	1479	
3033	33401	B	3068	1	1635	
3034	33402	B	3069	46	447	
3035	33403	C	3070	1	624	
3036	33404	C	3071	25	330	
3037	33405	C	3072	132	253	
3038	33406	B	3073	4	1011	
3039	33407	B	3074	392	814	
3040	33408	C	3075	414	557	
3041	33409	C	3076	74	328	
3042	33410	C	3077	1	678	
3043	33411	B	3078	1	5130	
3044	33412	B	3079	1	985	
3045	33413	B	3080	1	1671	
3046	33414	B	3081	146	556	
3047	33415	B	3082	1	732	
3048	33416	B	3083	136	753	
3049	33417	B	3084	1	1500	
3050	33418	B	3085	300	2678	
3051	33419	B	3086	1	1221	
3052	33420	B	3087	58	1287	
3053	33421	B	3088	1	933	
3054	33422	B	3089	1	1317	
3055	33423	B	3090	1	771	
3056	33424	B	3091	1	2241	
3057	33425	B	3092	1	642	
3058	33426	B	3093	1	2664	
3059	33427	C	3094	1	513	
3060	33428	C	3095	52	174	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3061	33429	C	3096	44	428	
3062	33430	C	3097	300	437	
3063	33431	C	3098	1	576	
3064	33432	B	3099	1	864	
3065	33433	C	3100	1	801	
3066	33434	C	3101	298	480	
3067	33435	B	3102	503	720	
3068	33436	C	3103	1	756	
3069	33437	B	3104	1	355	
3070	33438	C	3105	1	1143	
3071	33439	B	3106	1	2256	
3072	33440	C	3107	537	966	
3073	33441	B	3108	1	2009	
3074	33442	B	3109	1	3021	
3075	33443	B	3110	1	1085	
3076	33444	B	3111	180	2069	
3077	33445	B	3112	1	375	
3078	33446	B	3113	31	127	
3079	33447	B	3114	47	452	
3080	33448	C	3115	149	440	
3081	33449	B	3116	119	538	
3082	33450	B	3117	1	900	
3083	33451	C	3118	1	270	
3084	33452	B	3119	1	344	
3085	33453	C	3120	72	245	
3086	33454	B	3121	1	822	
3087	33455	C	3122	69	242	
3088	33456	B	3123	2129	2289	
3089	33457	C	3124	1	255	
3090	33458	B	3125	2129	2289	
3091	33459	B	3126	1	306	
3092	33460	C	3127	1	255	
3093	33461	B	3128	82	1254	
3094	33462	B	3129	1	468	
3095	33463	C	3130	2	250	
3096	33464	C	3131	166	357	
3097	33465	B	3132	423	3286	
3098	33466	B	3133	63	436	
3099	33467	B	3134	1	4578	
3100	33468	B	3135	1	4322	
3101	33469	B	3136	46	325	
3102	33470	B	3137	58	289	
3103	33471	B	3138	1	1695	
3104	33472	B	3139	89	1195	
3105	33473	C	3140	317	541	
3106	33474	B	3141	314	992	
3107	33475	C	3142	95	222	
3108	33476	C	3143	26	172	
3109	33477	C	3144	40	255	
3110	33478	C	3145	277	508	
3111	33479	B	3146	12	1358	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3112	33480	B	3147	602	780	
3113	33481	C	3148	1	306	
3114	33482	C	3149	1	771	
3115	33483	B	3150	149	360	
3116	33484	B	3151	1	567	
3117	33485	B	3152	1	345	
3118	33486	B	3153	1	1233	
3119	33487	B	3154	144	773	
3120	33488	C	3155	1	417	
3121	33489	B	3156	85	525	
3122	33490	C	3157	251	679	
3123	33491	B	3158	1	1185	
3124	33492	C	3159	541	729	
3125	33493	B	3160	211	382	
3126	33494	C	3161	200	409	
3127	33495	C	3162	85	423	
3128	33496	C	3163	243	455	
3129	33497	B	3164	152	437	
3130	33498	B	3165	1	816	
3131	33499	B	3166	79	294	
3132	33500	C	3167	6	353	
3133	33501	C	3168	82	405	
3134	33502	B	3169	3	191	
3135	33503	C	3170	204	413	
3136	33504	B	3171	75	1449	
3137	33505	B	3172	1	738	
3138	33506	B	3173	1	324	
3139	33507	C	3174	299	1009	
3140	33508	B	3175	1	447	
3141	33509	C	3176	1	570	
3142	33510	B	3177	1	703	
3143	33511	B	3178	142	744	
3144	33512	B	3179	1	237	
3145	33513	C	3180	63	254	
3146	33514	B	3181	185	330	
3147	33515	B	3184	214	1333	
3148	33516	B	3185	61	423	
3149	33517	B	3186	19	2467	
3150	33518	B	3187	4	1085	
3151	33519	B	3188	157	341	
3152	33520	B	3189	222	656	
3153	33521	B	3190	249	999	
3154	33522	B	3191	416	2447	
3155	33523	B	3192	187	1855	
3156	33524	C	3193	38	166	
3157	33525	B	3194	1	1449	
3158	33526	B	3195	286	663	
3159	33527	B	3196	255	556	
3160	33528	B	3197	85	591	
3161	33529	B	3198	32	404	
3162	33530	B	3199	185	253	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3163	33531	B	3200	202	2862	
3164	33532	B	3201	448	833	
3165	33533	B	3202	1	1275	
3166	33534	B	3203	1	591	
3167	33535	C	3204	1	291	
3168	33536	B	3205	1	744	
3169	33537	B	3206	338	523	
3170	33538	B	3207	1	435	
3171	33539	B	3208	1	477	
3172	33540	B	3209	1	2943	
3173	33541	B	3210	1	1719	
3174	33542	C	3211	113	280	
3175	33543	B	3212	1	1092	
3176	33544	B	3213	1	1470	
3177	33545	B	3214	1	426	
3178	33546	B	3215	1	747	
3179	33547	B	3216	321	2234	
3180	33548	B	3217	1	3057	
3181	33549	B	3218	1	537	
3182	33550	B	3219	1	2496	
3183	33551	B	3220	94	273	
3184	33552	B	3221	302	1432	
3185	33553	B	3222	35	1657	
3186	33554	B	3223	2	901	
3187	33555	B	3224	82	1479	
3188	33556	B	3225	224	411	
3189	33557	B	3226	328	429	
3190	33558	B	3227	27	1098	
3191	33559	B	3228	508	1765	
3192	33560	C	3229	1	321	
3193	33561	B	3230	251	415	
3194	33562	B	3231	695	1011	
3195	33563	B	3232	1	416	
3196	33564	B	3233	45	1340	
3197	33565	B	3234	65	2087	
3198	33566	B	3235	1	1149	
3199	33567	C	3236	1	108	
3200	33568	B	3237	1	384	
3201	33569	B	3238	80	383	
3202	33570	B	3239	200	409	
3203	33571	B	3240	14	419	
3204	33572	B	3241	1	888	
3205	33573	C	3242	165	435	
3206	33574	B	3243	452	593	
3207	33575	B	3244	1472	4415	
3208	33576	B	3245	103	207	
3209	33577	B	3246	242	292	
3210	33578	B	3247	1	306	
3211	33579	B	3248	1	684	
3212	33580	B	3249	1	838	
3213	33581	B	3250	215	2593	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3214	33582	C	3251	80	376	
3215	33583	B	3252	1	639	
3216	33584	C	3253	52	288	
3217	33585	B	3254	1	1197	
3218	33586	B	3255	39	2809	
3219	33587	B	3256	1	609	
3220	33588	C	3257	269	418	
3221	33589	B	3258	1	561	
3222	33590	B	3259	347	922	
3223	33591	B	3260	52	339	
3224	33592	B	3261	235	434	
3225	33593	B	3262	74	2676	
3226	33594	B	3263	90	675	
3227	33595	B	3264	1	1440	
3228	33596	B	3265	288	752	
3229	33597	B	3266	1	804	
3230	33598	C	3267	109	451	
3231	33599	B	3268	1	1122	
3232	33600	B	3269	1	768	
3233	33601	B	3270	380	2743	
3234	33602	B	3271	1	1296	
3235	33603	B	3272	322	591	
3236	33604	B	3273	174	464	
3237	33605	B	3274	1	384	
3238	33606	C	3275	320	385	
3239	33607	B	3276	53	485	
3240	33608	C	3277	175	205	
3241	33609	B	3278	216	316	
3242	33610	B	3279	1	921	
3243	33611	B	3280	22	453	
3244	33612	B	3281	168	817	
3245	33613	B	3282	1	477	
3246	33614	B	3283	190	1062	
3247	33615	B	3284	116	787	
3248	33616	B	3285	130	697	
3249	33617	B	3286	1	901	
3250	33618	B	3287	1	342	
3251	33619	B	3288	1	677	
3252	33620	B	3289	1	624	
3253	33621	B	3290	1	756	
3254	33622	B	3291	1	624	
3255	33623	B	3292	130	429	
3256	33624	B	3293	95	516	
3257	33625	B	3294	120	524	
3258	33626	B	3295	51	425	
3259	33627	B	3296	647	1015	
3260	33628	C	3297	518	841	
3261	33629	C	3298	67	294	
3262	33630	B	3299	1	1212	
3263	33631	C	3300	187	453	
3264	33632	B	3301	188	492	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3265	33633	B	3302	123	647	
3266	33634	C	3303	1	219	
3267	33635	B	3304	1	690	
3268	33636	B	3305	1	930	
3269	33637	B	3306	552	722	
3270	33638	B	3307	84	304	
3271	33639	B	3308	328	1104	
3272	33640	C	3309	300	593	
3273	33641	C	3310	1	87	
3274	33642	B	3311	1	819	
3275	33643	C	3312	122	334	
3276	33644	B	3313	1	318	
3277	33645	B	3314	764	977	
3278	33646	C	3315	379	471	
3279	33647	B	3316	1	1194	
3280	33648	B	3317	1	1800	
3281	33649	C	3318	273	506	
3282	33650	B	3319	1	1689	
3283	33651	C	3320	48	212	
3284	33652	C	3321	1	507	
3285	33653	C	3322	117	251	
3286	33654	B	3323	89	845	
3287	33655	C	3324	1	651	
3288	33656	C	3325	48	212	
3289	33657	C	3326	1	864	
3290	33658	B	3327	223	839	
3291	33659	C	3328	1	189	
3292	33660	B	3329	36	144	
3293	33661	B	3330	56	389	
3294	33662	B	3331	1	597	
3295	33663	B	3332	1	606	
3296	33664	C	3333	1	426	
3297	33665	B	3334	1	696	
3298	33666	B	3335	1	417	
3299	33667	C	3336	1	594	
3300	33668	B	3337	1	228	
3301	33669	C	3338	1	879	
3302	33670	B	3339	1	405	
3303	33671	C	3340	33	152	
3304	33672	B	3341	224	429	
3305	33673	B	3342	578	4588	
3306	33674	B	3343	1	288	
3307	33675	B	3344	77	1479	
3308	33676	B	3345	132	875	
3309	33677	C	3346	120	395	
3310	33678	B	3347	1	729	
3311	33679	C	3348	8	133	
3312	33680	C	3349	171	359	
3313	33681	B	3350	1	1098	
3314	33682	B	3351	1	1547	
3315	33683	B	3352	1	933	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3316	33684	B	3353	1	1989	
3317	33685	B	3354	1	595	
3318	33686	C	3355	62	559	
3319	33687	B	3356	1	153	
3320	33688	B	3357	1	768	
3321	33689	B	3358	1	969	
3322	33690	B	3359	217	358	
3323	33691	C	3360	449	961	
3324	33692	B	3361	1	1799	
3325	33693	B	3362	80	1327	
3326	33694	B	3363	111	258	
3327	33695	B	3364	112	429	
3328	33696	B	3365	147	390	
3329	33697	B	3366	1	585	
3330	33698	B	3367	1	2290	
3331	33699	B	3368	19	4071	
3332	33700	C	3369	1	183	
3333	33701	C	3370	1	183	
3334	33702	C	3371	44	283	
3335	33703	B	3372	1	954	
3336	33704	B	3373	1	384	
3337	33705	B	3374	709	773	
3338	33706	B	3375	1	3294	
3339	33707	B	3376	83	1229	
3340	33708	B	3377	1	1512	
3341	33709	C	3378	30	200	
3342	33710	A	3379	3	322	
3343	33711	A	3380	530	1489	YAGNESHPPSLPRYLRRSRHCG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPSVSSP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMPSA/SSPGQVPAQGD LSQEDSSDSPPAEQVLPPSSGSH NTLYLGCKRFSAFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRDGPCSTGRQSASKTPPPPS HPHTGHSLWSEEK*KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP APFSRMGPEQHLPVVVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3344	33712	A	3381	296	1255	YAGNESHPPSLPRYLRRSRHCG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPSVSSP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMPSA/SSPGQVPAQGD LSQEDSSDSPPAEQVLPPSSGSH NTLYLRCKRFSAFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRDGPCSTGRQSASKTPPPPS HPHTGHSLWSEEK*KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP APFSRMGPEQHLPVVVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK
3345	33713	A	3382	81	702	RAAFSPPAPVSSLPAPVSSPPAS TSCPPAPVSSLPAHASSPPASTSS PPAPLSSAPAHTSSLPAPVSSPP ASTSSPLVAGSGGSTTRSLPPGL GALLTHSVAPYPGGQPPPAAAD DP*TMAPAGWGSHNPRGCSCSP VAAGAGPFPASF*GPLR*AGSQ TFQILQVEVFLVVRHFSPSTP/PS VMLYPPPPSTPPTLRAPRPPIPPS P
3346	33714	A	3383	3	231	PMLLEVSVADRDAV*TFWQAPI GESQQGALGFWSKALQSSADN NS/PFQITMQPELPIMNWVLSVP SSHKMGHAQQH
3347	33715	A	3384	3	355	KIPGTSTSVKFLGVQ*CGTCQDI PSKVKDKLLHLAPPTIKKEAQR LVGLFGFWSQHIPHLGELLRPIY RVTRKAASFEWGPEHEKALQQ VQAALQAALPLGPYDPADQPL CNLNCLS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3348	33716	A	3385	2	1076	LCQRLLLAEPNEKPGSLGNVM AVARIEIGICEYYHEKTTEKALD SHGVLAGSTIKGVRSFQRNLEL KLPATERATANAIELLTVLDQA YENFAPQILPSTGSPTSQETAQF KANQNKPLVRGKGSPHEAIRYI SAAHREWKPAILTSAIRSFCST WLVFTSKNFPKLVTQHGSTIAG NGQSSDETQVQGAAWKSDSRG TKRQIPTWILAEGNNAGAQLDI PGPTIPAPNCSLKVPQSWSTTPS MPSSLGKAYWLLACYWALVET E/RLAMGHQVTM\KPELPVMN WVLSDPSSHKVGGAQQHSINK WKWYIRNRARAGPEGTTLPLT KALTLWLKKYSNVLMLVEFTG LTMFPDILKQLE
3349	33717	A	3386	1	1416	MAQYPILDFLKVGQLLGNCAL GKGNDQTFRGLLDTGSELTLIP GDPKHHCDPPVKCAAIDLANA FFSIPVHKAHQKQFAFGWQGQ QYTFTVLHQGCMNSLALCHNLI QRELDCFLTPEDITLDHYIDDIM LIGSSEKEVANTLDLLFWDYRH EPLRLANYSPFERQLLACYWAL VETECLMMGHQVTMRPELPIM NWVLADPSRHKVGNAQQHWK CAVHT/IIKWKWYIRDWAQAG LEGTS*LYWPRASRYQQGHQD LFILRSDLPSQVFIRDKLMERRN RRTGRTEKARIWEVTDRTVRT WIGEAVAAAAADGVTFSVPVT PHTFRHSYAMHMLYAGIPLKV LQSLMGHKSISSTEVYTKVFAL DVAARHRVQFAMPESDAVAM
3350	33718	B	3387	50	693	
3351	33719	A	3388	153	578	ARIQ/GSRNQGVEVEVAPLTVT PSDPLANVLLPVPATLPSAGLEI LVPEEGRLPPGDTTMMPLNWN LRLPHGHFGLLLPLNQQAKKG VAVLGGVIALDCQDEISLLLYK GDLTVMVEDKEEQNHILHGSR QREREPSKTGSPL
3352	33720	A	3389	3	402	GRHAVGDIEAEDGGGVRGPHP GGVYGLQQSHPGGGDPVWED GHPGLPGAQQRGQ*RQQACAH HKSPSGAG*G*LPGP/AQS/AGN PDPKSPGPAPCLVGSSRNETPG AMGAPSRNGSPPTAGLGVGDG TGSPSEAV
3353	33721	A	3390	141	320	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3354	33722	A	3391	1	464	HLKGLGNDTPRVCSCLIG*T*LC DCH*LQ\EASPTSVEVREPRTSV NKD/SPKSLLYSCSYSYFDEPVE LRSSSFSSWDDSSDSYYETHLL HLKLV*PNLAVFNCRPTARRKP DYEPVENTDEAQKTFCKTAHN LWSLTFPFPCLL*YETRARLER
3355	33723	A	3392	3	1189	
3356	33724	A	3393	1	867	PGRPT/LSEWI/QNTLGVNVEHK TTSKASLNPRDTPPSVVNEDFL HDLKETNISYSQEADDRVFRAH GHCLHEIFLLTEGMFERIPDIVL WPTCHDDVVKIVNLACKYNLC IIPIGGGTSVSYGLMCPADETRT IISLDTSQMNRILWVDENNLTA HV*AGITGKELERQLKESG\YCT G\HEPRFPWSSSTVGGWVSTRA SGMKKNIYGNIEDLEIVHFSDN DLSCIELDRLIEIVLPSSGIPLLD GYSTEIHMPVHLETSTTMCIVTP IHSSMKLETLRMSMSINCRKDK
3357	33725	A	3394	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
3358	33726	A	3395	2	441	DGMEKVDTAMNARPHKVDGR FVEPKTAVSREDSQRPGAHLTV IKM/FKE/DTEEHKLRDYIEQYG\ GGNFSGCAGFGGRSGGGR*GG SGNGYNRFDNDGSNFGGGGSY NDFGNYNDRSSNFGPIKGGNFG GRSSGPYGGGSQYFAKP*NQ
3359	33727	A	3396	3	404	

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3360	33728	A	3397	2	762	MNARPHKVDGRVVEPKRAVSR EDSQRPGAHLTVKKIFVGGIKE DTEEHHLRDYFEQYGKIEVIEI MT\DRGSGRKRGFVFVTF\DDP\ DSVDKIVIQKYHTVNGHNCEV RKALSKQEEMASASS\SQRGRS GSG\NFGGGRGGGF\GGNDNFG RGGNFSGRGGFGGSRGGGGYG GSGDGYNGFGNDGSNFGGGGS YNDFGNYNNQSSNFGPMKGGN F\GGRSSGPYG\GGGQYF\AKPR\ NQGGYGGSSSSSSY\GSGRRF
3361	33729	A	3398	1	3737	
3362	33730	A	3399	5	633	DLREWSWARRTAWEPRGKRV RGK*AFKEIQCP*QQKE/SMSGL LLLKVVAKEMTWLPPLSAIQAP GKVEPTKFPFPNKLMFSWWYIE TTTASAKVIGYKPSVLNCATLR VQIMSHYHSYRHLASLLVEGSA TLPGHSHILGPLIRHPDKVSAGK PRVLGLQLLKEDCSSQPAAKPQ GPHRLCSSLILHRARARLGPEQ RETKVPFSKGTTH
3363	33731	A	3400	2	816	QVPTMVDWAGWSPGLWTTCS GTGGGGAEQGWANWSLVLPG VLAGTSLETFSPLS*GLTFSSLLL MQISAASLNFSSENGIFFSTTLP GCKFSKFLCSASLLKWNAFSST QVTS*MLCCSEISSTRYPKSSL* SSKFHKSLEQGQNAASLFAKT* QESPLLQLPTSSSSPSETTSAWIS LSISLSVFLSKLFDKSLESSKLS\ TFSSVLLSPPNCSNLCLLPSFKV ACTFLGTFLRSTSLHWYQFTVL VCFHPADKDILKSEKKKRCKEK
3364	33732	A	3401	1	485	LFKAVLHDPHLKLLSLYGTSLS HTDVSHLCETLKHTTCKIEELM LGTCDISDEGCEDIASVLACNS KLIHLSLVENPEKDKRM\CCCA LETLMLMYCCLICVSCEDISHV LFCSKSLSLLDLGSNFLEDNEV\ HLLCEALKH*DACKTWRSLNF DWVGYLGC
3365	33733	C	3402	952	1164	

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3366	33734	A	3403	3	163	IAVSKQDPITSLEQEKEPWNMK ICEMVDESPAMCSSFTRDLWPE QDIKDSFQQVILRRHGKCEHEN LQLRKGSASVDEYKVHKEGYN ELNQCLTTTQSKIFPCDKYVKV FHKFLNANRHKTRHTGKKPFK CKKCGKSFCMLLHLSQHKRIHI RENSYQCEECGKAFKWFSTLTR HKRIHTGEKPFKCEECGKAFKQ SSTLTTHKIIHTGEKPYRCEECG KAFNRSSHLTTHKIIHTGEKPYK CEECGKAFNQSSTLSTHKFIHA GEKPYKCEECDKAFNRFSYLTK HKIIHAGEKP\YNCEECGKGFN WSSTLTKHKRIHTGEKPYKCEV CGKAFNESSNLTTHKMIHTGEK PYKCEECGKAFNRSPQLTAHKII HTGEKPYKCEECGKAFSQSSIL TTHKRIHTGEKPYKCEECGKAF NRSSNLTKHKIIHTGEKSYKCEE CGKAFNQSSTLTKHRKIHTRQK PYNCEECDNTFNQSSNL/N*/HK IIHTGEKLYKCQECGKASKQSF TLTKH*ILFNK
3367	33735	A	3404	3	345	
3368	33736	B	3405	282	694	
3369	33737	A	3406	586	1403	VSETALADGRCWFRKCQSHLC LASTTGKC*TSTLQSGRDYTEN GESAQEGETGLPERRLAHCT*L AEVHRRQPD*TQENRP/SKMGI MTSS/AAKDHLDNKCQRQDSIP GSSRGPSPLTMGAQDTLPVAAA FTETVNAYFKGADPSNTPSVLV EQLLSKRRSNPIMDHGGHKVPC SLPPLLTHPNRRQRELKMYGSH KAVAQPSPLQDRLQQCAVPTP VTGWTNSRAALGDIFSTWGSLL LRTSTPKKAAARARPMCPCPGA YNTSYPLAPYFWR
3370	33738	A	3407	1	421	FRHSMNGCEKDSSSTDSANEKP ALIPREKKISILEEPSKALRGVT GPNIEKSVKDLQRCTVSLTRYR VMIKEEVDSSVKKIKAAFAELH TCIIDKEVSLMAEMDKVKEEA MEILTARQ\RKAEALKRLTDL\A S\QMAEMQL
3371	33739	A	3408	1	403	MEILTARQKKAEELKRLTDLAS QMAEMQLAELRAEIK/*WFSEN ELGNSDLCSYSCYCLAAQKLSC QCYLGGTAHSAPGIAKRKTSQL I*PLP

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3372	33740	A	3409	1	756	
3373	33741	A	3410	2	1849	QRRRRNTPGWSGFQGLTRAPA LFPRLIFQSSSETRLLSGTLLWIP RAYSTRSKMAELNTHVNVKEK IYAVRSVVPNKSNNEIVLVLQQ FDFNVDKAVQAFVDGSAIQVL KEWNMTGKKKNNKRKRSKSK QHQGNKDAKDKVERPEAGPLQ PQPPQIQNGPMNGCEKDSSSTD SANEKPALIPREKKISILEEPSKA LRGVTEGNRLLQQKLSLDGNP KPIHGTTERSDGLQWSAEQPCN PSKPKAKTSPVKSNTPAAHLEI KPDELAKKRGPNIEKSVKDLQR CTVSLTRYRVMIKEEVDSSVKK IKAAFAELHNCIIDKEVSLMAE MDKVKEEAMEILTARQKKAEE LKRLTNLASQMAEMQ\LAELR\ AEIKHFVSERKYDEELGK\AAR FSCDIEQLKAQIMLCGEITHPK\ NNYSSRTPLQAPCWPLLNA\HA ANLWGKQSNF\SRKSSTHNKPS EGKAATPKMVSSLPSTADPSLR AMPANKQNGSSNQRRRFNPQY HNNR\LNGPAKSQGSGNEAEPL GKGNSRHEHRRQPHNGFRPKN KGGAKNQEASLGMKTPEAPAH SEKPRRRQHAADTSEARPFRGS VGRVSQCNLCPTRIEVSTDAAV LSVPAVTLVA
3374	33742	A	3411	1	489	MAEVQVPVLHGRGHLLGRLAA IVAKQVMLGWKVVVVRCEGIN ISGNFYRNKLNCSFRTPSCIFRW TVRGMLPHKTKRGQAVLDHLQ VFDGISPLYDK/K/KRMVVPAAL KVVRLKPTRKFAYLGRLAHEV GWKYQAVTATLEKRKEKA*IH YRKKKQLMRLRKQA
3375	33743	A	3412	2	260	
3376	33744	A	3413	1	612	AEVQVLVLDGRGHFLCRLADI VAKQVLLG\RKVVVVRCEGINI SGNFYRNKLKYLAFLRKRMNT NPSRGP\YHFRAPSRIFWRTVRG MLPHKTKRGQAALDRLKVFDG IPPPYDKKKRMVVPAALKVVR LKPTRKFAYLGRLAHEVGWKY QAVTATLEEKRKEKAKIHYRK KKQLMRLRKQAEKNVEKKIDK YTEVLKTHGLLV

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3377	33745	A	3414	734	1488	MTKDPWLKQSGSSDTSPAASP GHFRAVPRAPRARGTVVHHRH/ LCLSSWPSSS/RVPPGCASYTPA STAAGALPYQAQRRQGVLRRY TTYLRV*HFLPRGLPEGFQRGP RVPPPPPCPMAAEPELGHALKL LD\LREIVSFLYYFFFFLRRSLT LSPGWRDLGSLQ\PLPHGFKAIF /SCFSLLSGWD\YRHTATHAQLI FVFLVEMGF/TPMFARMASIS*P CDPPDSASQDAGITGVSHQVW RERLFLDEGGGGCP
3378	33746	A	3415	48	966	WSQVVTIVTVVVTVSGSNHGN HTQASHEGYRHPMRAQVSH/G ECR/PSHEGHRHPMRTQASHEG HRRPMRTQASHEGHRHPMRTQ ASHEGHRHPMRGTGVP*EHRH PMRAQASH/GEHRR/HH/GEHSC PMRAQASHEGTGVP*EHRC/HH ENTGVP*GHRCPMRMQASHAG HRHPMRVQASHEGHRCPMRTQ VSHEGHRRPMRVQASHENTGV P*GAQASHEGTGVP*EHSHPMR AQASHENTDVP*GVQASHEGY RRPMRTQASHEGHRCPMRAQT SHENTGVP*AAQYRP*EAGAPQ GGQGWQETGADRST
3379	33747	A	3416	8	432	NSKLPPVVTSQQMRFMY/DPQT DQHMKI\FPEQLPLDEFLQKTDP KDPANYILHAVLVHSGDNHGG HYVVYLNPKGDGKWCKFDDD VVSRCTKEEAIEHNYGGHDDD LSVRHCTNAYMLVYIRESKLSE VLQAVTDHDIPQQL
3380	33748	A	3417	38	2865	SFRWDSKKHTGYVGLKNQGAT CYMNSLLQTLFFTNQLRKKLL MGALPWEGALAPWV*ALDTDP SLPCSTCLTTARTCTSL\QQCHA DQCRWQTRWQGSSRW*WQQE EIGQEREEGVEYAKRVLLGPPY SISDCTHMESSLPPCSS*DPGSF QFHEERAEDEKSEGRGPSCSCT QPPPW*SLGEGLGECR*ESSSSY CSLAGLSLHP*ETRGERLQEAS QGQPESPFGEV*HPALVSLDLA E*QGRAEKHGCTETH

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3381	33749	A	3418	2	3515	YVRVSLPPPPPAAGRPGAAVAD DAREEEEEAAPPPPPPPPPRLAA ARPPGSQPRPPAAGEAQAAAD MNHQQQQQQQKAGEQQLSEPE DMEMEAGDTDDPPRITQNPVIN GNVALSDGHNTAEEDMEDDTS WRSEATFQFTVERFSRLSESVLS PPCFVRNLPWKIMVMPRFYPDR PHQKSVGFFLQCNAESDSTSWS CHAQAVLKIINYRDDEKSFSRRI SHLFFHKENDWGFSNFMAWSE VTDPEKGFIDDDKV
3382	33750	B	3419	36	335	
3383	33751	A	3420	2	1602	CRLKTTAFSSPSSRHITACLPRF WQICSLPKHLIPPEAPPVGMS*R RRKPVWVKSMMLG*RIP*GKR DPPTTAKCRTCSPQEETGPAGT QGQAARQLERRKLPPYVQT/PP RPDQLKGVCSLQTDAISLAPTA ERHSRLLPPPSRQQPTSAGTEA GACPNTRRPSGLQLPAAV\QTPS GQTPSVPKPGLEPTSLPVGSG/PI SASHSQ/PVSKINKK**VCESPY METFP*DAKRTRHKRADTARR GEPLRPRTSVPRRTVPAPSEKLR GSRRGEPTPAAPRRDPRRAGSL THAGPPGG*RHR*PGWPRGTA/ AKTPVAAEALIAAAAPLALHRI PLGAPPQLPAAPAP/RLALALRG ASAA/RPRVAPSAASPQRCLLR\ GPPSPQPSPAPGPVAPSAQGRG AVPGGVLAVLLPGAPRLSGKRP AAPRGGDTPAQGQVPLAARAP REGPGHGREPVIEELERRGAEL RSGKGGTRSEGVRGGRARGIV YGGAHGPEVGKDKMPLKPRNL SAPVAIGGLLHGAGIRFLNLAL HSPAVDFGQIT
3384	33752	A	3421	3	498	IIDPTQYRPMVPNKVSSPC*WLP TITQVHPDNEAEPIPS/PARSCAP ICGVP/AYGSPLSQSSVS*TRQ*F PSCSQSL**GSPTLVNPKTAYT* NSGSRGG/VSFDEDTSQHCYPG TG*GQQPLQ*SRNHAGPPGG*M T*VTGVAERDK/PPKTPVGRRG THSQPPRRSP
3385	33753	A	3422	1	270	

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3386	33754	A	3423	1	1899	MGFCHIGQAGLKLLTSKDLPAS AFQSAGIAGFWLLDGISGPILGQ REACCPAGNSNKELKQENSAL AEQLQVVLIDKAGMQCDLEEL KKKLELTELTLQQLSSWCEAPD ANQQLQQPTDERAQLEAHLGQ VMEWLKYLQMEREQYAEYLH GESAMWWQRMREMSEQIGHLI VPGICEMGGAQPEVVMGLGFV EVHTLREERVHSMSRVQELETI LAELRNQVAEPLPPEPPAGPSE VEQKLQAEAEHLWKELENLAG QLQAQVEENEGLSHLNQEQE\G LLRLLEQEEKLLEQEERLLEQE ERLLEQEERLLELQESLLEQKR KAASFLS*TPTPGAPSRALRGK YVTSYQSQRSV/REDVDRENEY ISRLAQDKEEMKVKLLELVLQL VGDCNKWHGRFLAAAQNPAD EPAPWDPAPQEIGAANKQGGLF PGCCLVTPGGFHGDCRGAYGA QSSPDSQQAQNPDLAVAGKAA FWEFKEHQESLTLLKSWGRRK SGSGQAAQLREGSRCAAARRH LARALPAARMPKRKVISTEGAA KEEPKRTSASLSAKPPAKVEAQ PKKAAAKDKSSDKKTQTKGKR GAKGKQAEVANQETKEDLPAE NELSSLYSFYARSLILAFIIHLRM
3387	33755	A	3424	198	364	FLII*YEGINCSRIVNLTRTAWCF FSG*IFRQKKCKQKGKGEQREN RPEVANPRN
3388	33756	A	3425	3	238	GVCPPRGRSCSDFKADSLYSFP CPSRCGS*ESSTQTCSGFWTGCT ALHRWRGMPERCPPESRDS*TR FPQSSLPGHKT
3389	33757	A	3426	3	681	HIRGPRYSGHHSAFGCPYSDMN LKKEATLHDRLREQTQAN\LES DSSHSKSKSLCSLNFNGKHEKV NSQPRLVQQAKCLKIKGKEDID LDNLFREYSVEQAQQVLHQSV SMSTVSAHPFRDLPLGREQHCK LLPGVADIRASQVARWTVDEV AEFVQSLLGCEEHAKCFKKEQI DGKAFLLLTQTDIVKVMKIKLG PALKIYNSILMFRHSQELPEEDI ASGQEVRG

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3390	33758	A	3427	30	981	TQDPWPSLPVLWSRASSDPAAG HRAEHI*TYWPWKLEGT\DIWL VLYMPLVQPDNFIKKHSHLPTY CLFKEDVKFPFRTCRLTYCWLN YTEEITYLHTKKVSVGQSAVRE EFAAACTWSIRIGEKLAILLSLY LCRQQALLNMRMSVPIHESGV AQRSPVMDKLAQYSVEQAQQV LHQSVSMSTVSAHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLIQTKQTPHLDESIS KGESPALVVTELRMCMTATEP LVPTKNPYQERGHIGDSFLHYT DQEPQPWDQSSVHPTPAPIYSV SSGFRVTRGSDI
3391	33759	A	3428	1	864	MVSALPEVGRAQILRLIAYIRSP APPVVGVERAARRPAQAFGLV ALPSTDATVFANQPLARACIGA ARHREPDAPGQSAWVGEECLK DALRSPETPKLGSLSPPCQDTRP GRASNDFSLEMGYSSLSAARLK IHGQVFQCCGPGPLRTL\HWTQ S*TYLNILALET*GAQNQP*EW QAVD*GAPGLFSHTLGVFPR/RL PQHPKQIICFQNYEYSVEQAQQ VLHQSVSMSTVSAHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSAPRGPELSAGANS SRGA
3392	33760	A	3429	201	336	QQTPGKAVHAPFIADQSLT*EL VSVFPQFQLFPYRR*DSHSGKS
3393	33761	A	3430	600	768	TDTSSYHGSG*PAR/NG*MHSFI RCLLLK*GIEPCALNGDSVLKS RTDVTFTPVNITTKVKSVEMHN EALSRALPGDNVGFKNVSKMF VMATLLFSDCIHNTFDQMWRT KEHNEARWSLQSSGDKVMKEN DELRDSVSQLQKQTLSLKSPKI ALGESLISCRERAEIEIVDKQTQ ALIMGVADLQGRVNAQLHQVS TVKVRDWKRMGPYNLECGTV GRTLIKLWTLSL
3394	33762	A	3431	1655	1841	EHQAEAEGGDGGPRSLPMKPG SPLMPDKAQRKQVRSRHGRGG RGGG*AGPGIPGKPGSPVSP
3395	33763	A	3432	1	1773	

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3396	33764	A	3433	648	1884	LDPEVAWAKWQHSTVKGPQK QFAFSWQGQQYTFTGLPQGYIN SLSLCYNLIPRDPD/RL/SLLQNI TLVHYIDDIMLIGSSEQELAYTL DLLVRRLCAKGWEINLTEIQEA STSVKFLRVQWCGACQDIPSK MKDKLLHLFPPTTKKKASLFGF RRQCIPHLECGPEQEKALQQAQ AAVQAAVPLERYDPADPMVL/ V/ELTWLWPLLSAQFASSGDQH *ALHMAPFLGVVSQLPGGKLIIL DIFHHGKGRVLFSLE*TLTPDM GLPILHIMLLPRLPSVNSQNALS TVMPGFTGPGIKGWKWHHSPS PLVIH*QNFCFLFP*HYVLLA*R S*FQRKEPCHQET*Q*FH*TGS* GCQLDTLGSCYF*VNKLRRELQ CWLG*LTQTIKMKSVYYSITEN CWMKRSPVKRRKILELEEA
3397	33765	A	3434	1	2223	
3398	33766	A	3435	1	1078	MNKEMSGQTFVGKQNSVRMP KIISGLGVQKPNRQWRLVQDLR IINEAVVPLYQAVRNPYTLLSQI PEETGWFTVLDLKDALFCIAVH PDSQFLLAFEDPLNPTSQLTWT VLPQGFRDSPHLFGQALAQDLS QFSYLDTLVLRYVDDLLLAAPS ETLCHQATQVLLNFLATCGYK VSKLKAQICSQQVKYLGLKLSK GTRALSEERIQPILAYPHPKTRK QLRGLLGITGFCQIWIPRYSEIA RPLHTLIKKTQKANTHLVRWTP EAEAAFQVLKKALTQAPVLSLP TGQDF\SLYVTEKTGIALGVLTQ HYGEERNS*LPTEYLSNIRKPLG DYYWLYRNLKRWQSYTARVIR KERKGK
3399	33767	A	3436	1	1677	

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3400	33768	A	3437	1	2052	MVLVVVAVVVVVLVVAVIVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATQALLNFLATCGYKVSKPKA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEK\TGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPLEMLTEGPLAFELA MATARAELSLAIHHCCLPPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEQGPPVTVQTHILRSHL

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3401	33769	A	3438	294	2340	EKCRHNCSSRVWQSLVSQSVW ATEGQYGRTKNARPVQVK\DS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINEAI VPLYPAVPNPYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLLLAAHLETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLLNQALLFKRPVLRLHTC ATLNPATFLPNNKEKIEHNHQQ VIVQTYTIQGDLLEVPLTDPDL NLYTNGSSFVEKGLRKAGIHPS RQWTPLWPKAGPEMLSKRQVL ESGILKAFLVPYLLVAVLGSIDF NGKPPVAVFSLSQAHRFLCAT WLLLGYGEVWIHSHTAIKTYQ RRRSQDGRIGTAPVYSSQRERR RRRVISAFPSEGIPTDLQLRVLS VRRKTNKQKGHPHQKPICTSPS SRPKVDKTTKMGKKQNRKTGN SKTQSASPPPKERSSSPATEQSW MENDFDELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSAMED
3402	33770	A	3439	2	350	YKVSKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIP\R*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
3403	33771	A	3440	1	897	
3404	33772	A	3441	1	429	

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3405	33773	A	3442	3	957	NKIPRNPTYEGCEGPFQGELQT TAQQNKGGHKQTEDHSMLMD RKNQYCENGHTAQAVPNPYTL LSQIPEDAEWFTVLDPKHAVFC IPVHPDSQFLFAFEDPSNPMSQL IWTVLPQGFRNSPHLFGQALAQ DLSQFSYLDTLVLRYMDDLLL ATHSETLCHQATQALLNFLATC GYKVSKPKAQLCSQQVKYLGL KLSKGTRTLSEERIQPILGYPHP KTLKQLTAFLGITGFCQIWIPRY SKIARPLNTRIKETQKANTHLV RWTPEAEVAFQALKKALTHAP VLSLPVGQNFSLYVTEK\TGIAL GVLTQELVLSWQN
3406	33774	A	3443	146	1303	EKCRHNCSSRVWQSLVSQSVW ATEGQYGRTKNARPVQVK\DS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINEAI VPLYPAVPNPYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLLLAAHLETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLLNQALLFKRPVLRLHTC ATLNPATFLPNNKEKIEHNHQQ VIVQTYTIQGDLLEVPLTDPDL NLYTNGSSFVEKGLRKA

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3407	33775	A	3444	1	1647	MNKEDYNDDDDNGDIKYLPDI KTGYNKTVQIPITSENSTVGLSN TEADEMDRLKCERDDALKEVN TLKRRTKGGKHLTLKVTYTLSE TNLHKNYLWECILMGQLGCYE ILRKPSPALGLTPEHKGNVGHT GEKTGAG/PATSRPPDSFPN**G PPFNPNGTKGDRQRGKQQTKE CQYSPIMPTPSSGRRRIWSSQ\R HVPFSLSDLIDLAVPNPYTLLSQ IPEEAEWFTVLDLKDVFFCIPVH PDSQFLFAFEDPLNPMSQLTCT VLPQGFRDSPHLFGQALAQDLS QLSYLDTLVLQYVDDLLLAAC SETLCHQATQALLNFLATCGYK VSKEKAQLCSQQVKYLGLKLS KGTKALSEECIQPILAYPHLKTL KQLREFLGITGFCRIW/NFQALL LERPVLQLCTCATLNPVTFLPD NE\EEYNCQQIISQTYATRGDLL EVPLTDPDLNLYTDGSSFVEKG PQKAGERRAVLASQTSLTPLGR NGRSIPATLALESKELVKSVRA LLDMDCAIPFLVGTSIVDPYLK YEPTTKNHLIMVQGEKNCITGR
3408	33776	A	3445	1	2217	
3409	33777	A	3446	1	749	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYLGLKLSKGTRDLTTFLP VNEEKIE/P*LSTSNCSKLRCSRG TSRGSLG

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3410	33778	A	3447	1	1374	MPLLQMIATPLQQSLISTEDEM DELTEVGFERWVITNFTEEPSPA LGFTPEHKGNVGHAGKGPLESS SPDPFLCGQEKQEKGAGLLHRQ YPLRLEAKQGLKKIVKDLKAQ GLVTPCSSPCNTPTLAVQKPNG QWRLVQDLRIINEAVVPLYPAV PNPYILLSQIPEEAEWFTVLDLK DAFFCIPVHPDSQFLFAFEDPSN PMSQLTWTVLPQGFRDSLHLFG QALAQDLSQFSYLDTLVLQYM DDLLLVTHSETLCHQATQVLLN FLATCGYKVSKLKAQICSQQVK YLGLKLSKGTRALSEERIQPILA YPHPKTRKQLRGLLGITGFCQI WIPRYSEIARPLHTLIKKTQKAN THLVRWTPEAEAAFQVLKKAL TQAPVLSLPTGQDF\SLYVTEKT GIALGVLTQHYGEERNS*LPTE YLSNIRKPLGDYYWLYRNLKR WQSYTARVIRKERKGK
3411	33779	B	3448	1	2862	
3412	33780	B	3449	94	1248	
3413	33781	A	3450	1	3805	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN
3414	33782	A	3451	1	444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFAFV*YVNE RNARAAVGGD\DSSSFDLDHDF QRDYYDRMYSYPAHVPPPPIAR AVVPSKCQHVSGN\RRGKSGFN SKRGQRGSSKSGKLKGDDLQAI KKELTQIKQKVDSLLENL
3415	33783	A	3452	3	93	
3416	33784	A	3453	117	316	SSATFSAL*ETLPSNTMASSSFD LDYDFQRDYYDRMYSYPARVP PPPPIARAVVPSKRQRVSGNTS

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3417	33785	A	3454	102	1059	ETLPSNTMASNVTNKTDPRSM NSRVFIGNLNTLVVKKSDVEAI FSKYGKIVGCSVHKGFAFVQY AYE\RNARAAVAG\EDGRMIAG Q\VLDINLAAEPK\VNRGKAGV KRSA\AEMYGSVTEHPSPSPLLS SSFDL\D\YDFQRDYYDRMYSY PARVPPPPPIA\RAVVPSKRQRV SGNTSRRGK\SGFNSKSGQRGSS KSGK\LKGDDLQ\AIK\KELTPD KTKKWDSLL\ENLEKI\EKEQSK QAVEMKNDKSEEEQSSSSR/VK KDETNVKMESEGGADDSA\EE GDLLG*MNDNE\DRGDDQLE\LI KDDEKEAEEGEDDRDSANGGG
3418	33786	A	3455	299	509	
3419	33787	B	3456	16	101	
3420	33788	A	3457	1209	1828	GNCDSPARPARPPHRQGCPRPS PPPRGRPRALGPTRASAARAPA DLPPPAAPHPAPAALVPHTAAP KA\RNALPGSPGALTEGAVLLP NAGARPRRPRSSEKP\GPAPSWP RIPGFRTGAPPPATPVLAAGGL APPSPGLAGQQVALPSQVPADT QSGVKSGSQDRGRN*QSAGSA GGGARTQVPGPLRMWKRAVW PGDWAPHPANI
3421	33789	A	3458	387	772	PHRKQAEPPRHHERLGRRVRH HARHGRGSRPDTAAEAAGGCG DPRAFQQLERRLRHPPLRWQGL LRRQRLLREEPRRSLL/QTS*S*C SPVTRPSSGCSSPRSWMETRRG APAPPAPRSRNKPTTWWPH
3422	33790	A	3459	362	608	FFFFFLNRVLLCHPG/WS*SGNH QWQSWLNS*PQTPGLK*SSFLC FRKWWDYKHEPLYPAKPHFEF LFGSSLQVREFFGKIKV
3423	33791	B	3460	1	612	

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3424	33792	A	3461	1277	2152	SRAAPTCFSWLPCGASTCPWL MWAMSGRMVAPLQRVLRAAP GLEGTLGGRQHPGTPPSVLHFS LTMNSMFGLQDFNVTPLAAQA TLPPGSPGRPTLVPSTAAPNSLQ MFTGGHGA*FPRWQPQPPSGVS /SHGAPPGVPHYCRQGRSPGKR\ QRKWLESEVQAQGP*EPDPTQL QTSTRTACG*GPPSQADPDPDP TRPRTPDLDPNCMRLRTPKPGR RQSRPH\GPRTPTQTDPDPPVQP PAPEVKPQRPP/WAARAPSDTA AS*GGLTCNSRPIREGQMGSPSP AGSLLLGAL
3425	33793	A	3462	1	2064	MDGQCSHYCVKTDLRVHSPFT TGAVHADQSCCKTTSARWEDT CDLTGSKKTLVISNIVIRTRSDD KLENEWETQSQNRNRVKPTAA DPCRNE/NEHSS*EKHPEVLQES ANDRLRDNERVSQRQSQPTTVS QRQSQPTTESEPTTES/RQRQSQ RQRQSQPMTESETMTELQKMT ESANDRVSQRQSQSQRQSQ\QR QSQRQRQSQSQ*QSQSQRQSQS QRQSQ\QRQSQSQRQSQ\QRQS QRQRQSQRQ*QSQSQ*QSQPTT ESEPTTEVSQRQNQRQRQSQP/ DDRIRDNDRVSQRQNQRQRQS Q\Q*QSQRRQSQSQRQSQPTTES EPTTESANDRVSQRQSQSQRQS Q\QRQSQSQ*QSQPTTESANDR VSQRQSQSQGQSQSQRQSQS/D DRVSQRQIQSQHQEDRPPKYQN KNVQVHA/DDKPRSDPQRRRNL TPPVKTAERRPHQEHVVKGEK ATSPSRHSTSTAPTRPPSAETAH VNVMCGGDMAHINQGHVEAP QGSHEKHVGAARDQYERRDA QSEKSQQVQTTGLRVHVSRRPP HDGSLTSTGLRVHVSRRPPHDG SLTSTGLRVHVSRRPPHNGTVT STGLRVHVSRRPPHDGSLTSTG LRVHVPRRPPHDGSLTSTGLRV HVPRRPPTTALSHPLDVSICRTL NAYPEMLTGERSTFPCVNVKN EKAVESKKDTPFKCESKESWI
3426	33794	A	3463	1	424	

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3427	33795	A	3464	1	492	MDESSFRGSITQSGSAKTAGLT GFCKLCKTSSWHTGAAQILEGG MEKANSPQYADPQTHLSWHTL PPGSQATSANESNVNFLSLPDT NSPEIRPDHSPPVPDRSVSPLEHI PRTFPKPGTG/PPHINTVTNPSA GAPR*E*PS*SGFNPGCFQLVRP SRISGTPV
3428	33796	A	3465	107	543	KREGWKEESDFWDGSHLPPLN SRCSTRKGRKTGRCGAATAAA SSPREGRRPPPSWAGHPCLGSC QWLRSCR/RGLAMAPGALPAL GEEEGPGASGLSAEL/RASERGL GQGLGPAALHS*ASPTPWAPVR PEPPRRAPPPAPWRPVPL
3429	33797	A	3466	27	1021	STQTWPVSEETGSPPQRNRC*SS HQPDTASWVLQREYSHRKGTA PRGMQGTLPLCPSLSGCRSPSCP AAARPPRPRAVRFPPPATAAAS SPREGRRPPPSW/RRPSLPRGLP VASELPEGLAMAPGVLPALFGS TLPL*AVT/PH*ECL/PASLLKPA RP*THREK*TTPDVQP*EL*HSP *RSAASLQEGPQLHS*SQ*DQEP TNSGHTYTLGTGR*FYTVCQFL WLG*TYRSSHRPGFACRCLEPG SAAPCPSHCLSAGPEGTL*AAC LGKVPGRSAPRSDQWSPGGRA PRGVPPPPLSRGHCKALASCAP SADA\REPPHRALLGSPKVHTP
3430	33798	A	3467	807	1428	GSDRLQPQPLLFGRDVLLLLPS GPAIPASGLASVFGAAGRAGHG SGGSA*TWGRGRTRRERPLGG AGASE\PGSVGPRGA\GWVSGP VRAPPRAAPGTLAPSSGRCRAP PPRRAQACVALTCPGPGGRCPL PMDRPALAMP/SHL/HPRPGQV APRWSPCSRRREEKGRHERVDI GHSHLVFALTLFLP*FGGGGKT EAAQNSWRIPPAG

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3431	33799	A	3468	68	1153	LLKMFRAKAACLTSMAWVLPP LSLIVLVILSPGSFILQITFTLLEP VLRRPSSAEKPLEPGPSSSPSSG RARGA\RPALPAAPKPLASPEA GMAVPGWGRR\SPSRREEAGA VACLSLTVFSGKWICQQAP/SA WGCCC*D*GKLVHRST*RCAR* KYPGLKPDQEGYCQPGAPVEV HPRCRDFPS/VLRRNLGFSALAQ SEYLW*DHS/CVLVVG/PVLFC* TLFASFPIRLYPEELLA/HKVTQ CPSLVSPCNWLSAGGGRKFEPA LRRPSSAERPLAPYPSSSPGAGR APQPWPALPAAPKPLASPEAG MAGPGGRRTTSLPKRRGCGCS RPASSCFSSLSGWAARVERRQM ASIPEIALLFPSPL
3432	33800	A	3469	1	248	FRPAPIPSSAPRGPTEPVLRRPSS AEKPLEPGPSSSPSSGRARGAM ASPSSSSEATGKPRGRDGSPRM G/VGGRPSRKEEAGAVAGGGK RTARGLRGRGGPAATGQEGDR HPYRWRRQRSGILHEF*AASGF PPPPNHGRHTVQAEPPEPWPAL PAAPKPLASPEAGMAGPGGRR TTSLPKRRGCGSCCRGEAHSPT TARTGEDAPRPGREETGTQTGG DRRGAA/RGSP/RSPWA/CIRAPL PSLGVAPG/VPSGRLAHGDILISP CTLPHSELGSPGH*TQANFL*DP GRRRTVLWKVFQGRSRKG*EG RGPGRGHNYDGSVTPGNFIA*S PS/PLPLPPSFTWTLPKTRIPECS GVTKCSGTLGTRVW/RPGSWG LHPGSAPP*LRRPSSAEKPLEPG PSSSPSSGRARGAMASPSSSSEA TGKPRGRDGSPRMGEEDVPPE
3433	33801	C	3470	365	589	
3434	33802	A	3471	1	465	MVTTTCYCKKAKPIPRRCSAKE WSCQLPCGQKLLCGQHKCENP CHAGSCQPCPRVSRQKCVCGK KVAERSCASPLWHCDQIKE/CR SQSCS*RRKTKTTG\ELEAFENR LKGRRKKNRKRDEVAVELSLW QKHKYYLISVCGVVVVVFAWY ITHDVN

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3435	33803	A	3472	1	444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFAFV*YVNE RNARAAVGG\MYSSSFDLDHDF QRDYYDRMYSYPAHVPPPPIAR AVVPSKCQHVSGN\RRGKSGFN SKRGQRGSSKSGKLKGDDLQAI KKELTQIKQKVDSLLENL
3436	33804	C	3473	190	265	
3437	33805	A	3474	144	316	
3438	33806	A	3475	3	342	
3439	33807	B	3476	180	1370	
3440	33808	A	3477	102	1054	ETLPSNTMASNVTNKTDPRSM NSRVFIGNLNTLVVKKSDVEAI FSKYGKIVGCSVHKGFAFVQY VNERNARG\AVAGEDGRMIA\G Q\VLDINPGLQSPKVN\RGKARC ETDLQAEMYGLLF*PWTYDFQ RDYYDRMYSYPARVPPPPPIA\R AVVPSKRQRVSGNTSRRGKSGF NSKSGQRGSSKSGKLKGDDLQ\ AIKKELTQIKQKVDSL\LENLEK IEKEQSKQAVEMKK**SQKEEQ SSQLR*KKDET*C*RLEVLKGG AD\DSA*GRGDLL\DDDDN*RS GGIDQLE\LIK\DDEKEAEE\GED DRGQRPMGGDDSLST
3441	33809	C	3478	216	350	
3442	33810	A	3479	1	3048	MGLMVLNVENCSSFGWIGRAP PRNTTVDLNSGNIDVPPNMTSW ASFHNGVAAGLKIAPASQIDSA WIVYNKPKHAELANEYAGFLV ALGLNGYLTKLATFNIHDYLTK GHEMTSIGLLLGVSAAKLGTM DMSITRLLSIRIPALLPPTSTELD VPHNVQV\AAVVG\IGLVYQG\T AHRHTAEGPVGLR*DGLLFLKC NTALTGSHTP*AAGLALGMVC LGEQGPCCGVWEELGERETFK DLIFNRKAPEGSNAT
3443	33811	A	3480	173	422	AAAERGAEEASGGAPPGILEDA GRERRGSGGGR*AGPVGDSKD GVGAV*PPQPHSHRDHHQ*PGP LGGPGCSG*PHLREGLET
3444	33812	C	3481	241	426	

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3445	33813	A	3482	3	826	RGEEAVSGKAGPDSPRAVLRG QGQVWGAAAERGAEEASGGG TQGEGGREVFDS*GTCSLGFPS* PGEQLMGLVYTLGG*PHSHRD HHQ*PGPLGG/HGCSG*PHLRW VPVSALGGRGVGADQLVRVAQ GSPETPCSLSGESWPA/GLPGPT PPGWQ**PGP*RAPGLQKAPKG PSYQQGPAPPSHRQSTAQRGVR PRTKRCPSLGCGDLSLLSLAVP VAQPAPRCAYRMLPLLFLLGRL TPVPSPLSSDKVIYNLHLQFIVF TSIKFSATPFKKKKK
3446	33814	A	3483	135	396	LCWLQIHRQGRKPCSPPSLKG* *ATCMPPRRRKGGFLSSVSMDII THSPGNEKIKMPPPTMSKQPGV LQQDCREKLSHCLVCSSLG
3447	33815	A	3484	256	1860	RAPETPRKILGEAGGCRGDGDR PAFQPVRNSRPFLSKLLGQCGR STLCRLCFRSLNHLFWLFPGPG WRGPGGHSTEDGSLQGKAGQD FSC*NLEISFFP*PSPTCSPTLHC GQKPRAGQGHLHSV\PGAPCW AEVPALLPRRVGD\PGPDILPPS TRV*RCPLDRNSPILL*VHFLKD RATTQNTARPPMGWRPLQQSR QISPAVGGKLCSLPVMI*ASPHP SASVVGETPA*IGGWGW/P*GF QLIG/LPHVRGTQPGLLESRVPS VRGTQPGLPGLPESRVPSVRRT QPGLLESRVPSVRGTQPGLPGL PESRVPSVRRTQPGLPDARVPY VRGTQPGLPGLPESRVPYVRRT QPGLPDARVPYVRGTQPGLPGF RPSRVPRSFCEGDAAGPPRRPRS YVRGTQPGLPAFPSPAFLVRVP SLRGTQPGLPGLPESRVPSVRRT QPGLPDARVPSVRGTQPGLPGL PESRVPSVRGTQPGLPDARVPY VRGTQPGLPGLPESRVPYVRGT QSSLPGLP/GVPRSFREGDVAGP
3448	33816	B	3485	111	258	
3449	33817	A	3486	1	4455	

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3450	33818	A	3487	1	2302	MTECLDRFIDSIAAVPRSTKSTV QKCLPCLSDGEDKIPDLIAITWT PRQGELLEKNVISETGTLLPTPC LDTSTKETADKSTSGKTIHQSIK TVLKDLSGSIDDLPTGTEATLSS AVSASGSTSSQGDQSNPAQSPF SPHASPHLSSIPGGPSPSPVGSPV GSNQSRSGPISPASIPGQDPGYG NS/DKSMGHEYSQR/SFLEDRFP IAVWWPRPLRLKNCLSVLSYSS PSEVTPHPKSESSGTS/SAAQDL QGCSQDVGQPASSSGGSTREQS TSSFIRIVAASSPSSCWKLQVLL SG/AGGDYSPVLLIGGYSRVCLP Q*SDASAATREP/GQNPVPIPP* ASHQCHRKEGPPCRQQAGASQ MLSRD*AKQLKPSSSHTLSKHK TT/GTRKSLLFGIKKAYNFTNKY YSELMTQTRPQSTPSIPSPLPLD DAGLERSQGNVSASSFMVLGN RERGEDTTGAGFGRSRNKEEVP CTIYVGAESP/EMC*WMDHT*R KEGKGGLVGVPCV/SREHLEEW QYQLQR*ISLKTQQV*RRKSEV LLGRS/SNTAQACSCWQLTCFM AGTQRNPQMAQYGPQQTGPSM SPHPSPGGQMHAGISSFQQSNSS GTYGPQMSQYGPQDGGGDVSD VVMAIDDDGSCHLLGSAVPGA VLVTFNLLLIIVVTLQMTEPQFR EYITGDPLESTCRHASLALAVV LHQETAMTMITDSLAVVPHSG

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3451	33819	A	3488	2	1427	EEPSRREPR/PPGHAPGAVAGG AGPMARAGARGLLGGRRPPGL RL/CARASARVAAG/CGRRRAA REPPRRRVPRRPARQPRRGATA AAATTT*WASGTRPSTAAPEPT ASAAAR\RLPLLLPRRAAAPRPE PLFQLRHAGLGPDRPAARPRPR HRSAPGPRPRAQPYGRLRCVRR RSAAGDGG/EPGLAFDEVGDRG PPLTAVPAG\ADRASEAAGPPG ATASHPGPTER*QRGRSEPGHR TEPRLTPRSRQEAPQQRAPGVG RPGAPARPAAAGRRDPLSSPEL GCSARRHSSLPCPRRGRPAGL\R QRFPALEPSPRQPPARAPR\HPR TCLRRWTPAPGPRRSTRPLPRR APMPPGPPVARPGP/PPLSHPTA RAF/HGTPATRARGPAPVQCED A*DLQPAAPRPLRQRGPRVPVP KDQ*QDRGHRVKRGRGA/RRG MGWGPVCPSEPQATGRGAPAV RPALLSASTAVVSWSLQAAGSS CK
3452	33820	A	3489	1	262	
3453	33821	A	3490	411	1919	RSYGVRWRRHAPPGRRSSPRIG KVKSASRAWRLRCCGCRRPSR TGMRWQMRWPMVTLARQPFW RRSVSWRGAWGSWRKSWRRS RATRSCSMTATASCSCRLSRID DISNYEVNLEPGGHDDITSCQG RGRSLPQRAPIGLCCSLGGGAV LADTPLFLPRPKPRDGPGSRAF QKRQQQQSALRVMQRNCAAY\ LKLRHWQWWRLFTKVKPLLQ VTRQDEVLQARAQELQKVQEL QQQSAREVGELQGRVAQLEEE RARLAEQLRAEAELCAEAEETR GRLAARKQELELVVSELEARV GEEEECSRQMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKV TTEAKMKKFEEDLLLLEDQNS KL\ARLGA*GQLGKWGWGALV G**MVNFTPWGLPHCGSQERK LLEDRLAEFSSQAAEEEEKVKS LNKLRLKYEATIADMEDRLRK EEKGRQELEKLKRRLDGESSEL QEQMVEQQQRAEELRAQLGRK EEELQAALARRQRFQ

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3454	33822	A	3491	3	266	KMRRLIKSKKDI\NRERQKSLSL TP\TRSDSGEGFLQLPHQDSQDS TSVGTNS*E\DGQTQHPRPI*DA QSSVCCAGSQHGM*ANHSQE
3455	33823	B	3492	1	241	
3456	33824	A	3493	1	1486	SRLHKLCNKPRRSGTTNAKRV GPDCHPMGREGAR*HHALRGR RGEAGTRGGRQRRREQDWREA GPGPRAEVGRTAASARRARGS APGPRGPSRGRSRWNTGQPRR NRGRGAERPRMQRSRPENGAR GTGAGLRGFQPRRHPGFPSRV* GSKDIPAARRRVETCPGPEPRPQ PQLPPRPWKGGGDARGDPKFP QAPNAVPGFCVIPAGGVLGAPT AAGLRPTGDVALRRPAGSVEPS GS/AGSQSQCLLCGPVPYRQQT STGP*PGGWGSP\SDVPCSALIS GTGC/PKAQHVSGSLSQRSLSL VDFGRPAS/RGSLFPWPLGTGG KS\PAAPSPQTLWQSS/P/GFLYF PGE/RKGKG*SGPGAGCEP\PIA VGCQEQPRGAEGNLPPKPADPC AGTKQPRAQRGVQQGTSQ*PST VVMTSGRGAHSRGGPVRRGAH SREVPAAVHGGD/GLLVEGHTA GRVQQPSTGG*PLVEGPPAGEG PFAEGHTAGRSSQLSTVLTTFLP
3457	33825	A	3494	3	393	
3458	33826	A	3495	145	1089	VYRTEFLQDRNYFFLSLVVSAP RTVPGTWTCLLSE*RNE*ILGCD SLFPKAGQAP*VAHITLGFQSSE YSKWKFTNSPTFLELLEEFPSLQ VSAGFLLSLLPILKPRFYSISSSQ DHTPTAIHLTVAVLMYHTRGL QPARATLMSTHSSSHPEGPLPA AVSGAQCASGFRLPEDPSHPRV LIGPGTGIPPFLSFWQQRLHDSQ QKGVAGGFPGVQGGRMTPVFE CRSPNEDHIYQEEMLEMARKG VLPAVPTAYSCLPGKPKVCVQ DILQQQLASEVLRVLHKEPGHL YVCRAVCMAWDVAHT/L/KQL VAA*LNLN
3459	33827	A	3496	292	478	

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3460	33828	A	3497	87	992	TACGFIACIG*QRLEYCY*DHK GKQQEVLSKHLQMAMDISHIR RNVSCSGRNKASSKAYGTGGS QGRACDLGHNF/TTPSSWERHC TLTSQGVDDFLNAKATFKIFDF SDAFVLSKVGFSGILIQKDENKE ELSDKDIYMEAGIFVSANRGPG VDYCGNRGLSIQGHGGWTLRP SILVSPGVEVRGNEDSVDTAAC IPAAPAPAPTLAERCTGTAWVT ASEGASYRPWLLLHSVKPVSPH STSLETWEPPYIFQKMYENAWC PDRRLPKKQSLMGNLYLGSAE GKYGVGAPTLETTIMQTPDS
3461	33829	A	3498	1	382	TADCAKPVPLAVVSLDSRYGQ WESRSSIHARH*LNSSSSSSSSSS SSPPAVYPRFIEFIHFDIQSTGQK SHRVNTRRGP\RDALF*LNSLIP LVRTSSKSAARRRP\GEAPRGTA VPGADPAGGTRPR
3462	33830	A	3499	229	367	
3463	33831	A	3500	233	525	WYFPAGRAGPADPGPGPLAGT PGAGAGGLPTYSTPLRVSSPVP RLESSSTG\SSFPADSAKP\VPL\A VVSLDST/RRDSGNSRSFHSWG VIN*MTRHLVH
3464	33832	A	3501	386	729	TGRGCCLPCTWRIRAQTCLT*T QCC/SCPTTYPGGGERRERERK RRGEKEKQKVLRKYKEAMSNK VCKYFDEGCGSCPFGENCFYKH VYPDGRREKPQRQKVGTSSRY WAQRSNHF
3465	33833	A	3502	63	559	HSSTCECT*DSRCGCKWRSAKQ FESKIIKSCPECRITSNFVIPSEY WVEEKEEKQKLILKYKEAMSN KACRYFDEGRGSCPFGGNCFY KHAYPDGRREEPQRQKVG\TSS RYRAQ\RRNHFWELIEERENSN PFDNDEEE/ALSPFELGE\MLLM LLAAGGDDELTDS
3466	33834	A	3503	374	656	RRVGCRCFHPSQTGTCT*RPPW NVHH*PATCHLAYNRHSWSPH RA/HWHIATAIQLSAHVF/ACHY QQLHHYHQHHHHHHHYRHHH HHHHHHYCHHH

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3467	33835	A	3504	1	1337	MQLQILTIFLDLHHNTNICNELE SSNVDDPCDIWEKVHISLIFTAK GSKIPKSSDFQADRELNMFDIIS QYDGCPGSIGLTSGAGSTHHRA PWTQTYPQGPTHLSGSPGCILA SITGRVTKMPESSESPAWELPRF TELFLSIKDEWTCIFLQLCCPTM LLSGFPPIRIEPWSPLSDQLNPIP LEAAIATHSRIHHCPLVFTASLP GPLTAGNQMADRLVATAVSNA RHFHNLTHVNASGLKCRYSNT WKAAKAIIQRRPTCQKRKIK/PD QEQPVQPV*AEGVRFWREDH*P /SHIRSRHSRMTSVSRRQSTWW LPSVTWT/CPTTEALEYGSGAC LGCPISGVSKGNKTRSGAAGFH /SPAFKSALCIWRFKQQHANRP YVCWGMEHRSPYSLLPRSSSSS HPQIHGNLDSDDLQVQRGECFI CRPCFHRLRSVPDTDTQCPQPR
3468	33836	B	3505	1	1158	
3469	33837	A	3506	35	369	
3470	33838	A	3507	345	564	PCASRTPVSSPWPV*PQPTSARR SPRCLPMVQ*AARASHDSQLCS CRFCVVVTPCAPQGQTCTRQV CARVTHG
3471	33839	A	3508	437	946	SFSSKIVQRMSSSCTENMHMSP SAPSSPQRPGALSLS/RPSGVGG LLKDPIAPC/SR/RLPGILSLSPQN PRAASPDSPAGFWDSVLCTCRL LRVACLCAVRSPRPRLCTRSCK GRGSSMVR*GGGLPIFSSSFSAT SLQLSSETVARVTPADECPAESP LPSHGPVSCQGIT
3472	33840	A	3509	1259	1497	KSNMSLLMVFSISSGITVTMCSS WGHLQCRQIFLSLEGLMKTSRS GPWAVL/RGWFSHT*ALDEDA ALGHPWASTRKQAPS

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3473	33841	A	3510	268	1278	SPSGPSSSHQPPALKGQVLQCL LSP*ISLRLNLHLWDVYLVEGE QVLMPMACTAFKV*WSKSTCA QWHWAFLLCLFFLLFLLDSKK DNRPPVLRAGAQCMCTAHVEV LPD\PSVFLSAKPRQGSSAARAV LASRGRKALCSG\IHVPTPSGLG CGGPLVP**FQTELLSSCPF*MC PGQPSCPAIPDTLENAVQ\EEAG PVKAMREKGEHGIPAAQPASS\ SPGSLVPTCGTVSPSQGTIRRPR GAWPRPQPRLTPLLSAPPWMR HLH/RSLWVGTISQEDQLATCW QANHTVEGAEIGFHCTKPQCGR GFAGPQGLGSATSTWNVLSSLQ ASRSIWDTAH
3474	33842	A	3511	1	1557	MSRISDDCSELCPLKAIKKERR KEKKQEKWETYRE/REKRQRG QRRRNGERKKRKNTKKR*NAG REGEKKRQKGKTEERKRRGGR RRRETKEEGGS*RNKKQA*SEE KKGRTGKNRKERRKEEGREKE RK\REKDRRGGRQKNKTRERD WGGEQQKTEREEEWARKRWK VPGGWEREAPHRELEKNEQLD KHSSSRAKLYDAGQLDLCSNLI QSCDPECPMQATSLTRYPTTTQ IFLRGAQGWVCVELFRSYGVE DTSAWERDMRNFGCMTREKQ GKPGQLLAHRHLCAHQKMSLL CADNSQKGCLSPANAAPCYGV QVAILTSAPTCPYHLEPLCRSFS LSDQQEAISDPRTAVRIARSGAS SNPRLCVTLTFPRVLQPFPHPPQ RWGEATKGGRLPAKGSPARTA AGRCGRSAGMPPDARAIFTSAA ALPKSRLVPSNIAFKGKRKDLS TKAAAPNLLALRYPRPSAPVGG SHAPSPGQQLQPEEEGNEEEEE EEEGDRAPVFTTGRKDRDSLAE
3475	33843	A	3512	1	525	
3476	33844	A	3513	69	707	LRQNQHEVLKDPRTHTHGGQM GTSSPEQRSTASGAPGWRATSS CVLLASPHHVHHAHGSQEAAS TPPVPWTQREYHGWPPGIYPFS SHLHK/RLLPNPAREEL*RRQQA PWKRHCWRDVTTPESTKNLVE SSMVNGGLTSQTKENGLSTSQQ VPAQRKKLLRAPTLAELDSSES EPRTAVHSSCTAHRCSAWCLA VSAVCPSRPCQSQRGLALS

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3477	33845	A	3514	81	446	TQGGRIKRHLGTSASPTGIMKY PPYCTCPCFQSALHPVPGGLSG KEAESQ*LSPHHPSSQAPGEDPT P/SQP/RLPKHSTLPALGFPATCG R\SPSPKPALPPRGTAPAPPHRY CCYYFPNRSHE
3478	33846	B	3515	58	1034	
3479	33847	C	3516	1	1470	
3480	33848	A	3517	1	606	MAGEDETPVPLPICGTRPI/DAA AAHMAPVPSHLRKHQRVEVHG FCQVQPSYGPGEDRGLADRGST DEHNPGAAQPRAAALHAHPGG VSQLPAPAH*AGQPPPTEPQLP VSPA*SNPQVSAPSLSPKQLPSP GS*DPAVPGLAE*K*TNSCPRD YTAVAAVLGSAPAAPAQLHPA CTLRAPSLRALQEAGAPQPPMG GSGQR
3481	33849	C	3518	76	1275	
3482	33850	A	3519	1	508	MTRQLSNCWVAAECCDPLRHV TQQVLQEAPIVSQAVGGPSRTN LATTPGSHRSTYCLSGAVSSRN LIEPAGEEAGATRARAEEPPGR LRAPSGGVPSPRPLCCRPPVAG CGSGLKMDEDGGGEGGGAVY CNLELKASGVILAVAAEKPSSG QAVLTNTEHSEPSHLKGKSSEK SYLHATPKEDIASFIAFLNVYKQ QGPP*APSYSTL/PPPPSPPPSSSI LRPLPQPATGGRQQRGRGLGTP PEGARRRPGGSSARARVAPASS P/DGLDEVPRRDSSGETVSRTM AARGCGQVGPAGASYSL
3483	33851	A	3520	451	487	SPLEKSWPGTSHTWFP*SRP*NP GRPLPDPLPADP/LRGVPPPNQR KGMSESSRALITPFHPPLTPAPL *NRPFLWSLF
3484	33852	A	3521	1	758	TPRAPLCRGAASAARS\CKWAP WPSRPRPRHP*SCAEAREGSAA QIPPASKLKHGGPSPPAA/PRRG HPRLLPAPP/VVPLPATAPAAVP SAPGKPFPTPPGLPKADPG/PIG GPLSAFSGSPPFPVH/EPTVLGSP QSTRNLPRPPAA*PPVAWARDA P\GSSPAAAAAKQTFASTQQTP KTT*EPRSPTGPAPALAKLFLTP GTCAPGQPSRKIKLPSRPVAPM GTIENIGYITKAFDWNVLFSDTT KGVRVDCMVQ

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3485	33853	A	3522	3	801	TLLMSHQKLLPLPQIKTPRSFHH SRHLHHQHRHHQKQHHKKHH HHFYYHH*NHHHHHHHCHTPS P\HHHHRHHYYHHHHHHPHQH HQHHN\NHHYHHYHHHHQHH QRHHHPSCTVCPQEE*/HNEHR KRPHRCWKVQDPR\NLGYLYIP TTHSELRLALSKHLPSFL*NKVS IYYRQSPDLCPHLNLNPHQYHH RYHHQYYHHHRRHKHYPHHH HHLHHHHHNHHHQNHHHHQE TPLHRTLGLPQGPRRRSSAAQP PPPPPPPLLSRRH
3486	33854	A	3523	3	229	WDPPPEFPGRRPRRESSGFPASI LLVTEPGARSPPRPAAHS\HPPS PLHRTLGLPPRHPDGAAAPRSS PPPPPPSP
3487	33855	A	3524	1	1257	MKAEIKMFFETNENKDTTYQN LWDTFKAVCRGKCIALNAHKR KQERSKIDTLTSQLKELEEQEQ TPSKASRRQEITKIRAELKSWFF EKINKIDKLLARLIKKKREKNQI DAIKNDKGDITSDPTEIQTTIRE YYKHLYANKLENLEEMVEFLD TYTLPRLSQEEVESLNRPITGSEI EAIINSLPTKKSPGPDGFTAKFY Q\MLEVLARAIRQEKE/VKGIQL GKEEVQLSLFADDMIVYLENPII SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNKQTESQIISELP FTIASKRIKYLRIQLTRDVKDLS KENYKPLLNEVKEDTKKWKNI PCSWVGRINIEKMAILPKVIYRF NAIPIELPMTFFTELEKTTLKFI WNQQRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKIA

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3488	33856	A	3525	2	2133	WRRIYQANGK*KNK/QKKAGV VILVSDKTDFKPTKIKRDKEGH YIMVKGSIQQEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRIKKLTQNSSTTWK LNNLLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCKA VCREKFIALNAHKRKQERSKID TLTSQLKE/LEKQEQTHSKASRR KSRRNG*IPGHIHPPKTKPGRI* VPE*TNNRV*N*GNN**LTNQK KFRTRRIHSQILPEHSAGSSGQG NQAGERNKGYSIRKRGSQIVPV CR*HDCIFRKPHHLSPKSP*AVK QLQQSLRIQNQRAKITSSPIHQ* QTNREPNHE*TFIHNCFKENKIP RNPTYKGCEGPIQGELQTTAQQ NKRGHKQMEEHSMLMDRKNQ YHENGHSAQGNL*IQCHPHQAT NDFLHRIGKNYFKVHMEPKKSP HCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMVLVPKQTYRP MEKNRGLRNNTTHLRPSSL*QT *QKQEMGKGFPI**MVLGKLAS HM*KAETGSLPYTLYKN*FKM D*RLKC*T*NHKNLRRKPRQYH SGHRHEQGLYV*NTKSNGNKS QN*QMGSN*TKELLHSKRNYH
3489	33857	A	3526	1	1896	
3490	33858	B	3527	1	1296	
3491	33859	A	3528	1	1095	
3492	33860	B	3529	1	1413	
3493	33861	A	3530	1	1539	
3494	33862	A	3531	1	1167	
3495	33863	A	3532	1	1575	
3496	33864	B	3533	1	1653	
3497	33865	B	3534	1	1932	
3498	33866	B	3535	1	2451	

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3499	33867	A	3536	1	2502	MTELTGIQQPQIVLFEHKGHKL VQGSSSDAGKVNRIYQHYEAS DKFNYTTGLAWKTAPEQTGKT VRKQQIKLNVKKMESRSKMQE HSSSPPMEQSWRENDFDELREE AFRRSNYSELQEEIQTKGQEVK NFEKTLDEYITRITNTEKCLKEL MELKAKARELREECRSLRSRCD QLEERVSVMEDEMNEMKREG KFREKRIKRNEQSLQEKWDYV KTPNLRLIGVPESDGENGTKLE NTLQDIIQENLPNLVRQANIQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITGS EIVAIINSLPTKKSP/GPVGFTAE FCQRK\EGILSISFCEASIILIPKL GRDTTKKENFRPISLMTIDTKIF NKILANQIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVIQHINR TKDKNHMIISIDAEKAFDKIQQL FMLKTLNKLGIDGTYFKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLAGAIR QEKEIKGVQLGKEEVKLSLFAD DMIVYLENHIVSAQNLLKLISNF SKVSGYKINVQKSLAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILSKVIYRFNAIPINLPITVFT

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3500	33868	A	3537	1	2197	MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFGVDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGRNQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRQLVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDLMEL KTMARELRDSCTSFSRQFDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLFADNMTVYLENPI ISAQNLPKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL SFTIASKRIKYLGIQLKRDVKEL FKNYKPLLKEIKEDTNKWKNIP CSWVGRTNIVKMAILPKIIYRFN AIPIKPPMTFFTELEKTTLKFIRN QKRAHIAKTILSKKNKAGGIML PDFKLYYKATVTKTAWYWYQ NRDIDQWYRAEASEIMPHIYNY LIFDKPEKNKQWGKDSLFNKW CWENCLAICGKLKLDPFLTPYT KINSRWIKDLNVRPKAIKILEEN LGNTIQDTGMGKDFMSKTPKA MATKAKIDKWDLIKLKSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NSINKRAKDMNRHFSKEDIYAA KRHMKKCSSSLAIREMQIKTTM RYHLTPPEVEVVLETL/NH/RSW
3501	33869	A	3538	3	242	NLEEMDKYLDTYTLPRLNQEEF ESLNRPITGSEIEAIINSLPTKKSS GPDGFTAKFYQSIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIISAQNLLKLLSN FSKVSGYKINVQKSQAVLYTN NKQTESQIMSEPSFTIASKRIKY LGIQRTRDVKDLFKENYKPLLN KIKEDTNKWKNTPCSWIGRINI MKMAIVPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKN

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3502	33870	A	3539	281	3228	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPQRYSSRRATPRHIIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASII
3503	33871	B	3540	295	2804	
3504	33872	A	3541	83	480	
3505	33873	A	3542	159	729	PTIVGVVIKFSVCISSPWSHLKP TFHATSWLADGDTDGCVLYFA SSCSSYQ*HP\CSSVPEPRYGRRI GSEFSAGSIVRFECNPGYLLQGS TALHCQSVPNALAQWNDTIPSC VAPELREECRSLRSRCDQLEEM VSVMEDEMNEMKREGKFREK RIKRNEQSLQEIWDYVKRLNLR LIVVPERDRDNGTK
3506	33874	A	3543	1	1116	MMARGAGVLIRKIYPLNYKHS AVEQVSRAYSFYTQRPVVPEPR YGRRIGSEFSAGSIVRFECNPGY LLQGSTALHCQSVPNALAQWN DTIPSCVVPCSGNFTQRRGTILS PGYPEPYGNNLNCIWKIIVTEGS GIQIQVISFATEQNWDSLEIHDG GDVTAPRLGSFSGLTPH/WKLS RCMAC/DPSERGLSCTWALVI/H KMEPEQPVCGKQHPEDSQGR/K GPGPGPQNHLLLPGF*VSDGRG RSRSELTPAGSFQWQHSPRNGV *LHQPSPAQVPQRLFKWRLLCP QFP\GDFVKYQCHPGYTLVGTD ILTCKLSSQLQFEGSLPTCEATP SSQCVWVSPHRPEARLPAHGPA PKRHVCQKASLLICGKEGMQL
3507	33875	A	3544	373	1051	RHLLGAQCLSRAPWCWNNQAS FPFPRCPRAKGQGTARASFSWL GCRIQHEGPIRVQGRRRPHRRE PAWAHLHPPMPCRQPNLRP/PG SLRVWPC*KSLC*PSPRPARTHP PGQRCHPYRVPSPPSPSPRPPS*F SRTFQPPGGPRTLTSGPRTQETL SPENVPGPGAP/PAPRHRSSGPK ADVALRMRGLSRAPPSAARKE RGSPESERPLNLSDGSGCCKHF TTVRA

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3508	33876	A	3545	1	411	RGREARNAAAVGAAQACT*FH RTQGPSRLGGVRGQLALPLRA GLGDCIFPV*AKSEFS/HSPLHAP ASLCWGP/PPHPVL/WATHRRQ DCGTLILQGSPAVSN*DSAPPAL ACRLSCGGGQGERTAPPSRCGE KTPWEVPG
3509	33877	A	3546	107	550	TFQMNSLTECCPSLRGWGAPQS LPMPALQTPGSAHLRCQGLLSV ETEVLWCHPTVIQSAVALKLH* AISPCF*LPPNYPLSGSSL\PTPH ACLSLPNLQCASPL*QPPPCPRE VAPLSLEIPESFVYGILGTHITGC LCISLVLPLSP
3510	33878	A	3547	54	825	VGGCLAGPQDPDGVFQTSLRK GVNRAQQQRRQLLPGPTPSKA KDSHP*EGG*GASPNAALLSGA GELPRACQCRLSRHLALPTCAA RVC*NPVKPRKGRSEPRSGWAS QLPGGDSRLPLRPGTSQGVFSP HRLG/EGGKLVLGVLSLSLKQR GFPGE\WGAAVLSPVRGPRTGW GE\DLPRALPDQSDGSGRMRKS AAEAETGPGARSAAGRSDSDS GGRPDSCQTVPAAR/SPPCLRRQ KLPRERLPRAPNP*GPRPLGR
3511	33879	A	3548	1	1335	
3512	33880	A	3549	1	903	MPAGYHVLSDVVSVETPGCPA EFLNIRIPPGDPVFDPDQRGDVP EPPRRVPPPAARRPIPSTTQGLR SVGARCGTGKQLHLQPQCEIH WVKPAGLLSLVGTWRTFMSSS ELVNIPIGTRYLAQAVTLTVKV CSFTAEASETTSPPGGTNNSRR AALRAVTLTAKVCSFTPEPARP RTHQKEETPNTSEHQKEQTPDT SAFKNCNTHGEGLQLHSLSPGR PPTPPGRPNNWRNPGLKSWNT YPGKVRNFHWLFSKKEIEDIRN TTLRDVLVAVINIDPSALQPNVF VWHKGGFLP\CPQFFP

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3513	33881	A	3550	1	797	ATRFGGNLVLVGLGFEMTTVPI LHAAIREVDIKGVFRYCNTTVT LTAKVYSFTPEARETTNPPGGT NNCRNAGLRAVTLTAKVRSFT AEPARPRTHQKEETPNTSEHQN EQTPDTPPLGTVTLNARVRSFIV EVNSQNPLLMWAAPDPAPGQN GPRGLYAFGAERGNREPFLQAL GLVLVRLH\NLWGQRLARQDP\ DWE\DEELFQQP\RQRVIATYQI TSPHTCTYSRTRCFPVKEIDKEQ SLTSHHYLSCSHCFGHEQSDHP
3514	33882	A	3551	23	3990	HGHFWLGHGPLWLSAPSWTLI LENTTGSRGGIVWGTRCPRKRA KSSTSPVQSLELRTPFRGRCSDL MGGTTTSWSTDG/CSKGYHVLS DLVSVETPGCPAEFLNIRIPPGD PMFDPDQRGDVVLPFQRSRWD PETGRSPSNPRDPANQVTGWLD GSAIYGSSHSWSDALRSFSGGQ LASGPDPAFPRDSQNPLLITGPG GCTQRGNREPFLQALGLLWFR YHNLWAQRLARQHPDWEDEE LFQHARKRVIATYQV
3515	33883	A	3552	2	663	VLLDERSAALDGAKRDGTLAL AAGALCREARAAQVFFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFPV SIPDHSTNSALSYLQSLITTSSHC
3516	33884	A	3553	3	669	GYEAFSASCPELCSKQSTPMGL SLPLSTSVPDSAESGCSSCSTPL YDQVSRCPCHREEVRTGKGME E*CQGGI*KVTCSIIYNGGDTGI* FIPQLSGLTEPSLQL*ALRK*TC WSCPGKWA*FPIYLSSSNRTEFT RYLKLTFPAESFCGYGHWPWL *ASLMNVGYFWISG\GPVEILPF LYLGSAYHASRKDMLDALGIT ALINVSANCP\NHFEGHYQYKS

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3517	33885	A	3554	3	1377	WAVCATRVGGAVGGTAKKPR SPEPRVTLLSQSKSGFWFGAER PGGLAFPRKAPPCPWPREQTKS TAGPITLGALRPAMVMEVGTL DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIAGSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAG\LD GAKRDGTLALAAGRA/LCREA RAAQALLPSKGGYEA\FSASCP EL\CSKK\STPMGLS\LSLSTSVP D\SAESG/CASSCSTP\LYD\QGG PVEILPFLYLGSAYHA\SRKDML \DA\LGITALDPNVLSQIVPNHFE G\HF\QYKSIPVE\DNPKADISSW \FNE\AIDFIDSIKNAGRRVFVHC QAGISRSAT\ICLAYLMRTNRVK LDEA\FEFVK\QRRSI/LSLPNFSF HGASLLQFESQ\VL\APHC\SGR GWGAPANAGLDRGTSTTTVFN FPVSIPVHSTNSALSYLQSPITTS
3518	33886	A	3555	450	719	
3519	33887	A	3556	63	332	
3520	33888	A	3557	573	1309	WCKGEGEATEKGPRAEAQASP LSEEAGAGRCPGCPYRDAQPLL GSGHTLKRAIQDICYGPGHYQA RAAREVHPPGRKIGKQSLRRPC KLETDDHLSRSLRELD/SW*FGR KCAGAGLTERTQGRLRRKRTL SSEGALPQVLELSAEASKRGSL GKPRKFGKKNPGHGAPQPVVF QSRQCLQRILGEHPRTRPCLRN DNPGASSAPAQATFISPSEDFSS SSQARSPALSLSFREGLVMTHG

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3521	33889	A	3558	1	1797	KDSAGPGPPVALLLPGAA/CLSP APGCRRAAPRWSSPGPRTAAG* RRMWCASASLA*SPCRPPRSRW WRDAGSGWTPHCPASAAWGA EQEPVRSWGPRASQSHCPGGLR APPPGSVRCSTQ*DCSSVRPAW SRS*GAC*QV*PRCPCRTPATG WAPPPQGRCGPTTAPGSTGPAG RASLCCPRRAHLPG*WPQKLIC AHPGAKSLGLACQPHRG\KGTP IEG/PACGT*GGRRGSGCPGRPH TRRRC*PPAPCGRRSAGSAHPA RPWPHGPGGQQRDPGPAYRGG QGGRSPASPSGRRLPASRAGRS RAARGTPGRPEPRSPQRRTGTV QPARCPWPPHRAAAGPPRRGS GAPAPLGRTRSFGTAGKAHPW PRRRPGHW*SAAAAPATGVPA CRAGSWVSAAPPAEGRPARAR RHPGRCPEASGPRGRRSAAHGH GARAGSPQPGAPPCHLPGIPAR QPLGLPRRTRCFGGIAQRGRAA RHCLLSRPSAKAKRNSSYREPG MGGWRSPQALGEYGKGSQAG SARLSGAASQGRRARHLRGKA PAWNPAPPPSPPPPALGLPLRTQ REATRKPRREEARRPRPRPLRP GGANGSPGPPRAARA
3522	33890	A	3559	1443	1871	PFVYTSSLGRPPSIS*QPFVSGSG CSCP*RSRPSGAWRA/RSASSPA PPP/KAP/SPRPGPRATAGASRRT AGPALCGRPR*GSRGRHLFSRP GGTRRRRRAAR/SAGLPAPGGS EPPKSGSGFPSSPYASSSGLIPGN RSPAAAGEL
3523	33891	A	3560	62	864	ALAESRGDLEAGPSSNTWEFW ELAGFSVLFLGNRRAALGLCEL PSLRAGVEFTAVQRLWSSAGA TWWSKLAVPLAGSAGRENPGS LLDGLLFTLENNLSRGQGAPST PPAARRAAR*DGGQSASSS\PAL ESPPERHRRLALVSEQKPQEPA/ RSSRRSCGTRLPRLVFCSKVCR RAEPGGSVTRREGGAEREAEER KRGR*GEARR/RQGGRKSTRRK KQAIKGKRESQKRRGGRQGRG RAASPPL*EPRARQPRGSAAPSL LRGLSGCL

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3524	33892	A	3561	3	2701	TGLWCRCPRSARRSVGRRPGT APAARPPRPAAQKQALGSRERV GTGPGRILRPGGWGCFP\GPRGT EDADQRAARGPVGAGTQQHG RAVPR\GPQNEPDETLLP/GGPS PRGGELRGRSGARGLP*SLTGP APGPQRGG\G*SPSPGRASSKAG PWKRPGASRASLQRASSM/PAS QVDWGG/PGGSPRCNRCRERKP GTGPGWPPRLRSPGNLRPGVGG LGLALPARTAAAAPRPRERWRS PGAPCLGAQ*PSL
3525	33893	A	3562	2	905	HEGFFFFILGCPFPNFIPPNLVSV RKLGVKPAWGAA/RPRLPLAP MPSREGAARSREMRRPRGIRRS PKEGLFHPEGSQGKSQNGADPQ RM*REPGSSKSSEPLPRLLGVH QTA*RWETGETGPAIGGPAELD AVHVGL*CNRGFPSSKQRARRR ARVWPGPKKRPPARAARMARL ASDQRDFSVSRKAGDGRFPVIG IRSGGGAATGSSSRLSVSSSAVL RKPGRTTGAVPAGGSARKGPSL APMLGPGSVRSASSPSPGHNPG AGS*ERAGLGERPRQKPLAVPA AAIDFPQSPASRSNI
3526	33894	B	3563	149	283	
3527	33895	A	3564	269	452	AGILFLSSSQ*SNARRPTHGALL GDWGPRCSPSPYANRSPSSSLA RQCRTRGSTRDLRVRT

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3528	33896	A	3565	1	1877	MDPQLERQMETTQNLVDSYAA IVNKTVWDLMVGVTPKTIMHV MINNRHAPPHGSRGLLWHWGC RWPCWPGGDAGQPYGTSILIEK KREKNQIDTIKNDKGDITTNPTE IQTTIREYYKHLYANKVENLKE IDKFLDTYTLPRLNQEEVESLN RSITGSKIEAIVNSLPTKKSPGPE GFTVEFYQRYKEELVLFLLKLF QSIEKEGILPKSFYKASIILIPKPG RDTTKKENFRPISLMNIDAKILN KILANQIQQHIKKLIHHDRVGFI PGMQGWFNTRKSINVIQHRNR TKDKNHMIISIDAEKAFDKIQQP FMLKTLHKLGIDGTYLKIIRAIY DKPTANIMLNEQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLARAI RQEKKIKGSLQRVLSFLTTQRG LRRSLQPSIPFSFIILVRAMFLLS GLVAVTLGSPSAGNQSTVLSSW SLVAQQEKAVPTLPLQSARPPH GSAVQAAVWPDTLYQSCCPLA ENQTHFWMTGKCVLCWLCSL WSSGEGKGQAISRVLFGGVKRP YPFQGTLFLESPWNLAGSCPVK PALATRGQG*SSAYSTEPVIVQ RNAT*LKGKARVQLGAKKESG
3529	33897	A	3566	770	949	IRYVLCGGALR\MELLTKQG*SS AYSTEPVIVPRNAT*LKGKARV QLGAKKMMSQSVTPD
3530	33898	B	3567	507	1436	
3531	33899	A	3568	43	421	TSAHPGGEAVPS/LTTSTTWSRS SSLVTFTLMPPRGCSTGPPVTSP LCRMPRTTTMPASPVGSSIGQT STTLPSCPQRQT*PSACTGSG*A SAVRCAPKSSSSPATSSSMTTTT PGRATTTTTQTRC
3532	33900	A	3569	210	610	TRKSRRNG*IPRHIHSPKTKPGR S*ISE*ANNR\TEIVAIINSLPTKK SPGPDGFTAEFYQ\STRRS*TTT MPASPVGSSIGQTSTTLPSLAPR QT*PSACTGSGNHKSLTVKSFS QGCAGLPASLTGPLWWRC

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3533	33901	A	3570	1	718	MENAGEREDPTVGNEGEVRLA GPVLRTQDELSWEEDEANPTSY PKGADSYCHSDCQTIMDFSNFN AFSTPNTFALMNTYSCPQHPNS KQFQLPTFVKMGEAVSVFFIGL PHATPIVEHQNDLIAGSVRMQN QPKGSTLQCIILMPQRPPGQTLE DMDYYYSCFSDEKNLGTKKLS SFPWSHSKEVKATFKGRYPGSH ALNRHTTLPGTAWILLLGGELA FLTVKDGSPLALPSRPADGMRG RNKARVLSSLNLTASWG*QAQ SSELRTSSPGKRMKQTQLLIQK EQILIVTRIARP*WIFPTSMHFLP QTHLLS*THTA/VPQHPNSKQFQ LPTFVKMGEAVSVFFIGLPHAT PIVEHQNDLIAGSVRMQNQPKG STLQCIILMPQRPPGQTLEDMD YYYSCFSDEKNLGTKKLSSFPW SHSKEVKATFKGRYPGS\QPLT ATPHYLALPGFSF*VGNLHSSQ* RMEALWPCPPAQLMG
3534	33902	A	3571	719	1643	IQKRACSVSARRGLRTGRCGCT AGTTTMPASPVGSSIGQTSTTLP SCPQRQT*PSACTGSG*ASAVR CAPKSSSSPATSSSMTTTTPGRA TTTTTQTRCASTPPSPSTPGAAT AAGGPLVQGHGRHRVRVQSES HEGHPHGMRPQPHCSTSSTGM SAGPRVPGQV\ASSRMLTHTNG LRGPGGFKLPSHGVLDLQNGT GMPGGAVCCSTVRGPATGPAQ TGQRREPRPTRCPWSSVPPLRR GKKDLARRQVESKPVWPGPWE GTPWSLLLGCNLPALSLCCIGTS ADRSFRKFYFFQTRIPLLLTDVL
3535	33903	A	3572	1	933	MPEPPP\PPWAPARPKPPRRAPP PAPRRPVPSTTQGLRSAGT/PAR DWQAAPPAALSSPEPHFNLIAS VQTVMCPVGAPAGMQGSG\PK PSGCRLVLWTPG**KGSIWGTA ASMTRRRWTMRSRTAMSPGPQ RVPSAPKPSSAPCA*MEGKRSL LPA/TVPGCKKRYKVTWVAVG GPDPTREASLCQPSLLGTDQDL QSSPFHWHLRIRQKMRYRTPRP HAEQGMGEGSHCLMSEHHFEK TQRQFSPDYYPNPSSQLNVNGI KYHAKNGHRTQIRVRKPFKCR CGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ

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3536	33904	A	3573	2	316	CLSLPTPPWTPVRPEPPRRAPPP ALRRPVPSTTQGLKSAGARRGT GRQ/PPPAAPDCVAQ\SSTVHLA ARATK*PSAHSVVSSSPMGVLF LHGLDFPRMTRSQGLR
3537	33905	A	3574	3	1078	SLPPPPWAPVRPQPPL*VPPPAP RCPVPSTTQGLRSAGA/PARDW QAAPPAAQVFTLLKNIKMLPCL EKPGKFGSLVIMREFNNHMWQ VELKMPVPSDLPKGTGKTLILP ECIQAPCMKSNNA\PSSSSAPSP WML*A*AWLCRYCRASCGISSI PTASPVTMACC*RYMRWGILPI SEPP\QTGFSPAGANQRGPLAAT LSGPGGEGQSAVARLTGEKKN HPGAQYANRLSPRVGRFINAAG TTGFPTGKRAGHKKEPIPQSFIT RAARRSR*PSKASELGRKQRRP V/PVR*LLRSAQEEISAVGKTPG FCQGGNTGYQSQR\RKK*PANR PVKRLP*GGI*SLPGSKTYAVSV RCPDQKI
3538	33906	A	3575	2	969	VSTWETPQYRRPPSPS*RGSREQ PCSFSSPRDTPGENHWLSLPQR D*AGPPVRRALGAS*PHATRRP NRGGAS*PDLQPNHTRPFRPFPS KNPCFRFPEPLRAPTLVPGPCKP HSPAASGRVPPTHPGRGLGKSE G/SKEKPMRRTAAPTPIRFPKIT GT/PSTQTAADHALLGMRDQSL SGQSPGPKSPDADDQLQNRDH TETEQRISSGRSSALAPESQLQQ GCAGIHFRGRFCKAPPLVCERL RGW\PRGKRKGVCESAAQASP MSAAPCSTVPSPINHPRAEECG RTARDWQAAPLAALVRDPLDE ASWAPESGGDVENLYV
3539	33907	C	3576	1	444	

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3540	33908	A	3577	227	2141	FCPVATSASVTPVQTRCATRPT TAPSADCVSPRAAGGLPSGHCF RSEP*GKNWAPCPQPALTPSS/P SQTSDSEEHPSSENIPPGYEVVS LLEALNGPLTPSPAVPPLHVL/E RWPPLRNAPFIWQ*WPPAPRQD DLAS*PPV*/PAAVRDSNSKRVS PNPLPKTLPCCMKRKMSIPAAS/ TETQLSQRPSVQHLGEECGVTP ESENLTLSSSGAIDQSSCTGTPL SSTI\PPQKALPAAAWPSLSCPW HPPRSALTPSPPCLAPTSPLALK RRERLSLPPSLPAGPPQKK/REG LPAESPDSNFAGLPAGEQDAEA ALSSHYQPISHASKGDCKSGME QQGVCEREWGPATVQSDTPAA AVGLAAPGRQAVEGLSVCSLR PPCSSRCDGSGCSGQPTTVINIS LRRPTSPRTREDSEKPGQYPKG HTEARQMPGQKDKVAKRSRK V*EEKENGKGPIRRQ*KQAAPR QLGQAGLTHSLKARV/RGGTG G/AAGVLG/GAWAWRAPHQW/ PGLIALPARGNEGLSTRASGCG GCTGSPSSASPPALRSISRRALA AFPRGRARDLQPAMPEPPTPSV GSCAAPASPMSAAPCSTA/LQS HRPPKG*GVRAHGAGLAGSST CSPSAGSTG*S*LGS*VWWGRG EPLCPAQGL
3541	33909	A	3578	26	1141	VLQLLRWRVWSLFFLMFRCVR SFFLLTQKPSWLHPVDPAPGLQ VELPASPAPCARTPQPLGGRWD WAPWSRGRRSSGRLGLHRNLR RPGAQAWRAAGPGPCPAGRQL RPGEKSSAAPVGWHCWGTEYT FPSSRWPGC*APHCPGLAGPAG\ SPSAGPAKPTPTWNSSWPASAA RSPGSYS/PPLPPY\PLQAEGAGS GLGQPRKGLLHL*DVPAEPVLA GPLASGSIPLAAPPAGRGLLAPG PCPGLDLRLL*QLPPPSVFPTTP KTELVLGTPGHGQPHRGGHESS DSAGG/APTPRALRSGWDPSPPS SVCATPTSSGLSSTPQLPLHQRT SSSTASWSPGWGMGSC*VLVTS GAATVGC*RLPSISTS*SPI
3542	33910	B	3579	1	1234	
3543	33911	A	3580	443	865	

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3544	33912	A	3581	2	1524	CLSLPSPPRPPHPWAPVQPEPPR RAPPPAPRCPVPST/TPGAEERG RTARDWQAAPPAAPKEETPNA SEYQKEQTPDTPPLRTVTLTVT VHGFILEVSETKNPPIPDTGLQV VPKPLPRHTRGRVASSSIHHIRF PVSPSARAG/APPGHTPCQGTW QIQSSPAQGGGAPN\PLYSAGSA LVSSLVLVLQFVDPFVRS\PEHS VIARPSPARPGTWELGRRRTRP SQDPPRGPSGGPWPGRGRGPW RSKTDAAPGKA\ARSPAPGASC ELARRGASPGREGLAVGRAAG RGVASG/APSPAEGP\QAALGAP PGTHRSSSPSAQVPSSGARTESP W*P*LLASAGRPRPQPGYHAQE WRKRPRRPVRTRRRFPTKAPAR SAGSFETSTFSAHDPGSRGHPW GPKPLPAGGDRTAPPGAQGRGS A\SKAPARIHEPALRGHSGSRGG TPG\GSSALLCAKNCAPGDPGT AGVGR*SGTQLPPRAPLEPLSAP RRVRPVGSGRRREKVPRPGRPR
3545	33913	A	3582	1	3339	MSVRKDVEKLEPSDIVCGNVQ CYSCMETNLTVSQKVKHEVTV GPREGATKPNRMKGKEGRSGS LLGEGDFFKDESVMSSQGSSKD GEKRRGKAQRWKWPMQGICR QLGVAKSMEGYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDIESSSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPRC
3546	33914	B	3583	1	503	
3547	33915	A	3584	1	787	MIKWVSYQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSSYKAPSVVAQAAPPSS PHKTSSLCTTSAP\SRPSMRTTS APP*\SSAARPSI*NISS/SPESSAA TI*N*NMSSSPGLQLHDTQTRTS APPRVLNSAT/SQTTTSAPPRAR TPVPPGSPAPRPSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT\PDLN SGSTTS/SSRSSAPRPSLNNPFS* NSAVKKSAAEVNE

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3548	33916	A	3585	746	2018	THPQERGTWGNRQLFAVLPLPF YTSLETMSMGCGAVVAGQYQ KCPFFTIPSANFPWQKQEGMSG NPPRVRRHISLSRSCLTLAVPMT IRRSWEGAPFVGAQDGCRPLLP GRRALLLHLGLAPLL/GPPPPPV SPPWPPCKATWVSAGGRCLY/G CPSAPAPR\APPEFPAPPGFPAPP AASSPSTRCSRGT*SCGPGRPGP LGPAWSA\GQRGQLAVPEPLQA VLGALGLLRPLGERR/PAQAGT FSPTAPGRGAPGASA*GGRISG HSSGDIPRRGPSRGHPPLLAQGS DAIRSTLH/ERLSTRTRPSFKIKT PSPHQRPQQPHASWTPSSGTLS KPSTPCSSSSCAPRSGDGGG/EG HAGLPSQPAAGSQPAAPCQRPE AWAGGRGNRPGKPGAPQGPCF SLPRPQRSR*LPPPARQKPPFFTL LSLFSF
3549	33917	A	3586	1	1911	TIYAVNLFPILPQGDL*PFTMVT MHWGEGNGQIFRGLLDTGSEL MLIPGDPKCHCGPPVKVGAYES QVINGVLAQVQLTVVPEGPQT HPVVISPVLECIIGIDILGSWQNP HVGSLTGKVRATMVEKAKWK PLEQPLPRKIVSQQQYRIRGEIA EISAKIKDLKYAGVVIPTTSPFK SPIWPVQKTDGSTKIPGTSTSVK FLGVQ*CGTCQDIPSKVKDKLL HLAPPTIKKEAQRLVGLFGFWS QHIPHLGELLRPIYRVTRKAASF EWGPEHEKALQQVQAALQAAL PLGPYDPA/DQATVQLKLPVIN WVL\SDPSSHKVVMHKLREEV GQMTMVFTPATLSSLPQHAMM VSWGVSYDQLTEEEKTRAWLT DRSARYAGTTRKWWTP/HQSLS PATPVI/SQWA/HGHGGRGGGY AWAQQHGLALINADLATASAE CPICQQQRPKMSTRYGTIP\GKV LQKAVCDLNQHPIYGTLS/PIAR IHRSRNQGVEVEVAALTITPSDP LAKFLLPVPTTLRSTGLEVLVPE GGKLPPGDTTTIPLNRKSRLPPG HFGPLLPLSQQAKKGVYPPKKK SLYQKHALSYMSLFTAVPFTIA KTWNQPRFPSMVNWIENMWYI YTMEHYTAIKMSEIESFAAIWM QLEAI
3550	33918	C	3587	44	310	

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3551	33919	C	3588	20	328	
3552	33920	C	3589	288	542	
3553	33921	A	3590	332	528	
3554	33922	A	3591	3	1717	NVCQSHRIPEHCYDSLNVCSS* GIPEYSCCDLNICPSHWTPEHCY EGLNDCPSSNIPEHCCWGLNDC SSRSIPQHCFWGLHVCPLHRIPE HCSWVLSVSPSQRILEHCDENL NVCL*HRIPEHSRCCLNVCPSHR IPEHCCL/ESESLSLTQDSRTLLR L*GSECLSET*NSIILPPLFECLSH T*YSKTLHLGSECLSLT*DSRTS LLWSECSSYD/VENTTA/EGLSI CPSHRVPEHCYEGLNDCPSRRIP EHYRWGKNVFLSQRIPEHCYE GLHVRFSRGIPEHSCCRLNVCPS HRIPEYYYECLNICPSKRIPEYC CLVPSVYSSHRIPEHCY*VLNVS PSQRIPEHSCGGLNFCPSHWIPE HRYEGLNVCLSHRIPEHCYEGL YDCPSHRIPEHSCCGLKVCPSHS IQEYCCWVLSVCPSHRIPEHCY HCLNVCPSHRIPEH*EDSRTLLL LSECPSQRISEHCYEGLNVFPSH RIPEHCYEGLNDSPTHRIPEHCY EFLNDCHSHRIAEHCFSGLNLC LSHRILEHFRWGLHVCPSHGILE HCCWDLSVSHSH/SNSRSL*RVS
3555	33923	A	3592	3	191	
3556	33924	B	3593	58	477	
3557	33925	A	3594	19	367	AIQSWCHHVLQAQPHVELLVP RFIEELGSLVHGH*PRHRLPPAH SHVLHHCQLQLGHTLRPRHCIL QEHACG/RVRCLLQRQAGSPGG WCKRECLFLQE/VKPSVRICTVE MCTISIS
3558	33926	A	3595	55	555	NHFVAEAASCPPRCPFRLDAKK LVRSPSGLRMVPEHRAFGSPFG LEEPQWVPDKECRRCMQCDAK FDFLTRKHHCRRCGKCFCDRCC SQKVPLRRMCFVGPRAAVRGS APWVFPQGGGVFTD\NSSKCS* AEPPSSS/QFGNSEKPETMT/VSS FQ*PEILVSGWRQPL

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3559	33927	A	3596	182	696	PVFWIRNL*SMASRGLRRD*EH LKEAILAHSL/KAKRGGEAAEE ESEASRGWLVRFKGRRCLRNIE VQGETASAAGEAAAGHPGDLA KITGAGGYYTQQIFSVDETTLH WKKMPCRTFTATEEKISAYFKA SKDGLNLLLGVNAPGTYVLRS NISVFLSEEMSSDKRLTEMGY
3560	33928	A	3597	74	2521	RERWAAGPVTCQVTTWPGAAT TRVTWPMTRPATPCAVHGCSC PRSHWSQKCGQPASRAV/SPHP PSTCGSSA/APGPTPKQEAPSAL WPLSGFPN*EPGPGQPGD\VVE KATERMAAMKTEAGVPLVEV QDPVEVPSGR/PAGTCPAQPQH RTPAPCTADP/PALDTPTTTHPA PAPCPTAIAASWPAVW\LPQPG Q*PRCPRLIATCEGQTPAGEEPQ AAATAGEGR/VKASVSPAPRGT PCCGIRWVARPAFSGHRSSPCP GSQGCWA/PSSGVPEASEPRPGE QEPIFRKREFNKEIKSL/PEPAGV PRPAWLLSAP*APSHAELPG*PP PLPCPAKRGQPGCG*APWRPLP RRPSSV/PPPAWSPP/QDLPPLGS EPAKPTNGG/PALCFPPPHSLQP QDASEKTQG/PEEAPPPCLVPR WPPDSNSR*HPRRSPMSPAPHS TPGRRHLTQIPNYKTHLFP*APA RGPSPGRACTSPCPRQGLWWR WPAARATSGALSHLHFPPPTPA LPATFSLSSLQLPLHLPPHCVQR APAAAAGSRRRSRCPPSRRSPA CLTSPTAFMRSSPTS*PSRQPPW SSASTSSKRTSVSSWASSPSPSP TCSGTFPWA*RR*KAPASTCPR RPTGAACCVNWRSPKGPGRPP GSAPPTAAQRHPLCSRNQPPTL PRTRPQSPAAPSTPTCQPAGSSA LWSPSSTCLPAPAWVPVPPSPR
3561	33929	B	3598	1	588	

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3562	33930	A	3599	357	1011	FLPLGELYAEGSRMIWSDGFW AGHLHSCSHPRSSSFSPTCTYPL PPPPPWVERQGTRGSG\P*PGKR TSSPFRVSPGSNTRECTPS\GLLD CIPSCISLSEKPQNDSSSESA*KIP ASSLVTSGLGFCKNPQWSNTSC TSLSCDA/CPPWND/CCQMPVPC SWTFQPPEP*AK*TSVPYKLPSL WYSVSQRGKDSPSPAPPGPGRR AQPASRAAAAPPAVGP/SDRAA DPLSPLQAPIWAPRHQHGRSPR/ VR*GLRWLHGALRVVVILEGG RAQ*PPWNDFVRCQCHALGLSS LQNHEPNKLLFLINYPVCGILCP NAGKTARAPPLRARVGAPSLPA ALLLLLLLWDR
3563	33931	A	3600	63	660	KPQVNKSASCAQLAGPVSQRG KDSPSPAPPGPGRR/CPACQPRC CCSSCCGTADRAAAPLSPLQAPI WAPATSMDARRVPVRVFALTE ART*GRAPWAFPGDVNPSLAPI P*TCSYTELIPPVSFSFPPSTSGN SPTACLDSGVQLASPSGSRTGA TGGAAHSPARAPA/PPQPLGSR WDQGLRWLHGALRVVVILEGG RAQ
3564	33932	A	3601	202	515	FCKHEAAVSSGKAVGTRSQCR HSGPLRVAMKFPARSTRGATN KKAESRQPSENSVTDSNSDSED ESGMNFLEKRALNIKQNKAML AKLMSELESFPGSFRGR*PRGCS AAPRSKRRSGHPPPAWT/CSPR AAERS/PE*RRT*RNSDM*S*FP ARSTRGATNKKAESRQPSENSV TDSNSDSEDESGMNFLEKRALN IKQNKAMLAKLMSELESFPGSF RGRHP
3565	33933	C	3602	40	186	
3566	33934	A	3603	1	3189	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3567	33935	A	3604	1	1821	MLKNFKKGFNGDYGVTMTPG KLRTLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIQMPLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWKNNTPSCTEKPQALIDLL QTIIQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGEHAP ADYQNPQEYGKEESPAQFYER LCEAYHMYTPFDPDSPENQRMI NMALVSQSAEDIRRKLQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHSVVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTW LPQGFKNSPTIFGEALARDLQK FPTRDLGCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSKKK\AQICQQQVRYLGFTI RRGV\RLGSERKQVICNLPEPKT
3568	33936	A	3605	1269	2463	GVQEESSDLPTAVDSSRPDIRD QAWASVHWELYVHGSSFINT* GERGAGY/AVITWT/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHHARQG PAVPPGIQAYGAAPFEDLQVDF TEMPKCGDIRKIVTGDVNTPAI LGVVSSSPPSHIGNNITEDPELQ PILAGLSLSMYLVTVLRNLLIIL AVSSDPHLHTPMCFFLSNLCWA DIGFTLATVPKMIVDMQSHTRV ISYEGCLTRISFLVLFACIEDML LTVMAYDCFVAICRPLHYPVIV NPHLCVFFLLVYFFLSLLDSQL HSWIVLQFTIIKNVEISNFVCDP SQLLKLACSDSVINSIFMYFHST MFGFLPISGILLSYYKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
3569	33937	B	3606	1	1830	
3570	33938	B	3607	1	459	
3571	33939	B	3608	30	440	
3572	33940	A	3609	1	279	
3573	33941	A	3610	2	500	

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3574	33942	A	3611	370	464	GHACGAERDHLQPHSPAHLLL LLLSV*AVW*PRYTVKMATAC HQW
3575	33943	B	3612	1	780	
3576	33944	B	3613	1	610	
3577	33945	A	3614	1	1896	
3578	33946	A	3615	2	1418	
3579	33947	A	3616	314	720	GVQEESSDLPTAVDSSRPDIRD QAWASVHWELYVHGSSFINT* GERGAGY/AVITWT/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHHARQG PAVPPGIQAYGAAPFEDLQVDF TEMPKCG
3580	33948	A	3617	1	1029	
3581	33949	A	3618	1199	1758	KTLSFLSDQPLRARSCLPFSGKI RS/RALAKTVRQRCVSCRQHHA RQGPAVPPGIQAYGAAAFEDLQ VDFTEMPECGGNKYLPVLGRT YSGWVETYPTRAEKAREVTRV LLRDLIPRLELPFRIGSDNGPAF VADLLQKTATVLGITRKLHAAS RPQSSGKGIQNNRTGGVYTPCD IESHVILFRSGY
3582	33950	C	3619	499	831	
3583	33951	A	3620	410	1144	LSIQQYLTRP/PLLGFPPAEDSW FTCLDLKDAFFPIRLAPERQKLF AFQWEDPESGWPPCWRALAAT ALLVQEANKLTLGQKLNIKASR AVVTLMNTKGHHWLTNATLT DYQTLLCENPRITIEVCNTLHPA TLLPVSKSPVKPGCVEVLDSIDS SRPDLWDQPWASVDWELYLD GSS/FLQPPRRGGGYA/VGDTSE LPPCWVCGIPALTQRLEKQHLP PSGHQGSLKHLIWDLLLLTKKR TFSSMI
3584	33952	A	3621	1244	2690	
3585	33953	B	3622	1	1114	
3586	33954	B	3623	1	1863	

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3587	33955	A	3624	3	2056	REALQGIQVRLKHLRTFGIIVPC QSPCNTLLLPFPKPRTKDYSQV QDLRLLHQATLTFHPTVPNPTT LLGLLPAKDSGFTCLDPKDAFF PIRLAPERQKLFAFQWEDPESG VTTQYTWTGLPQGFKNSPTIFG EAWARDLQKFPSRDLGCVLLQ *VDDLLLGHPTAVGCAKGTDA LHRHLEDCGCKVSKKKAQICR QQALAATALRVQEANKLTLEQ NLNIKASRAVVTLMNTKGHHW LTNARLTQYQTWLCENPRITIE VCNSLHPATLLPVSESPVEPRC VEVLDTIDSSRPDLRGQPWASV DWELYVDGSSFFNPQGERGAG CAVITLDTVVEARSLSQATSAQ KAELIAFIRALELS/EGRKGLSPG RGKDK*WRKDGFGYRMGEYC ATAARSCSCTGCARNHPSTSGV TGKVVRPVFLHLAFVS\FAKTV RQRCVTCRQHDARQGPAVLPGI GAYGAAPFEGLQVDFTEMPKC GGNKYVLVLVCTYSGWVEAYP TLTEKAREVTRVLLRDLIPRFRP PLRIGSDKGPAFLAALLQKTAK MGTRSDTQLAHIGTVLRDIHVS VCSDGPNLRTGLNVILGGVEW QSTPGNLVRRQGETGLHLHIYH WWQAVAIFPVYLGSSLHMKVG GRSFEQEEDTEHIPVSYDREGQ ECDTELKGQEGDELEAGSVVP
3588	33956	A	3625	491	964	RIQLCCRTRGTGAQKKRMKVS SRCTPAPATRGTGAWQPQAQQ APGVRATEAPRL*AHDEVSQPA PAPPSTRHSPRR*PVAGKEHLE AAVDKERHEVAQAVVTHVLEG QLEDVAPAHAAQI/GSPPWAGK RLRTNPAPRPCHPIQTLSRRLGP QNHTLLH
3589	33957	A	3626	131	351	NVGLKGTAGER\GGSGPPS*PPA GRNSGPAGRRPPAARAPTPGSA AR*PAPPGPPRPPAGRGAAAAA GPAGGGA
3590	33958	A	3627	3	428	GEWEAPPLLRHTRPGPA/PAPPA PSGASCAPCGGQTCRPRPLRQA PPSPITTGHARIWLGQPRPRSSS ATPPKELP*GPTE\PHTGELWVA SGSCPSGTKLPEEGSGSNTYFSA VSAGDTQSNIIWNGPPANSNRP AAEGPDC

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3591	33959	A	3628	2	425	YLASAAIFRNMSSVVCLVCFFF TSQICLQTDNAPYTVLSINENLS VLGSMFSNFLRSFLRSTKASAK PFIVTLLRSSFFSVSSSLASSSAM HSCSSSNSSSFFNSSRTTSKSSST SSSFTPS/SESF/SS*VSSSRFHSYT PW
3592	33960	A	3629	81	594	LPAGFGPCGAWNQNQREKRPQ SPGAESAA*SGGGQQRGGRAG AGGHGACASLGSE/PQGREPAL GAGGETALPSGSGSGRPPRPQR PRDSGPEALPSAAFWKRRR*AS ASAPALTPVPDSVRGAQPGGG GAEPEGKAVRMRGASRPALSQ LSGREIGPCPQGRVVAPSGTAC
3593	33961	A	3630	317	778	PMVWSCASAARLPEPGNGALL RTSSPRCSP/CPSAA*LTRLPPT/P /PGDPSAAPSPGQRPAGLAGAG GAERSGAVEVGPREPGRDGAG S*SWI/AGPPGRLEAGSA/GVLR SPVAGWRPGTCAGRP/GKAGDL GPSAPPQAPHPPPPSWSPLSPLA SPPTK
3594	33962	B	3631	1	1068	
3595	33963	A	3632	1	730	LALTARSSHPQRATVPKASVVA AASPTKFRHSGAALQWRNLGP VRAQGRRLSTAAPAAPSRRLFP PPPFRGGRGGGWSGSRGRRGA EPGRSHGAGGPGDDGRCGWGE GAGTSTPARPSRGPG*RPEIWTR GGGGSAKSQG/PAGAPGCAGPR GASSFGRQRAPAVLGPG/SSTA VCPLPRRTWNLRAPGGAPSYA QVAAAHQAPPGRPPWSPRGAR GSGRSRTFAPSTPAVVAGAASA VAPPRLRPSPPPAPAPAAAATA AERRGREEAPGRGCGSGRAEPP PLGPDGTQVSPLQRSSRVTEFC GGSGGHYARFWHSSPLRVGAS RSQS
3596	33964	A	3633	70	792	HGLVLDVRGPLSHAAPYWAPY PAATAAAARTAPLPPRSAIV*/S GPQPDFQELRKTWPSQC/GMAR REPLLPITAIPRVVVETTP*GFA KQEPSVAGLRCRGSEAPA*LLH GVHRNVS/ETPGPEMGRPG*GN HRQRPGKQRGIPSSGLPGRCSG SRGPHSSPGQKPHGSTLSQRRG ADPRPRRRVYLSTPLLCEKKPH HDTILKRKPGMGDGNNPCPWN AGLYGQATRFAPLPLCPRRRHG

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3597	33965	A	3634	2	339	WPCGWTGRGGCRQ\RGRERRL GSGVRFGDVSFRGRGRGRARA SWKPPHQGPGEPKSGTRNRPP*\ GGGAPAGIRGPELGTGNMKKL LLSLPIYYHLAGEKGQVAKIVRI PSADV
3598	33966	A	3635	31	438	MVTDVVTRGGELGQRHVPPGE SSGLFCGQCGERETRDPSYRG/ WSRRFRFRALKNGAHWSPRLA VFGDLGADNPKAVPRLRRDTQ QGMYDAVLH/VGNFSNYKARF SMPGDNEGLWYSWDLGPAHIIS FSTEVHFFLH
3599	33967	A	3636	1	422	LRRDTQQGMYDAVLHVGDFA YNLDQDNARVGDRFMRLIEPV AASLPYMTCPGNHEERYNFSN YKARFSMPGDNEGLWYSWDM GPAHIISFSTEVYFFLHYGRHLV QRQFRWLESDLQ/QSQ*EPGSP AVDHHYGAPAHVLTK
3600	33968	A	3640	1	319	FRREPPRGAAAAAALPRRNREN KRSKNRPCCEGPRGSARMKELE *PRPLQVLCLLPEMCSPRLADS YSPVSVRPISAPVRFLHRCCPPP FAEFPACRLLQHSRVPL
3601	33969	C	3641	214	363	
3602	33970	A	3642	1	3390	
3603	33971	A	3643	396	766	ERGLGRSEIPRKEVEHFMQLGS AVAGP*LLP\LVGPAGECFHGW LEPLLARIAEDKTVVVSPDIVTI DLNTFEFAKPVQRGRVHSRGNF DWSLTFGWETLPPHEKQRRKD ETYPIKQPVGVIGD
3604	33972	A	3644	105	786	VGPEHCAGAARWVTSPPRSWP DAGQSVN*PDLP*REKHPEG/G* KLQGQGAKTAGNAVVWKPLS K/PQGSSALSGGHWDRLPAPDP GKMPNCDRAPPKIASRVSPQAC FPRPSPPVPSAGPLRASTPADQA RRPARAARPPDALSKRGPCRIS AKLHSGGGGGGGCREKAQEEP EGRTARSLTPPLPLAPRPGPAGR RLPPAHTTQPPGRTGCPSPAGR DTSQLPYFLLK
3605	33973	A	3645	313	546	RNKVGSRGRAKQLKFSGQSTR VHRSESREEEEEKEEDEEEEEEE EEEYEKEEEKEEEEEEEERDLEF SKGPFLSS*SSQGK/GTRVHRSE SREEEEEKEEDEEEEEEEEEYE KEEEKEEEEEEEERDLEFSKGPF

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3606	33974	A	3646	3	1332	PLGPRRQQSECGAPTLTWPPGS NGLPGQQGASPLSASPGAGAGS GRGPAA\GGSGASCTPSPRGPAS WSRSAAQVPRSSRWRAGSASS* NAGSP/TPPTSQPPRA/PALCAA AGTLAPVEKGVEVPAGRGLSG APS**GKCPLPEAPSGGSAPLS* GGTESGAGAPEPRKATGRPGPR VPGGAGAA/RGLPAPTSGCAAP FPPRPCPGLCVLRARPAGAAHP CPGPGWPG/PGPGAHQTLRAAL REPSPLASPLVSGRPGPRLVFNR VNG/AAGPLHVPILRGDPGDLH SGPRGECPLCVRSLAAGATAA\ DGGPAGEGRPRPVYTMERTAN PRLQNFVPH*PR/PSGGRKQFLA RITS\FPSGCWEGGAATRPTCRQ EKGMAALPTHCAWLGAGHT*K CQHLDFCTFFFPGPGCGDGRCH VQGPNPSDLSPAHCAQGPATSP WGWQGGAPG
3607	33975	A	3647	102	788	GHCGGGTQCSWPAPWCQNLLP PSASPTLSTQRQLWHAWPGAH RNPV*QVPSLDS*ARAQLSVPA QGSLPLC/ASLTASPWCSCSSLA VLLFGK*PFCVNLF*RASLMKS SSRARVLPSLRPVRWPAVG\RG WQGMERGQGAWPWLCGAVCS RA*SVHMTTLPSGPALCGIQRR LQSSTQRRPESLHPLQLGWEAA QAGEGLPHPAVVHLPASPRLQL SQLHQSRPRLPPG
3608	33976	A	3648	114	1309	TNCSCLRDRPLDSSHVPWVEEA QSAHNNKEIVPQKGPWSSKHN QARGPPRSESNTNKAVNCAGRS TKTQTPRGTSGT/TEGNT*VHTR HTKMSTTNTNTSSLDAPPTTQQ MRSTRERGTS\PAPPSSALKNTY TLPLPTS\SNDTTIYQLTVVPGP GPRTGELPRCHARVTPRVSGEE ALPPPPRSPENSNTHLRTPSQTR TPTRARPPL\PETSPQQPWPDPR VGFFLRSSPVWAPSSQQYPWW SPSLSTNMTIPPESS/SLLPTLAY YTSLTSHHGQRMPA/PADHA*A QSTPSAHRHRPQYVQWTTDPPS THGTFEESSGR/YPQTHTVAVK KKTIGTPARDSHSFPTTPTTRM VKSLKTSTGTSTDLSSSRSILKS PTSSIFTSLTIFSIWRDPDSMDLC V

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3609	33977	A	3649	3	1777	NVAGNPARSMAETQSRAGTAG PGPRTKQTPGTWGSGQAGAPA HPPCYIQESRSGFSAPGRARNA\ PGAANPLCMAPGGAEGSGVIQ REVEGRPRSHSAPMLSLWSERP PSCVCLGPDGAADFPRRGRGPR PPLQDSPASPSAPRCSPARCSRL PL*PRPRDKDAPGTGGRPG/PPG TLPDSRLECSASRPCGEGCETL VQFPDRRGPGCGPLQGPGRGNP ARPQPRLTRAAP\GPTAPAALVS SGGAAVPPRRTR*PLLAGAVEV ASPRPGSVQSLVPEHPGPFKELR NIVLSNSPEASYSAPAN*RPPPA EIRRREWQELRGGVLGGGLVFS FPPHSCVGSTGAWGLPTWRGV GSGIQGFFSVPP/SGRETSRGGR TATAPWSSTPDCPSHWREPSAG SLRRG*GRRDAAPGAR*SRAPP TRPGSRASPG\GAGEAGVEGEL LGPRGQVVTG/PGRPTAPGIYRP GGRRKASAAGSRCATGGSRSSC PRRGSRSPGWRWTRWGVP/GR RGTLARPAPGPGCPYRRRPGGA PRGAGGRPSTGCGSRSRQWLA GQLLPRPSMLGALPGLAPLQPP PAPPVPPPPPPPPPMPLSAALSS
3610	33978	A	3650	3	922	NVAGNPARSMAETQSRAGTAG PGPRTKQTPGTWGSGQAGAPA HPPCYIQESRSGFSAPG\PRETHS GAANPLCMAPGGAEGSGVIQR E\GKAGPDPTARLCSAFGPSGRP PAC/RLGPDGAADFPRRGRGPR PPLQDSPASPSAPRCSPARCSRL PL*PRPRDKDAPGTGGRPGRLG HSLTRAWSAQHPGP/AGEGCET LVQFPDRRGPGCGPLQGPGRGN PARPQPRLTRAAPAPDSAGSSG/ APPEGCCAPAKDEMTPAGRSC GGCLAETRICPVARP*APLEKSF PNVVNPGKKKAQPTLSPSNMT
3611	33979	A	3651	1	542	LPGAGHRRVLDAGGPRGAGLQ PQLPARQVGAVAELHVSGPPG AGLA/GSGSGASGVGLGAAGW GSGPRGVRAEGEGAYSGPGQV FPVQGNVGNADAGTTGVGVPA GWWPPLPTRLQTLSVASPWLCP *AAASARSPPSGLSGE*TLFYTF SFLPPVVIAASPPAGLASEARPC FPRFHSYP

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3612	33980	A	3652	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFPVQNCLS LARSDSREQGLVLVMESRNRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSTFSQFSPISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSSKT GLSPSGNMEKNKVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
3613	33981	A	3653	1	847	MENKKVASPGWTCWECDRLF MQRDVYISHMRNEHGKQMKK HPCRQCDKSFSLSHSLCWHNRI KHKGIRQGPDSRRTFTKRLMLE KHVQLMHGIKDPDLKE/TDRCH P*GGNRNKRRQPRSPVPSRSWK NQFWSSGLPKEQSLNH*KS*KS MFLRFTSALVRGFTTENLLQFH EHIPQHKSDGSSYQCRECGLCY TSHVSLYMHLFIVHKLKEPQTV FKQNGAGEDNQQENKPSHEDD SPDGTVSDRKCKVCAKTFETEA ASNTHMRIHGMAFIKSKRMSSA EK

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3614	33982	A	3654	854	3009	VNSHSQLLQRE*NT*ESNLQGM *RTSSRRTTNHCSMK*KRIQTN GRTFHAHG*E/RVNIVKMAILPK KIQSDLTSHEISLEEMKKHNQG KEAAQRVLSQIDVAQKKLQDV SMKFRLFQKPANFEQRLQESK MILDEVKMHLPALETKSVEQE VVQSQLNHCVNLYKSLSEVKS EVEMVIKTGRQIVQKKQTENPK ELDERVTALKLHYNELGAKVT ERKQQLEKCLKLSRKMRKEMN VLTEWLAATDMELTKRSAVEG MPSNLDSEVAWGKATQKEIEK QKVHLKSITEVGEALKTVLGKK ETLVEDKLSLLNSNWIAVTSRA EEWLNLLLEYQKHMETFDQNV DHITKWIIQADTLLDESEKKKP QQKEDVLKRLKAELNDIRPKV DSTRDQAANLMANRGDHCRK LVEPQISELNHRFAAISHRIKTG KKPSWRRGVSNLGEMLVEVYL KALMSEDLRKGINQDEFSPTIY YFPITVFGSEGDLLLGKIRWIQG AYCLMIGQDVFMDTRLRVSAC FLKTKMKTVLVVFDQNEDNEG TVKELLQRGDNLQQRITDERKR EEIKIKQQLLQTKHNALKDLRS QRRKKALEISHQWYQYKRQAD DLLKCLDDIEKKLASLPEPRDE RKIKEIDRELQKKKEELNAVRR QAEGLSEDGAAMAVEPTQIQLS KRWREIESKFAQFRRLNFAQIV
3615	33983	A	3655	44	953	GVHNGVEELILVRRMQKSPGP GEMESGSLEKEPLGTQTGPVPS E/EYGIGLSQSISTKHPETSPKDS RIRENDVTADGRTTEDHITADP GTTEDSVTADPGTTEDNVTVDP GTTEGSVTADPATTKDYVSADP GTTKDSVTADPGTTENFVTADP GTTKDSITADPRTTENFVTADP GTTKHSITVDPGTTEDSVTADP GTTKHSITADPGTTEDSVTADP GTTEDETTKHGDTHLL*TTSVT AVKPTRLLTPMGIILISLAATTV TVVLFVGLGFIVKECFLPPLNPS TRVIYHPHVMDYSTP
3616	33984	A	3656	200	542	CSPPSTRPGPGP/SGTAWPGPRG TKRSSPSSSSSSPSTTSTTTSSSSS SSSSSSSSAPPRGFSSTRPSPLRR LLPPSSSSPSSSSSSPSTTSTTTSS SSSSSSASAGGRRAGTRG

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3617	33985	A	3657	132	853	EIDKKHRFLVSISLNSPSK*GEG DTPSRPHRARTGASVVPSPKFPT SLGRSALSRHPHQTTNPTRPLR KAGAAAFNAPRAGPLGTAWPG PRGTKRSSPSSSSSSPSTTSTTTS SSSSSSSSSSSSAPPRGFSSTRPSP LRRLLPPSSSSSSSPRSSSTGDEA AAAAPVA/SRGAGPGA/SAAAA AAAASSSPG/SGAGAGPGTGGG SPGRAASLAGAGAGPAGCSAA PPRRLPRLERLARRRAC
3618	33986	A	3658	222	373	
3619	33987	A	3659	3	513	IPAALSCCCPEWQALV*QILQDS SCCQSPRVPGHSCGKGTTLCVF SREWSLVSGSRC\SDGETSCTGR CCNAFLCYDLRFSWLFCTLDVR RGVA/GQGGRLGLDLGLSAVCI HQVWVMGSRCG*QLLAPGRVS RPRGRERGTHWSCWCRSPWM GSGWEAHSGAACLSGVFVP
3620	33988	A	3660	3	463	
3621	33989	A	3661	263	1020	SGLREPKQLQMLEL*RKMSQLS LEG**SSHNM/V*RL*KKCSDYS YRDYILSWYGNLSRDEGRTLPS ALGR\FWEIARQLHDRLSHVDV VRSCLQGCCEDLYSLISVT*KLP MPDMKNSQDLLCCT/PCLRNSD DEVRFLQTCSRVLVFCLLPSKD VQSLSLRIMLAEILTTKVLKPVV ELLSNPDYINQMLLAQLAYREQ MNEHHKRAYTYGPSYEDFIKLI NSNSDVEFLKQLRSVEGTVEKS GRRCVLVVFNN
3622	33990	A	3662	1	4314	
3623	33991	A	3663	2	492	ISAGVTGTSGLSAEATGIPGLSA GVTGKTGLSAGVTETIGLSAGL SARVTESTGLSAGVTGTIE*SAV VTETTRLSSGVTGTIGPSAEETG ATGLSAEVTGTTGSLAEVTGTT GLSAGVTGTIGSSAAGLSS/AP*I PSIPAFSGLVFILSCSTKFKAKE WLFFV

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3624	33992	A	3664	1	959	AGLSLMGSI*ACHTGLESSLPV WILSAPSFPPHPVTSSPPISFHLC/ KLSLSH/CT*LGTVGALLPASSA THVHQAWPQWPATLMSHWNC YPREGEEIGYLPTSHPTPHYIPV LTTSA/HSAAPSHFGQSQAPIRL PPPPGAPSISLSPLPQNLCKGYE RDPLPSRPPLRAVRSKKQKLGW RLAGPLSKSPDGINLPFLTSPLG CLDLSLPPGPGPTVLFSVSLWH STKLCQHQSLTGLGGQPGQQG SSSPSAVFRGSRDVSGVIAQRQT SQEKELESGL/CVLTSGAPSPSSP HPPYRGTSLFLFYLCILEKGKM VNKRDLCC
3625	33993	A	3665	2	2180	CPQSLIAVEQRKPPPTGSQVLLQ PRAAQGTPLPTATPHGTSGDAQ KHLLQTW*NTWP*KKPGPSPT/ VRRTQDTDQTTAQHPEGAKVQ GHDQFPGGSVHFGCRPAPSPPR RQG/PLAWHGAGADGFPH/GSP FPSSLTRRCTATPSVLKTSPYRK PLLHSCPSN*MYP*PTRPPPSPTS PTQLSLRT/ANVATCPPLWPLPL RRHLSQWVPPNWEPGAASGSS REHGGI\PAMPQPQCSAPSY/PPT EACLQSADGDQALSKHSADTN AS\RPKPRGSWCPPVTDEDAES DRGSGQQQSQRTPAEVLGKPQ VLERFLLPTQTKQEGSHDEETR HVHNCREGSTEKQGRHPLPARP SPASSKRLL/TPGPSPPAAKRLL RQGLLRPAATPCSASGGYLGTR QRALGAGALGGCEPTPATGEES RPCHLR*PLSPSDSSSLCPLGFA K/PHQARNAGLLGASTGMKAT KWAGACRQRTAKTEAWASSW QRVSDTKP/GSTRQKNKDSGSH PQYQAFDLRLTITAGFSAAEAS ELEGSCAAATQISSLQVACHGT SRPHNHVVDDIMNSTAGPPSGV CGELENVMSGKPTQLVSEMLQ VR\PSPSGASFQQSLRMT*VSVN WTPPRPCI*NRP\AAPAETSPAPR TA/STPNASPQGPSARGFVEKW NGSHAARHPRYKPGTQ*PSGA ASTG/SPGTPPSPALPPCRASSLV
3626	33994	A	3666	3	426	
3627	33995	A	3667	3	266	

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3628	33996	A	3668	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL\PIYRV SRKAANFEWSPEQEKALQQVQ AAVQAAWPLGPYDPADPMVLE VSVADRDADWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGQRRWWQLAE RQDSRDREAAIGERQETAVGKT ARDGEAVCD
3629	33997	A	3669	349	718	AGPEGTTTAECP/I/CQQQRPILS LRYGTISWG/DQSATWWQVDY IRTLLSWKWQSASAKTTIHGLT KCLIHHDIPHSIASD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHHPCSFPN
3630	33998	A	3670	667	960	
3631	33999	A	3671	1	1371	
3632	34000	A	3672	1	942	MVGKAKWKPLELPLPRKIVNQ KQHHIPEGIAEIAATIKDLKDAG VVIPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHQKPFAFSW QG/QQYTFTVLPQDYINSLAL*H NLIWRDLDYF\LLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSII KWKLYIHDQAQTGPEGTTTSVI AQWAHEQSGPGSRDGGYAWA QQHGLPLTKADLATTTAECPVC QQQRPTLSPRYGTIPSLPLTKAL TLQLKKCSSGPMLMEFTGLAM FPIILKQLD

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3633	34001	A	3673	1	1270	MGDPSRRRTCRAMQAKYPLVF KGCGVCWGSLDPRCRVASQV WPIPKRLSRGWPFHNAVGRQV SDWKSGQDFADFGTTHQTGFS PAGANQRGPLAATLSGPGGEG QSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAAGTTGFPTGK RAVSATQLMILCLLPGYLCNGK RKLSAIQGLLDNGSELSLFPENP KRHCGLPVKVGAYGGQKTDRS WRKTVDYCKLNQVVAPIVAAV PDV/VVSLLEQINTSPGTWYAAI DLTNAFFSIPVHKAHQKQFAFS WQGQQYTFTVLPQGRWEINMT KIQGPSTSVKFLGVQWCGACQ DIPSKVKDKLLHLVPPTTKKEA QHLTGLFGFRRKYIPYLGVLLC PIYQVTRKAASFQWRPEQEKAL QQVQAAMQAALPLGPYDPAGP MVLEIAVADTEAVWGH
3634	34002	A	3674	1	1978	LTIYAVNLSLILPQGDLWPFTRV TVH*GKGNDQTFQELLDTGSEL TLIPGYPKRHCCPPVKVRVYGG QVINGVLAQV*LTVGPVGPRTH PVVISPVPECIIILSSWQNPHIGF LTGRARAIMVGKAKWKPLELT LPRKIVNKKQYHILGGTVEISAT IKDLKDTEAVTPTTSPFNSPIWP VQKTDGSWRMTVDYCKLNQV VTPIAAAVPDVVSLLEQINTSPG TWFEWSPK\KALQQVQAAVQA ALPFGPYDPADPMVLEVSVAD RDAIWSLWNAAIGESQRRPLGF WSKALLSSADNYSPFERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSGAQQ RSIIKLKWYIHDWVRAGPEGTS KLHEEVAQMPMVSTPATLPSLS QPALMASGGVPYYQLTEEEKT RAWFTDGSARYAGTTQKWTA AALQPFSRTPLKDSCEGKSPHH PVIAQWAHEQSGHGGRDGGYL WAQQHGFPLTKADLAMATAE CPICQQQRPTLSPRYGTIPQGDQ PATWWQVDYMGPLPSWKGQR FVLTGIDTYCGYGSAYSARNAS AKTTIHGLTECLFHCLGIPHSIA SDRGTHFMDKEAPSASVLGLA LALLAPQLADSLLEDPVIVKGT DEAEYFQSVREEPDSGVKRKK MLKSGKNY

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3635	34003	A	3675	1	746	MGKIVQPEKAVSAKAGVCLKG CDCSEYKVQCEWQDTSPKYLG IVLSFGEEPVTHLRWDLHAWSY ALSKVISTICRRGKFSEFKAHTA PVRSVDFSADGQFLATASEDKS IKVWSMYRQRFLYSLYRHTHW VRCA\KFSPDGRLIVSCSEDKTI KIWDTTNKQCVNNFSDSVGFA NFVDL*PPSGTMP*PSAGS\DQT VKVWDVRVNKLPTALPRMVY YGAKCHLWGCWSFTENSELSF QLFCTSIPIWF
3636	34004	A	3676	5	812	AAGSAGLPATPQPRARRVGRR RLGPGARGAGGAGGAAGCRAL RATARAAGSQPGPHSPGRTARS ARK*RLRRPESNKVRVCGPHSP APRTPPSSPGIQHAGKPRARRPL PPPGAGVGLGIVPGLGLGRAGA DVAGRVGPGAGVPGCCREGAR RPGSGRRAAPVLSPLC\PGLQTA RAAAGPAPGA/GWP*VRRLEPA EALPSGMFMMRKSCSVALTSSL SSSPSSSSSSSSSSSSPSLTRPDVS PRVTAATGDMYRGSFSGLTKA LRTWPR
3637	34005	B	3677	1	1071	
3638	34006	A	3678	1	169	
3639	34007	A	3679	2	189	
3640	34008	A	3680	3	352	SKHNLKLTATSQPHRPMQLKP ACVPPVLSSPHMWGRSDTSEGP AH*PPA\AWRVCVVLGL*ASPP AKLQAQHQAGSTRPVDRQAPS VLTAPPLVWPPFPQGICSKWGA QHGKRGQGH
3641	34009	A	3681	8585	9026	ERYKFFSAASPNILILLTFFKIVV RPLITKENLYLEILIRHSLLCSVL TLVCVFCCPVFIGSCSSKRLTTA WTHSTGLCAAMSSPRPGGGGG KGGPAPWAGKRAGSGG*GEGR GKERVCGVQAPSVPTGVGMGG QRRAGVGGPRAAP
3642	34010	A	3682	2	484	
3643	34011	A	3683	1499	1793	IHSIESSPIPHWIGGLRLMLCIVT RLNFEICLVKHFIKQCKVVEHT QQYEWHRVLHLKKK*QALNLK KNLQT\GDKKL*VSSLVHGETN SCRSKALAL
3644	34012	C	3684	1	1044	

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3645	34013	A	3685	8504	8970	ERYKFFSAASPNILILLTFFKIVV RPLITKENLYLEILIRHSLLCSVL TLVCVFCCPVFIGSCSSKRLTTA WTHSTGLCAAMSSPRPGGGGG KGGPAPWAGKRAGSGG*GEGR GKERVCGVQAPSVPTGVGMGG QRRAGGGEGKGALARRLGGG
3646	34014	B	3686	1	2178	
3647	34015	A	3687	1	2424	MLTVIHSEMQAAKVSDGNEELI GKWNLLGIERPWGPRRDWSGL HGPGPGTPTARPRPLRDSSQNT WRLQLKPRLKGGPGAQNARM NEAWQPLPRFQRIYEKTWVPW QKHDAGAEPSQRTSTRAVPRGS MELEPPHRAPRAVRRVPQFSRF QNGRSTSILHPVPGKAAGTQLK PVRADLVAALYKATGAELPKA LGAHPLHQCPLDVTDELLEKIA SRSQNIIEINISDCRSMSDNGVC VLAFKCPGLLRYTAYRCKQLS DTSIIAVASHCPLLQKVHVGNQ DKLTDEGLKQDNQPQCIEGNFE SRMHAQGRTLVQERPKKTVNFI TVCLLGPVQAGSKGQGRVVNG KVLTSTANLRRISVDGKSEKSV KDAEKAFDKIQQPFMLKILNEL GIDGMYLKIVRAIYDKPIANIIL NEQKLPWVVDGTGRCGAGGS VTGEARAMQ\GPQWGKGRLRH GGLQVPIPALQGGS*GPARN*A QQLLAQRIKYL*IQLTRDVKDL FKEN*KPLLKEIKENTKKWKNI PCLWI*RINIVKIAIL/PKVIYRFS AITIKLPLTFFTKLEKKTTLNFI WNQKRACIAKTILGKKNKDGG IMLPDFKQYYKPTVTKRAWYW YQNRYIDQWNRTETSEITPHIY NHLIFDKPDKSKQWGKDSLLN KWCWENWPAIYRKLRLDPFLT PYTKINSRWIKDLNVRCTTVKI

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3648	34016	A	3688	453	1508	KAPQAPNINSYCLQVEECCQKG ISVDLSTGMTSTGVVP/HYNEQ VAGEKEEETNSVATLSYSSVDE TQVRSLYVSCKSSGKFISSVHSR ESQHSRSQRVTVLQTNPNPVFE SPNLAAVEICRDASRETYLVPSS CKSICKNYNDLQIAGGQVMAIN SVTTDFPSESSFEYGPLLKSSEIP LPMEDSISTQPSDFPQKPIQRYS SYWRITSIKEKSSLQMQNPISNA VLNEYLEQKVVELYKQYIMDT VFHDSSPTQILASELIMTSVDQI SLQVSREKNLETSKARDIVFSRL LQLMSTEITEISTPSLHISQYSNV NP*RGCFHYCLAFT*T*SNTLSI YSENVQEGLVKGN
3649	34017	C	3689	57	230	
3650	34018	A	3690	2	123	WWKV*KKYSGFKVFL*HQH** PRRPLQSLFS*MPWKRIAK
3651	34019	A	3691	94	360	LMSLLTSPHQPPPPPPASASPSA VPNGPQSPKQQKEPLSHRFNEF MTSKPKI\HCFRSLKRGVSSAPE SCLSGVLWLHVWFCITNFVCE
3652	34020	A	3692	1	2037	
3653	34021	A	3693	2	1079	NLSKKYQPKKNSKEEEEYKYTS CKAFISNLNEMNDYAGQHEVIS ENMASQIIVDLARYVQELKQER KSENDHRVSGASRRAPLPGPFR RLRPFTPDVGGEEAAANQAE\Q *YPSLKWNSKGKTNGTRNGTK CGKEHSPTLHQSRQGTVIQSAN RPSVA*SYRAPLHPSPH*KLAP* VPAFSSSRVFPMLSSFSL/YISTD DQEGLYSLYFHKCLGKELPSDK FTFSLDDSQLVIEAYKSGFEPPG DIEFEDYTQPMKRTVSDNSLSN SRGEGKPDLKFGGKSKGKLWP FIKKNKSPKQQKEPLSHRFNEF MTSKPKIHCFRSLKRGIQPPDG NEKQDDTMASSFTFSLSLDYEM PVIEKAE
3654	34022	A	3694	1	215	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVVLSRHQAP/C*PPA FAHAAVAAHSKVFSNIVRERV KTQEAERA
3655	34023	A	3695	1	208	MAQDYGAMGDLVLLGLGLGA\ ALAVIVLAVGLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT

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3656	34024	A	3696	1	164	MRYRYIPVRMAEVRT/SDETKC W*ECGATGTFIHCWLANIQQHT LSRLFTCLCSC
3657	34025	A	3697	146	659	LAGPRCTTSLTPSEGG/LPPPDSL GYTVHPPDSQGHTGPLPAREGT GSHRFGVE/VRQRRWERGEAPL LQLSPPAGRPPRRPHPCRPQHLP SAAISEAATARGPRNRSQAAAA AADPDNLRVARG/PRSTRSSAV DAGPPP\SASPGFP*SSSQQRPSP EKTGSEVYSAYIPANC
3658	34026	A	3698	32	376	
3659	34027	A	3699	1	2148	MALSPWTPGLGAGEKLVQAAA VSTGPSLELCTLPSTLGSSVAVE ALEQLFVVECVRDARRLNLFEI NTIKMRITRTENEIELLKKKITD LTKYNEALGEKQEELARKHAR FVLSLNQTMEKKATTTVYINET YTKINLKREDIALQKKCIQEAEE LMEKERAEYLIRKQELTAQINE FENTREVKRMETYQKK/QRIG*I TN*NVKNKRNSY\FSAAVLSDH NLEIARLHESIRYWEQEVSELK KDLAILEAKLCFFTDNKEKLDD ISNDEKNEFLNKIKQLVETLHA ARMEYKDLREKMKTLARQYKI VLSEEEKAFLQKQKIHDENQKQ LTFISQKEYFLSQKRVDIKNME EGLITLQELQQVILSFMSSVYSK PNLSHSRGLTCCSFPLYLQMMT PFPCVITQWKMACLRKKHARW TAKIKAEIQAITEKIQNAEVRRI ELLNETSFRQQEISGFVAQIEKL TTELKEEEKAFVNKEKMLMKE LSKYEEIFVKETQINKEKEEELV EYLPQLQVAEQEYKEKRRKLE ELSNIITEIIWGFLFEQEDVKQEL QQLRDQESKKNKDHFETLKNL ENGFYINDQKADLLLLENKKLK EYILYLKNNIEKYREGQEALMH TSSDLSRQLIAQEGLLQVEEQGI QWWIRQSPKASQVGKPTVQPS VCGQRPKSPCQTTGVNPRVQK LKNLESNVRGQEASSTGERGIL

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3660	34028	A	3700	1	2658	MQAPYRCQRTGWLQQKRLKA GLWGLESSSWSLGPLGQAAQQ ELTSAPGQFRLPPPPQAPERPTA GGSASLGPPLP/PGKLSEVPEPS RPGRPRRPPSTWAPPGGP/GASA LPVVPG/HRGARTRGASTRGAS/ EAGPHLPIPVTSNAPGHAGGW\ GAPSHQNHASPCTGRGPQPAGE LRQA/GEQFPNSWGRRGSCRTC SVVLGHTEPRPEPAHVLVR\GN PGSPVGAAWGNEA/GHPRAPG AQRGG*RSPGLRE
3661	34029	A	3701	31	556	
3662	34030	A	3702	3	1394	RKKELQHKIDEMEEKEQELQA KIEALQADNDFTNERLTALQEN QTRAKESDFSDTLSPSKEKSSD DTTDAQMDEQDLNEPLAKVSL LKDDLQGAQSEIEAKQEIQHLR KELIEAQELARTSKQKCFELQA LLEEERKAYRNQVEESTKQIQV LQA\QWQRFHIDTENLREQKD\ NEIASARDELHSARDEMWLVH QAAAKVASERDTDIASLQEELK KVRAELERWRKAASEYEKEVT SLQNSFQLRCQQCEDQQREEAS RLQGELEKLRKEWNALETECH SLKRENVLLSSELQRQEKELHN SQKQSLELTSDLSILQMSRKELE NQVGSLKEQHLRDSADLKTLLS KAENQAKDVQKEYEKTQTVLS ELKLKFEMTEQEKQSITDELKQ CKNNLKLLREKGNNPSILQPVP ARIHRPIPGFPDMVIRSIVERKK PWPWMPMLAALVQVTAIVLY VPGLARASP

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3663	34031	A	3703	1	1133	LEEKEQELQAKIEALQADNDFT NERLTALQEHLLSKSGGDCTFI HQFIECQKKLIVEGHLTKAVEE TKLSKENQTRAKESDFS\DAVSP GKD*GSDDSTDAQMDEHDLNE PLVKVSLLKALLEDYRGGYRN QVEESTKHIQVLQAQLHRLHID TENLREEKDSEITSTRDELLNAR DEILALHQAAAKVASERDTDIA SLQEELKKVRAELERWRKAAS EYEKEITSLQNSFQLRCQQCED QQREEATRLQGDHTDEAADLP LSRHSVSDPGVSCTQEEIQEAR GLTLLCFSKIKCSQKQSLELTSD LSILQMSRKELENQVGSLKEQH LRDSADLKTLLSKAENQAKDV QKEVKRKDIMSPIMVGLKAKS
3664	34032	A	3704	1	540	
3665	34033	A	3705	1	280	
3666	34034	A	3706	2	416	
3667	34035	A	3707	309	908	LPSRGAGLGTCRPPCLSLPLLP WAPVLPEPPRRVPPPAPRRPVG STTQGLRSASTRR/VDWQAAPP AALVWDPLGEASWAP/GVWCA AIDLANAFFSIPVHKACQKQFA FSGQGQQYTFTVIPQRYISFPAL CHNLI/RRDIDCFSLLVVHFAWK EKWSDVRLGTDSWAAASGLA GWSGTWKKHDWKTSPLVIHEQ KFCFLFP
3668	34036	A	3708	1	2973	
3669	34037	B	3709	1	1053	
3670	34038	A	3710	1	1178	
3671	34039	A	3711	3	247	DCLRVLWCPPV*F/QRSPSLQQP L/RPGFEPLVGRHLMRPARSWR PQPSSASAGLPSSPFRDGCHRFR ASWALGGRAAEGEVAI

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3672	34040	A	3712	137	2176	LKNPPQTHPRRGHLLLISVWGH ILRACGAWQEAKPKAKWPQIP EEKEEGQAPRACTLPGCWRLL RRGQEEKEENWVPPACTLSGC WRLEAVRQQQREGDGDFGAAS CSDLAFRCASSQNPRSLEPVASS PERRRRQPSRAPLGWALKEPGS ERSPPLLSCVEALQPPFLLGLGS GAFCLTRGEKGSPDQDPFCLHS PWMLEAGGSDAATARGDFGA ASYSDLAFRCASSQSPRSPEPVA SISERRRRQPSRGFQILRSSGAFL LDREHVCLASSASTTGLGSPRP SWSHQVASNKGLKPGLRGCWS DGERGTTLEDTRVLLSNPLLLR KGGRKVSTSRLMQLCSVVEKY CPWFLDQGTMNIEIWEKVARA LKKAYRDGAEDIPINIWSVWAL VHPTLEPFHTDHDEEESEEEGE YNEVTKEVTEQFCLPAKAAKE GGNPSLTSPQQLTTETEAEIQLI EKQVHKAQINRIDPEKTLDLLIF PTQHSPTGGVVQEQDLVEWLF LPHSNSWTLTPYLDQIATLIGN GRTQIVKLHGYDPGKIIVPLTK AQIQQAFINTLNWQTHLADFM GVLHNHFPKTKLFQFLKLTNWI LPRITKFKPIECSENVFTGRSSN GKASYSRSKNKVFQTSYTSAQ KAELVAVIEVLTAFEMPVNVIS DSAYMAHSTQLIE/TAQL*FHTD
3673	34041	C	3713	1	784	
3674	34042	A	3714	87	447	AVQRRSGVGPACLSCGSANPGP PPGTSPGAGAAPGGGRWARAK SGPESPPGT/GPPQPA*APQ/AAG PKTRAGVSFLSPPLASSPGHANF GPDSFLGDGVMRQA*RSENKQ DPA\GTPGTWVR

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3675	34043	A	3715	3	1435	RGPSGPRTVSPSPAGASSVGGPP VQAWPCSLCVGSLEPRGSIGGP PKGLQLWGPRASWFLGDYACP LLASAPVLAACKTLCQTPAVPA SL\G*RPLVAVKTHVAAQPFLRI KHLAAVLADKSAPGLRPVCGT A/GFAGYLCLPHSLPSPDG\EPV DVSTLDSAEYCQLGLGGICRGP GR*EGGHGY/RGSEKPHSTYPSS PSLSG/EPENRG/DPGVAQEP*P PPREQAGPFSPFVILEAAPFSAG ACFPGSEAPGGSSPPN\GSAVGL WRGRCPPGPRSL*RIAAAWPEK RCLDSWKG/RRDGAARGVGTA ATFSPPFASRLVLPGEASLGTPG VVFLLRAGEPSASGFPGPAWRE STAGASGGGCCGHGPCSGLRA AGLPSGAGSW/RGDCCHLGMG EDPLG/PW*SSGTPASARGSQEV PAT*GRAGGRAARHPQGARLPS GPPG/EPGSPGFWHRKESQSTLT FLGAQGSSSPLADLGSLGASAG
3676	34044	A	3716	1	756	MNDAGNHHSHQTNTRTGNQTP HALIHKRKLINENTWTQEGEHH TLEPFGGTTDRIVSPSHTRSPDM AIANFQSSGCSVVPDTIPRPQYQ CRSRHSVLLTSNLTVPMQSCVK PPYMLLVGNIKIWMNNQTVRCI NCHVYTCITSHFDSRKSVMLVL AREGIWILVTLPRPWESSLSIRLI NEVLQRILKRSKRFVFTLIAVIM GLITVTALATTAGMALHQSVQ TAHFANDWQANSNQMWNSQQ GIDQ*EHMDTGRGTSHTGAFW WNNRQNSFPFPYSQSRHGNSQF PKFWVFCCPRYHPSPSV\QCRSR HSVLLTSNLTVPMQSCVKPPY MLLVGNIKIWMNNQTVRCINC HVYTCITSHFDSRKSVMLVLAR EGIWILVTLPRPWESSLSIRLINE VLQRILKRSKRFVFTLIAVIMGL ITVTALATTAGMALHQSVQTA HFANDWQANSNQMWNSQQGI DQILAAI
3677	34045	A	3717	3	131	

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3678	34046	A	3718	2	424	CGRKSRGTALPTGSSPQSGPAA PGHSAASALHPTP/SPPPHPL\PP AATGDIDGNRYPATPMTKYPS ASARRPVHRPTCSGGGSHTNHA ESLPPLTPLEEADTHPPGGSQ*T RPPHCIRTGSCLPPPREAPYTRR ERRRHPP
3679	34047	A	3719	1	418	
3680	34048	B	3720	361	1371	
3681	34049	A	3721	1	469	PGTCRGSTGQP*EACWRSP*SV RNTRCPVREEPASPGWSSCLTS PSARGWWACS*RLPSSSCPGST AGSSSGTLCREAAPCHR*AACS DGKPPGMPRSTRRLGPSGARSG SARRCPCGDGPESLRGHAPARA ATQAPDPSTQSSASSATPRAPPL L
3682	34050	A	3722	117	871	GPQSSAGNAGPQRRRTTLGVPR TWHPGPAA*AGNSCHISFYSSR FQPFLGVTSVLRGSSVSVSGIPD HLGQPRSSQEPSRPENAAAQM* TGCPGYAGCTVA*MKGRAELQ GLRTIAAQPGQWLTLLPRCPST RRLGPSGARSGSARRCPCGDGP ESLRGHAPARAATQAPDPSTQS SASSATPRAPPLLGLCGGGC*G DRRSQQGTE*A/VAVPGMLGGP SPFSQPEHPSAFAQPSSCLPLGL DFKLLIPSQ
3683	34051	A	3723	110	1017	EAANEPKHLHQLRHAGLGQHR QAPRPQGRPFARPHQGQDQTD RLHHLQGGGRHGARGHLHQA GAGQSAPAPKGAHVQGPCGCH ESTGPVEH*SHGERPKHRCPRP AL*EHGHENPHK*SSPHDQR*Q TADPEGDN*SQCCPTAN*IPLRK LWLRG*DLCGRSHGQQ*PHQG W/HLDAQLLTPASSSTLCPTPLQ QPLHQLRHAALAQHRQSPPAA RT\PLARPHQGQDQPDRLHHLR GGGRHGARGHLHQAGAGESAP APKGAHVQLVSKQLGGVAAEA HVDSSGLWVSPGPRHN*YKSKS SRL

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3684	34052	A	3724	3	1092	LVEPGRLLEAQGFDKNKR*RRR GRVCGRGGEAPAPGQGQGQPD *NKGKEEV*NSSE\EESSEVSLP KTSREQEIPSLACEFKGDHLKV VTDSQLQDDASGQNESEMFDV PLTSLTISNEESLTCNTEPPKEG GEARPCVGDSASTPKVHPGDN VGTKVETPKNFTEVEENMSVQ GGLSESAPQSNFSYTQPAMENI QVRETQNSKEDKQGLVCSSEVP QNVGLQSSCPAKHGFQTPRVK KLYPQLPAEIAGEAPALVAVKP LLRSERLYPELPSQLELVPFTKE QLKILEPGSWLENVESYLEEFD SMAHQDRHEFYELLLNYSRCR KQLLLAEAELLTLTSDCQNAKS RLWQFKEEQMSVQVF
3685	34053	A	3725	182	771	QTALSCARHGRSAAFVWRPNR APVWRSGFRGVAAGSALVHST ALPSRRQPPERRSEHDCLRCRA LCGTKPQGLSY/TGP/WGLGKV PEAAAALDLGVH*PLFHLPLLD SESRKPGRGLAAPPPMPARWGL SCLEQVGHTRKEGGGQGCRPW PPCWSPVSGTRGGPITTRLRRGS AALHVRASYCLMENPPEPPSIV
3686	34054	C	3726	769	981	
3687	34055	C	3727	70	197	
3688	34056	A	3728	1	158	LGSVSSFASCTLGAPGYSPTAP VAL*SVGPWGRIVKVPGHPGS WEMHFIISM
3689	34057	A	3729	229	496	VTGLQNLVLSIVTESGKTHLLSF SSHGLEEIISQLPGCSGTLTVRP QGPT/GSQGNRGCDRVAQGSQ GAGGERGDRSQAPVPAPARDS
3690	34058	A	3730	167	769	FLTRETGDPTGRSSSHGKHPVA VFP**PTRPP*TIWEITHGCGRR AGRCPGTGPDGP\SGRGGPRCW PSGHLAATGGLGPSCGRLGAN RGEAGPAGFTVCSPLSGWRTPY THHFPASRMSWHLDYASPRTY RSQGNRGCERVAQGSQGAGGE RGAGSQVPVPAPARNKDPAKR QKPRPPLLSSPTARLIGLFPRAD SCRSC
3691	34059	A	3731	234	543	ALDQVASLPIMVPASKQNTATS CCRLGYNSFDLGPAAATIFFPSP AMVISQLPGCPGTLTMRPQGPT /GSQGNSGCERVAQGSQGAGD ESGDGSQVPVPAPARD

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3692	34060	A	3732	1	3695	MGKRSFERVLVDKCDSGRSCL RKQHENECAFIQILDTQSLMIPG QRGSFRLADSQHTDRVLCTLM AEKWDRKALSYTRNSFRAQIRL RKTRFQGKGCMICKKSRVLPY QAAYVSQHGSACQPSSHLPSVG SLSSTGDDEEEEEIVHMGNAIM SFYSALIDLLGRCAPEMHLIQTG KGEAIRIRSILRSLVPTEDLVGII SIPLKLPSLNKDGSVSEPDMAA NFCPDHKAPMVLFLDRVYGIK DQTFLLHLLEVGF
3693	34061	A	3733	1	2523	MKQFLLYLDESNALGKKFIIQDI DDTHVFVIAELVNVLQERCHTR LGYTEFLVAWRVTFGLCVEAV TLHLKYQILIRGLLEMMSFSDA DILKQLPVTVPGLFPASLSPSSL LGNSPPSWLRHNSESKVSAVSS PSATKTLSTGIGKLDPGHKEMA EESELLKNKMQAPPLSRCPESQ KCQHQLRLHHWKPSVRHQVKR RSPAVLRSAMPPADCPAVLEAT TATHPEKGTALSKHLPSSDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKEQGKGDLKKKKK GKLPKNYDPKLTPDPERWLPM QECSFYQGRKKGKKKDQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIPPRH QRPAGAPATKKKQQQKKKKG GKGFPVLREITVVKVDTLVVFQ ILEERLSVFHIQYDTSYPFSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQQPFMLKTLNKFGVDGTY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNTV LEVLARAIRQEKEIKGIQLGKEE VKLSLFAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTESQIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL

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3694	34062	A	3734	1	6208	MILDQAFKYITELKRQNDELLL NGGNNEQAEEIKKLRKQLEEIQ KENGRYIELLKANDICLYDDPTI HWKGNLKNSKVSVVIPSDQVQ KKIIVYSNGNQPGGNSQGTAVQ GITFNVSHNLQKQTANVVPVQ RTCNLVTPVSISGVYPSENKPW HQTTVPALATNQPVPLCLPAAI SAQSILELPTSESESNVLGATSG SLIAVSIESEPHQHHSLHTCLND QNSSENKNGQENPKVLKKMTP CVTNIPHSSSATA
3695	34063	A	3735	164	415	EYWGWLLRRINIILTGNCLRG/ WPSLLPQAEESLSPQTKVERLK AAWIEEGILPLLGMRKLFLLAR KVHQSLQAQCPQLHQGPPT
3696	34064	A	3736	1	886	MLDLPWFNVEEGIQRLREIGML EWLSHFRPTRLSREDPEDIPFTN TLPNKFVRGVPASLKSSFIGLLC MPDLTKTVGSWRMTVDYHKL NQTVTPIAAAVPDVVSLLEQIN TSPGTWYAAIDLANAIFSIPVHK VKDKLLHLAPPTTKKEAQCLV GLFGFWRQHFLHLGVSLWVIY RVTLKAASFEWGS\EQEKALQQ AG\QAAVQAALPLGP/HKDPAD PMVLEVSVADRDAVWSLWQA PIGESQQRPLGFWSKALPSYAD NYSPFERQFLAYYWALVETERL TMG/HQVTT*PELRIM
3697	34065	A	3737	1	1815	
3698	34066	A	3738	1	988	MPAEFFQRCSVIMVQLPWKEA HVERPHGERDYTPDLQPDMWE KFPGLRRALRPVVKTLLVQLEY RQAEKCEKRDWPSLPDYIFLLC WMLPALEYRTPSSSVLELRLAL RAPQPADSLLWDLVIVPITSLKS WQTPRGEVEGVTHEEICASLKS LAVALLSMSDLTVGTPVTQPQT LNTMGIIGSRGGRGQVAALNR QRQVPELIIGIDILSSWQNPHIGS LNGRGYINSLALCHNLIRRDLD RFLLPQDITLVHYIDHIMRLDSV KDKWLHLAPPTTKKEAQCLVG L/FGFWRQHISHLETAL/RPVTG LWWKLNI*LWAIKSPCNLNCLS
3699	34067	A	3739	26	318	RTAWMQYSPLHSAYGRVPTVT SSH*LLPLRSHPRDSRPAPCP/RA GPARNRQSSA/SRNRSPRRRNPE ASRGRPPGRGVASPAPSPPTPRE TRTAATRRP

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3700	34068	A	3740	425	588	IWSVPFAPWRRRGHAGSRCSRR SRSR/TPRRNELSTAALGAARG HARIWREAGNWP
3701	34069	B	3741	465	1623	
3702	34070	A	3742	667	960	
3703	34071	A	3743	1	2021	MTVLTQTSSQHSTGCHAKPAIT TPWLLAVFFQGPGVLQSVGGK ASQADIILGLSPVSAIFQLYDVS FPPGKQGRPGLGSAGRIEVARD CGMLWKQRGYLISSSQPIKNGQ QVSDLFEAIPEPKSLAIIKISGYS TLETPESKHNHFTNTLAAIDLV NAFFSIAVHKV\HQKQFAFIWQ GQQYTFTVLAQGYINS/PPALC HNLTQRDLDCFWLLQDNTLVH YIDDIMLIRSSEQEAANTLDLLV RHFCATGWEINPTKTQGPSTSV KFLGFQWCGACQDIPSKVKDK LLHLAPLASKKETQRLVGLFEF WRQHSPHLRMLLQLIYQVTRK AARFEWACTDGLMRSPYDQLT KEEKTRARFTDGSTQCEGTTQK WIAAALQPLSRTCLKDSVHQR VSSAEEDFNNQVDRMSRSVDII HPLSPATPVITQWVHEQSGHGG RDRGHAWAQQHGLPLTKADL AMFTAECPIFQQQRPTPSPQYG TIPQGDQPATWWQVDYIGPLPS WKRQRFVITGIDTYSRYRFAYP SFNASAKSTIHGLMECLIHSHGI PHSIAFNQGTHFMAKEVWQWS HAYGIHWSYHVPHYPEAAGLIE LWNGFLKSQLQYQLSDNTLQG WGKVLQKVVYALNQCSIYGTV SPIARIHGSRNQGVEVEVALLT VTPNDPL/GKY*LPVPVTLHSDR

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3704	34072	A	3744	3	1197	TLGPGTGPRAGTGSSSSPSSSPG TGSVPGAGPGANSVVHPGADS GVRAGAALAPGLC*VKLLGQM SPPGGALGPHNARQSAVAGGF GRARRPGRHE*LQGTWWSGPG QPLGAALQTATGPVVMNQFLR *TWHHEGHSRAPCPRFWGWF* TYSGEKPLPAAVQPSSSSVF*SL QQRCPFFLGVPCQACSSACPLL F*GL*W*PGVHEDQ*ASPAGSA LTWP*LHHDPPPSSGA*SDATG PG\GPGSALAGFQQLGSGGQVL QQGQLGSQTCRGGSPRGRRHC* ASSWG*G*AGRLLPWA**PPAR SAGSPHRLRGLS*ARPCGCAPR CRAAGGAGP*SSAPRT\GDGDV GQLGERE*EAHPARVGQWGW GSRCPQGQGVAFSGSESYMDW SSRNRRFRNT
3705	34073	A	3745	1	98	
3706	34074	C	3746	439	1053	
3707	34075	A	3747	48	751	EGDLVFPLGRGMLRLVSFSKMF KLLKRTMDYGSGSPSVSGHIPL PQACGPPQLVCSRRVRGQRPRP HSVPGSRAAPGLSGDTGRFLSG FGKFCFGSRKGALLTKGFSVSS GWPAAKFPPAQRVQTIVRSR\P RRPGKRVL*GEK/GEWAASLPT PLPLAGPSLPSVPGPVPVAPQTV RAVSPVTPQGPSSPPFLREHSTQ PRPGCREIYQHPRMGTGRMRTP WPWRLSARPAAAAA

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3708	34076	A	3748	1279	2791	QAAGGAAGAERDEGAGVA/GA HGPSRSTARRGGRGAGPRPPPP PRSLGTGSAGRGAAEGTGRAR RPAGAAAGRALRAGRAGRLGA CGGVAAVGARGLRAAAAGAR RRGAPATGAPPP/PSAAASPTAP\ PGPRHPGRVSGAAARAPPGTAP RIGERRPGGGAPATEPPDSRTPA AARASSA/PGAVSGPAAAPGPP GRRENAEGR*PQDAG*RGLWE GALPVPGSSPQTSSSSTGRTSGG SRAPSHMVPGTGSPPG\RGGEA GAR*AAAPAGVKPSSLWKK*L ALFRPCFQEPTPG/SVGCRGPLE CFTHSSPVGV/NGHRHCDNCCR/ PLKPPSPKAAWAVPRAAVPEA HA*K*RAEDQRGLRVLGPNVTL SNPPTRGFR*LGTGVPGFQDPC VDS/GL*VEEGLCPEASRGNGE RNKGTWGIPPQPPLRPSSRWLQ E*PTPLPGSP*DATSPPAGGGRH RSRLPKPALVGNAGTSSLPAPE PCFPHLYFTTFLLSLDSSLKFRD LAGILIPE
3709	34077	B	3749	71	285	
3710	34078	A	3750	417	1208	GPQRVPTLWWEDAEARSQRDG VGGRAEAPGARIPRDLGAAGG LRGHPRLVRGHCRRRLRCSMA RTLVLRVTPVPGGAPLALRQPP VPGGSRQEWPAFSRVGTGLPLT PTAGPSRARGARRPCPPALPGH CLLDRTYTGLQTLGAETLLAVV NSAAMNVGVQVVDVELHRHS LGEDCIYPQSSESDISDAPPSLPL TIPAPVKASSPIKQSHEPVPDTS VEKGS\PGSCPFHL*GPLSHLGS SPGFLLWRPPGLLSSVALVASC

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3711	34079	A	3751	10	932	LQLCSMWLLRSWVQAEGAVSI SDSPFSLHQCWAVLHKAWCVF LQLPGGFTFTLNPLSDNLLGKR VDSAPSWGPLGSAFRGVHMPC VGAAWEGKGPNLLRPSGKLGP SGSRPTPIGQQQLPEVPRAKGPL GPAAVICQ/HMPAPSTGGKRGS FSGRYLSASLELGGLPMAPTGP SALSAPPSVSRGAR*STREKPGV YASAT*AAEIREGQALGG\PRPS RNG/SGGPLGPDFGPNGPKLRRS KAGCPWWHLSSVDAGE*LWK QHSTAVFSMPGTQPPWRGLITM PISPRGTEPTAHPGPRSPGLAYS LTA
3712	34080	A	3752	3	650	GTVLDDPHLTGYCWHPPCPPNS VCNGSLSPVLREEAESSEAPVQ SPQRSWTPSAKSPPLPASPPCSQ LKAGGDQEGLQRGALPVGMD RGGPGGCGGHCQCSRPRILSPV VPVPQVCPSSEAPGPPRQVPHTP RPQEPSRTRGRLEA\SAPSWQ*P APPAGSLPAWP/PG/RPAPTGSR AR*AGLEASETTWSTNGPTTVH P*TL*AGSLGAPQTSAAASEHSP CPNLPLPL*KPWCATNLSCRI
3713	34081	B	3753	1	1812	
3714	34082	A	3754	1	209	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVVLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT
3715	34083	A	3755	2	462	PPLPGCLGDTGAPWPGPGCTGP PPRTRSPPRLPG*APASRLQNPH PRGRPWPAGHSRCH*SQPWLA GPTGS*HLPDASGFCPGALTGS CLPSLGGAGGGW\QSAPPDVGS KWNTPRRSGAPAPPGGRLLPGP ACRAPPRSDLPLS*AGRVGRPG
3716	34084	A	3756	129	616	NRIFLNCNMVHKCKCKTPMVV AGASLVETGQDESIKDE*LNGIP GPVATPSRLPPQRTWN\PGPHP MP*RRPQSLPQPSQAPPGPFLS* GSEGEGTQPKP/P/GLPGLGPPR QPGRCGFAVD/PPRCGVSPGPG VPGPAGPAAGAAPG*PKLRQRP GPSIGDCGDAP
3717	34085	A	3757	59	292	YCNVSFGPILSARKPASPRSS*T SATWLQNHPLMYLTPGTGTLW RFLTTRENVPYGPVP*WNRTIC GVANWPYWPSV

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3718	34086	A	3758	177	448	GTGGWVAMLQQYFA/TAWIPH NDGTNNFYTANLANGIAAIGY KSQPALWVTGGLLVIIITFIVRGI VYPLTKSQY\TSM\AKMLVL*P GAEGL
3719	34087	A	3759	1097	1206	
3720	34088	A	3760	2	505	QGSRAKLSTPLGLSCTRSTAGP SRFARCSLGGCSHPSRHSPHLPP PPPVQFRAGPRGRQGSPSRGSPS \GAFPAGPGGAAAAAVGDDQQ QQEQHGAHEGEENNEGNSVPC G/PGKTGGSSVSPGLPEPWPPAP LWTQPSWSAPCH\P*KPPIPPTR QVLGRTGCFLLPAP
3721	34089	A	3761	181	581	ADELNVPLT*APAIPLSKEMKL HVPTKPARKRLKWLHSQQPTC PSTGEPVSNCG\PPPVPQPTTQQ YQGLDAGATTRVPRSLLRSEGS QTQKSPSCGSHSQDNSGG/SQSS PVTPQHLLSPRAPQAAPSPDRA PV

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3722	34090	A	3762	18	2104	RWQGDKRDSA*RGNLRARKPS KRGK/DR*RRVSPTRSGKRRGA EEKNRQEKKKGREKERREKRS ERQRDRRRRKEQRKEEQRRRA RTNERKPRQTQANGATSS*KAS AQQAGMWGGSP*TDATAIRRG GAPCSSRRTCLNQGTIATPSGR\ RRHGDAG*PGLASEHDASGHG CLRTGAG*PSDSTESVCRRPLA MHVPTHESHGPVFTRLVSHTFH CG\SKLPAVGRPVACRPTYSPSL CHNPQRPAQLLAHSSALQCAPL SWDPQRCAPPSPRPHRRGPPSP HPHRRAPPSPHPHRRA/HTTART DPTTSAPPP/RQTQRRATREPAT KHTRNAHPRRSACNRGTHTHP RRRRTTERTTHHARPRNRGQAT PNTRQPTAGRHEETDGATRRR QHGQTRGEGG/RRRGRAAKTR QRERQEPPHDNTRRTRRRPKRR DRTGAPAGTRNRTSGHKKRQP GTRASTGTAPASQQQQTPTVLS RCISRFGVFYGPDFSGG\NSFCS LPLMSDSTLSTYGGQRRG/RSR ARKTQDTGVLSPLRRERSCPPA HGRFPGLFLSTHRQVGPAALRP PELSCE*LPQDGDFCVWLPSLR SRLRGTRVVAPASSP/CGDWQV TAVAP*PQTQSPSLSQSRDVEK RHRGQHPSVGSV*LMKAA*RG PSGAKRPKTAPRPQCRARVLPK RSGPTSPGRGSCGSQSRTRGF*D
3723	34091	A	3763	1	446	MWESLELPRDLLNGFDQNADN DMDNEIQAEVVSDGDEELVGN WSKGKQLKSSENLQLDDATEK KNLFSEEKFKLAEETYLSNEEP NINSQDNGKNVSKACQRTLEQ AFPS/SGS/GGLGGKNGFVG*AQ SPSAVCSLGTWYP\CPSCCSHG
3724	34092	A	3764	186	529	GTCWKLEQSTLPLLHWAGLAC PLAPGTCTSGPLL/TAPQR*MQL CGSPGWHWKRSVVVAPGRQLP GSGECMFQLPLPCRQPSLCAIPP ILQANLPLNGRQNCCAQISCKE DQSFH
3725	34093	B	3765	73	1374	
3726	34094	C	3766	1	873	

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3727	34095	A	3767	603	1208	FTTCSKHQTRPGHRPEQQHPAE KSVSGIFCYAEEMESSQLPDPGS GQPPRGG/ALGPPYEPLSNRIPD APG/EAGPASTPGH*SLDQGIPG *PGLAPRGHRLWKSPETPAPSP APRGVSGGLPGSRSAQVGSGDP SPHHL*QPAAAGRKDSSSF*AT WRPP/GPPGPAAAAGRKDSSSF* /GHMASPRPPGPAAAGRKDSSS FMVLP
3728	34096	A	3768	872	1015	VIRSRMLIPKTMGKVSPGHVRG LHSRPSQHRPRGLGGKNGFTAA PAMAEGSNI/GALAVASEGASP KPWQLPCGVEPS/IRRCMETPG* PGRSLLQEQVPHGEP/PARAAQ KGNVGLEPPSTVPTGVPPSGAV RRRPPSSRPQNGRSTDSLHHAP GKATS/SSMPAPESSYEGGGTL QSHRGRAAQDHGNPPLASA*P GDLVKLQLLTPQSDNSCTHIGD NGTYRSQLKAAFAEKLNMGKL TFFITGVNHKWGLPLSLTWLPA NSWESLLSFPPPSPPQQLNDKPG RRSNITHSSKEDKKTEESLELPR DLLNGFDQNADNDMDNEIQAE VVSDGDEELFGNWSKGDSCYV LAKRLVAFCPFPRDLWDFGLER DDLGYLVEEISKQQCIQEVTRV LLKAFSFIRETDHKSSENLQPDN AIENKIAFSKKKFKPVAEICISN KEPNVNPQDNGESVSRACQRSS QQALPAQAQRPRRKKWFHSCS
3729	34097	A	3769	234	636	GPVSGHHRVNCLPCTILPLRR*R AKGHLCRLLCPAGEATGARWR HSPQPLALLQRAPEPAHHHPAA PPGRLHHAGLRCSPVRPAEEGR GPRPQQRARTASLQLLRRR/SLL QPQPPD*\RDKMAEPQRRSRQP AHL
3730	34098	A	3770	1597	1878	DTPRFHSRSKRGITLQEYASSRN *RTSSAVPVF*RMSVRGMEVPC SNER*TQSISGDQVRPAEEGPGP RPQQRARTASLQLPRRRYFLQP QPPD
3731	34099	A	3771	97	471	GVEELRNVNVFFPHFKYSMDT YVFKDSSQKDLLNFTGTLPVM YQA*ICHCWSSSSSSPQVSRGTS HVFSI\TSDEARQVDLLAYIAK\T LKVFQIQIQRAGQIMRIKQSIKL LWLEVENSVLPAH
3732	34100	B	3772	1	1449	

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3733	34101	A	3773	1	927	MQRWFNICKSISVIHHINRVKT YMIISIDAEKAFDKIQHLFMIKT LSKIGIQGTYLHVIKVIYDKPTA NIILNGKKVE\AFPLRTGTRQGY PLSQLFFNIALEVLARAIRQ/EEI KGIQISKEKVKLSLFAGDMIFYL ENPKDSSKKLLELIKELSKVSRY KINVHKPVALLYTNSDLVENQI KNSTPFTVAAKIIKYLEIYLINY MKDLYKENYKTLLKKIIDNTN KWKHILCLWIGRINLV\KMTILQ KAINKLNTIPIKILP*FFTELEKPI LKCIQNEKRAHIAKARL/SQKN KSGGIRLPDFKLYYKP
3734	34102	A	3774	1	639	MGRNQSKKAENSKNQNAFSPP KENDSSTAREQNWMENEFDML TELDFRRSVITNFSKLKEHVLTH HKAAENLEKRLDKWLTRINSV EKTLNYLMELKTTLFMVDNG/C R*LENSHDL*AYFLHLLGNTGL *CCVRGQIGDGKEKREQRDSRS MG/EILRAQLEPFAFHQRSVQC GDIRDLWMGYFLLNLMKKLTF Q*FP*QDT*QLKELKKIAST
3735	34103	A	3775	3	1079	APGPRGAGAQKACGASAGGDP ECAAY*GGAQCECGPTVGPGE VPRAV*VWVHGGPWAGGYPV Q*CDAGGREGSFAGAAAAPGG AAGEPAGPCPGAAAAEPAGAG AQQPPAGREVCAGDSGPGAAP EAGGAGGGGAGGTAVPGGDPR AAAGPASGPQGPGTAAAAAGG RARGTAGAAPRPQGQHAGTGA GPPGAAGPARAAAGPAGQRGG TGGGPAGRA*TPDARWASAAG PGGGAAEASERARQGSDAAGR VVSGAG*AAG*TRGATGPAGA AGAGAGTAGDAEPAAARVQPA AGPERLPADHAV*AIDTAAKCP GRGEPAAAG*SSGPEPGEQGAP GAQPGESGPPAPRTAGVPGPA
3736	34104	B	3776	45	149	

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3737	34105	A	3777	3	442	EGKDERND\GKDEGKDEKKNE RNDGKDERNDEGKDEGKDERK DERNDEGKDEGNDEGKDD*KD EGKDEGKDEGKDDGKDERKDE GKDEGKDERKDEGKDEGNDEG KDERKDERKDEGKDEGKDEGK DERKDEGKDEGKDEGKD\EGK DEGKDEGKDEGKDERKDEGKD EGKDEGKDEGKDEGKDEGKDE RKDEGKDEGKDEGKDEGKDER KDEGKDEGNDEGKDERKDERK DEGKDEGKDEGKDERKDEGKD EGKDEGKDAGKG
3738	34106	A	3778	459	660	VRGHEWAQKKYHKFSLWSVD ST*N*QPSPHASGCHWLEEPAA FCHASPAASGIFAAAASDRPLLP SV
3739	34107	A	3779	2	440	RPLSLINIHANFLSKILANSIKQC LNRIIHHDGVRFIFEM*E*FNIHR SINVTYYINRMKNKNMII\DAEK AFDNIQHPFIIKILIKLGIEGT*LN TIKALLMAAAACL\NSCCKDAR SSRGGMAEGCRLSASSELWAP MSMGGGLR
3740	34108	A	3780	1	1145	RHPGWPTPAACPTTLRWLKAP VWTPGP/QKMEKEPAARGTPGT GKERLKAGASGFAGGMGPRSV PARKKAQTAPPLQPP/RAAPGPE RGAALGRPVAQQVPGARLAGG AAGLGFPAVPRVLPPFPCALSG DRSARERPPGALLRPLPC*GPPT \PVVGGKNDQLKERADSGPDPV AADAVPGEAALQARVP/GALGP AKLSPEGAIVAPA*VRGPGRLH QPGLRPGPRQRSDPRFPGSREPA /GERGRGARRGHRRGRPGGPCD PRRPGTQGEASERGEAAEGEAA EGGET*ER/GGRGKRRGHGPPG SPGKPYPSAGSHAKGATGRGH GTPGTPSPGRSRPGCPRGVPTRS SGLGVARSSAQARGGTEPAPRR SPGAPSGRPATLAK
3741	34109	A	3781	218	376	TRNKILYRQANAERFCHHQACP KG/RS*RKH*TWKGTTGTSHCK NMPNCKDHQG
3742	34110	A	3782	2	187	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL*RILFLLHL* SLVWLDMKCWVENSFL

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3743	34111	A	3783	1	220	IALMVSTIWHVFAVAGTGCFFP CLVLPSGALVRQA*W*QNLSAF ACL*RILFLLHL*SLVWLDMKF WVENSFL
3744	34112	A	3784	713	997	KFFSLRMLNIGPHSLL/CLQSFC Q\RSAVSLMGFPLW\EPDLSLW LPLTFFPSFQLW*1*QLGFL*LLF LRSIFVAFSVFPEFECWPALLD WGSSPG
3745	34113	B	3785	1	1698	
3746	34114	A	3786	948	1121	
3747	34115	A	3787	1211	2437	LTKRWPGTNTSPESG*SRRAAC AGL/LIPFTSRSSSPTWTRPLLS/ ACASSHDPGHHNSP*VLVPPDG GTQGFLVLHQADDLHRFLIKILI DIVRQRRENGVKILLGNRVMY HEHSPQVRGGQQLEQLPLITVH GGGLQLLHHVLSEGHSAVQNW GWTLPFIIAKLLMNLH
3748	34116	A	3788	1	1908	
3749	34117	A	3789	1	1788	MTGVSRGSGLPISMAENRRPLP VSAGSKPVIPILQSPLQILNTTH YFLKSLLTPTSSFAHVISSAEDL VQRRNVIGDVYSQGPASPFEIN NGLGSPLKYTAWRKQEMGPW QWLWQQDFHLFLGAPLQRYAE PLPVGTISPGWGSCVVDSSQES LPNDKHLRAAKEVPLQLQWQR SFQLPLGASPQRNTRILLTGMFS WVWLNIHPGTLLGEKLGSWGS KGRTTAGAIAERLLVSSESSIPG NPEQLPRNAELPLTEVFRCG*IFI QGPCLVKSWGPGAARAEPLQE P*RRGCWFLLRA/AIPGNPEQLP RNAELPLTEVFRCGQCSYAAGT PQKAPCPVRSSRARDPCRKPSD CLLGTDEQKDSSNLCRLKCPCL TALKRAVFLPARSWRSENGQT ASSSGSLSPEQPKWEAPPSRGRL TPHTAGSLRSQCDQREEWVSA MEDEMNEMKREGKFREKRIKR KEQTLQEIWDYVKRPNLCLIGV PESDGENGTKLENTLQDIIQENF PNLARQANIQIQEIQRTPQRYSS RRATPRHIIIRFTKVEMKEKML RAAREKGWVTHKGKHIRLTAD LSAETLQARREWGSIFNILKEK NFQPRISYPAKLSFISEGEIKYFT DKQMLRDFATTRPALKELLKE ALNMERNKRYQPLQKHAKM
3750	34118	B	3790	116	885	

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3751	34119	A	3791	593	883	
3752	34120	A	3792	47	716	EAPACL*KALSPLAPTTISSVDC GFRASTGITLLPRTGAAHGAAG *DRGGRAGVLTMTASRACCAG P*SS*RYLRQ*TPNSLEGPTGRS LRSRASPGF/TLRDPVTQPSSPV AAVS/ALGVEPGLAPAL*SQRV* ALPR*TRRKSKATAPTATKPNA GHNTTKKARPGQGPTPEIPALG SPREVDPEVAHPGAFLSQPERR RCVLGSSFPPGYQQRRVDPLPV
3753	34121	A	3793	2	829	GTRAGWRRRRSGRDGPEVTPQ PPGAARDGAG*TGPSPPRCAGP A/TAAKPSGHPPPGDFIALGSKG QANESKTASTLLTPAPSGLPSER KRDAAAALSSASALTGLTKRPI LSSTPPLSALGRLAEAAVAEKR AISPSIKEPSVVPIEVLPTVLLDEI EAA\SWRATMTGSRACCAGP*S S*RSPAPSLTAPST*ASCTWPRS SPTSSPLRASLRLCVASCGGTPP STSRPRGTAWCLCWPVTSSWPP TRRTRTGPRSLSRCTSRTPWGS GSGWTALT
3754	34122	A	3794	114	254	
3755	34123	B	3795	1	2052	
3756	34124	A	3796	860	1090	
3757	34125	A	3797	2252	2557	LNPLSMGRRWPGEETVTDPGW KRLCHPLHWVAETVPVQAVGA PWSLQMGGWNWGGRCPQHLA PSKGVM*RLPGQFGRTPSWKE VPEVWGMFRRPACGPRLS
3758	34126	A	3798	444	854	VSHLEAQK*PSWTC*HQCQWA LPMFPHHSEADGLIE*WNGLLK SQLQCPPGGNIL*G*GKVLQES VYAQNRHLIYGTVSPISRTHRPL CSQSTQDSCLLVANPSQICLVHI PFP*VQHSLGL*ISWDWTGEVG PFL
3759	34127	A	3799	1169	1881	LEHPATVIFCFSWETFDPQGFCF SLPKVSGTCLISLLLHAFPFVVT SAPCPQEFPHSPHLCFHVP\HHS EADGLIE*WNGLLKSQLQCPPG GNIL*G*GKVLQESVYAQNRHL IYGTVSPISRTH\GHQVTHGQPV KTT/LL*SPSMGSWGIALVLPPL\ DLLLSG*SLTLPLAFLLRTHPLL TTVQRRAELPFTSWICFLSLFER GKGPGQPLVTWTECQALTLLPS PGSHTQGTWRIPH
3760	34128	B	3800	65	1324	

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3761	34129	C	3801	1	1263	
3762	34130	A	3802	1	2845	MAPRSLRMEDAIESLAVVSSEY VGAGVNWMFLPPSSKSTCKILT PHVMVLGEQGLAPPTVFLKALP IPLYHTVPPGGLQPRAPLVTGSL DGGNVPFILSPVLQPEGPGPTQ VGKPAAPTLTVNIVGTLPVLSP GLGPTLGSPGKVRNAGKYLCP HCGRDCLKPSVLEKHIRSHTGE RPFPCATCGIAFKTQSNLYKHR RTQTHLNNSRLSSESEGAGGGL LEEGDKAGEPPRPEGRGESRCQ GMHEGASERPLSP
3763	34131	A	3803	1	279	
3764	34132	A	3804	2	517	KGLAFEVSLADLQNDEVAFRK FKLITEDVQGKNCLTNFYGMG LTCDKICSMVEKWSTMTEAHV DVKTTDGYFFHLFCVGFTKKH NNQILKTSYAQHQQS/RQIQKK MMEIMT*EVQTNDLKEVVNKL IPDNIGKDTEKV/CPIYPLHDVFI RKVKMLENPGFER\MELRGGGS
3765	34133	A	3805	18	602	PAPWRLACNKRLTKGGKKGAK KKG\VNPFSKKEWY\D\VKAPA MFNIRNIGKTLVTRTQGTKIAS DGLKGRVFEVSLADLQNDEVA FRK\FKLIT\EDVQGKNCLTNFH GMDLTR\DKMCSMVKK\WQTM IEAHVDVKTT\DGYLLRLFCVG FTKKRNNQIRKTSYAQHQQ\VR QIRKKMMEIM\TREV\QTNDLK EVVNKL
3766	34134	A	3806	525	1173	GEPHSQATSGHFASSAGDTQAN RVWSGPPANTNRPAAEGHDC* KEN*ETERTSTPKPHLYVTIIKD QRKGISD*RSNE*NEARREV*R KKSKKK*TKPPRNMGLCEKTK STSDWCT*K*RGEWNQVGKHS SGYYPGERPQPRKAGQHSNSG NTENATKILLKKTNSKTHNCQI HQS*NEGKNVKGSQRERSGYP QREAHQTNR*SLGRNSTSQKRV

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3767	34135	A	3807	111	1329	RNRRRERHKEREGGGTGGTDW *RRGNRRKRTQRGRDDERRGR DDDQNHTTNTRRETTKTKRTT NRTQQKREQKRNETSKRNETK RATEQNRRERTGTRSGRSAKRQ RTEPERERAARRARAKRTASAA RDRGLSSTFQLPTRSGNSVHTS KKPLSRKYEQDPWADS/GSEGV WKPVPRRLEAKVMRESQGSSR SCCNSRTSARLITRTMR*ATLSS NKWSFCMPAGRCLTVTSPCCTP CALVTRKMLVTLGL*SRSRELT T*GTFVRGKQK\SVFSAAWGPG HQAQCSEQPSRGRFHRAQPMA *EPCCKSRHPRATPLHPRPSRPK SPTTPPPTRQNANNKGHNTTHT KPRAPPEPQTTQHEHTPQPPPDS HAQDNNNKNTPQQPPTKNAER PPRPTAHPPPAHKPLL
3768	34136	A	3808	2	517	
3769	34137	B	3809	1	1008	
3770	34138	A	3810	139	1407	WRGGLDSALRAAVTLQGCAGC DRPGSA*SNNYSI*I*R*RW*SN YSEK**GNEGNAVILLFHSNGT ASKWTVNRASADISKSLQASW GTEHTWPEGEYS\AGPSQHSSP AVSDSLPSNSLKKSSAELKKILA NGQMNEQDIRYRDTLGHGNGG TVYKAYHVPSGKILAVKVILLD ITLELQKQIMSELEILYKCDSSYI IGFYGAFFVENRISICTEFMDGG SLDVYRKMPEHVLGRIAVAVV KGLTYLWSLKILHRDVKPSNM LVNTRGQVKLCDFGVSTQLVN SIAKTYVGTNAYMAPERISGEQ YGIHSDVWSLGISFMELALGRF PYPQIQKNQGSLMPLQLLQCIV DEDSPVLPVGEFSEPFVHFITQC MRKQPKERPAPEELMGHPFIVQ FNDGNAAVVSMWVCRALEER
3771	34139	B	3811	1	1134	
3772	34140	A	3812	374	931	WRGGLDSALRAAVTLQGCAGC DRPGSA*SNNYSI*I*R*RW*SN YSEK**GNEGNAVILLFHSNGT ASKWTVNRASADISKSLQASW GTEHTWPEGEYS\AGPSQHSSP AVSDSLPSNSLKKSSAELKKILA NGQMNEQDIRYRDTLGHGNGG TVYKAYLCPEWENIICKGHTTR YYTGTSEANYV
3773	34141	A	3813	3	444	

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3774	34142	A	3814	75	807	GIAGFVNIHLDSLSFLTGVPGVK AERF\E*RMTAKHCALSLVGEPI MYPEINRFLKLLHQCKISSFLVT NAQFPAEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRF LDSVKALAVKYLQRIGSRTPM DTKIYSYCPAVHPAEPTDMKS WPSLFEVPTSLEYCPFYLQLVES ADAEGTQKYRRLTAYYIPVYTE PPLITKEPSCLWKQAEFGDLGK HVWLVEQFSSTRVQEHGVGW
3775	34143	A	3815	35	2088	KVMNKRSQTQNGTRYMTPPPR SSHTKQHLL\PTPPPRSSHTKQH PLHDPITTKLTHRT/CTRYTTPSP RSSDTEQHPL\PAPSPRSSDTEQ HPL\PAPSSRSSDTEQHPLHDPT TTKLTYRTAPATRPHHHEAHTQ NSTRYTTPSPRSSDTEQHPLHGP ITTKLTHRTAPATRPHHHEAHT QNSTRYTAPPPRSSDTEQHPLH GPTTTKLRHTTAPATRPHHHEA HTQNSTRYTAPSPRSSDTEQHP LHGPITTKLTHRTAPAT/PAPSP RSSHTEQHPL\PAPPPRSSDTEQ HPLHGPTTTKLTHRTAPATRPH HHEAHTQNSTRYTAPPPRSSDT EQHPL\PAPPPRSSHTEQHPL\PA PSPRSSHTEQHPL\PAPSPRSSHT EQHPLHGPITTKL/STQNSTRYT APSPRSSDTEQHPL\PTPSPRSSH TEQHPL\PTPSPRSSHTEQHPLH GPITMKLTHRTAPATRPHHHEA HTQNSTRYTAPSPRSSHTEQHP L\PAPSPRSSHTEQHPL\PAPSPRS SHTEQHPLHGPITTKLTHRTAP AP/PTPSPRSSDTEQHPLHGPITT KLRHRTAPATRPHHHEVQEQA KPIK*PPRPSPETTRAQPREPAV TLLPSGALGQACPCDATAGPHG TTLWPAVPPRWQQHLTRELLH PVPRACP*QGQGQPFTAGPGRG SHPYDPTGASPKGQSSIL
3776	34144	A	3816	83	184	RLTLPDRLGSPPDTH*AQHITRA VLPQGFTDSPH

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3777	34145	A	3817	1	811	MAEEDSGNLQPEGEGEAGTSS HGGAGERVKGKVLQTFKQPDL TKQTRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIIHPHFKGVR PRRDACLGPSPLAASPAFLGKG QHALKRLKPIITRLLQHGLLKPI NSPYNSPILPVLKPDKPYKLVQ DLCLINHIVLLPIHPMVPNPYTL LSSIPASTTHYSVLDLKHAFFTIP LHPSSQPLFAFTWTDPDTHQAQ QIT*AVQPQSFTDSPHYLNQAQI SSSSVTYLGIILHENTRALPADH
3778	34146	A	3818	2	324	HFEARRQAGPPKPSPQPPFR*LP TAGT/RGGGGEKAAGGFRWGR FAG/MGQGPDPPGAHGQNPASP SLDFPWGPICASQGVTDQSPSTF QGPLGEA*KPTAGAKPGAGAG
3779	34147	B	3819	206	1391	
3780	34148	A	3820	229	792	LGSSAGNSAPDPWRPTSSGVFS FHNTSHSHWILRLRTQERFSEV CVQGTWPTRPLWALPPP*FPFPS PAPAAFASCQSLPPHSPQSPRPG AGIS/RPRSQEAPDSSQ/PAPTRP SVPSPMANQGSGDDRQPPPPQD TPPRPNAASQSAGHNYASLPAP RGRVGVGIGFPGSPACAGGGIW HFHTLSFPAF

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3781	34149	A	3821	3	1676	KDNERRLNTCRSTRSHKRAHTR RSIRAHRGSAAAPPAAQAPGW RWASSCPRVQSAAGRGGRSGA ASGR*APRWGCPP*CGSRPGKC SPSPAPLASTFPRPGTEPPCRL*R GTCLGSACSGGSGRG*RR*GTG TQRRCPLPSARPRTRRRQISCQG KFS*CPSASSTNVCSPTGRGL*K PVPWAPGGRRRRPS*GRSSGDL SSGTWWP*S**ELGIPEYSHST/Q G/LVGVAMPPHRRAVTGNVHIA GQARKKDSP/GGRSPAWL*SPL FCAPGGRGASHLLLSFP*ESPAP *TARP/PLPARKLTVPVVLLRDG LGRGGLGRR*PCSAEKS\GRGRS GWRRARRPPSEAGTRGNRTSSS WRAPWRPGLGTGEPPGAPPGF APSSSPRRTPISPLSPASGSGGSG LGRRQRAADRARTKPGGD*VG SWAGRRPPGGAEGP*GQRRPRP YAVLLLSGWP\GGEGGGSLQPS VQLLVQGGPVGLTG*VSPRLLT REALKQNGATEAGGEHWPSCP PSH*/PGAGEHPGAADTLQVAS PA*GHGTAGRQGRAPAAHPAH RGQRAHSTRQ
3782	34150	C	3822	78	371	
3783	34151	C	3823	349	591	
3784	34152	A	3824	822	2114	AGRSVRIQAMTCLHPAHLGYP GSFQAPESSCPGQ*GRMHSQPT P/AGRRDMQDEPSFSNNIGVAG PGAMSRYTCPGCKNSNQRTEEP KKMR*TF*SLSSFPWGSGSPHP VPSFLWVPPSQLPNT*KLRAGL GTSGLAPGGTQKLRFMRASLW QSKKSRLCPRWGPSGPVGSV*G VEGVAE*RQGLGT\AGSGHQPE RTGHRLWPAASG*SLACSAPSR KGSCFSRPSLRSTETSLPAPGSL SAVGH*GVESAWPAAGRAGNH FGPEVADNLYEMKPPEPQVKP GLGRRQRAADRARTKPGGD*V GSWAGRRPPGGAEGP*GQ\GGP GLTLSFFFQGGQSGEGGGS/PAA ECISGGDSDVALQGSHCVHSEQ GCLAELEDPG*EPGVAVPGWG SQERNVAGTGGVSAHGDTACR PAPPGHW*PTGRGDEIVEAKTK

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3785	34153	A	3825	3	452	PRHSPGCRCPVAEGQSSGRALP PRLILLAVLLLLLCGVT/CWLCP VLLPPEAGTGPATSATSTAALR CGSHPYGQ*QPCTQ\P\GPPTAP CSTHWACGCPAFGSWNWTPW/ PPPAYSLYTPEPPTSYDEAVKM AKPREEGPALSQKPSPLLGAS
3786	34154	A	3826	16	118	
3787	34155	A	3827	292	1047	SWQELESRAQAPNVGQRDGPR RGLSYHVAAEVNELLVEGQHR LEGDKHFTGHSG*QGARGVKA AGRDP*\PRGLVKAVGRGAMES RSSSPKGRGNRMPSGYCTEL*A AGNQSGFVEAGLAFTPAIST\PT GGPLGTHRSQCCVQGCHCP*G* LPRRRAAVLVADVAGPVPASG GSRTG/AQPAVTP\QAEAGGPPA G*APLATGCSSGPRAGTGPRGR SCRPRSPAPPAAAAGAAGAAG AAAAAAVRGRSAAPGP
3788	34156	A	3828	2	462	GPVSIGEPEIGPPGPVSIGEPE*G PPGPVSIGEPEEGPPGPVGIGEPE EGPPGPVSIGEP*EGPP\GPVSITE PE*GPPGPVSIGEPEEGPPGPVGI GEPEEGPPGPVGIGEPEEGPPGP VSIGEPEEGPTGPVSITEPEEGPP GPVGNEMSSR
3789	34157	A	3829	3	374	YRALVFSSSTQ*VSKNFLYSGSS SMLPVLASFFLSFFLAIFWNGA NSATAGYSRPQVGGEELEVVV CWQRAQLLLQLLLGEARRQAA DDHLRGARGRSHRGGAWTRSS KGTAYRAGRPGPRPTK
3790	34158	A	3830	66	619	VRSLFSEMNVVEFQNGFWNMF PVKRPKISCSGRVCSIPEDSQKE AEKKRCQDWKHRR*SRI*EVFR NL\RVEEEKTSANPETLLGEME AKTRELIARRTTPLLEYIKNRKL EKQRIREEKREERRRRELEKKR LREEEKRRISVEDRWLYTIRINR RKSQRKK*GLRSHSGSDKEHRD VERSQEQ
3791	34159	A	3831	253	482	QVSTCYHSQEKEKKRISSTSKSL NKEKRRNEQ\KDQ*ALLSSPPSP PAESQGWHWSSLPPHSRFLKTS YILDLDIKK
3792	34160	A	3832	156	443	
3793	34161	B	3833	426	513	
3794	34162	B	3834	47	1311	

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3795	34163	A	3835	1503	1652	NCGNNQ*LTNQKKSRSRWIHS QILPDVQGGAGTIPSETIPINRKR GNPP
3796	34164	A	3836	1	1986	
3797	34165	A	3837	1	1116	
3798	34166	A	3838	1	546	ERSSSPAAEQSWMENDFDELRE EGFRRSNFSELKEEVRTHGKEV KNLEKRLDKWLTRITNTQKSLK DLMELKTTARELHDECTSLTNQ FDQLEERLISNFSKVSGYKIN\G KNHKHSYTPITDKQRAKS*VNS HSQLLQRE/YKYLGIQ/AYNGCE GPLQGKLQTTAQGNKRIQTNG RTFHAHG
3799	34167	A	3839	1	987	
3800	34168	B	3840	1	1593	
3801	34169	C	3841	1	1479	
3802	34170	A	3842	129	368	
3803	34171	B	3843	1	1884	
3804	34172	B	3844	1	471	
3805	34173	B	3845	1	675	
3806	34174	A	3846	1	410	
3807	34175	A	3847	250	880	GEVTKPQFAQFFHGSLASLTIRP GKMESQKVISCLQACKEGLDIN SLESLGQGIKYHFNPSQSILVME GDDIGNINRALQKVFYINSRQFP TAGVRRLKVSSKVQCFGEDVCI SIPEVDAYVMVLQAIEPRITLRG TDHFWRPAAQFESARGVTLFPD IKIVSTFAKTEAPG\A*KPQVQN SEFSL*AFENPVSCQISNSGHVP NFQFRV
3808	34176	A	3848	890	4889	
3809	34177	A	3849	1	799	MYAQPPNCKREKASGDVSLYW WKLAKGCLQMEVSEGAPNSAS TPTGNTVSQELNRPLP\QPPYPR RFSWVCRSSLQA*VAESATKTS AFRAPNSFCRLQPRPCCRASPAS PATSCTCPGSLAWARPAPASH WARPHRPPPCPTSPRP\PRGRDA PER*AHGPPVPDAR*GALAPQA TGGGQPPGAQPHHARAGPGQP RTPL/Q*GLCARPGEPQLRVTPH GPQAGG/HTQRLPPMGKPGVSG GVCPHSDFPQPMPTVEMTGPRS GVQRPT*DGTGWLAPDAESLV SFEFSSPT*VL*QQWK*RSGVQR PT
3810	34178	A	3850	212	361	

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3811	34179	A	3851	3	909	GGRQRGKDTGHMAKQEQERE VGGATHL*TTRFRSCSK\SALIP VIPITKSTGSRFRNSVEGLNQEIE IIIKETGEKEEQLIPQDIPDGHRA PPPLVQRSSSTRSIDTQTPGGAD RGSNNSSRSQSVSPTSFLTISNE GSEESPCSADDLLVDPRDKENG NNSPLPKYATSPKPNNSYMFKR EPPEGCERVKVFEECSPKQLHEI PAFYCPDKNKVNFIPKSGSAFC LVSILKPLLPTPDLTLKGSGHSL TVTTGMTTTLLQPIAVASLSTN T\SKTESLEEQVQSCHQLLYSHH QNQLRKLKD
3812	34180	A	3852	189	454	LWKRFNSWTSLRHPYQPYQAE QIAPQTCGSQSDGGLPSSSGPAP LHHAGLGYGTEGSPGARRRVE GQDP*VLEQAAGPTPPRYLVRP
3813	34181	A	3853	17	561	IPGSWRQKMPVPPAA\PAHAQG RPGALQSPGSSTPAQPGSRWEV GGPAAPWGSLRHP*QPYQAEQI APQTCGLQSDGGLPSSSGPAPL HHGGLGYGTGGSPGA/LEEGGR PRSLGPGAGSRAHAAEVSFPSG PPSRGLTGSGFCACSEERAGFPR ELMVIKNTVTPTREATTLILTKA PAILP
3814	34182	A	3854	1	540	FFQPIFWGKDPQSGTPPHP/RPG PAPSGPEPSISMVTRRWLRAPN CSDRRGEGPRTEADRHGSCCRF RSRAGTAVHSCRRRHPRAAGLP SSLCAEAGPRET**LEGGCREG AEPRP*RPGSGAHAHTDPERAH RSGARTQ/HPERAHRSGARTQIR SAHTDPERAHRSGAR\HRSGAR RTLPL

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3815	34183	A	3855	1326	2409	GRPPGVPPATAPRAAPGAGDGE AGTPAPGDHPEPVCRIQPG*WG T*GWGASQHWGGH\PALALAG RRPSRGLAGASGRSSEEPGVAT QRLWESMERSDEENLKEECSST ESTQQEVLALEEERAQVLGHVE QLKVRVKELEQQLQESAREAE MERALLQGEREAERALLQKEQ KAVDQLQEKLVALETGIQKER DKDLQRQCCGMMGDRAKASP SWTSTVILKFPLIKNCLNPKDIS LMAKELWSLRTMDALNRNQIG PGCQTQTMVQKGPLDLIETGK GLKVQTDKPHLVSLGSGRLSTA ITLLPLEEDCLPSLVDDLVPRLG LKISLETRRRGQLMLCTPKFEN QWPTTDKMPETSTGSH
3816	34184	A	3856	240	639	DHGRSQ*EPNRPWMPDPDHGA ERTLGPDRDRQRAE\MQTDKPH LVSLGSGRLSTAITLLPLEEGRT VIGSAARDISLQGPGLAPEHCYI ENLRGTLTLYPCGNACTIDGLP VRQPTRLTQGLSMSLPSQLIQET
3817	34185	A	3857	1	1758	MALLPTVLCLWAQAQVGVQR HNHIFWNEKEHGHGKSGSCHN GASCSAEDGACHCTPGWTGLF CTQRKPHLLASQPLRIPCCGLL ATVGIVQTSREGGMQAAPGLV VPDSCPTRTEELCRGSSRPDWIQ GIDKPKVLQGCPAAFFGKDCGR VCQCQNGASCDHISGKCTCRTG FTGQHCEQRCAPGTFGYGCQQ LCECMNNSTCDHVTGTCYCSP GFKGIRCDQGIMLLLFLIV/CAA GPICLASAAAEREGPRPGSPCLL HTCHE/R*PAPTTPSQDLTDHYL RFSMPIMVLT/CLQGAFPGSPGR \PG*TWAPLCGMNVNRPGT/HE LGCDSDHWGPHCSNRCQCQNG ALCNPITGACVCAAGFRGWRC EELCAPGTHGKGCQLPCQCRH GASCDPRAGECLCAPGYTGVY CHPVTGACTCQPGWSGHHCNE SCPVGYYGDGCQLPCTCQNGA DCHSITGGCTCAPGFMGEVCA VSCAAGTYGPNCSSICSCNNGG TCSPIDGSCTCKEGNVPSLPSPS LTYEHIPQVVLPAEGSQDGTFG LNCSEHCDCSHADGCDPVTGH CCCLAGWTDIQEGFLEKEGPKR
3818	34186	A	3858	2	2414	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3819	34187	A	3859	1	852	DEEEVVAREEEEEEEEEEMVPE ESMASAGPEDFEQDGEEAALA RGAPAVDSLGMEEEVDIETEPV AHEKRPSMLDEPPLPVGVEEPA DSREPPEEPGLSQEGAMLLSPEP PAKGLAHPNGSQKVIFRVPLRV IHGPKAVELQVFPGLHKQPTNQ PK/TEPCDPHSWFKSCYHLLFIP VGISRPP/HNPTITATIFASTASV LW/PVLDTCMSSNSGYFKAVLE SYSSKVLSVTQYGNPRATGSAG LRGRPGS\PGSSGSRGPAWP*PQ AAPRCPPSSGRPGPTSQSPS
3820	34188	A	3860	3	1997	AQGSVVPGLFWAFLQLEVNCL LESPIIQGKFHFRLERISVVEPQE RKRLSFRKSEI*P*K*SLVKKL*E RLKTRKQMQLANRLRRYGYSV VES*FPNLKVSSSVSTTPTTTYIP MTHKAIFSSYFLWDGRSAFLTI YKMMSSHPQEEEEEEEEGGE GEERKRRKKEEERGKRRKRRR RMK*RRRRTRKRRKRRKMK*R RRRRRRNMRKKRKEGKNMKK KM/REEIKRQNALYEIEMRKKL EKKREEMHESRRRFLAPLFSSP TANCSTSLVPRLRLASLPAALPS NRVVRVTTPPAGVRGAWRHSH FSRSRSIMDTSSEMLVRFGRRC GRAKESTGRDWNSLKSSEEDR KMWESLELPRDLLNAFDQNAD SDMDNKMQAEMVSDGDEELS GNWSKGDSCYVLAKRLASFYL CPRDLWNFEKDDLGYLAEEISK QQSIQEAQRSRRKKWFYGPGPG SLCCVQPIDLVPCVPAAPAMAE RGQCRAHAVASEGGSPKPWQL PHGVEPVGAQKSRIEVWEPPPR FQKMYGNAWMSRQKFAAEAG PHGEPLLGQCRRELWGRSSHVE SLMGHYLVELLSIGAMGIKVQR PRCFFDIAINNQPGEKGTGKSTQ KPLHYKSCLFHRVVKDFMVQG GDFSEGNGRGGESIYGGFFEGP AMGPNATNNFTKLAG

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3821	34189	A	3861	86	1120	LVLSKGKEHLLGIKEHEEEEER RKKYE*KDAEEIKRQNALYEIE MRIKLEKKREEMHESRRRFLEH MQDKHIIKAVEQQQ\RQRKKM KR*ENSSKQKKRLIQMGKEKEA ETHRLMEKRRERIHNFLSELLK EKLDNEDMIIARDIAEAEAEWE KREREKDEKNQAELKTIAEYRA IVMKNKEEEERQRKIEAKEQLL AVMKADQIFWEHEKEKKCKA DKEHQEVQDAHIQQMAKNKFN AKQAKQAELDYCRLTEALVAE KEKEFQDYAREVIELESETPNK YIYPLVKAVQEGPGGGRGPVFV DRGGLRPSYQANDVTGVQLPF YNSQGPKYNFQKSKRRLGFTW
3822	34190	A	3862	591	2805	WVHQPAGS*GEKPT*ISAPPWP EAPTSELWVLTPPEAVQEAAAR VGQEVPAAP/RGPLPSSATGAK SLGQGSPTPSTRSMSLQSCAGP QHP*TLRRGPLWGTSRWKMVL T*ASRTSSTPGLT/QGPRVTVLL GKAGMGKTTLAHRLCQKWAE GHLNCFQALFLFEFRQLNLITRF LTPSELLFDLYLSPESDHDTVFQ YLEKNADQVLLIFDGLDEALQP MGPDGPGPVLTLFSHLCNGTLL PGCRVMATSRPGKLPACLPAEA AMVHMLGFDGPRVEEYVNHFF SAQPSREGALVELQTNGRLRSL CAVPALCQVACLCLHHLLPDH APGQSVALLPNM/YSALYADG ARPQPPWALAHLV/LYWTWGR WP*GAWRQGRLSSMQKILLHP* *LLGPLTAC*LPSASAQALGTS/ ETGYAFTHLSLQEFLAALHLMA SPKVNKDTLTQYVTLHSRWVQ RTKARLGLSDHLPTFLAGLASC TCRPFLSHLAQGNEDCVGAKQ AAVVQVLKKLATRKLTGPKVV ELCHCVDETQEPELASLTAQSL PYQLPFHNFPLTCTDLATLTNIL EHREAPIHLDFDGCPLEPHCPEA LVGCGQIENLSFKSRKCGDAFA EALSRSLPTMGRLQMLGLAGS KITARGISHLVKALPLCPQLKEV SFRDNQLSDQVVLNIVEVLPHL PRLRKLEQGRSGAPGVGDSTPD
3823	34191	A	3863	1	2784	

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3824	34192	A	3864	727	1715	YLSKGLKEVREGSLQIPGEIIPG RKKLMQMLSEKTL*SQHHY*K GFLQRQIHQKMIAHLVEQRNK DCMFLQIMPAATS*/TEIQATIR DYYKHLYANELENPEEMDKFL DTYTLQRLNQEEVESLNRPITG SEVEAIINSLPTKKSPGPDGLTA EFYQRYKEEL/PKPCRDTTKK\E NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSINVIQHINRTKDKNH VIFSIDAEKAFDKIQQPFMLKTL NKL\GIKYPGIQLTRDVKDLFKE NYKPLLSKIKEDTKKWKTILCS WVGRINIVKMAILPKAPLPLPP
3825	34193	B	3865	1	1908	
3826	34194	B	3866	609	1658	
3827	34195	B	3867	61	234	
3828	34196	A	3868	1	978	LFTDDLCQPVEATSGQAMVQS RGATTHGGGRGGSCKLLGDRG QGSTSQVGRWGSSCHPPTGG\P ARSPCWPTARKPLRGVLQGASL GSTASMLGAASGTPRPPPSWLV SVPSPRAPCWGVPGAG\EQGGP ETQPPGAREYPQPAGREGRPQI LRFPKSSSSQCLVEFCSLASSCF ALEAMKTRRSPSS/SGSSGSDG/ SQRTTRSGPAQRPRVSGSSEQG\ DGMRGGSSGGMKGRRVPKREP RTEAASSSTA*RQPPPPPSPLPH ARRHFRFRPCCGPARDAAPSRA QTEAPPPLRTQSALSWPLCSRT DGKLSRGQSRDGSRAPTPGVL

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3829	34197	A	3869	1	1919	TPVSDEEEGSLHHTTWRNLRIG VRIACPAGENAQSSESPVRACQ PGTKTQYGLNQAWSPGVRRDL IQGSAERPARYPAPGEMGVGAF IPLGHDKRRAASQHLHVSGREG PEALGSRGSALRKQVPAWLPHS LRTCPVDRNPQAPCARTGLMV ETPHHEQWVRGEHYRYKFSRP GGRHAAEGKWWVRKRIGAYFP PLSLEELRPYFRDPHTLMLGQR VTERELDGEPRGPVTVEGRSAT TSGYPTKVTKIGGPLDPAGGLE GPLHGALGSDPLEVSDCPGPHL SRKVWENGSFGASDQQHTR/YT TDGSSWPTVAEKKAPSSKQYH SSMET*R*TGHSNHPRNRPTCG QVPPNENNTRNRPTHTARYLPT /ENNPRNHSTHATRYLLTTTTTE IIPHAARYRPTRTTRYLPTRTTR YLPTKMTREIVPHAATYLPMRT TREIIPHTATY/ASNENNQYLPM RTTSQVPSNEDNPGCLPTRTTR HLPTRTTRYLPTRMTQEIVPHV AWYLPTKALRPFNGKRTAFSA NAAKRSEAPTLR*ALRT*CPVN PPDTEGTGPAMPSLECPEQGNP QRRWAGRRRSSGAQDAGQGTR FTPSLWRAWGWSRLRPRLSAP GCWLTRKCRTEPPVVPQALMM AAVTDMQTLIH
3830	34198	A	3870	295	457	
3831	34199	A	3871	296	1057	GNEVKMPARETTPHRVPTGAQ PSEAGEKGHHPPDRRMVDPLTL ALCTWKSCRHSMPDCKAAGRE AVPCKVTGAERPRPRAPTSA*P SGKLEGLSLWCTQSCSCMLHR AGVISVFFTMEDVAPTRGLLH* RAAIGIISPITISVTKTSNNCRWC RVGGCAN*LRGALEAGG/WLQ NQKGRDAFNKRLRGGMDKPG AGGTCGSGRRNRPLRDRS/VPE VKGGTGTG*KTGSGGLKRKYV GDGTTASFESLRVLIKWPL

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3832	34200	A	3872	3	913	GGADSGERLGPHALGLGAGSG GGRGRYGPSRSRPSGRAADPGG VRPFPVAPRGARARRGGRVVP AF*RPAGAA*AAQHHVVVSEP AAAARGGGGPGGQGSRAWRG VRRLPGGAGGLAGPPGRVPVL GPPGSGPAAQRPPGRGQGAGQ EPPPAGDAAAA/PSSGSASCR/G PGAA/GPRALCPGPAPPARRGPR AGLGRPAADRGAPAAAPVRAE PHGLGGAAGARPPHRLRGGAG H/SGALVVLLTLWITGGGGDGD RASPGSPGPLAT/GAGLVGNKA APS*RAARAPGGLGCRWARFSL TSQCPCPQL
3833	34201	A	3873	2	484	TPWRRKSTE*PTLGVRRPVPRN AMPHHCSFFTGRTVPSMATPG YNEGWDKFRMKCHLCVNYIE MQTDPANCDYVIVSGAQRKEE RWDMADNEQVLTTEHEKKQK LETDAMFRLEHGEADRSTLKK ALAHT\DHIQEAQSAWKDDFAL NSMLRRRFRVPSKP
3834	34202	A	3874	3	531	GRKRSKRMEKGERGEPYSLSLR NHQGSWEPEHMS*KPEGG\VLA FKGDDGFSVWESNAIATYVSNE ELWGSAPEAAAQAVQWVNFA DDSQYQGVPTLGKMHHDKQA TQDAGEEV/QPQFQAVLG\EMK LCENMAHFDAKIFAESQPKKDT PRKEKGSREEKQKPQAERKEEK KVATPAP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3835	34203	A	3875	2	1326	TMAAGTLYTYPENWRAFKALI AAQYSGAQVRVLSAPPHFHFG QTNRTPEFLRKFPAGKVPAFEG DDGFCVFESNAIAYYVSNEELR GSTPEAAAQ\VVQWVSFADSDI VPPASTWVFPTLGIMHH\NKQA TENAKEEVRRILGLLDAYLKTR TFLVGERVTLADITVVCTLLWL YKQVLEPSFRQAFPNTT\RWFL TCINQPQFRA\VLGEVKLCEKM AQFDAKKFAETQPKKGTPRKE KGSREEKQKPQAERKEEKK\AA APAPEEEMDECEQALAA\EPKA KDPFAHLPKSTFVLDEFKRKYS NEDTLSVALP\YFWEHFDKDG WSL\WYSEYRFPEE\LTQPFMSC NLITGMLQRLDKLRKNAFASVI LFGTNNSSSISGVWVFRGQELA FPLSPDWQVDYESYTWRKLDP GREETQTLVREYFSWEGAFQH VGKAFNHGKIFK
3836	34204	C	3876	58	222	
3837	34205	A	3877	6	153	
3838	34206	A	3878	2	889	CPPWELILDQFRKSLGISPANTG PLCPAPPSCMYPPSPQMPAKAP/ PDHPPEGRPGTTPEPFPRVTCVT E/PVGKGLSRDSQ*ETRGDLQE* SLAAPKSAPCFTHSAICPGAPSM SRHPERSVFLLFQAPVQEPPAPG PP*WVLREPDFGTGVFPEPSW* KAADFEPLGLCPGRSLSAQCPS WWPPTSSDPG*ALLKSGTGTPT VAPRQPAPAAPRFQRPPQPRGL ASTCPAGPQQKGSDPPGRSAGS E/GSVSGKSLKPCLSSPLIPPPQS STQKKASVAKFVEFSPYTKQKS QLSVP
3839	34207	A	3879	1	391	MAKAVEKPESTLEATKSKESV MSRVEWIGTAHMWVDDETGD NASKTQQTLEPAELATKYANFS EGACKPGYASALMTAIFPRF\C KPIRLSP*PRHLAHWCKKWAPK ILGSSAPVALQGAAPVAALMG WR
3840	34208	A	3880	1	346	
3841	34209	A	3881	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
3842	34210	A	3882	25	302	
3843	34211	A	3883	1	2235	

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3844	34212	A	3884	1	2724	MGGMVESSRHNWSGLDKQSDI QNLNEERILALQLCGWIKKGTD VDVGPFLNSLVQEGEWERAAA VALFNLDIRRAIQILNEGASSEK GDLNLNVVAMALSGYTDEKNS LWREMCSTLRLQLNNPYLCVM FAFLTSETGSYDGVLYENKVAV RDRVAFACKFLSDTQLNRYIEK LTNEMKEAGNLEGILLTGLTKD GVDLMESYVDRTGDVQTASYC MLQGSPLDVLKDERVQYWIEN YRNLLDAWRFWHKRAEFDIHR SKLDPSSKPLAQVFVSCNFCGK SISYSCSAVPHQGRGFSQYGVS GSPTKSKVTSCPGCRKPLPRCA LCLINMGTPVSSCPDRSTRQKV NKDIQELNSALHQADLIDIYRTL HPKSTAYTFFSAPHHTFSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRIKTFTPNRSTTWKLN NVLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVF RGKFIALNAHEKIQTTIREYHK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPITGSEIEAI LNSLPTKKSPGPDGFTAELYQR YKEELVPFLLKLFQSIEKEGILP NSFYEASIILIPKTGRDTTKKEN FRPISLMNIDAKILNKILANQIQ QHIKKLIHHDQVGFIPGMQGWF NIRKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQPFMLKTLNK
3845	34213	B	3885	1	1971	
3846	34214	A	3886	1	1146	METRPSRGPLTPHTARCQSETK LPEEGSGSNICCSAIFAILQPPLV IPRQTGSGVDLQQTPTDLELRD LTVRRKTNKWKGIASTSTKRTS TPKRHLSWFFEKINKIDRPLAKL IKKKREKNQIDTIKNDKGDITTN PTEIQTTIREYYKHLYANKLEN LEEMDKFLDTYTLTRLNQEEVE SLNIPITVSEIEAIIKSLPTKKSPG PDGFTAEFYQ\ASIILNGQKLEE FPLKTGTRQGCPLSPLLFNTVLE LLTRTIRQEKETKGI/QLGKEEV KLSLFADDMIVYLENPIVSALN LLKLISNFSKISGYKINVQKSHA FLETNNRQTESQIVSELPFTITTK RIKYLGIQLTRDLKDLFKENYK PLLNEIKEDTNKWKNILCS

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3847	34215	A	3887	66	1392	QVLLSFGTPLVLTTKREKNQID AIKNDKGDITTDPTEIQITSIEYY KHLYANKLENLEEMDKLLDTY TLPRLNQEGVESLNRPITGSEIE AIINSLRPISLMNIHAKILNKILG N*IQQHIKKLIHHDQVGFIPGMQ GWFNIRKSINVIEHINRTKDKN HMIILIDAEKAFDKIQQPFMLKT LNKLGIDGTYLKIIRAIYGKPTV NIILNRQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAKAIRQEKEI KGIQLGKEEVKLSLFADDMIVY LENPIISAQNLLKLTGNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLVKENYKPLLKEIKEDTNK WKNIPCSWVGRINILKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRACIAKSILSQKNK AGGITLPDFK
3848	34216	B	3888	1	2868	
3849	34217	A	3889	1	1218	
3850	34218	A	3890	1	1893	MKEIETQKTLQKINESRSWFFE KINKVDRPLARLIKKKREKNQI DAIKNDKRDVSTDPAVIQTTIRE YYKHLYANKLENLEEMDKFLD TYTLPRLNKEEVESLNRPITGSE IEAIINSLPIKKSPGPDGFTADFY QRYKQELVPFLLKLFQSIEKEGI LPGSVYEASIILIPKPGRDTTKK ENFRPISLTNIDAKILNKILANRI QQHIKKLIPHDQVGFIPRMQS\W LEVLARAIRQEKEIKG/IQLGKE EVKLSLFADDMIIYLENPIISAQ NLLKLISNFSKVSGYKINVQKS QAFLYINNRQKESQIMSELPFTI ASKRIKYLGIQLTRHVKEHFKE NYKPLVNKIKEDTNKWKNMPC SWVGRINIVKMTILPKIERIGKT KGTETQRGKSCKPTHPVSVISL AESIARDFCLQLNRARSCDQSS YNEVLEADNRAFSLCKGMPFD RLSPISQTPGPSWYQSSPYQPMF LAAPIDIGSRPASMDPIHSRTWH YVTVVILARSRKHQELILSESKQ FEEAPPELRSRAPGGFSKPAAG QIKVGLRENLTASMQISPADAN LILQDSFLAIFLFQALIVTIYKEN EKEEGQERREEALRSTGKNNV WKNTDIDRPESISDSESAGCDY

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3851	34219	A	3891	2	1562	WGEIRAEKLKIPKTGAPLFLQRI AAPRQQRNKTGQRMSLTS*QK *ASEGR**QT/LSKLKEHVLTHC KEVKNLEKRALAKLIKKKREK NQIDAIKNDKRDITTDPTEIQTTI REYYKHLYANKLETLEEMDKF LDTYTLPRLNQEEVESLNRPITG SEIEEIINSLPTKKSPGPDGFTAE FYQRYKEEL/PDKQLQQSLRIQ NQCAKITSIPIHQ*QTNREPNHE *TPIPNYYKENEIPRNPTYKGCE GPLQGELQTTAQR\KRGHKQM EEHSMLMDRKKQYCENGHTA QGSTDFGEVQRLRLWQEDDVA EEVSGFFEEDNLKSVAQDPFWE SRQVKTIFNCVDTYIAGAKAIA GITQVTCTGNQFAEINQRFLKL KKSWSLYRRFQPWQEECGPSW NPSWTHPSVASSRKDAAAQRE AQEGDLQGQEGAEASHAGGPA ADHYSGTAHAGRGRALDRGVC VRGHAPPPITELSRPAGCGPHR QGEEAREGDANKKNGFHIQRC SCCLSCKQEHPVLPLVFGLD
3852	34220	A	3892	2428	6109	YPESTMNSNKFTRKKSNNPIKK CQQASQLKALPTQSCSPSSNSY ETFLVSPLHPFQFYISFPHYTEM VPPLTPEDYNSRGDFGGDTETN HIISKFHRSLEQVQNAASRRSQ DGRIGTAPVYSSQRERRRRRVIS AFPSEERSSSPAMEQSWMENDF EELREEGFRRSNYSELREDIQTK GKEVENFEQNLEECITRITNTEK CLKELMELKTKARELREECRSL RSRCDQLEERISVMEDEMNEM KREGKFREKR
3853	34221	C	3893	13	391	
3854	34222	A	3894	117	704	WLSAWPRACPDCRVRFPHTSPP CLPCGPEAEPGPGPALRELVQP LPGQLQPPFGMPLPLVPAGSFLI CTVWERPRPGLAVGSPPCFPSL H/PTVPVGCPPPSPCL\RPPA*PT THLHIWPSLLFGPLPALPPPLAA SASAGLRKPWLDGLHPSVEPSG LGAAPSPAPPACAWTRPPHLHP SSFSSCVPQISSLFLCF

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3855	34223	A	3895	1	1185	SAASSVLYVHNEPQVHGAHQK IHPIHPSLHYCLAHIISQDLHTS MNALGLFGVG*EQGLQEKSNL SSTHHEPGHGGQDAAGARDGA RGRGGS\TGSAAGERGGRTVPH WA/GQPAEAGGAG*PRGPQLRR SPPP/RLPPRAGSSANTRNSVLL* FF*AVCLWADHYPL*TLISSS*M AGRWRSVPGIPTSPTK/PPPPPPP PPPPPPPPPPGSFLSEP\VWSTA* NSTCPPRRCRSASGGPIWCPCRP /PAPPPAPPAPPPLEATEESLEEG \GGRASRSANMFAPTAPAGSSW HRARWG*PAWKAGAAGTRGA KCGQFVPSASSAP*LAGGWPGA GGQRGARRAQKAWCCRPGTSL /APGPELFPESALVQAGSAPPPP PPPPPPPLCLLLLRAESEGAVLM
3856	34224	A	3896	192	477	
3857	34225	A	3897	2	1782	RAAARKEHQGSAT/RAERA/PR TPKAS\GRG\SPVPTSGTVTART GTAPRGLSAEDGRRRGRP\IGIP FTDHSSDILSGLNEQRTQGLLC DVVILVEGREFP\THRSVLAACS QYFKKLFTSGAVVDQQNVYEI DFVSAEALTALMDFAYTATLT VSTANVGDILSAARLLEIPAVSH VCADLLDRQILAADAGADAGQ LDLVDQIDQRNLLRAKEYLEF/ YYQSNPMNSLPPAAAAAAASF PWSAFGASDDDLDATKEAVAA A\VAAVAAGDCNGLDFYGPGP PAE\RPPTGDG\DEGDSNPGLWP ERDEDAPTGGLFPPPVAPPAAT QNGHYGRGGEEEAASLSEAAP EPGDSPGFLSGAAEGEDGDGPD VDGLAASTLLQQ/MDVIGGPGG G\RGGGQRRGVAGRRQGRHGL LPEVLQRRPRRRRLPGLVAEGG EEDPSQGLPEVPHLREGHPGRR QAAATHPHPHGREALRVQHLQ GPLHQDTSTSTLQKPGSPRPL*V TAGR*AGQAEGAHAEAHGREA VPVPAVRRRLCPQLRPEEPHAR AHGPAPLPVRQLLQDLRPLRPP AQTPQERRLQRRPLAPAVPASP CVLWAGGCPDPQPW
3858	34226	C	3898	162	356	

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3859	34227	A	3899	3	2289	GELHGVAEQAEGDPREGSPGP AEQASGTELREVPGPHWPLHPP EAPVCQHYHRPMVQKGN*GSV WGRGESLVQG/AHGQTSQRSV QMTGGGAWTGQTSQRSVQMT GGGGTPRGSRSSSPRTT\TPGTA EDTEGEPAGAGEQAAGRPVRP LHGHPGAGQEAAAGVRELPPA EPAAHLHPQPALLIQQHPISHAR SQHPRRPCCLPGPGLRAGGTAE GLPCAFCSQRDERAEGRERDLE GGGEAASGPGRQAQAPGQGGH LGPPLTPAAPLPWWLEGHHRE ATGRPRGG*GRPPGRGPTGRRK ASRAQDISSGQNLPRGHPA*VA SPRHEPPAHLQPAARDHCRGA\ PGSQACPADRGPANGTPPPLPA RSSPPSP\GMSVASPWTASCGPP GPPP*P\IGPEALPEGGPALPPKP PPVPAPSEPPQQPPGPCCSPQRP PAPGPEGQRSRGLGGAHRTAG AAQCPGGHAGPSPGGGTAPAP GPAAAAG*GQGRQCQAKGPAH TRGDAALPTSRLRL*GP*E*GD QGSSG\AAGLSGGRHTQPAGPG RAQRTEAAATQDCALDKPLDL SEWGRARGQDTPKPAGQHGSL SPAAAHTASPEPPTQSGPLTRSP QALSNGTKGTRVPEQEEASTPM PPDLDGHP\GPARLKC*DQSPTN WMRQTPQAA\SGPELPGGG\PT STTGEGPECICTQEHGQGPPRK
3860	34228	A	3900	3	3169	ASQLVLTLAYQANCVSVSYTD LLGKPGGSYFTFLYVLNIRSRSR LKKDYDDFRRQPDHDTFNREL WTTDEGEGDLGKDSPKGEISKS IDSTEPLDILEKDHFDSDDMKLS EIDFPMARSKLLKKELPSKDLP KTLLKTLKRQSKQTDYVDDST KELSPRKKAKLSTNETTVENLE SDVQIDCFSESKHTEPSFPESFA SLDSVPVSTLQKGTKPIQALLA KNIGNKVTLTNQLPPSTGRNAL AVEKPVLSPPEAS

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3861	34229	A	3901	33	1227	HHLRGTGQRAGQQLPPGMKM GRAGPPGPWCEHTT/PPSRGRPT SSGGPTLAPALAELSPRPQTPSP SISSLPMITSLPGGTGPLCLRPLS WEKPGSATGK\RGSQQEVDVG PSPGHTAPSKSHGQGPVGSPSA RQGCGPASSALQRRREPGGGPR GHPAGPHGGCVLPPWPGCPGN TMQRL*GFHTRAMNTQSGAGP RTAPSPRAQGAQGRPSKSCSGA SQGPCPAVGPH*APGEDRVRHP LASISGTTRAHGRPSQQREPRN KSTRADSRSPRTVPPHGPPGPSL PRGR\PAQPGPGV*RNGISVGAG RFPPFTAPCGQQARPGAG\NRG AGSGA\PEL*GGLGRDPGSSGCE VPGGRAGG/PPRT*HFLARPAPP SPPQGLPRPPKVLGLQA*ASAPS
3862	34230	A	3902	124	1183	DNRAVFSPTGRR\DRGGGGPAG TLARV*SAPGAFGV*STRTHVA GVQMPPVPGTCDVCTRPCSPVS RPPRASTAVAAAAS/SGPRQPR HPRHTSPMPPPAALRPPAGPRG LAPGG/HTAPPATAAPVELQHP LLRLQTGPPLGPPTGPA*EPRAH PCIRGLLPAGSGPPPRRQGHPEP PRLHTAACSPCQPQRALESSCPP RAFPGTAAHWLLGTGDWLL*P AAQAALASQEWALPGICLCNSL SEPTGRVILASQLAPCIRLGCRK RSLAKAPKLISGGAGAHTPTPE PTCFSVSVLGTSPPAAGGPRGQ ESVVSSPVTMGT/VPAWAIPSLG CRGEASLDHPAGQLPARGQRSR RH

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3863	34231	A	3903	174	1599	VLHAVGNQVQGCPGPEVHVCG WRPGCVRLLQLHVVGRADGPE CDLCAVWPGGGDV*PAVPGAV PHVTQCEPQGHPYGEGTGAGA YCAALCGPPGARGHCGQEARQ PQVRTCQGQERRRDCQDLL*E AGGQEAPGAERPSAG*ASRGTP RAAATHPPRTASPGEGQHV*VP AHVGGARPGAWQRHPGLHQY HRPQHLEPPAQPDEPHQDP*HL PGQRPAPAVEAEPGQQAPS\KP CPPPEPSAPQDGVPAENGLPQG DP/GAIAPRAQAPDSPCGRCTSP GQQ*YWLGPGAPQRGSSPEWD RP*ATQDGRPRPRPTPAAAICDP G*PREPRGGAPQWAGWGGRRR **RLRNPQ*PGQP\SGSSGRGPG PRRPSVASSVSE/RVLRGERALS PSPEAPLRASGQRANPTTAPAA ECPPYNPRDLCWTPGWLPMGP ESGKRRSRCVEEDAGPALHRQ GGTDGET**TGRGGNRPGPYGR
3864	34232	A	3904	331	1120	HKDRFWQLQNDSCFLHSPGER QWLGGPRSDTFGPQVLFGHVGI CSQRA/HPAGPGHRGLPEGR*PP HRSQRHPPRSRKPYLA*PPDMC VATDRRTQTPRDFPPLGR*KPH GTLRSAACPAGRVSPSPRPRGL PAPPPKSHLCG\PGVRGR*QLLP PHPGSPKGERGWTASPGAARG GPGPAPAPRP\RASWSQPSVTFP LPLAGLA/GHPGSRTEPAWKAG GAAARPGPELPRDLLQAGSTDT ASGEQLAAGPWTGKEISGRARP RL
3865	34233	A	3905	2	415	YTILTEK*KLSKLST*W\VHQDQ LQKREELSMEILNK*DQDSEAY PQRTVTGEETWLYQYDPPPLPR SLPPPQTHTAPVGA*S/DWGG*E LPPGLNGDKLAHHSPTPFLSFSG LLFVDWL*SQLLSLFGLFTQGVI RIFI

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3866	34234	A	3906	1	4527	MGFCCRECRPRLLKGRPCIQHA GPVAAFKVATPYSLYVCPEGQ NVTLTCRLLGPVDKGHDVTFY KTWYRSSRGEVQTCSERRPIRN LTFQDLHLHHGGHQAANTSHD LAQRHGLESASDHHGNFSITMR NLTLLDSGLYCCLVVEIRHHHS EHRVHGAMELQVQTGKDAPSN CVVYPSSSQDSESNHGNNFRIH VSNGLLMRGPRPLDRERNSSHV LIVEAYNHDLGPMRSSVRMRK LRQSTALAQHWTGTALDR
3867	34235	A	3907	1	2180	MALTFPCRKFEWYGRRQPEVR YSVPASHQLKATDADEGEFGR VWYRILHGNHGNNFRIHVSNG LLMRGPRPLDRERNSSHVLIVE AYNHDLGPMRSSVRMRKLRQS TAL\DSTGQAQHWTESRSGSPG SPVAPTCSART*QTSAS\VHLCL SGKSHHAWPP*TPFKLYYVH\E YSAHIHKENLVLVIVYVEDIND EAPVFTQQQYSRLGLRETAGIG TSVIVVQATDRDSGDGGLVNY RILSGAEGKFEIDESTGLIITVNY LDYETKTSYMMNVSATDQAPP FNQGFCSVYITLLNELDEAVQF SNASYEAAILENLALGTEIVRV QAYSIDNLNQITYRFDAYTSTQ AKALFKIDAITRILGTQMDTKM NKTLLSPQRVLRLEVEMELIQD ANQSATRRCAENYNRGVVEPL RAQQSYLAGEAGRLHGRGGFP VECEREEGIQQTECPGEVMPDR GSDMEGVITVQGLVDREKGDF YTLTVVADDGGPKVDSTVVSG TRVYITVLDENDNSPRFDFTSDS AVSIPEDCPVGQRVATVKAWD PDAGSNGQVVFSLASGNIAGAF EIVTTNDSIGEVFVARPLDREEL DHYILQVVASDRGTPPRKKDHI LQVTILDINDNPPVIESPFGYNV SVNENVGGGTAVVQVRATDRD IGINSVLSYYITEGNKDMTFRM DRISGEIATRPAPPDRERQSFYH

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3868	34236	A	3908	603	1395	RGRPRGSPIFPTRAPREKKR*EE VGGHKREQTG*GGGERRKPPN PQHEPKERGWCSRVPEEPQ/RK RRSARARPKKL*REKRRRGRPK RCLW*TGRHPSHHPRTHQC*F* WRK/REEGKERKKEQPAHAGQ KRRKAARHRRRRRRRERTDEK NRTWTRRRREKAGQDEKREGE HGQKRSQQGRESRRDGRARTR KERRQKRENDNRARRRQQAER EKTKSVKRRQTTQQAEEVRQA RENEAREPQQRRQHSRRRKEKE EMRAPRSKQ
3869	34237	A	3909	1	548	
3870	34238	A	3910	1	1803	
3871	34239	A	3911	1	279	
3872	34240	A	3912	1	506	MCYSRQSNLGTFGEGKIKGSEV IDECPRSSRYQDLQELQNKTKL TVLEGDILDESCLKRACQDMSV IIHTTSIIDIIGVTHRESIMNINVK RTQLLLEACVQATVPVFIYTSTP EVAGPNSYKEIIQNSHEEEPLEN T\WCSPS/PYKKA/LARSGI*ATL QLGGSQEECT
3873	34241	A	3913	3	621	AGQQTVEIDLRHRIQLP\DLENQ RNFNELSRIVLEVRERVRQEQQ EGGHEAGEGRGRQGPRESQPSP AQPRAEAPSKGPDGTPGEDGGE PGDAVAAAEQPAQCGQGQPFV LPVGVSSRNEDYPRTCRMWNS TFQTYKKEVCLPRHSMHPGPW AICCECQTRFGGRLPVSRVEAA LPYWVPLSLRPRKQHPCWMHA AGTTAGGSAVMS
3874	34242	A	3914	1	430	RHRIQLPDLENQRNFNELSRIVL EVRERVRQEQQEGGHEAGEGR GRQGPRESQPSPAQPRAEAPSK GPDGTPGEDGGEPGN\AVAAAE QPAQCGQGQPFVLPVGVSSRNE DYPRTCRMW*GCGGYWGLKV GQHGLQRGPQPHT
3875	34243	A	3915	2	1175	
3876	34244	A	3916	1	256	HLRIHTQESSYVCDECGKALTS KRNLHQHQRIHTGEKPYECSKY \G*PFGLLPQLGHLEHVYSGEKP VLDICRFGLPEFFTPFYW

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3877	34245	A	3917	1	1396	MRPQLAGRDHHRGAATLLLER PGRLVTHFRQRRGAVRYGGGK STTQHLSQRRLSGPNDHTKGLV WLLEHILQRLVSFVKLQATRTF TRTYITYAWFLPWGFSGVLCGT PVDTCWALKHQRIHTGEKPFEC SECGKAFNGNSSLIRHQRIHTGE RPYQCEECGRAFNDNANLIRHQ RIHSGDRPYYCTECGNSFTSSSE FVIHQRIHTGEKPYECNECGKA FVGNSPLLRHQKIHTGEKPYEC NECGKSFGRTSHLSQHQRIHTG EKPYSCKVCGQAFNFHTKLTR HQRIHSEEKPF*L/CVDCGKAFS AQEQLKRHLRIHTQESSYVCDE CGKALTSKRNLHQHQRIHTGE KPYECSKYEKAFGTSSQLGHLE HVYSGEKPVLDICRFGLPEFFTP FYWKEEKKCGRKMRNEVVHK VSFFLVVPIALSSLLKKKWKML KKEKAQDPTEYGNLEDDNSQQ
3878	34246	A	3918	1	547	MDSQRPRER/QRERERQSERQR HTQRMHREAETEDERDWKGH DTKTRRQRQRKRAEEGQCREH DRERRRD\RTGERREKQRKSTQ QSRKPSEEPHREKTQIKRERGPE QGELERGQCTERNRKA/GTPEC *TDPHIWTPHPARSAPAHPPDH TAAKYRPPYRSHHSGITHQHPR AASTLKLWPKP
3879	34247	A	3919	1	399	
3880	34248	A	3920	3	872	KSKLKSEQDGISKTHKLLRRTC SSTVKTDDVCVTKSHRTFGRSL SSDPRAEQAMTAIKSHKLLNRP CPAAVKSEECLTLKSHRLLTRS WSGDPRCEHNTNLKPHKLLSRS YSSNLRMEELYGLKNHKLLSKS YSSAPKSSKT*/VFSKEP*RRRG RKALSLPQGLFGYP*HHLHPSSS QLAPNGAKCIPVRDRGFLVQTI EFAEQRIPVLNEYCEVCDEPHV FQNGPMLRRGRDVCEWAKKY ANSVVRKKFCRLSIARRSRYRA DMDLLRMSNFILTIIYKQKLNL
3881	34249	A	3921	3	218	CCRSHQGAGEGGHLSVQLLWQ YRWMWCSWGPV\FQFHTDLEL VAWRCVGLDPGCQQLDIGMQT LIGDHICVF
3882	34250	A	3922	1	1055	

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3883	34251	A	3923	3	962	RSMRQKVNKDIQDLISALPQAD LIDIYRTLHPKSTEYTFFSAPHR TYFKIDHIVGSKALLSKCKRTEI TTNCLSDHSAIKLELRIKKLTQN RTTTWKLNNLLLNDYWVHNE MKAEIKMLFETNENK/DETYQN LWDTFKA/PSIILNGQKLEAFPL KTGTREGYLLLPLLFNIVLEVL AMAIRQEKE/IKGFQLGKEEVK LSLFADDMIVYLEDPIISAANLL RLISNFSKVSGYKINVQKSQTFL YTNNRQTESQIMSELPFTIATKR IKYLGIQLTRDVKDLLKENYKP LFNEIKEDTNKWKNIPCSWIGRI KIVKMAILPK
3884	34252	A	3924	1	1452	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSKEYTFFSALHHTYSKIDRT VGSKALLSKCKRTEIITNSLSDH RAIKLELRIKKLTQNRSTTWKL NNLLLNDYWVHNEMKAEIKM FFETNENKDTTYQNLWDTFKA VCRGKFIALNAHNRKQERSKID TLTSQLKELEKQEQTQSKASRR QEITKIRAELMEIETQKTLQKSN ESRSWFFERINKIDRPLARLIKK KREKNQIDVIKNDKGDITTDPT EIQTTIREYYKHLYANKLENLE EMDKFLDTYTLPRLNQEEVESL NRPITGSEIVAIINSLPTKKSPGP DGFTVEFY/QEGN*AGEGNKGY SIRKRRSQIVPVWR*HDCISRKP HRLRPKSP*AGKQLQQSLRIQN QCTKITSIFIHQ*QANRKSNHE* TPIHNCFKENKIPRNPPYKGCEG PLQGELQTTAQ*NKRGYKQME EHSMLMGRKNQYRENGHTAQ

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3885	34253	A	3925	1	1251	MKAEINMFFETNENKYTVYQN LWDTFKAVCRGKFIALNAHKR KQERSAMNTLTSQLKELEKQE KTNSKANRKQETTKIRAELKEI ETQKTHQKINESRSLFFEKTNKI DRPLARLVKKKREKNQIDAIKN DTGDITTDPTEIQTTIREYYKCL YANKLEYLEEMDKFLDTYTLQ RLNQEKVESLHRPITGSEIEAIIN SLPT/KKSPGPDRFTAQFYQRY\ DGMYLKIIRAIYDKPTANIMLN GQKLEAFPLKTGTRQGCPLSRL LFNIVLEVLARAVRQEKEINGIH LGKQEVKLSLFADGMIVYLENP IVSAQNLLKLISKFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTITTKRIKYLGIQLARDVKD LFKENYKPLLNKIKEDPNKWK NIPCSWIGRINIMKMAILPK
3886	34254	A	3926	1	1203	
3887	34255	A	3927	1	1233	
3888	34256	A	3928	1	951	MKREKNQIDAIKNDKGDITTDP TEIQTTIREYYKPLYTNKLENLE EMDKFPDTYTLPRLNQEEVESL NRPITGFEIEA/INSLPTK*SPGAE GFTAEFYQSVGSSGQGNQARE RNKGYSTRKRGTQIVPVCRWH DCIFRKLHGLSPKSP*ADKQLQ QSLRIQNQCAKITSIPIHQ*QTYR EPNHE*TPIHNCYKENKIPRNTT YKGCERPFQGELQTTAQ*NKRR HKQMEEHSMLMDRKNQYREN GHTAQGHL*IQCHPHQATNYFL HRIGKNYFKLHMEPNKSLHSQ DNPKQKEQSWRHHAT*LQTILQ GYSHQNSI
3889	34257	A	3929	1	814	

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3890	34258	A	3930	1	1545	HQLKVQFRIIISIRSSCDGSAWG VAPTFKTRGARSRSRAAIRLGA ADLDEVKSSLVNESENQSSSSD SEAERRPQPVRDTFQKPRDYFA EVRRPQDSAFFKGPPYPGYPFL MIPDLSSPYLSNGPLSPGGARTN SSPAPKETWICARFGGVSLSFLE IGSRVLLLGRDVNRSSSLLPAQI PIACHFAVDGGNFIRGKGAYLL TFDLFGNWGLFFLIEIAVWELS AHSSGQSEDALELSRGTCSSSL QLCWTAKALVGKGLDGGPVC KNSGICSTRTKTQEQMSFMEAL YQEGFLRETVVQAVRKVPQTP RKAVLEVLARAISQEKEIKGIQL GKEEVKLSLFADDMTVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQAFPYTNNRQTESQIMSE LPFTITTKRIKYLGIQFTKDVKG LFKENYKPLLNEIKEDTNKWK NIPCSWIGRINIVKMAILPKVIY RFNAIPIKLPLTFFTELEKTTLNF IWNQKSR\IGKKILSKKNKAGGI
3891	34259	A	3931	693	1464	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFFIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATK/DQKS FCTAKETTIRVNRQPTEWEKIF AIYPSDKGLIS

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3892	34260	A	3932	211	2519	ENRKSNCLCLQMA*LYI*KIPSS QPKISLS**ANLAKSQDTKSMC KNHKHSYTLITDKQRAKS*VNS HSQLLQRE*NT*ESNLQGM*RT SSRRTTNHCSTK*KRTQTNGRT FHAHG*EESIS*KWPYCPSKC/K RTEIITNSPSDHSTNKLELRIKKL TQNHTITWKLNNLLLNDSWVN NEIKAEIKKFFETNENKKTTYQ NLWDTAKAVLRGKFIALNAHI GNLERSKIYTLISQLKEPERQEQ TNPKASRRQEITKIRAELKEIET QKTLQKINESRSWFFENIKIDRQ LARLIKKKREKNQIDTITNNKG DITTDPIEIQTTIREYYKYLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNTPITGSEIKAIINSLPT KRSPGPDRSTAE/FYHRYKEEL VLFLLKLFQSTEKEG\GRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIYHDQVGFIPGMQ GWFNICKSINVIFQYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPVLNEIRGHK QMEEHSMLMDRKNQYCENGH TAQGNL*IQCHPHQATNDFLHR IGKEEVKLSLFADDMIVYLENPI ISAQNLLKLISNFSKVSAYKINV QKSQAFRYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYRPLLNEIKEDTNKWKNI PCSWVGRINIVIMAILSKVIYRF
3893	34261	A	3933	2	1304	
3894	34262	B	3934	141	2008	

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3895	34263	A	3935	1	1845	MVISVDAEKTFNKIQQPFTLKT LNKLGIDGSYLKIIRAIYDQPTA NIILNGQKLEAFPLKTGRRQGC PLSPLLFNIVLEVLARAIRQEEEI KGIQLGKEEVKLSLFADEMIVY LENPIVSVQNLLKPIRNFSKVLG YKINVQKSQAFLYTINRHTESQI MSELPFTIATKRMKYLGIQVTR YVKDLFKENYKPLLNEVKEDT NKWKNIPCPWIGRIN\ILKMAIL P/KELEKTTLKFIWNQKRACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSDIIPHIYNHLIFDKPDKNK KWGMGSLFNKWCWENWLAIC RKLKLDPFLTPYTKINSRWIKD LNVRPKTIKTLEENLGNTIQDID MGKDFMSKTPKAMATKAKIDK WDLTKLRSFCTAKETTIRVNRQ PKEWEKIFAIYSSDKGLISRIYK ELNFTRK\NNPIKKWAKDMNR YF*KEDIYAANRHMKKCSSSLA IREMQIKTTMR/YHLTPVRMAII KKSGNNRTRENYFKIHMESKKS QNSQGNRKEKEQSWRHHATRL QTIVQGYTVAKTACYWYKNRP TDQSNRTENQEIRLHTYNHLIF DKPDKSNGETTPYSINGARITG
3896	34264	A	3936	1	700	
3897	34265	A	3937	1	3489	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAYLGV LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRS

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3898	34266	A	3938	120	1331	TSLGPIYCAVRHTSSCRKVGSSR CQHGCQLSVRLQLDQAHHKQL PWLAPKNAVVPKSLEDPQGRK EGVTALTPEAPRSGPPKRLQLFP PSLCPNCSKQGAYFSPFGVTAT LLATPFSRSRVLVLQPGRMRYA DKWRVSKMKRCCIEQWNSSEK THSARASHSLQRQRGGPRVGGS SLQAGCHVISAALSKEEALEWV ASFCRQIVQSYLRPLLCSGADP GAFMDLRGEELRSLELSLSYTP PSNEFKISMKLEAQDPRNTTST CIATVVGLTGARLRLRLDGSDN KNDFWRLVDSAEIQPIGNCEKN GGMLQPPLGDSFHCDVRVSILD LFCFLLSELPFTIDTKRIKYLGIQ LTKDVKDLFKENYKPLLNE/IK/ EDTNKWKNIPRSRIG*INIVKMA ILPKDFG
3899	34267	A	3939	1	1421	MDSMSGGGQYRKINGNPTSVK CPLLLLPAILTPEPVNRWRQSC KAFARHSPLAFRVTISTSTFFDG LLVTGLYTSTSVQASQSIGGSSA FGFVLEVLARAIRQEKEIKGIQL GKEEIKLSLFAGDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FK\ENYKPLLKEIKEDTNKWKN IPCSWVGRINIVKMAILPKNWK KLKFIWNQKRAHIAKSILSQKN KAGGITLPDFKLYYEATVTKTA WYWYRNRDIDQWNTTEPSEIM PHIYNYLIFDKPEKNKKWGKDS LFNKWCWESWLAICRKLKLDP FLTPYTKINSRWIKDLNVRPKTI KTLEENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQTTKWEKI FATYSSDKGLISRICNELKQIYK KKTNNPIKK

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3900	34268	A	3940	3	1566	IQTTIGEYYKHLYTNKLENLEE MDKFLDTYTLPRLNQEEGESLK RPMAGSEIEAIINSLPTKNSPGP DRFTAEFYQRYKEELLISNFSK VS/VIQNQWEKITSIPIHQ*QTNR EPNHE*TPIHNCFKENKI\LGIQL TRDVKDLFKENYKPLLSEIKED TNKWKNIPCSWIGRTNIVKMAI LPKDKTSKYIDVDENEGSHCGK RKYKYGMEKALEILARAIRQEK EIKGIQLGKEEVKLSLFADDMI VHLENPIISAQNLLKLISNFSKV SGHKINVQKSQTFLYTNNRQTE SQIMSGLPFKIATKRIKYLGIQL TRDVRDLFKENYKPLLNETKED TNKWKKNILSSWIGRINIVKMA ILPKVIYRFNAILINLPMTFFTEL EKTTLKFIWNQKRACIAKTILSQ RNKAGGITLRDFKPYYKATETK TASEMKYYLENKIPFKVLHMV YNVPTHPPFIGDLHPNTKVVSL PPNITSLIEPMNQGVISAFKDCY LRKTFVQAVATPEGETEMTVM QFWKDYNT

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3901	34269	A	3941	1	2580	MVKGSIQQEELTILNRYAPNTG APRSIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVSKDI QELNSVLHQADLIDIYRTLHPK STECTFFSAPHRTYSKIDHIVGS KALLSKYKRTEIITNCCSDHSAT KLELRINKLTQNRSTTWKLNNL LLNDYWVHNEMKAQIKMFFET NENKDTAYQNLWDTFKAMCR GKFIALNAHKRKQERSKIDTLT SRLKELEKQEQTLHSKDSRRQE INAEKAFDKIQQPFMLKTLNTL DIDETYLKIIRAIYDKPTVNIILN GQKLEVFPLKTGTRQGCRLSPL LFNIMLEVLARAIRQEKEIKGIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQESQAFLYTNNRQTESQIMSE LP\FTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIP\CSWVGRINIVKMAILPKVI YRFNAISNKLPMTFFTELEKTTL K\FI*KQKRACIAKSILSQKNKA GGITLPDFKLY\YYKAIVTKTA WYWYQNRDIDQWNRTEPSEIIP HIYNHLIFDKPDKNKKWGNDS LFNKRCWENWLAICRKLKLDP FLTPYTKINS\RWIKDLHVRPKT IKTLEENLGNTIQDIGMGKDFM TKTPKAMATKS\KIDKWDLIKL KSFCTAKETT\IRVNRQPTEWK KIFTIYPSDKGLISRIYKEPKQIY

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3902	34270	A	3943	5	2130	QRLRRQHRLEQKTRSTTCHMR QSTTRSAERADTRIESMPT*TTP *HTDDVP/SHCTNSTHTATTSPS THNHQQTLTRVANVAQIRRTDI SSIAATEWISTINTHNYACRTRA VSQRRYVSDFEKRERPTSNTPE PRFRLVVSTPTLVGTTQGTYQP PPARSRISIASHLLPPLSLLPSSL DLDGRSTLACSSSVSQFSGSRGS PSSYIVATTRVISDVDYDMTTY YNSTITPIS/PSARS*CQRSVHLL LSSHRTYRHPLVSRHTSQEHSL GGPLHRH*YNPVGSRAAAWAS KSALV/SVSLEALVVSALI*LVA TRQRLVGICRTTPIRARSSVVR* VTRYQPNQRAPLIHATYHLLDR GQHPQSMQTISHWTTPPCWCL VCGKKSSLPCCSTSSMSTRRNQ YDTLSLTTSWVL*SSIFWLAFIL LPRTSLPWPTVS*LAANA\SSGS TPVNSSFRT\SVRRSKLVVPANE IETPSFVVVTKFSRSASSYDCSIE YASTYAINITIVNSYVFA/PTHTT REHTISYALTSPGQPQNKTRIPE LQWAF*AVRPSTQ/PSTVIYHAP TSQAIASCALHSLLGCLLGSAT APLPPTWTTPPPPPQLRTT*STG SLPHPPSC*TRP*PLAPRN*PFTG MSSQHCIPT*PQLASHSIALRG/S RARPTTSQTSIAS/SHSHS*LSHV Q*RPLSDQRSPLDHHAHSSILYA RASRISCLRVCAV
3903	34271	A	3944	254	884	MTPNYTSRLFLHMGVLFYPFYR RLT*HIRTHINLKGWK/NRHFM QMDTKNAEKALDKIQHRFMIK TLSKISIQGTHF\KIIKAIYGKSTT NTILNGEKLKAFPLRTGIKQGCP LLPLPFNIVLELLARAIRQEKEIK GIQIGKEEVKLTLFADDMIIYLE NSKDSSRKLPELIKEFSKVSRYK VNLHKSIALLYTNSDQAENQIK NSTSFTI
3904	34272	B	3945	52	843	

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3905	34273	A	3946	1	831	MEMLYCLIAEAGHISSRMATNT ANSAGLKPTCVCVALPLPPGRS APHRSCSQAGRELPGQGPRYYR HLPQLSILHSIGEGQGCGFWSER SFKGYPERPAGAAGVCRLQGC GRRGRGAPFRTTDFSSRPRGAA ERADQGPRAGSPWPRTTSGAQ RGRAQGQGHTARRRGNSNPGP SRARQASRRRRPATSGPPRGSP RPDRPRRRSPFYRSSSRETSRPP EGPRRPRAPALSAPAPGQPARP RPREPVPCGAVFTARDRLRPPA ATSHAPFSAANPRR*HRPGGPG ARRLGDAQLSRRST/SGAPRCS QTRSR*PTCVCVALPLPPGRSAP HRSCSQAGRELPGQGPRYYRHL PQLSILHSIGEGQGCGFWSERSF KGYPERPAGAAGVCRLQGCGR RGRGAPFRTTDFSSRPRGAAER ADQGPRAGSPWPRTTSGAQRG RAQGQGHTARRRGNSNPGPSR ARQASRRRRPATSGPPRGSPRP DRPRRRSPFYRSSSRETSRPPEG PRRPRAPALSAPAPGQPARPRP REPVPCGAVFTARDRLRPPAAT SHAPFSAANPRR
3906	34274	B	3947	250	281	
3907	34275	A	3948	3	639	DHTCRLRQRLRLRVLVGPVPG AGPAG*KGCYGGRSANHHGAP ASCHLARSSCGPRLPGRYSAQQ PRARCAASGLCGWTAPAADPV PSEVLASQEVQLLCAGE*SGSC GPTHADLQPSPGGTGEDGAAR AKRDLPGSVGERAAAPASGRL RACPGRPAGAPGPRARPPGGTA ALAQPPRPQGAAARPPSGIGWP\ GNNGSAQSKGRALMEQAAG

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3908	34276	A	3949	161	2377	SLFHGKVCHFLHEPLPLVYLSL CTGYQLFKPSLISWLEEEEELST LPRVLQEWKMCLKTKGPALW QDNFCLKTLNGIQLARNQNGEE LYDCKQCEDVFCKHPCLKTNM STQNRGNTSECIQYAKDLLSLY NKTSTIRKVSVFSKHGKSFRL\F *MFRSRESVHKINPLK/CTDYGK AFIYQSYLEAHRKTQSGEKLNE WKQCGEAFTHSTSHAVNVETH IIKNPYECKECGKDFRYPTHLN NHMQTHIGIKPYKCKHCGKTFT VPSGFLEHVRTHTGEKPYGCKE CGKAFGTSAGLIEHIRCHAREK TFKCDHCGKAFISYPSLFGHLR VHNGEKPYEHKEYGKAFGTSS GVIEDRRSNTGQKRFDCDQCG KVFVSFSSLFAHLRTHTGEKPF KCYKCGKPFTSSACLRIHMRTH TEERLYQCKKCGKAFTKCSYLT KHLRTHAGEKPYECMKCGKAF TERSYLTKHLRRHSGEKPYECK KCGKAFTERSDLTKHLRRHTG DKPYEYKDCGKAFVVSSSLVD HLRTHTGYKPYKCNACEKAYS RSCVLTQHLKTHAAEKTSECN ACGNSFRNSMCFHDRLKTLTKI KPYKCKDCGKAFTCHSDLTNH VRIHTGEKPYKCKECGKAFRTS SGRIQHLRTHMGEKPFECDQCG KAFA\FSQLVLHI*KHTREKPCG CEECGKTFAVSSSLTEHVKIHR
3909	34277	A	3950	6	455	GLLHERQAEARCSICLDYLRHP MTTDCRHYI*SARIHQCW*ELQ DISPCPVCLQHCPDKNLKRNFQ LCHMTDIAKQLLTTARRKRKL QGEEPVCRKSDVALFCEKDPEL LCHQYRVSLDH*DH/SPMPIEQ AAAKHRKQFESYIEPLEKQV

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3910	34278	A	3951	2	1009	WNGHRMN*MQSSNGLEWN/QS SNGKEWNHRIESNGIIIAWN\Q WYQHQTEKNGIFEWNRRESSN GPEWNHVMEWNG/DNPWTRM QSSSNGIEWNHRMDSNGIIFQW NGNGNHRIGIEWNYDQ\SNEWI\ QWNQHQTEKNGIIKWNRRESS NGPEWNHLMEWN/ENNPWTR MQSSSNGIEWNRMESSNGLEW NNH*TESNGSVESSSDGNER/QS SSNGIAWNHHKMESNGINIKW NQMESWN/WN*MNRMELSSNG IEWNQHQTEKNGIIEWNRRESS NGPEWNHLMEWN/ENNPWTR MQSSS/NWNRMESSNGLEWNN/ QLNGIEWNHHRMEMNGIIIEW NRIELWN
3911	34279	A	3952	1	1494	MASLLGAPRLAGWASGAGALS RGWAIRPADTGGNLGPVPRVPL PPDPVLTARWAPGVNSGSQFSC HCQAPILEMGHKGSSPGLGDAE VRAITVQCIRPIDGPQQPPGGGS AGRRLTIPASTQEWAQLPVGRV LANVLTEGGDTGNQPIPQRSLC RPQPCSHAETWGEVEAQVPAQ SNREQPAAAPGCGPGRGETGA RPETTFSPRRAPPNPYDEEGVR WSLEFMLCGTDGPVQPVQHQE GPAARLQLIRGGSLILESEGTLR G/SPVLQTDQPASHLLHTQGFW A/AALSAVCL/HQNIIHSGSALL APATRAAWEQIQRSEGGTAQL LRRLEGYFSNVARNVQWTYLQ PFVIVTTNMILAVDIFDKFNFTG ARVPWFDAIHEAFPRELESSISF PANFFKPPEEKEGPLVRPASRK TTPQTTRPGPGTEREAPISR*KR HPDDTG*FTFTLGIVYCTPGQLP PEPYDPNRRSLWLPHWPIINTS MVSALVYSEGAPLPSPL
3912	34280	A	3953	1	681	MGQLLDKNTPSHGARTREECG RERLCVSPSQTGDTPRTSAYLC VGGPAWSPLSESRPAGSSGCPW IKPPDPRYSPIGLCSLLTTEMMS RQPRTDLRGQTNPAA\PSAPVPL SCSQNLPVWPSLMAGTTWHSP L\SPSCFWHSPGHN*H*CCVSKD *KSLFWEPTA/YSPLLPSTSP/SS KSMQPPKPRSNADSSVQASLIP RAMSSPTVSPWIMGNGSQGFD HIAVSMWDD

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3913	34281	A	3954	136	420	RESRNLSRGEESEDPAEPS\RNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPPSPAPPPETHTGSPRPPSGRSR IRAYLH
3914	34282	A	3955	1	1782	
3915	34283	B	3956	1	3070	
3916	34284	A	3957	104	279	STTHPSVHE/QEEEEEEEEEEEE EEEEEEEEEEEEEEEEEERKKEC SKAQCKHFPLSEVL
3917	34285	A	3958	1	252	MTVCIHIASEDLPVGRDVEVED SDIHDRDPGLGDKSETPSE/EKK EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEES NFLQHYLHL
3918	34286	A	3959	2	368	
3919	34287	A	3960	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEKIFLGHRVGI
3920	34288	A	3961	1	577	MQIPSLHKLKKEEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE\EKKKKEEKKKKEE EEEERRRKKKKERKEEEEEE/G KEEEEGEEGEEEEEEEEEERRK EEEEEEEEGEEEEEEEESCLMGP MCVHIHP\DKDLYSLGPPAQRF TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3921	34289	A	3962	327	559	PKGRTPSPSCIHRYPCQTPRPHE P*GCHCPEEK/PRPRVWGPSRC MPLGSVQEKRPCPAPGGVQGSF RVSPLMMLTRL
3922	34290	A	3963	1	577	MQIPSLHKLKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE\EKKKKEEKKKKEE EEEERRRKKKKERKEEEEEE/G KEEEEGEEGEEEEEEEEEERRK EEEEEEEEGEEEEEEEESCLMGP MCVHIHP\DKDLYSLGPPAQRF TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3923	34291	A	3964	157	272	WCNGSPLYSGW*LVGMESLGR MHKDLWTRQPNQDQDLQ
3924	34292	B	3965	1	3723	
3925	34293	B	3966	1	573	

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3926	34294	A	3967	3	424	AGGQALQGPGQGRGSQGVVG/PGTGSSGAQHLGKHYPVLSGGSERSWGRSHTPAGAGC*VRGRRAGGRPGTGHSRPPGGSCLSPAPPNSARWLGLGAPWQAGAGLRDPGDWRRGQGGPGWAWCPGQPPAQPHTCPPNSTARY
3927	34295	A	3968	3	1238	RGAERRAWSRGPACTRRGPADWAAAGAGRPCPQRRGVCCTAAVPGAARLSCPTGPGPGDPGRRSLTGQGS*GLGAAFGGWTGALPSWHS*SQGWQTDPVR*VRGTERDICTGL*QPCPPGGLQTGSGGLEHSLPWPGIGIQAP*GPNHPCRLPRS*ALSAGG\SGGQALQGPGQGRGSQGVVG/PGTGSSGAQHHCCPPYTPPG*HPIPSLLALGPQSLQPEWAHSGTASGEQHSAGEHGMGTTGH*LPGLCSRCVLGKHYPVLSGGSERSWGRSHTPAGAGC*VRGRRAGGRPGTGHSRPPGGSCLSPAPPNSARWLGLGAPWQAGAGLRDPGDWRRGQGGPGWAWCPGQPPAQPHTCPPAGSLPGAAPGVLCAA*GPAAGV*AGPGPGPGSRR*TRGPSPGAPRPA
3928	34296	A	3969	3	415	ETGRHRSQQSVSSPPVQPRGKRAMYHSAAELVSRGFPRPPVQAPAEPAGAAEGVHSQPASRQEA/GS/TEVRGQAHRFVSPPNAAGAGDG/PDPQSLLAPTNRPCPPGGISPARSEPVPPAPGRAAP*CFPDLPGLAPPLC
3929	34297	B	3970	1	657	
3930	34298	A	3971	125	524	EAEALENQSQPCDTG/PQSAFSPPGSTQHPRSQLSQCKQRYQDLQEKLLLSEATVFAQANELEK*RVILS\GEPLLKQDSKQVQVDLQDLGYETCGQSKNEAEQEETTSPEHEEHSSRKEMVLVEGLCSEQG
3931	34299	A	3972	1	648	MGQVWGLVHFTLEVFHTGDEEEQEYSEVTEDVTEHVYLPAKAKVAKEEEAGIQQARQEGDLEAWQFPVRIHPPDQQENITATFEPFPFKLLKELKQAINQYGPGSPFVMGLLKNVTVSSQMIPTDGDPLTRACLTPAQFLQFKTWWADEASIQAARNAWAQPQINITADQLLGVGGWAGLDAQFVMQDDAIEQLRGVCIRAREK\IT*CGEQYPSF

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3932	34300	A	3973	350	1078	GSNRRSNRAEQLRGVCIRAWE K\ITSGEEQYPSFSIVKQGPREPY TDFIAWLQESLKKVIADSAAQD IVLWLLAFDNANPDCQAALRPI RGKAHLVDYIKACDGIRGPAG RLSWLSLQGRPAGAARCTSSSS DWKAQLAPGPHAGPLRCPAFR ARQPRLPAVLSAGAAFRDCPLS CVQALLGGSAGPGDRLPGHYS ALVALSLPFVKEATMNRWSRN HRSAFFLFSANAHGAEGVLSHT VASR
3933	34301	A	3974	2	630	WDNCGLWFIPSWNLFTLMMRR KESLMK*QKK*QSRFVCQLKLK /PAKEGEVYPYPSAPPPYFEEKE WPDPPDLSFLEDAGQKVIAPVT VQAAPQAIALSSIQAGIQQARR EGDLEAWQFPIRIHPPDQQGNII ATFEPFPFKLLKESKQAINQYG QGSPFVMELLKNVAVSSQMIPT DWDALAQACLTLTQFLQFKTL WADEVSIQAACNA
3934	34302	A	3975	264	634	WSSRCQHSSRPQASESWFPG*G PSFWPRIQGDEKTGAGGHP*LG C*PGMTGQGFSTKCQHTCLMW GSHWAQEAPENAPGTSCPGSSG SWVLRSSLQRQKSAWSPG/ASM PAPKMPFLTPSSGFS
3935	34303	A	3976	3	410	KKKVWREEKERLLKMTLEERR KEYLRDYIPLNSILSWKEEMKG QGPK*\EENTQETSQVKKSLTEK VSLYRGDI/L*VDAIVNAANASL LGGGGVDGCIHRAAGPCLLAE CRNLNGCDTGHAKITCGYDLP AKCEYN
3936	34304	A	3977	74	432	MLHNLRPRTLTTRTRCPSTPS*T TT*ATPPTTTHGSAGPRAAHLR RTGTRRWRAPRRARSCTRSSPR RARAASTPPLAPARELRSPASPP SCEQSAAPPSGRNGGNFPESIFV KTINSN

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3937	34305	A	3978	2	894	WGGYGMRTGPRTLTTRTRCPS TPS*TTT*ATPPTTTHGSAGPRA RTCAAQRTSGSHPSQRRTSSAA PGV*RANVFPWAH*MKRV*TT LENLTA/PEMAMPPAPHVIFAT DDWAAMVHPSARVPGLDGTG ALLVPTGVCAPGPCKCPLTSSS VTHTRLKTTLSVPPSARQTGRC RSPSDLRCSYPPDEQPVCVPKC GSPWVSVLVAWIQSESAVLDPR HPQHPYLYPVDMQNLLTNLGE PPQARALAAKLLGRPSSSQSGS RVPAVWAQAGNATYITVHTLC SHNTHMSPVRVKRFTHLG
3938	34306	A	3979	157	570	
3939	34307	A	3980	1	936	
3940	34308	B	3981	257	3934	
3941	34309	A	3982	210	4286	MPLKTRTALSDDPDSSTSTLGN MLELPGTSSSSTSQELPFCQPKK KSTPLKYEVGDLIWAKFKRRP WWPCRICSDPLINTHSKMKVSN RRPYRQYYVEAFGDPSERAWV AGKAIVMFEGRHQFEELPVLRR RGKQKEKGYRHKVPQKILSKW EASVGLAEQYDVPKGSKNRKCI PGSI\KLDSEEDMPFEDCTNDPE SEHDLLLNGCLKSLAFDSEHSA DEKEKPCA\KSRARKSSDNPKR T*L*KRATYNFEAH
3942	34310	C	3983	163	309	
3943	34311	A	3984	72	424	RNCGTARSQHEPLGSWLQDTP QPP*TLELAGNLPGD/F*PGPGK EQGMFVCHPIRQPLPRPLPGSSH QSMPTAQPPLSSSSALLPALPAG FPVTQGQWTKLQVQAPAPFHL PPQVEAV*AFYQKQMLVPCSL* SMPTAQPPLSSSSALLPALPAGF PVTQGQWTKLQVQAPAPFHLP PQVEAV
3944	34312	A	3985	1	347	KWQRFVLTGIDTYSRYEFAYPA CHASTKTTIHGLMEFLIHHHGIP HSIASDQGTHLMAKEVRQWAH AHGIHWSYHVPHHPEVAGLIER WNE\GLLKSQLQHQLVNRLRRE LQCWLG
3945	34313	A	3986	1	1716	

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3946	34314	A	3987	1	737	MSSVLLRLIYQLTQKTASFEGG PEQKALQQIQAAVQAALPLGPY DPANPMVLEVSVADRDTVWSL WQVPIGESQLGFWSKALPSSAD NYSPFERQLLACYWALVETEY LTMGHEVTMLPELPIMTWVLS DPSSYKPAPMASWGVPYGQLT EEEKTRAWFTDGSARYTETTR KWTAVAIQPLSRTSLKDSNEGK SSHQQAKNGITVLAGVIDPDYQ DEISL/LTPQWRCHPGSSVWRAS SLGISHPP
3947	34315	A	3988	2	384	CGRSGYWHSSVATKITRLRML RPREGRKLPPGDIMIPLN*KLRL PPGS/FLLLSHQAKKGVTMLAG VTDPDYQDEISLLLHNGGTGKS PHISDTFYGSKVASCQNTGPEK QDETQAQETAVYKSQIFGS
3948	34316	A	3989	3	1273	
3949	34317	A	3990	3	341	GLGRRQPAGSWPERRPGPSA\R RSTAPRRCGQAES*TERGSQPH QVQGQGRWGVCMKIPSHSGKS PDVSEVSKSRNSIISTAVTHAVV APEGLKRNGGGSHLRSSRGHR AVIF
3950	34318	A	3991	44	243	
3951	34319	A	3992	40	558	LGSIQVMQAVRNAGSRFLRSW TWPQTAG*QMTAPSSPPPPPGL CSYSCPLSHP/SLPVTVRPWPSPS FSSQQGRGQNA/APGPSAQALD SSKTLRPSRKLNRTRLPATPSSG EPHLDQPSGDPQPLTLARHPPES EPVNFQLCHLLSVGPYANKSEP QPSHLKMRIMLREVVRIT
3952	34320	A	3993	335	581	RRHLFLQWGQRAWRLQVAAA GTTRPTSAMGIRCSEGAAARAT AARA*TAGPEPLE/PAANPPPPL TASALRAPPSFVLPQCTR

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3953	34321	A	3994	216	1159	SWHGPPGANTVAAAAGPEE\K AALKLRPTHGWPVRATDVHDV ILKASGESEWRGGSRASHQMSP VAMATALGEGVPVRGPAAGSL RLLPGSSAPLGRDAISSCNGVN GLETTGGRCRHNAPNKRHGDP LLEGAAAR/AQAARA*TAGPEP LE/PAANPPPPLTASALRAPPSF VLPQCTAAPRDPSAAGAAN*G KAQSRNC*NEPFAYGGGTHGT GAGAAVTVAADGN*LGSIQVM QAVRNAGSRFLRSWTWPQTAG PWPSPSF/VFPAGSWPERRPGPS AQALDSSKTLRPSRKLNRTRLP ATPSSAFTLPFQERRAL
3954	34322	A	3995	1	738	MTKRGHGTAWAVASKSASPKP WQLPHSVEPVGTEKSRIEVWEP LPRFQRMYGNTWMSGSSLLQG NQNLHAERYCNSTLERNDTPIE SLKPKRESEDGLGEHNGSTMEE VGAETRVQRHWVRVSMTELAL ASDAHMWGSNPGQRVTGVMV GECGTMLGDTQVLLSNPCGDR ARRAYSTAPDYAVCGNGGKVK LNEQRFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGEDS*AIPVVTE LGERIAQLLIMLYV\KWGKSEIK RT/G/GFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGEDS
3955	34323	C	3996	87	329	
3956	34324	A	3997	3	122	
3957	34325	A	3998	1	156	
3958	34326	A	3999	1	353	
3959	34327	A	4000	1	201	
3960	34328	A	4001	56	207	EEKKEKEKEKEKEK/EEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE
3961	34329	A	4002	1	174	MNRC*RHIYSSNEVH*KEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEIPLSSL
3962	34330	A	4003	1	278	MTSYKFTEPKNGIWQLHEAAQ LDTTYNKLNKKEEEEEE\EEEEE EEEEEE\EEGEGEEEEEEEEEE EEEEEEEEEEEEEEEEEEGVIL
3963	34331	A	4004	144	429	DLPREEYALLPAGPRRRCRHTH RYEPNPEFGAKHSCPAA*HRAA PATSDTQE*HRSNAFGEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEETLFSNM

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3964	34332	A	4005	3	122	TEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEGEEEE\EEEEE
3965	34333	B	4006	1	300	
3966	34334	A	4007	1	1226	MPSSKGVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGIDSNFEPELVFLEFFEALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYTILNQDAQNKSP SAVMSHESDAAHSDSARSSSSK LELSPDVNKIRKSEAMVKEKKK ADKKGEKSARSPSSLSDNLDFS KQDGNTTRQEMSPAGVPLLGM QLNEVKPKKDRQNVQQNEDAT QYEESILTKLIVESYEGEKVRGL YEGEGFAAFQGGCTYRVSCPFE NLQEGEEGRLCEECPDEPRRVH VAGRSMYEGEVVNGMRNGFG MFKCSTQPVSYIGHWCNGKRH GKVGEVATWRAEKKKKEEEEE EEEEEEEE\EEEEEEEEEEEEEE EEEEEEEE\EEEEEEEEEEEEEE EEEEEEEEEEKIRP
3967	34335	A	4008	453	705	LLSIVQAEAVSENSHPILPRVSR SGWGQKEEEEEEE\EEEEEEEEE EEEEEEEEEEEEEE\EEEEEEEEE EEEEEEEEEEEEEEGRRRRRSSP SCYSITPELSCKLGHR
3968	34336	A	4009	93	705	ESSTQTCSGFWTGCTALHRWR GMPERCPPESRDS*TRFPQSSLP GHKT/SEKEEEENRKEEEEEEKE KEK/EEEEEEEEEEEEEEEEEE EEEEKEEEEEEEEEQEEEEDDEE EEEEKSCSVNVSLIELPWDPKA YSRLAPLSSQPGPAVKVPTEHLI AKLEDCVQGFTYLTVEKRWAR AVTGAQELGVDYPRNEKCKPH NNGYDND
3969	34337	A	4010	1	3189	
3970	34338	A	4011	1	5127	
3971	34339	A	4012	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL

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3972	34340	B	4013	1	3570	
3973	34341	A	4014	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQHFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSL*RRI/W KRLQRTLSIPVLDAV*PPMF*AS
3974	34342	A	4015	1	5073	
3975	34343	A	4016	1	3297	
3976	34344	A	4017	1	3514	MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFFSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRIKNLTKSRSTTW KLNNLLLNDYW

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3977	34345	A	4018	1	2666	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITTDPTEIQT TIRESYKHLYANKLENLEEMDT FLDTYTLPRLNQEEVESLNRPIT GSEIVAIINSLPTKKSPGPDGFTA EFY/PESYL*QTHRQYHTEWAK TASIPFENWHKTGMPSLTTPIQH SVGSSGQGNQPGEGNKGYSIRK RGSQIVPVCRRHDCLSRKPHRL SPKSP*ADKQLQQSLRIQNQCT KITSILIHQQQTNREPNHE*TPIH NCFKENKIPRNPTYKGCEGPLQ GELQTTAQGNKRGHKQMEEHS MLMGRKNQYRENGHTAQGNL QIQCHPHQATNDFLHRIGKNYF KVHMEPKKSPHRQVNPKPKEQ SWRHHTT*LQTILQGYSNQNSM VLVPKQRYRSMEQNRALRNNA AYLQLSDL*QT*EKQAMGKGFP I**MVLGKLASHM*KAETGSLP
3978	34346	A	4019	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YTFF/LAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
3979	34347	B	4020	1	3765	
3980	34348	A	4021	1	4791	
3981	34349	A	4022	1	3297	

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3982	34350	A	4023	1	3170	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLKELEKQEQRHSKPSRRQE ITKMRAELKEIETQ
3983	34351	A	4024	281	3030	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPQRYSSRRATPRHIIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASII
3984	34352	A	4025	1	3290	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
3985	34353	A	4026	1	3573	
3986	34354	B	4027	1	4251	
3987	34355	B	4028	1	3065	
3988	34356	A	4029	965	4089	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFF/LAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID

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3989	34357	A	4030	523	3981	
3990	34358	A	4031	1	3429	
3991	34359	A	4032	1	3156	
3992	34360	A	4033	2	4943	
3993	34361	A	4034	1	6747	
3994	34362	A	4035	1	3928	MAAWNLLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKLTTRKDIYTENPSV HHHHQRPKVDKTTKMGKKQN RKTGNSKMQSASPPPKERSSSP ATEQSWMENDFEELREEGFRRS NYSELREDIQTKGKEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRSLRSRCDQLEER VSAMEDEMNEMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
3995	34363	A	4036	1	3638	
3996	34364	A	4037	3	3585	SNSHITILTLNVNGLNAPIKRHR LANWIKSQDPSVCCIQETHLTC RDTHRIKIKGWREIYQANGKQK KAGVAILVSDKTDFKPTKIKRD KEGHYMMVKGSIQQEELTTLNI YAPNTGAPRFIKQVLRDLQRDL DSHTLIMGDFNTPLSTLDRSTR QKVNKDIQDLNSALHQVDLIDI YRTLHPKSTEYTFFSALHHIYSK IDHIVGSKALLSKYKTTEIITNC LSDHSAIKLELRIKKLTQNRSTT WKLNNLLLN
3997	34365	B	4038	877	8907	
3998	34366	A	4039	1	450	QGSPSGSRE*NSQSSAGPQCALP PAMA*VPLSWRSMGKWWKRT SCTSDST*PPSERRHWRSRKSPS AMPASFRCSSASAREMLP*KKG RCAAGSGIAPGPPETWGRTGGC PGKQATCGVSGPNANGEPVL/K YPSSSSEAHGGPGRNGRSD
3999	34367	A	4040	2	522	
4000	34368	B	4041	102	186	
4001	34369	A	4042	2	5417	

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4002	34370	A	4043	45	1585	KQPSGLLKFGNLILKCHPPSLTH MLSQPCA\EAPTPDPNWELA\LY IHPSSGIMSATVSFWSIGTA\YLE AQGIWEP\FRRRLS\FEASNPPFD VGRPFDLRRIVGISSEGNLNTLS CDPGHSRGFCGAGGSSSRPSAG SHKQ*GPSGHPHSSHSNRNSAD VDDVRAYNSGRTSSMTSAQAA SSQPANKTRPLVLDSNTGAQGH SAGRKSKGAKQSQHGSQHHAH SPLEQHPQPPLPPPVPQPQEPQP ERLSPAPLAHPSHPERASSARHS SEDSDITSLIEAMDKDFDHHDSP ALEVFTEQPPSPLPKSKGSTEGG PASTFTQAVDGGIQFFTDCWTE GPSSSLLAVAREVQLALCIHELL IHGFSQLQVSGGPGAMPDPAAH LPFFYGSISRAEAEEHLKLAGM ADGLFLVRQCLRSLGGYRQLN GTYAIAGGKAHCGPAELCEFYS RDPDGLPCNLRKPCIPPSGLEPQ PGSSTACETPWARPRSRPSSARP RRWRSSLLRRTTSGCPGTTAA
4003	34371	A	4044	1	1773	
4004	34372	A	4045	1	663	MALWTLRPTPLLVTCMLICAPG VMGAVVAPLTILGGPLLIRAAW YTAGIVGGLSTVAMCAPSEKFL NMGAPLGVGLGLVFVSSLVDQ MGRWFVAGGAAVGLGALCYY GLGLSNEIGAIEKAVEYWFNSF VCHSNQQNACSHELHDERLLG DMGLPILHAMLLRRLPSVDSQN ALSSIMLLHTALP*QSAERLFS* TS**EALG*YGFAYPACNASAK TTIRGLTECLIQHHVTPHSIASD QGTHFTAKEVQQWAHAHGIH WPYHVPHHPEAAGL
4005	34373	B	4046	147	330	

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4006	34374	A	4047	485	1568	GEGYKADLAAATVECPICQQQ RLTLSPQYSHIPQGDQPTTW*Q VDCIGPLPSWEGQRFVLTGIDT YFRYGFAYPACNASVKTTIHGL TECLVHHHGVPHGI\ASVQGTH FMA*EVQQWAHAHGIHWSYH VPHHLEAAGLIEQWNGLLMSQ LQHQLGDNTLQGWGKVLQKG VYALNQCSIYGTVSPIARIHGSR NQGVEVAPLKITPSDPLAKCLL PFPKALHSACLEVLVPEGGTLP PGDTTTIPLNWKLRLPPRHFGL LLPLSQKAKKGATVLAGVIDPD YQDEISLLLHIGGKEEYAWNTG DPLGRLLVFPCHVIKVNGKLQQ PNPGKTANDPDPSGMKV*VTPP GKKNPRPAEVLAEGK
4007	34375	B	4048	182	662	
4008	34376	A	4049	1	2250	
4009	34377	A	4050	1	1326	
4010	34378	A	4051	1	1614	
4011	34379	A	4052	1	2586	
4012	34380	B	4053	1	1954	
4013	34381	A	4054	1	705	
4014	34382	A	4055	1	1833	
4015	34383	A	4056	1585	4128	
4016	34384	A	4057	1	1425	MARG/NAITLPV/CGRAVKFT/L EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLLTGQQT PAFGRRVSGVIEIADGSRRRKA AALTESDYRVLVGELDDEQMA ALSRLGNDYRPTSAYERGQRY ASRLQNEFAGNISALADAENIS HKAHKYFVFEANTGTETGYQG EESLFNKAYYGGGTNFFRKESQ KLQQSAKKRDAELANGALGIIE LNNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQQSSKQKKAIQTAI RKNKEANAVLARLNSELQQQL KGFADFREPPIKQDFRLLGQTS VDRLLQLSQGQAITELCGAKRV GYFGPTQFYIALKLIAAAQSGLP VRIESIKCGNSYDHDYEFELGTL VLPRSLEGFALSLNCGEHYWL

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4017	34385	A	4058	1461	2496	NKRNHQSVCHAFIRIP\AAPMV DSLIARVGVMARGNAITLPVCG RDVKFTLEVLRGDSVEKTSRV WSGNERDQELLTEDALDDLIPS FLLTGQQTPAFGRRVSGVIEIAD GSRRRKAAALTESEGTPAFGRR VSGVIEFADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAENISRKIITRCI NTAKLPKSVVALFSHPGELSAR SGDALQKAFTDKEELLKQQAS NLHEQKKAGVIFEAEEVITLLTS VLKTSSASRTSLSSRHQFAPGA TVLYKGDKMVLNLDRSRVPTE CIEKIEAILKELEKPAP
4018	34386	A	4059	340	2067	
4019	34387	A	4060	1	1959	
4020	34388	A	4061	1	2319	
4021	34389	A	4062	1	1587	
4022	34390	A	4063	964	1757	GYSGSKPDVITLLEQGKEPCVV ARDVTRRQCPAAPMVDSLIAR VGVMARGNAITLPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADANN ISRKNITRCINTAKLPKSVVALF SHPG/ELSARAASQRQQCGYHK LHDKQRLLRG*KGNICAKLLNE
4023	34391	A	4064	1	1554	
4024	34392	B	4065	1	1599	
4025	34393	A	4066	1	682	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGRDVKFTLEVLRGD SVEKTSRVWSGNERDQELLTE DALDDLIPSFLLTGQQTPAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQK\HTKKRT ASLILHAMICCRSLNSSKTKNT KCLNSINQRLKILSLQKDLMCG TAGRCKTLTEQ
4026	34394	A	4067	1	2448	
4027	34395	A	4068	1	2541	
4028	34396	A	4069	1	828	
4029	34397	A	4070	1	1899	
4030	34398	B	4071	1	1686	
4031	34399	A	4072	1	1437	

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4032	34400	A	4073	1	3417	
4033	34401	A	4074	1	3826	
4034	34402	A	4075	812	2578	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGHSNGN GQVSPIFHQTSSSTIRSCSCHLLT LNFLTLQLNTSDIAVFHSTPKLL LVTSTITHMGLNTSQAQSVPVI NSVAGSLAALQPVQFSQQLHSP HQQPLMQQSPGSHMAQQPFMA AVTQLQNSHKFSHRSHGPGQS NDACSEPTNKKMRRNRFKWGP ASQQILYQAYDRQKNPSKEERE ALVEECNRVWQARRLGAFGKE DVHVSFAARRGAKFRHQTLLG RRSSIPAAPMVDSLIARVGVMA RGNAITLPVCGRDVKFTLEVLR GDSVEKTSRVWSGNERDQELL TEDALDDLIPSFLLTGQQTPAFG RRVSGVIEIADGSRRRKAAALT ESDYRVLVGELDDEQMAALSR LGNDYRPTSAYERGQRYASRL QNEFAGNISALADAENISRKIIT RCINTAKLPKSVVALFSHPGELS ARSGDALQKAFTDKEELLKQQ ACKL\HEQKKAGVGDNSIDSW KNAGRVFKDSDKFDANDPILK DQTQEWSGSATFTSDGKIRFIL

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4035	34403	A	4076	1474	3367	REEGANSECLGRHGFKKMLYV KRDEVGKGQIRLETVFEQAIDQ RFSTDTSLSTPAAPMVDSLIARV GVMARGNAITLPVCGRDVKFT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDDLIPSF\LLTGH KTPAFGQRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGE\LSARSGKCMVPTESAPH VTVLGCQCGPLGLENGLKEGY LGRSTLDMEAWQPLQEFYLHN LITGQMFEIAVTQNNSKINSSSP TTEQSWMENDFDELTEVGFRR SVITNFSELKEHVLTHRKEAKN LEKSDGENGTKLENTFQDIIQE NFPNLARQVNIQIQEIQKTPQRY SSRRATPGHIIVRFTKVEMKEK VLRAAREKASLAPENLDNSKIR PVVILFHYGESWNLLRADQRLI FAKSWPRASRYQQGHQDLFILR SDLPSQVFIRDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSVPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
4036	34404	A	4077	794	4235	RVSRGRKWFFIALKRMPAMKK AMNLFLGLSNVRTVHPEGFTV YISTHISFPSLSGYRTGLRSFGLV KQKKSPIRMPCVYTNTLCQYR KPDGSGIVSLKIDWIIERYQLPQ SYQRMPDFRRRFLQVCVNEINS RTPMRLSYIEKKKGRQTTHIDL ALKGLRVLLVEGNDPQGTASM YHGWVPDLHIHAEDTLLPFYLG EKDDVTYAIKPTCWPGLDIIPSC LALHRIETELMGKFDEGKLPTD PHLMLRLAIETVA
4037	34405	A	4078	1	2574	
4038	34406	A	4079	1	536	

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4039	34407	A	4080	368	1449	LKSTNLITFLRLFVPQMPLAYM KFTPSGLVAACAPWLRQRRVV QLGQIAFSAP/YLSQMVRQEMY NRYGESAYEDGYRIYTTITRKV QQAAQQAVRNNVLDYDMRHG YRGPANVLWKVGESAWDNNK ITDTLKALPTYGPLLPAAVTSA NPQQATAMLADGSTVALSMEG VRWARPYRSDTQQGPTPRKVT DVLQTGQQIWVRQVGDAWWL AQVPEVNSALVSINPQNGAVM ALALLNNARPWYLGAQPRDSTI IFCQFGAHPLLDPKTQPVGCRN AARKSCAEIRLVPDARANSGKL VRRYRKYRRQYHKSKSRHQPL RQQQPVRLDWRNVDNQYALT TRFLYQSLQRHAQLNVPLFHVL
4040	34408	A	4081	1420	1842	
4041	34409	A	4082	407	1347	GRIRVHIHKDGRADGGSQPGVT AIQQQLPFAFAFPN*SY*TESAW AQSIK\GPWWLRDQVDGPAGR LAALPQR/SLINAVSTRMEGISG AFNTANPACST*FLCSLLILPSLF STALPNFRLSAMVSDCTISNMV WST/SAVTDWSCTPLD*ERKHR GTARLTTGKGVGMDRDKQVST LFLGFCYAHLQWNEDVFIARH VHLHIALFLDQRAQTASYLQYH IFFARFVFPHRTGVFATVARLK HNDNRTIAPCFTRLWTTLRWR HLLFEVAFVVILQQRQQRVLHI LCIGRIEVHHQTLFKPGDRRKG KQLRFYVLL
4042	34410	A	4083	1	649	MRHGYPARANVLVKVGESAW DNNKDYRYAKALPTYGPLLPA AVTS/ANPQQATAMLADGSTV A/LSMEGVRWARPYRSDT/QQG PTPRKVTDVLQTGQ/QIWVRQV GDAWWLAQV/PEVNSALVSINP QNGAV/MALVGGFDFNQSKFN RATQALRQAGAHLPAHSQSGH HQQTAR*KSNFCARM*TPDQLS W**KNCPFRLSPT*QRQWSLRR YRPVSQRTSF

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4043	34411	A	4084	2	551	WRAAGPEPCPTGRQLRP/AGDL ACSAAAGPGAEPFTAPLALAGR SKCGAAEPAPTQNSRWPMSPH LSLHASPQAEGAGSGL/VPAPR AAAG*RAPQMRP/VVGAEAEE APGP*EPCRHPAPHASQHRYGC HPS/AAEPCRHPAPHASQHRYG CHPSGLNPAGTQHPMPASTGTA AIHRG*TLPAPSSP
4044	34412	B	4085	1	1029	
4045	34413	A	4086	1	2157	
4046	34414	A	4087	1258	1838	TQVVFITSAWGLGEMVVQGAV NPDEFYVHKPTLAANRPAIVRR TMGSKKIRMVYAPTQEHGKQV KIEDVPQEQRDIFSLTNE\EVQE LAQQAVQIEKH\YGSPMD/IEW/ AKDG/HTGNGHVQALRNRCPE ARQHRMRIPGRILPRPIGRMAG PKTRIEHTSVTVISNRRKIKTEN RGHKGYEDRKLHEDLQLRHQS
4047	34415	A	4088	2806	3540	
4048	34416	B	4089	1	1251	
4049	34417	A	4090	341	946	GLSSVGQSVNDHLPWT*GLSSV GQSVNDHLPWT*GLSSVGQSV NDHLPWT*GLSSVGQSINDHLP WA*VLSSVRQSIDDHLPWT*VL SSVRQSIDDHLPWT*GLSSVGQ SVDDHLPWT*GLSSVGQSIDDH LPWT*VLSSVRQSIDDHLPWT* GLSSVGQSVDDHLP*M*GLSSV RQ*VT*AKVNPKISAVTRNRGS VESPHLEGRSLKVQVFIPQVED MSWGPPWLWVEGESWT
4050	34418	A	4091	426	706	VLGGGSEEKAPLWWSGPMVLP GAHSMKT*LPHTHVEFGFACLA SAGAQDVGMEGPRHTTENSVT GSPSHFPPRASQHRRGICRPHAG RATADF
4051	34419	A	4092	596	905	GLSSVGQSIDDHLPWT*VLSSV RQSIDDHLPWT*GLSSVGQSVD DHLPWT*GLSSVGQSVDDHLP WT*GLSSVGQSVDDHLPWS*G LSSVGQSVDDHLPWT*GLSSVG QSIDDHLPWA*VLSSVRQSIDD HLPWT*VLSSVRQSIDD/HSSMD VRSV*CRTISR*PSSMDVRAV*C RTINR*PSSMDVSAV*CKTINR* PSSMDVRSV*CRTISR*PS\P*T* GLSMSLIPSQLCGLSAVTPFSAV TRNRGS\ENHPILKAAASRSKSS FPRLKT

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4052	34420	A	4093	3	1194	SLGPRSHSCCRSDYRSGTTVPL VLLPVCGVPALLVFALLSPLCV VCSALCGGLLPVLRASLFLWCV AFLAGLVFVFGFAFFGSLVRGR FLVVVPFFLLFALCRLLFLVCW LRSFGACPVSVCVAGFACFAGL FLVLVSLLSSGFGFRLSFSCVVG SLCLPGFAFRAFCLFFLPCVGPA LLAFPGFCGPSSPSLSYGGLFAP WSCALLGFFGCLGWSAPGFLSS FGLSVRVLSLPCASGLRSLSGC ALVPGLFLPWVFSPRSLRPLVSF GCLLCSFVSH\NMDWIKES\AG KVIQGNP*WLPVILFFGSVPLTS KAATAKPLMRMG\RALTVSQL T/AVASFAAVYGLFILPT*PTLV GAVQMDDTGTTRIGKLVSNHP FFIRVLLGVALTVCFGFVLGSF
4053	34421	C	4094	70	1950	
4054	34422	B	4095	262	4347	
4055	34423	A	4096	2	458	
4056	34424	A	4097	2	445	QPTERGLCASLKPSRAAIKSQSS KVISFDSMSHIQGTVVQGVGSQ GLEQQYRSGVAVFRLHSFSHRL LSACEFSRCRVQAVSRSIILGSG RWQPPSHSSTREWPSGHTVWG LQPHISPLHCPSKDSL*GLCLCN KLPPENLGFSYVL.

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4057	34425	A	4098	1	2589	MVWFLKNVNHGTHTNAKKYN DVENKERTGWKWGSTEYLLCA RPLRKGNVGLSGDVFLTVFVM KTGHSSSLLPSTTTSDSTAQEGY ESRGGMLDWKHLLDSPDSTDP LGAVSSHNHQDKKAMLKDGEE RPFNEPGVFHLLADHQLTQKV ASIPGSAVCAYDMLDIASVFTG RFKEQKSPDSTWTPVPDERVPK PRPGCCAGSSSLERYATSNEFPD DTLNFIKTHPLMDEAVPSIFNRP WFLRTMVRYRLTKIAVDTAAG PYQNHTVVFLGSEKGIILKFLAR IGNSGFLNDSLFLEEMSVYNSE KKWSTAKPVRVTIILNPGQASF CITLRETV/C*RRKHIWCPPYRC TLQ*HFCPCH\CLSGKETLCRVT GGMKVKADRDESLPYAAMLA AQDMAQRCKELGITALHIKHR ATGGNRTKTPGPGA\SRPSSPCP LGCLK/WQTLFPRRRLRWPQGG RRKRSQLEAQRVIRESYLKGHD QLVPVTLLAIAVILAFVMGAVF SGITVYCVCDHRRKDVAVVQR KEKELTHSRRGSMSSVTKLSGL FGDTQSKDPKPEAILTPLMHNG KLATPGNTAKMLIKADQHHLD LTALPTPESTPTLQQKRKPSRGS REWERNQNLINACTKDMPPMG SPVIPTDLPLRASPSHIPSVVVLP ITQQGYQHEYVDQPKMSEVAQ MALEDQAATLEYKTIKEHLSSK
4058	34426	B	4099	1	1299	
4059	34427	A	4100	95	502	FPEIPQSCREGAPGPAKPGGPRA REPCPNRTAASWGVHCEDGGS TVRTGGPL*GRGVHREDGASSP QHPPRRGRGLGHLGPRPL*GQG DAAAAPGHRGKS/GGKGFLPAL RVQRGERGRVSRRAVCMWTSL CASVPS
4060	34428	A	4101	2	653	DSFGSMSVLIKNPRTLFGGKPY VCRECGRGFTWKSNLITHQRTH SGEKPYVCKDCGRGFTWKSNL FTHQRTHSGLKLYVCKECGQSF SLKSNLITHQRAHTGEKPYVCR ECGRGFRQHSHLVRHKRTHSG EKPYICRECEQGFSQKSHLIRHL RTHTGEKPYVCTECGRHFSWK SNLKTHQRTHSGVKPYVCLEC GQCFSLKSNLNKHQ\RSHTGEK

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4061	34429	A	4102	8	389	LPASASQSVGTTGVISFENTCNI CHFFFLLLLFFSSSSSFFFLPFSFS FRVSLF*IQPLKTTASTVQGRQH SGGYRASPERRADQRAHTGEK P/YVCRECGRGFRQHSHLQLSV YPHSFWTQDKRSNH
4062	34430	A	4103	1	740	EGKRGRPFRIPRPAHPFPHELQS RLCILKPLHHPTPSSCPSS*TPVA PLPSHPCAPH/SARSCPVSDEAA L\P*SMALWARAGLLEAPTTLL PAAPDASSPA/MPPSRKLPPPLP L/CPEPLGPSPAAPSPPAPPGPNA AARPPL/PPSPSAAPGPRRPGA\R PVGPSRGPG/PRNSRSLRAPDVH TAPMRCLPSVRPPLPVLSAL/PD PLPRPPSFVPSLPSP/PSSGPSCPP TSAPPGSPRPGFVRLPCLLFWGS
4063	34431	B	4104	48	272	
4064	34432	A	4105	2	622	CPLSPLLFNIVLELLARAIRKEK */LKGIQIGEEEVKLSLFGDDLIV YLENPKYSSKKLLELVNEFNKV SGYKIYVHKSVALLYTNSDQAE NQIKNSTPFTTATSSSSSSSSSP QGIFLTKRLKNF*RGKFKTLVK KNQGDPKKGKNPPGPKMGKN NFGKTPFWAKKI*KFHSI\PKKT PPFFFQKLKKTGVKFFWAPKGP KGFLSKK
4065	34433	A	4106	39	1043	QKQPVWQRCREIGTLGYCGWK WTLDIHGRGHRILSGGVEIPGP WTEGFIQGRDVGELQEPGLSGR ESIH*\GKSYEYECSEDGEVFRV RASLTNHQVIHTAEKPYKCTEC GKVFSRNSHLVEHWRIHTGQK PYKCSECDKVFNRNSNLARHQ RIHTGEKPHKCNECGKAFRECS GLTTHLVIHTGEKPYKCNECGK NFRHKFSLTNHQRSHTAEKPYK CNECGKVFSLLSYLARHQIIHST EKPYKCNECGRAFHKRPGLMA HLLIHTGEKPYKCNECDKVFGR KF\NLTNHQRIHTGERPYKCNA CGKVFNQNPHLSRHRKIHAGE NSLRTLQME

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4066	34434	A	4107	3	941	QQHQQQQHFVGQVAIQQQQQ QGPGVQTNQALGPKPQGLMPP SSHQDLLVQQVSPRPPQGPQG MVGPAQVGVLQHQLHGALGP QGLH*QVFMP\QSRVFSSPQLA QQGQGLMGHRLVTAQQQQQQ QQHQQQGSMAGLSHLQQSLMS HSGQPKLSAQPMCSLLQLLQQ QQLLS*QQHLQQQQQQQLQQQ QQL*QPQLHQQQQQQQLQQQQ PQQL\QQQHQQLQQPQINSQ/HL FPSRRPPNHMGLLTHSPNLTAS LRLTSTHKAALGPGLQAALGHP KDGLLWKTLGTWRARGLICTG GIISYFTQHSWEVKVFTTL
4067	34435	A	4108	1	2255	MEKNKVVKREAEANSINLSVY EPFKVRKAEDKLKENSDNVLE NRVLDGKLSSEKNDTCLPGTAP SKTKSSSKLSSCSSAIMALSAKK AASDSCKEPVANSRESSPLPKE VNDSQARAPLQSTVMTNAVSP AELTPKQVTIKPVATAFLPVSA VNEMKTAGSRVINLKLANNTT VKATVISAASVQSASSAIIKAAN AIQQQTVVVPAPSRANAKLVPK TVHLANINLLPQGAQATSELRQ VLTKAQQQIKQAIINAAASQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPPTNAG ITLPTRGYKCLECGDSFAVEKS LTQHYDRQSMRIEVTCNHGTK NLIFYNKCSLLSHARGHKEKGV AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKSLYTCPECGAI CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGSHCEVFYKCPICPMACKSAP STHSHTYTQHPGIKIGEPEIIYKC SMCDTVFTLQTLLYRHFDQHIE NQKLSVFKCPDCYLLYAQKQL MMDHIKSMHGTLKSIEGPPNLG INLPLSIKPATQNSANQNKEDT KSMNGKEKLEKKSPSPVKKSV ETKKVASPGWTCWECDRLFIQ RDVYISHVRKEQGKQMKKHPC RHLCQHNRIKHKGIRKVYACSH CPDSRRTFTKRLMLEKHVQLM
4068	34436	B	4109	1	411	
4069	34437	C	4110	54	146	
4070	34438	A	4111	1	1937	

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4071	34439	A	4112	1	1830	MCIEVTCNHCTKNLIVYNKCNL LSQARGHKEKGVVMQCSYSIL KPVSAGHIIVSPSSNSSSSSSTLQ SPVGTGIHTVTKIQSGITGTVISA PSSTPSTTAMPLDEDPSKLCRH NLKCLKCNEIFQDKRSLATHFQ QAADMSGQKTCTICQMLLPNQ/ CQRIHQHKSPYTCPECRAICRK KRT\QIHEWERETGKEISISFEKK SMETKKVASPGWTCWECDHLF MQRDVYISHLRKEHGKQMKK HPCRQCDKPFSSSHRLCWHNRI KHKGIRKVYACSHCPDSTGTFT KGLMLEKHV\H*CMASRTLT*K K*QTPPMRRKQK*K*TSRSAVP SG\VERTGSGVQASQRSNNSTT EKAENQCF*GSQAPLCCTQVKG TSASAQAKWGWRR*PTGEQTQ PRGRISQW\VMSDRKCKVCAKT FETKAALNTHMQTHGHAEGCL KQPCRSLLSQPRIKTEARNLIRN ADFLNSILRNGEGYSKEKKNGT GFLGRSARLALGAQGGKSWRF LFWVLLPNVLVLRVGMHDVN HRLINAAGCVSQLAVTLSTEPH GISSAISRVPRHCHPSGENSMAT SLNVNRSISRLAAGSGVLAMDL PIPAGHRAIETGLLGTEDTEQ
4072	34440	C	4113	217	510	
4073	34441	A	4114	210	281	
4074	34442	A	4115	1	675	
4075	34443	C	4116	126	434	
4076	34444	A	4117	804	2061	WERREAGGEDEGINIHEP*VEE EMKKHESNNVGLLENLTNGVT AGNGDNGLIPQRKSRTPENQQF PDNESEEYHSLGDKSKTSFQNS NNNNNKQQEQQQQNPTFSNTR KLTKLYKAPIPPSIILSGCPNIND SNWQEIEHGMQTAGLPTRPLSH GLQQKGAAFRCLGCKCSEPFTG SLILQKAKTNTQKWQATYPKS QNEQLVPSVGKSYRCSTPAQP MKTAVGHKPCKATGAELPKAL GAQPLHPCALDVGQGFKKGNF GAVGLNGLLGLEFHGVSGVLL VGPGDGGLISEGVVREDLMCG VWSAGTWSVGTAERCLEKPGA LHVIEGPLDSWDGPVMPNGPV KSRQSSCLDGPGRCCSEILTGQS HGNKKPARASSKSSQSINDRPL AVLTNQYQCEQLASERQPSSNS

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4077	34445	A	4118	1	357	GKLMLPGSTRKPQVPVDRKMG HEGVFVWQAGLRARPGPSLPFS HGLTLHLHWPLALPV/GATSSP CEAGDLGV\PLAAGTWCPWEA *RQEEAGWQAPGRAGPARVG WGGTGLTSAEVIITI
4078	34446	A	4119	1	771	MLISHKQLSPQLLSLTLPLSEGK AGWAGECPNPPSKDSPVQGIG/ GPPP/GYQKCR*DTASMLTMAP CHGPVCPPHPGWRPRSGSRVIL PAPPGHHPWP\GPRARNGLGTF QGCSTGWQVQETCFGPGGWLG DRHLVGPAATGARCLPAARGP/ DGALHPAVPTGKLKGQP\GPGA RHQRTYD*LPRPCGAAGLGSPP A*HPISEETENQWGLHGPPQPA WARPDHGCQ/APTLSPSLKRKP GRVTAGGPMPGCFSTSSVPTT
4079	34447	A	4120	1	402	MLISHKQLSPQLLSLTLPLSEGK AGWAGECPNPPSKDSPVQGIGD LHQLPKMQIRYSIHADDGSVPR AAHKRGLRKRTLKTISLPRQES AFPFHGQGGDPGVVPGSSFLHP LGTTPGQGPRARNGLG\PSRAA PPAGRGVAGGSPSGG\PAATGA RCLPAARGPVGPYTQQSQRAS* KGSLGPGARHQRTYD*LPRPCG AAGLGSPPA*HPISEETENQWG LHGPPQPAWARPDHGRQPLRC HPP*RGSQGGPQKAAVSQQIPR AGQEGTH*DPTEWGPPDGDQG GPRESCRGLQGGRGQCLCDWS PNTSEI*YPHA*NGD*KAG\PPM DTKSQLQVSTPKSPASHGEDVA RLEEPEASGD/RSVP\GLPGASLI PIWRPPFSRISVRTFLPSPWNLL RDCGFLGTSLASSSGRVTA
4080	34448	C	4121	111	218	
4081	34449	A	4122	2	453	WWPVLSVPPECRLPGRLPSG*V RGPAPWWPEPASQDKSQLSSR GFPGKVSLGKGMAFSPLQTAP* KWLGLSPPLSSTENTASRGHTS PSSRNGFDSQPRDSRTGRECQA TQLPAQHSHAEVLHFGGAMSG QLSLVGPQDSKRTARLTDSQ

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4082	34450	A	4123	1146	1775	KGWLEGAPEA*ERYPG\PPCVV CSLSDAPWVGHPAPSLGV*EP NPP*SRGESQGPTSSICRQSSGD LG*KLESPIHTVIPRHTSQARQG HTAPFPPFQVPS*LLV*LKAVSL APAEAP*PASGLHAPWPVAPRV TCAI/PAKGTTVPAGPAELRPVS PPPILLP/PDSRSSAFPSRKGPASP YETCSPPTS*/EVPS*TYKSMGP GIRLPALPASPRVPSEGPGLSEH PEGPPALPPAIPFS\SPSWFKQCS FSIRPGWLLHGAPQGKGWPQA SWVGKTG*PEKRGSPRGPEHSA LNLRVALPGVAV*EGPACVGW GGPPQPPGAICEATAPPSI/VPPL SLPAPFPGTLP/PPTPAASP/PPAL PPLLRRGRPRPCAALALPALSSL FS/PPVFSLLSLQLPADRVRQVH PVLRAPGPPFRPPKQIPPSSSGDL PFPSLPGR/PVL*LEKWLPPAPK ASPPSSVNLILLVVVKLNTFRCG PLVKNLVPPSVVCPCPCSYKYL *ILIYIHTLHMGQPPSPSSAGNQ SLCYPCGGLVAQPTKRTLVPPTI QLQSVPPPV/KPPCHARPVDSQP PPSLPPPTKHGGAVQAAVWPDS FYPVLLSLG
4083	34451	A	4124	146	1701	TFLGYLETAHGPSAQQCPTGLF AFRSLGRGLLLTSLPKQPARSPP REDVPRSTTQEMTRPRHPPRKP AQPGLGARRRGAPV/RGLSKSR ELNSGNTSDSGNSFT\PPHPRTR GPCWRISPPPAGAESQGDAMLL ARMCQMPSLGLMSRTFPHSST GKARGFQSPCLECAEVKKSSLV PSTARSSPMKGCSRSSSYASTRS SSHSSQSPNPRASPRVRTIITCIL *TRKRPRETKSSAKVT\HYYSSK SGKRSPPSRSSRSRRSPSYSRYS PSSPNSPADIPQNSHPQPSASTD RPHIQSPQFLPTHQGLRNIHVLT PAAPALL*CPPANADTPAQAQP PPLRY*QPSQTLTAAPSSSLRSP LRQRADPIP*PSGGAGSQIQ\WK DSQQRERERARRRRRSYSPMR KRRRDSPSHLEARRITSARKRPI PYYRPSPSSSGSLSSTSSWYSSSS SRSASRSYSRSRSRSRSRRRSRT RTSSSSSSRSPSPGSRSRSRSRSR SRSRSRSQSRSYSSADSYSSTRR

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4084	34452	A	4125	1	1068	MLLLELNAPEHVLETINFQTLT AFCNTFHILRPTKAPGFVYAWL ELISHRIFIARMLAHTPQQKGW PMYAQLLIDLFKYLAPFLRNVE LTKPMQILYKGTLRVLLVLLHD FPEFLCDYHYGFCDVIPPNCIQL RNLILSAFPRNMRLPDPFTPNLK VDMLSEINIAPRILTNFTGVMPP QFKKDLDSYLKTRSPVTFLSDL RSN\LQVSNEPGNRYNLQLINA LVLYVGTQAIAHIHNKGSTPSM STITHSAHMDIFQNLAVDLDTE GRYLFLNAIANQ\LRYPNSHTH YFSCTML\YLFGRRANSGRPFQ\ EQITRVLLERLIVNRPHPWGLLI TFIELIKNPAFKFWNHEFVHCAP
4085	34453	A	4126	1	984	MQANLEMAGNGVTSMGMEPL AIPHIYCCSEGTCNFSNTENHCL RAALSMLLNGTPFAFVIDLAAL ASRREYLKLDKWLTDKIREHGP SVHGLFPSRVLSPALGPGAFPG RHNCGSCVAPQSGLPGVHPVEL PWSISKLFRLRSPANFSDVLGSR SKVLLLMCTLKYCGMQLGADA TRVDMLTFLPTLGFIRNNDYTD DTKASELTELSHNLHAYDSVTG VPGDETECSKTVSTWAYTAESL QGYMAAKLLGRNLTVPSRYLF LNAIANQLRYPNSHTHYFSCTM LYLFAEANTEAIQEQIT/RLVRE RI*S*ANAYWHSEKFYQFTCEL
4086	34454	C	4127	1	399	
4087	34455	A	4128	1	868	MANVCNPSTLGGRGGRITRRPE DPGSPVYSVPPASYHPKPWLGA QPATVVTPGVNVTLRCRAPQP AWRFGLFKPGEIAPLLFRDVSS ELAEFFLEEVTPAQGGIYRCCY RRPDWGPGVWSQPSDVLELLV TEELPRPSLVALPGPVVGPGAN VSLRCAGRLRNMSFVLYREGV AAPLQYRHSAQPWADFTLLGA RAPGTYSCYYHTPSAPYVLSQR SEVLVISWE\TLAPPTTPGGT*S AWGWPGWSSSPWARWSLLTG AVRTALLLFPQVPHRATTPWVT SYDWVWLP
4088	34456	A	4129	1	270	
4089	34457	B	4130	39	919	

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4090	34458	A	4131	3	466	GRALCPPRLLAAGRVLGPGRRS PG\PGPGVP/GG*R*GGAEPRPG APRGRVLPPSAGSGQFSAATPA QNGLPALRGPGSRPGIRSKAVR PVPLGRVGVYFRDALRASGQS GRKLCCIGNTLSPTSFSVGKEVP RKHETNQKHEKGILCMEAVKP
4091	34459	A	4132	1	1647	MWRWLYAGARMTVRDKQPLE QMLAGCTHASLVPTQLWRLLV NRSSVSLKAVLLGGAAIPVELT EQARDMGIRCFCGYGLTEFAST VCAKEADGLADVGSPLPGREV KIVNNEVWLRAASMAEGYWR NGQLVSLVNDEGWYATRDRRE MHNGKLTIVGRLDNLFFSGGEG IQPEEVERVIAAHPAVLQVFIVP VADKEFCHRPVAVMEYDHESV DLSEWVKDKLARFQHLVRWLT LPAEPKNGGIKFHVSAKRVGAL TTRMEAAQQHADDKIRQMINS EQRLSEQFENLANRIFEHSNRR VDEQNRQSLNSLLSPLREQLDG FRRQFRTASLMKVAGWDYLM NSLYNANSSALVNRVRYKWIA AFEGGFTGIVATLDTGRPGPVM AFRVDMDALDLSEEQDVSHRP YRDGFASCNAGMMHACGHDG HTAIGLGLAHTLKQFESGLHGV IKLIFQPAEE\VRVARGRWSMQ VS*MMLIILLPCTLALAYLRALL CAAVIILWQPPNLTRTSPVPPLT QAQNQKTVTMPCWRHTSHSCT ACNRPAQRRSFQS
4092	34460	A	4133	864	1128	TGRSTIRRQRREPRRKAATLRF DRNGCRARCTPP\GRKEQRYQQ TADGDKGAEFYRRPEGVEIVA VMEQRDEVIQADKLAGETKRI DAL
4093	34461	A	4134	618	1102	HSNAAPTARSSFVQNTPSSCGY SRRAWRISSIPEETDRTSYRNIQ CGNHPPVPARLPAGQTGDGDIP PRPRWQSPQTAPRKPPDLP/LIR KNKIPMFRSATTQPGLTGTIAK ASSSEVKAIIGARVKMTRSENF GIQSSLKNILIMSATSWSEPPQP TRLGP

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4094	34462	A	4135	2400	3201	VGGGRNRSPGVACWVEDGNG DAVRDGW\ALDADWQASQAM RRKQQPE\YWQHDAATADADR QMNMPV\LH\RALVAGRAQEM NGAQGKTLLKGW\DEASARRG T\KTED\FCEEDTRDDAMIAWM PR*PGVLPRADAWANVLNHGV GWKKAQLK\STWM\PQVQQ*W RGD\KAANSNAAVAHTVVLLN SGGDATQ/TAAFPISSPLSV/EEV CVTMVIA*FWMWDSGSGGVVL CSSSGRSLTSWSATKVRG/SGH KGRWCSRQGVTCQVRHGGHV APH
4095	34463	A	4136	118	1008	
4096	34464	A	4137	3	1140	KHTYMLSILKPVRTSALPPPAP AQTLCTQLSRVSSRLL*DHPSR WGLR/PSTGMSQARACSPGSLG WMQRSSFTPGAGRVRHIPN\SA GSTRRPACGSRSAAAPVRPCRR TR*G/RSSVVERFMTALSLACR ALPGP*AAPGPSITRRFTISAELK DTRL/PREHVVPLVCTHAIAVPD RGAAVRPTRRRDAAAPPSPLVG DVTLQCPSQ*RGSNAPDQVRLP CVG*RPRSSLQRSGLSVFSADGS TSGPEPASGRKDAGWPARVLRF GTLSRGAPEAGADWGPYSPGSP GAAASGAPWLGQPQALQGAG GQLVGSENGERGTGTKPRVSVS VAYGEIALPADTSWSSRAGAA VLLGLSRSTGGEGPGNMGHGG QSQMLTLEVL
4097	34465	A	4138	10	585	PLEMELNLISIEVWGERLGISTG TEKMPTLKHRTWPVECSKASSL EGDLRSL/S*LEVISAFSADPASA DDSPGCWKKKDDCSMVHLHR QEWQQQQCCQ*K*RKQPPGER RNKCGSHPVCGTVLWQP*QTH\ QISSCPTVGCPPSHSSFSILDGAN AGQEKQSTTEPEPALFLLPPSRG AFGPFGLLSDLRRQL
4098	34466	A	4139	1	474	
4099	34467	A	4140	458	612	ASCMASVDISVLTCMWRCTIEQ SSSFLCLLTPLWE*SWCHVTRIC PFISLG

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4100	34468	A	4141	1	829	MGRPDLILSSILGLRWLLLPQSS RAGRRGAIREASDAEQVTFSGG TVPARTSSGREWRSLLGPDMET TSLFCIDTKTTFLFVYRYGDHIP LVPEQSGLEPLLIWADPGLFHV RLFHLLTIDDNFCGLDMNAPLG VSDMVRGIPVFTEDRDRMTSVI AYVYKNHSLAFVGTKSGKLKK /VRSSAAP*VWDQDTPRSLGQQ GAQRQP/ILRQCVYTFFQLN*RC PHSTARRELRTGGFIPTRSHQD GLRSAARCTQGTTQ*ASWSCV HVCASVRAMCSYC
4101	34469	A	4142	5	237	NFGAMTRIR\DLPWEINPLSSCS SLCEKDPPTTSSPQTN*PKEHHT NFQSETGDEFYPWTQNFSTGHG LGKTVFPWCL
4102	34470	A	4143	1125	1190	
4103	34471	A	4144	306	573	RNFGAMTRIR\DLPWEINPLSSC SLLREKDPPTTSGPQTNQPKKH LTNFKSGKRPLLTLFSNLSHCPS TTFFFPFFNLSLLLISIPFIFW
4104	34472	A	4145	1	329	ASHSWQTLQHSGRYSRSSG/SA GSPRDCAARAPTISPGCAMAWL NLDSISPSSQSKASPLSQLTCPET SYTGCP*SAPHSPPPPWCPQERC ACKGHCLHHRDGCCGYGYN
4105	34473	A	4146	2	336	SILTRKCKYGMEIPT/NIPGLGA AGPTGMFFGSAPSPMGGISPAM TPWNQGATPAYGAWSPSVGSG MTPGAAGFSPPKA/PTYSPTSPG YSPTSPTYSLTSPAISPDDSDEE
4106	34474	B	4147	1	1260	
4107	34475	A	4148	150	335	SFQQSAPW*ASGQSCASDPAPP ATARGRFGPHQSQAFHSRHSPIP DPLPPPCSGGWGHSRW
4108	34476	B	4149	1	3267	

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4109	34477	A	4150	1528	2973	GKQIFSLIIPGHINCIRTHSTHPD DEDSGPYKHISPGDTKTVINNW LLIEGHTIGIGDSIADSKTYQDIQ NTIKKAKQDVIEVIEKAHNNEL EPTPGNTLRQTFENQVIAVVGQ QNVEGKRIP*LPPPL*WGAGRR EGVG*CGRFSEHSRSSAAGYRG GRPCC\PSWEDDP/GAPPDPPAS AQIPAPTRSGCVRCSARPSPGPP AECAAGPSHWYNQSGTSSQKP CWKA*AYPGSGTQRSRGSQAR SHP**SEAESGA*SQMESACPRR SAVQRQQ*PDSQTSAAECSLG WAPAHCCVPSR*PLLRPAWPS* *CSECPGKS*NQQWSPQCQ*YD PNPQSTVVAEDQEWVNVYYE MPDFDVARISPWLLRVELDRK HMTDRKLTMEQIAEKINAGFG DDLNCIFNDDNAEKLVLRIRIM NSDENKMQEVMGVLEVSVSHV
4110	34478	A	4151	459	940	HLPGGGVPGREGGSPDQHVAP GAVSGGAGGGSTRGRGSRRRR PGRPRPGPRQPRRGALPGGEHG LRASARCAARAQQRDPG/TPSC SSWACPTPRRPWAPAASSRLRR PPRGPACATPPPCRPPARRTCTG RCPPSCCLCGSPTTWRRPPPTG GALESPKRR
4111	34479	A	4152	264	1386	SSRCQPVCESGHPGYGQSPA/YT TAGRTESGGTGST/GDNHPLWP CI/GGAPCPAQNTPHLRCV*RSH ALALDSAGSSSPESPH*RASIPH TTLGQKRRSWAGTAHS\PMAPC AAASISTST*LSHHHSPAAQSVC PSSHTTPSFCPIQKFHCFR/SPQR NTS*VVLCPGG*LRVG*WPSSG HDRSWYHTREPSVGN*HRSHQ RR*RGTAPAPGPSARLQCPARG SRSSHSAPASSSRRPFPGSTPAG LGFPSARFPVGKPVVPAALMNR PTRGERRFAYWAPGWFFFSPVR RATADCPSP/SWP*ESCSKRSTL VCPSRRKSCLMVVPKSAKSPVL AK/YGPVGHDHGTEHDVVLGE VQGKRPVAPTMGTPKHKAVHP RAPH
4112	34480	B	4153	52	363	

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4113	34481	A	4154	321	802	HLPGGGVPGREGGSPDQHVAP GAVSGGAGGGSTRGRGSRRRR PGRPRPGPRQPRRGALPGGEHG LRASARCAARAQQRDPG/TPSC SSWACPTPRRPWAPAASSRLRR PPRGPACATPPPCRPPARRTCTG RCPPSCCLCGSPTTWRRPPPTG GALESPKRR
4114	34482	A	4155	15	263	CGRFSEHSRSSAAGYRGGRPCC \PSWEDDP/GAPPDPPASAQIPAP TRSGCVRCSARPSPGPPAECAA GPSHWYNQSGTWKCKG
4115	34483	A	4156	3	518	SPSVGSGMTPGAAGFSPSAASD ASGFSPGYSPAWSPKPGVPGVP QVPSKPLKSLHPGGVVRHLSGQ VCFLHSSG*VCPLLISFVGCFPT GGAMSPSYSPTSPA\YEPRSPGG YTPQSPSYSPTSPSYSPTSPSYSP TSPNYSPTSPSYSPTSPSYSPTSG SYSPTSPSYSPT
4116	34484	B	4157	620	6763	
4117	34485	C	4158	430	870	
4118	34486	A	4159	1	3039	MDSETRRTAKVRLLMTVLRDQ DRVSGVQAHPEQFQQAICPLCG VSLTRSGTTFGSPSEIYSPLGESR ASSGLPRRDGRLIGEEPPEKKFS RSPKGD/LSSGGQRIDYRVCVPT KFNL*VLSF*PRGQGAGGQSPG FSVRRLLVLVWSSGTFV*NGK* QKLL*TLCECVHD*GVQGPASG SPVCSSTAKATEFEKDPSGPFSS SSLPLTPYISFSRVTASSASPGLG SALTPQTLKRKGRI*AICL*VVE TPKVFR
4119	34487	A	4160	1	772	MVARAFLWSQVIRRLGRKGGL SQGDRGCNTALAEGRLDPDLT RGHPALCLPRRPAPRPAEVRRE GEAEQPEAGQPPGAAPRRARD NGAAAAAAGGRLLQSVRPAVV CPHPGPQASYGLRYIAKVLKNS IHEKFPDATEDELLKIVGNLLY YRYMNPAIVAPDGFDIID\MTA GGQNNSDQRKNLRSTAKVLQH AASNKLFEGENEHLSSMNNYLS ETYQEFRFKNVTFDIIATEDVGI FDVRSKFLGVEMEKVQLNIQ
4120	34488	A	4161	174	444	YHRHDSWRNTRR*\IKLDGKGE PKGAEESEATSKYTAAKLHEK GVLLDIDDLQTNQNAVNDFSV GPQDEVIVEDITNCYLCEIFKRY EWVT

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4121	34489	A	4162	379	520	GTSHRGASQRRCCPPLSKTGPK TPCGKGAPSAP*QGGLDVQGEP GGK\GDSSGECVGGNVAGLHK GGGTRADSQVPGGMRGGRMS Y/GG/HLTAEGPMGRSGPR/GAV PSLYPPGFSRGSCSRQYSGAHM PILTGHVGWSESSLDPPRAGQD RFLGTARP*GTSHRGASQRRCC PPLSKTGPKTPCGKGAPSAPFIP AGPTFDHKALM
4122	34490	A	4163	455	798	
4123	34491	A	4164	32	2109	WIGGCPGSQPDATAIMGWTLA PHSSRCHRCCHYRCHCRCCLCP AEMTVGRPEGAPGGAEGSRQIF PPESFADTEAGEELSGDGLVLP RASKLDEVLSPQEEIDPTSDSTG SIYHTLLDLAQKGRWLSVWSLS FSLTQRVMKTSLKMRRTWRVS SKTRTGGWCRSSARRL*GVAPQ GAA/DSLNNLPSNIPRPQTQPPS GSRPPSQHRSVSSWASSITVPRP FRMTLREARKKAEWLGSPASF EQERQRAQRQGEEEAECHRQF RAQPVPAHVYLPLYQEIMERSE ARRQAGIQKRKELLLSSLKPFSF LEKEEQLKEAARQRDLAATAE AKISKQKATRRIPKSILEPALGD KLQEAELFRKIRIQMRALDMLQ MASSPIASSSNRANPQPRTATRT QQEKLGFLHTNFRFQPRVNPVV PDYEGLYKAFQRRAAKRRETQ EATRNKPFLLRTANLRHPQRPC DAATTGRRQDSPQPPATPLPRS RSLSGLASLSANTLPVHITDATR KRESAVRSALEKKNKADESIQ WLEIHKKKSQAMSKSVTLRAK AMDPHKSLEEVFKAKLKENRN NDRKRAKEYKKELEEMKQRIQ TRPYLFEQVAKDLAKKEAEQW YLDTLKQAG\RRKTL*ETRVKA PGLFKRKRPKSRIFPGSKKLQNS ASEIQSR/RLEGSLEQPASPRKV LEELSHQSPENLVSLA
4124	34492	A	4165	251	637	

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4125	34493	A	4166	1	1344	PGRTTRSMAEDVFLSAPIPRGC ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEEE EEEEDAVLVAEAEAVAAGWM LNFLCLSLCRAFREGRSEDFRRT RNSAEAIIHGLCSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKEHDKLHE EIQNLIKIQAIAVCMENGNFKG AEEVFERIFGDPNS\HMPFKSKL LMIISQKDTFHSFF\QHFSYNHM MEKIKSYV\NYVLSEKSSTFLM KAAAKVVESKRTRTITSQDKPS GNDVEMETEANLGYKKKC*LT NSLR*LNPQRVQYPY*GSHKNL FLSKLQHGTQQQDLNKKERRV GTPQSTKKKKESRRATESRIPVS KSQPVTPEKHRARKRQAWLWE EDKNLRSGVRKYGEGNWSKIL LHYKFNNRTSVMLKDRWRTM KKLKLISSDSED
4126	34494	A	4167	1	1345	IPGSTISCLKGQYPSEPFNMAED VSSAAPSPRGCADGRDADPTEE QMAETERNDEEQFERQELLEC QVQVGAPEEEEEEEEDAGLV AEAEAVAAGWMLDFLCLSLCR AFRDGRSEDFRRTRNSAEAIIHG LSSLTACQLRTIYICQFLTRIAA GKTLDAQFENDERITPLESALMI WGSIEKEHDKLHEEIQNLIKIQA IAVCMENGNFKEAEEVFERIFG DPNSHMPFKSKLLMIISQKDTF HSFFQHFS\YNHMMEKIKSYVN YVLSEKSSTFLMKAAAKVVES KRTRTITSQDKPSGNDVEMETE ANLDTRKRSHKNLFLSKLQHG TQQQDLNKKERRVGTLQSTKK KKESRRATESRIPVSKSQPVTPE KHRARKRQAWLWEEDKNLRS GVRKYGEGNWSKILLHYKF\NN R\TSVM\LKARWRTMKKLKLIS SDSEDWIVFVKL
4127	34495	A	4168	3	378	LTSGSRADQGEGQEEGAEGGR ASSSSSSSSPRGPQHHPHLHGDP AEHRPGHPLCSPPDLTVAYQ/M PEVPAEDM/SDPSFCSARQGGQ RGLDSGPGAPWSSSHSPHSRFQ EASHGACAGWRWCRQEEL

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4128	34496	A	4169	1	1044	SGQEVNKEDGQADVQQDHHA DEDGVGDLARQPHLFHLHLRL CRQCGLLPRLLLGPRLGQPSSLS LAGLGPGLGFGDDGLGLQLGG GLACRLGASERGGLQRGGGRG RGRGLGPG/GPRARAGPQRVGA RAAWCAQHSCGSPGKAPPPAP A/TGAGGACRASMAMRSVAGR AGLRRPAPSDGVTDRLPSPLGS PFQAP/EAQQAVLGHPGPGPLG LRGRPGR*RGATLGPRGLT/PRA AAGSRGAAVGGPLRRRPGRGA PAGSPSSPGSPAAAGASDIPDLA GRSPEPAPWPKCEQCWTPGWQ PGRPVPLPQLWPWRGLSISGSM PLGEGLEDGSDPMTPSCCLPGT
4129	34497	A	4170	1	732	SLTQAGTVSLGLDAEGQEVFVP FSAVLPMVAPNDLVFDGWDISS LNLAEAMRRAKVLDWGLQEQ LWPHMEALRPRPSVYIPEFIAA NQSARADNLIPGSRAQQLEQIR RDIRDFRSSAGLDKVIVLWTAN TERFCEVIPGLNDTAENLLRTIE LGLEVSPSTLF\AVASILGGLCLS FNGSPQNTLVPGALELAWQHR VFVGGDDFKSGQTKVKSVLVD FLIGFRLQRP/VSIVSYNHLGNN
4130	34498	A	4171	1	908	MEKAPPQTQHEGLKSKEHLPE QTDEGKTEYRRVPSLRAVVLFR QRSCIENILRACVGLPPQNHML LEHKMERPGPSLKRVGPVAAT YPMLNKKGPLVWEVSPATLFA VASILEGCAFLNGSPQNTLVPG ALELAWQHRVFVGGDDFKSGQ TKVKSVLVDFLIGSGLKTMSIV SYNHLG\NNDGENLSAPLQFRS KEV\SRSNVVDDMVA\SNP\ML YTPGEEPDHCRMGRNLPE*GSS
4131	34499	A	4172	85	529	ECGARPGSSTRPPARLSPRLFCS AIRAALKTRPAPALACTWRTG* RASLPTTRCAGSGLGTCTAEGS EGCSHPGPLTGTG/RQEACPGT APAGSPSCLHPRGRPRPCPPGTL APRMSCPWPRSPPLTRYLPSGE NLQSKLESLNTSEKF
4132	34500	C	4173	215	324	

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4133	34501	A	4174	2	505	YKCEVCDKVFNQN*FLVCHNR CHTGKKPYSCYECGKTFSQTSS FTCYRRLHTGGKPYKCSEHNK TFG*NSALVIHKAIHTGENPCKC NECGKVFNQKAHLARHHRLHT REKPYKCEECEKVFSRKSHLER/ HKLKRGGVALV/C*ECPTVYQN TSCLRSLSCSYPMSLNG
4134	34502	A	4175	1	6192	
4135	34503	A	4176	2	3389	
4136	34504	A	4177	3	875	GEEAALSLCMHSTDDATRLGA RDTEPLWHVPAQ/ARLSAIAGS SGNKHPSR/QDAAGKDSPNRHS K\GSKPSAGSLRLSSREGEDRTA WTGPRGAVEQEVTGPDLC*GR GQQGLLVGWT**EQKRGQGKP QYSSHSSSNTLSSN/ASSSHSDD RWFDPLDPL/EPEQDPLS/KGCM SLAK/APRPAKPHKPPGSMGLC/ GGGREAAGRSHHADRR/REVSP APAVAGQSKGYR/PKLYSSGSS TPTGLAGG/SRDPPRQPSTLWH RTWYL/YHTASAAVHRGLCRE LEQADQIPPSWYGRRPMGNS
4137	34505	B	4178	108	318	
4138	34506	A	4179	103	540	RRGCESHKTLRRGTSWGLDAR GGGPGPGQVSAGRDGAEVWLS TCDRGHALSGSVEELLFLQN/G ARTER*EGPGEWPRPPPPGLASP ALWRFWAEQVGGSFQELESPS CRTARGSSRTWGSILQNSSWLF QDLGLHLAEGCFLETP
4139	34507	A	4180	33	896	KITRHCTAPGKIRIVPKESQEST PQQDGAPGPGRATSCSARWSPR SWKSHELFCKMEPQVLEEPRA VLQDGAPGPGRATSCSARKGR GPEKPVQGLPN/GSVRAHSGGR AAPQPSPRGHGPGRG*TAAPLP HLCPLTPVLLQG*GPD*WPLGW ATMRPLPLRAQPAPPPPHWML LTPSAPPPGTGKPQGGRGQTSG SCVPATDPHCRLSAPSPGKLGPP CDFLEPP*QRTTNWGSSEAGSP KSRCPRGHVPSGGSKGGIFLSL HFPGAPQSLEFPGSQPHGLIGAS
4140	34508	B	4181	1	625	

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4141	34509	A	4182	160	1149	FASERMKVEPWRAGPGRRAWS EGAGQAPQKRARAGAEPQLPA TPALPGGKMVARRTKLA\RGTR RT\YPEPTV\YAAIPIKFSEKQQA SHYLYVRAHGVRQGTKSTWPQ KRTLFVLNVPPYCTEESLSRLLS TCGLVQSVELQEKPDLAESPKE SRSKFFHPKPVPGFQVAYVVFQ KPSGVSAALALKGPLLVSTESH PVKSGIHKWISDYADSVPDPEA LRVEVDTFMEAYDQKIAEEEA KAKEEEGVPDEEGWVKVTRRG RR\LCSPGLRQPACGCWRGRDG SAA\KRAAQLLRLAASREQDGA SSAA\RKKFEEDKQRIELLRAQR KFRPY
4142	34510	A	4183	2	361	GTMVARRTKLA\RGTRRTGIPS PPC*A\AIPIMCSEKQQASHYLY GRAHGIQQGTKSTWPHKRTIFA FNGPPYCSEQESLSCLQSTCGL VQSVKLKEKLELGWESRSKFFH PKPVPVTEEQ
4143	34511	A	4184	917	1128	
4144	34512	A	4185	1	660	MAWQMMQLLLLALVTAAGSA QPRSARARTDLLNVCMNAKYH KTQPSPEDELYGQ/C/SWRKNA/ CSFTSTTQEAHKN/TSHLYGFN WNHCGEMVPACKRHFIQDTCL YE*PPNLGPWI\RRYAWLPGIQE LAEELNFPGVSAGSNPSSSSIQG WVPGILEPEPFFSTKISQVDQSW RKEWVLNVPLCKEDCEQWWE DCRTSYTCKSNGHKGWNWTSG SNKCQVAAA
4145	34513	A	4186	216	781	MDMAWQMMQLLLLALVTAA GSAQPR\SARA\RTDLLNVCMN AKHHKTQPSPEDEAVWPDP/W MCKGSCRKTKSWNI/HRKSKCE VGLA/WEACSVSAGTGRGPGC GRWVGAPQGP/CPRKCSSG*PT W/VQRSQNMEEMAVVNQSWR KERILNVPLCKEDCERWWEDC RTSYTCKSNWHKGWNWTSAPS AVCDPLL

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4146	34514	A	4187	3	625	QCRPWRKNACCSTNTSQEAHK DVSYLYRFNWNHCG\KMAPDC KRHFHPGTPALYE/CAPHNLGA WDPAGWIQSWRKERVLNVPLC KEDCEQWWEDCRTSYTCKSN WHKGWNWTSGFNK\CAVGAA CPTF\HFYFPTPTVLCNEIWTHS YKVSNYSRGSGRCIQMWFDAS PGATPIEEV\ARFY\VAAMSGAG PWAAWPFLLSLALMLLWLLS
4147	34515	A	4188	1	268	EQGRH/GSSTPVGPRGGPR\GAE HAPKHQGCGDRAGPQVGMDQ RRRDPPRAPAAPRPWCGQRAA LSSLGGSHLCDDA*VQPSAGLG KVLKF
4148	34516	A	4189	2	1632	WKRCPGLPRAAATFPSGSGAG GARREAGGRAPTPGPASPRTAR GHARNSPAPARTAGRTGSAGA WQTPCPAPLFPMSAGLPAACH WNPV*LRALKTG/LEGVLGGSA DTQHNRVTDGSLAPN\AACVYT PKINGNRHPNTCTKMFIVSLDA KGKKWKQPTVHQQRKRETCG LHPRKCLQYTPS*WSTTTGILPS RTPRISCVQFVKKKLGQAGLLG HPGACLLCTLP*\PAGVGTFLFP RGC*GVVH*LETHTCG
4149	34517	A	4190	2	87	
4150	34518	A	4191	3	291	
4151	34519	A	4192	112	286	AWLLWLTSLPWGSLYALALLA NKPAL*SLLLLRYTLLPPHHQC EKVPRWNEPQPTLFP
4152	34520	A	4193	1	933	
4153	34521	B	4194	1	999	
4154	34522	A	4195	135	1160	VWALVRSTLELFHTDDEEEGE YDEVTEEVTEQVYLPAKAKVA QEEEVHPYPSAPPHYYFEEKEW PDPPDLSFLEDTGRKVVAPVTE QHLERLLSVLFRQEFSRLDERD DAVEQLRGVCIRAWEKITSGGE QYPSFSAVKQGPKELYADFIAW NLLRQESLKKVISDSAAQDIVL QLLAFGNVNLDCQAALRPIRGK AHLVDYIKACDGIGAKQDSERF AFTIPVVNNLQPAKHFHYFTDG SSNGKASYSGSKGQNQQPIWIL SRHLKPYHEPDAKEEIPGG/CPR TPWLQPCRD*C*GGP*/PVTSNT R*TQPPTWGQIKKLSQMVEENL RKAGQLVTMTVYWN

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4155	34523	A	4196	502	578	LV*EDCIAERAEVLRNESYGIIID WSP*GMFSLNCTSQSACHGHT MFSW
4156	34524	A	4197	2	408	
4157	34525	A	4198	3	853	LLKVIMSAKIFTKKNENSTERL CGDGEKRGPDFRTERSVWLLR LEEAVAMVQRGSRAPESRVVA QVLTLLDGASGDREVVVVGAT NRPDALDPALRRPGRFDREVVI GTPTLKQRKEILQVITSKMPISS HVDLGLLAEMTVGYVGADLTA LCREAAMHALLHSEKNQDNPV IDEIDFLEAFKNIQPS/LVFEASL GLMGIKPVDWEEIGGLEDVKPE VKTAH/WSLRQKSGHC/RSCAR LPTGLLATLGSGSGSGRATEAV SGPAG*KRASIGGSSQRPRRFPT
4158	34526	A	4199	266	370	AERINSITVFSETLKRFLQASGK *FHRDIHNSRN
4159	34527	A	4200	1	1780	MGDVNQSVASDFILVGLFSHSG SRQLLFSLVAVMFVIGLLGNTV LLFLIRVDSRLHTPMYFLLSQLS LFDIGCPMVTIPKMASDFLRGE GATSYGGGAAQIFFLTLMGVA EGVLLVLMSYDRYVAVCQPLQ YPVLMRRQVCLLMMGSSWVV GVLNASIQTSITLHFPYCASRIV DHFFCEVPALLKLSCADTCAYE MALSTSGVLILMLPLSLIATSYG HVLQAVLSMRSEEARHKAVTT CSSHITVVGLFYGAAVFMYMV PCAYHSPQQDNVVSLFYSLVTP TLNPLIYSLRNPEERSHRGVKL NECNQCFKVFSTKSNLTQHKRI HTGEKPYDCSQCGKSFSSRSYL TIHKRIHNGEKPYECNHCGKAF SDPSSLRLHLRIHTGEKPYECNQ CFHVFRTSCNLKSHKRIHTGEN HHECNQCGKAFSTRSSLTGHNS IHTGEKPYECHDCGKTFRKSSY LTQHVRTHTGEKPYECNECGK SFSSSFSLTVHKRIHTGEKPYEC SDCGKAFNNLSAVKKHLRTHT GEKPYECNHCGKSFTSNSYLSV HKRIHNRWI*/YYCRNFWRKAL IDLSSLR*FERAHTGYISYLLQH
4160	34528	C	4201	18	182	
4161	34529	A	4202	1	389	
4162	34530	C	4203	114	548	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4163	34531	A	4204	122	735	LRAQQQHN*VLTLHKPACTLST TS*K*LHKIRK*LWHLRDRAPFI FTSEMEYFITEGGK/NPQHFQDF VELCCRAYNIIRKHSQLLLNLLE MNSYNGYVGLLHNILQLEREG LATKEELQQNFPPLSVSLPFDQS INQISEHRSLIFNGQYPYGSCWF RQAVCKLIQKYAGEWGWIATA ELRAEIDLNVLKFTIQVLSWKV QASLQ
4164	34532	A	4205	139	4496	KMAYSWQTDPNPNESHEKQYE HQEFLFVNQPHSSSQVSLGFDQI VDEISGKIPHYESEIDENTFFVPT APKWDSTGHSLNEAHQISLNEF TSKSRELSWHQVSKAPAIGFSPS VLPKPQNTNKECSWGSPIGKHH GADDSRFSILAPSFTSLDKINLE KELENENHNYHIGFESSIPPTNS SFSSDFMPKEENKRSGHVNIVE PSLMLLKGSLQPGMWESTWQK NIESIGCSIQLVEVPQSSNTSLAS FCNKVKK
4165	34533	A	4206	1	3150	MEKPRPLEAPSAWPQDDVQCG VTVGMDGAAVRANRTPWPQD LEQTKWIEIKKSAFTWSSQLSL NRGFLTCKDENNNAGLLRVSS YSSREDQLKNIASDSLFMLPGG LCQSPTGTSHCSNQMETQGQGS PGGAVRGDKALGPEKARQGCG MNGSGKYCKFRVLAIQGKPEC LATLMQPDLGDSPGLREMNVV EHLRASFPVEQWYWRGGQRGE AEGARSSKAENNTSLICNFRLD YAPIEKQWDLHFADYFAEDLK
4166	34534	A	4207	1	1203	

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4167	34535	A	4208	1	1470	MLHSRGFLAEVFGILARHNISV DLITTSEVSVALTLDTTGSTSTG DTLLTQSLLMELSALCRVEVEE GLALVALIGNDLSKACGVGKE VFGVLEPFNIRMICYGASSHNL CFLVPGEDAEQDGTGTSGIGAQ KKKMYANNGAIDRKLLFEATF VTIEKCCDTNQKGDDTHALGQ PIRGHDKSLAGSFCYACRSEEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNIAGDLTAVIAPDGS RNGTQYDAWGKAVRTTQGG\L TRSV\EYD\AAGRVIRLTSENGS HTTFRYDVLDRLIQETGFDGRT QRYHHDLTGKLIRSEDEGLVTH WHYDEADRLTHRTVKGETAER WQYDERGWLTDISHISEGHRV AVHYRYDEKGRLTGERQTVHH PQTEALLWQHETRHAYNAQGL ANRCIPDSLPAVEWLTYGSGYL AGMKLGDTPLVEYTRDRLHRE TLRSFGRYELTTAYTPAGQLQS QHLNSLLTYRHANFAL
4168	34536	A	4209	757	907	RRYCRITVRWQSM/WADNRIA VDAHYPYR*CRS\GRVTEKND\ LIPKG\VIRTDDERTHRYHYDSQ HRLVHYTRTQYAEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPQVTWYGWDGDRL TTIQNDRTRIQTIYQPGSFTPLIR VETATAVMDRILKDHQIVVDIP HGEAWLRDDEERPMILIAGGTG FSYARSILLTALARNPNRDITIY WGGREEQHLYDLCELEALSLK HPGLQVVPVVEQPEAGWRGRT GTVLTAVLQDHGTLAEHDIYIA GRFEMAKIARDLFCSERNARED RLFGDAFAFI
4169	34537	B	4210	1	3258	

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4170	34538	A	4211	281	1571	CQCPGAACPTTSCRVIPHWA\Y DEADRLT/HRTVN\GETAERWQ YDER/GWLTDISHISEGHRVA/V HYRYDEKGRLTGERQT/VHHPQ TEALLWQHETRH/AYNAQGLA NRCIPDSL/PAVEWLTYGSGYL AGMK/LGDT/PAANLDIRIPYAT DPA/GNRLPDPELHPDSTLSM/W ADNRIARDAHYLYRY/DRHGRL TEKTDLIPEGV/IRTDDERTHRY HYDSQ/HRLVHYTRTQYAEPLV E/SRYLYDPLGRRVAKRK/DRTR IQTMYQPGSFTPL/IRVETATGE QAKTQR/RQLADTLQQSDGED GGS\VVFP\PVL\VQML\DR\LESE SSADRVRSFISLANQSKCVEHA Y*RWQCHLGVCWWSSHQIPAV PLTGSVTRWHCHLASSSEAGSV AWLPHLSEGHSNRTSSPELLRS RMCAWHTLSAQSVHLVSLYIL EILALMNSINSL
4171	34539	A	4212	311	788	
4172	34540	A	4213	29	395	RIFHSVI\GVAAHKGGVYKTSVS VHL\AQDVAEIT/LLEGNDPQGT VS*YQGPGRTLIPLEAALRNIAH SLSIPPPKIFAAPTLRHYFALFFC GHSLFAPHIELLEAGTVLQLPQ GPWSSPTSF
4173	34541	A	4214	1	1033	MKMPEAIATKEKIDKWDLIKIK SFFSTPKETINRVNRHHTEWEDI SAIHLSDKGPISYIYKNLTRFTR KKQPHYKVGKGNEQTRILESHP HLLKGLASTPFDSEGVRTERRD IIKDGILTQWLLTSYSARKLGLK STGHAGGIHNWRIAGQGLSFEQ MLKEMGTGLVVPGTAENARSC IRAYFYDIHETLCRQEEMALSV VDDHVREKLIWLRQHQEDMTI LLSEVSAACLHCEKTLQQDDCR VVLAKQEITRLLETLQKQQQQF TEVADHIQLDASIPVTFTKDNR VHIG\PKM\EIRVVTLGIGMGAG KNLLSLF*V*NRVEFHGSPFPTI WFLTWETVGFLK
4174	34542	B	4215	414	1022	

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4175	34543	A	4216	896	1626	NATTIRYEHQRVLKAAQYLHQ QGITRCNSSSTLTSAAPGRVDSP PTSMIVAPALIIRFACFTASISEL CVPPSEKESGVTLRIPITHLMRE LTCRLIRDKSATVTGSHTLVVA RHCCYAAPGGCCLLANWLKPG LFGPIGVLSRRGTSVILPIGGFY QWNPMICPNGVVPMQHG*RRG LAQERPLEEWLPVCRDMLNAF FLPDAETEAAMTLIEQQWQAII AEGLGAQYGDAVPLSLLRDEL AQRLDQERISQRFLAGPVNICTL MPMRSIPFKVVCLLGMNDGVY PRQLAPLGFDLMSQKPKRGDRS RRDDDRYLFLEALISAQQKLYI SYIGRSIQDNSERFPSVLVQELI DYIGQSHYLPGDEALNCDESEA RVKAHLTCLHTRMPFDPQNYQ PGERQSYAREWLPAASQAGKA HSEFVQPLPFTLPETVPLKRYN DSVRAPTCAESRAIFTSTRNNTL QLFFNANFRRPWARGLATNVN DRRASVDHQIRMFHRIYQRVM RATIRKGIRRDVEDPHYSSDAG TYLSPNSRQISNGNWQSHIGRSP SLLLCRTWGLLFTGKLVETRFI WPNRGVIPTGNERYIAHRRFLP MEPDDMPQWRCPHATWLAEA KMFDSLAKAGKYLGQAAKLMI GMPDYDNYVEHMRVNHPDQT PMTYEEFFRERQDARYGGKGG
4176	34544	A	4217	838	1575	CFFLSPSPPSSPPSPNRSQTTEEE TKRQE/ERERKREEEEEKKGRR KETKKRRNRQEGKQHRKEEKE GEKQTKQRTETERETKRRRENE QAKAHKGTRKRKEEQKKAKA ARRRTHKRQNPSRGREGTHPK QRQGKEE/VNRQNKEEAKQKR EEAGRTRR/EDRGRKDDKKERR QQQTEKKAKPKAEHGQERTDT TTKKARQREGRPSERRRREREE/ MSKHDPQNRAEKTNEEKEEGR QHER*TQKSSTGI

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4177	34545	A	4218	1	692	MNALHAEALEMTSQFDQELAA KFEADHEMALLMNKDFDRDRE EQRRLAEQARREHEERIKREAA EQARRDAEAKHKAEIEAAARR EAEEKARAELAERQRIEAEQRA EREKKETEERARREKEEAVAAE RRRQEEAEAARLVEEQRKAEE EARRAADKEHRRTVNRR/GLRR SDCSGHPRRIRTESSAGDRWRQ SAGRAHQILRQT*THTSLTTAS KNGAGLSSNSPTRKRS
4178	34546	A	4219	3	1120	
4179	34547	A	4220	1	831	MVKARKIMETPQPAWEMRVRI CTVDWSKLNPYIPDDFSLIKSEK KYDHPELIVDESNLRVVYAPSR YFASEPKADVSLILRNPKAMDS ARNQALLEGYFSFTATEDQLEQ AKSWYNQMMD/SPEKGKAFEH GNMPA\QMLLQVPYFLRE\ERE H*IIITPILHMRKQEQSG*/RNLP KAAQLSMMQDLQTLLMAASY CSELGHVATQFQGMLACTRNP NSWDRNSETSGKAEGFIPMQLG DVADPSVRCSSVSSLWGHSSPK LLRSVCMANRICVKLQRWT
4180	34548	A	4221	1	1503	
4181	34549	A	4222	1	1113	
4182	34550	B	4223	1	760	
4183	34551	B	4224	1	1755	
4184	34552	C	4225	1	4215	
4185	34553	A	4226	1	3240	
4186	34554	A	4227	1989	2144	
4187	34555	A	4228	1	1203	
4188	34556	A	4229	1	4767	
4189	34557	A	4230	31	512	EYRKSPDIRPIVIQHGEEAEITH HFR*QELADKTLIFEITHREMQR FQPVGTGDIREPVFVFFRWRLT NPFNILEHGEPEGIRVDAAVPR AVIGGLEDHIGVAVQKLQHKTF RYFPFIIQMVKDGVVPEGRPAF VHHLSLFLRIKILAHLTHNTQDF
4190	34558	A	4231	369	918	RPGMSNPWRDLFRTGVDPTND RLSALVEI/YRMMRPGEPPTREA AE/SLFENLFFSEDRYDLSA/VG RMKFNRSLLREEIE/GSGILSKD DIIDVMKKL/IDIRNG/KGEVDDI DHLG/NRRIRSVGEMAENQFRV /GLVRCTGTVPPFLHQQKCEYH L/PQRPVASTLSRYF*HFRLRNF SMPRANEIKKGMV

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4191	34559	A	4232	3	1012	SVVLKIVERVDGYFPSPPLFLGA AFGSHVRSRALPDPCVLFRVTI YLCVLASVARTFSPLLPVSRKK HITPLGGFQLHETHLCLQDCRTI ILRPRLGEFGNKFSQLVDTIDLH \NQHGLAHL*KESARGQYSLLL LGMVSLCALILILWRVVYRSVT CPLADQTQALHRLLDGDIVSPF PETAGVRELDTIGRLMDAFRSN VHALNRHREQLAAQVKARTAE LQELVIEHRQARAEAEKASQAK SAFLAAMSHEIRTPLYGILGTA QLLADNPALNAQRDDLRAITDS GESLLTILNDILDYSAIEAGG\K NVSVQSYVARLEPVAASGWHK YPWLN
4192	34560	A	4233	1	502	
4193	34561	A	4234	1	653	
4194	34562	A	4235	2	300	YALATPPLSV/INQWQLALDKG QLPTF/VAGLAPQHPQYAAMHE SYWPYSALR/EILQRTGMLDGG PKITL/PGDDTPTDAVVSPSAVT NSHGR*VPTLGGVWGL
4195	34563	C	4236	40	105	
4196	34564	A	4237	355	526	
4197	34565	A	4238	116	949	RPGTGRCSAVQLPVLLLRGPHS SHTVGTH\MVDLDSGQLCVYP GNSDESMPAATQARERLLADT AKKKAQIAELQSFVSRFSANA* KSRQATSRARQIDKIKLEEVKA SSRQNPFIRFEQDKKLFRNALE VEGLTKGFDNGPLFKTLNLVL\ EVGENLPVLGTNGVGKSTL\LK TLVGDLHPDSGTVKWSENARI GYYAQDHEYEFENDLPVFEWM SQWKQEGDDEQAVRSILGRLLF SQGDIKKPAKVLSGGEKGRML FGKLMMQKPNILIMDEPPTHP
4198	34566	A	4239	1	319	MVKKMARAPMI\L\ALANPEPEI LACRHGRKEVRPDAIIC\TPGRS DYPNQSETNVL\CFPANVHRIPQ AASHLRAHQSRIPISLMSISAKIL TYLLANQIQFLVKQH
4199	34567	B	4240	263	1390	
4200	34568	A	4241	1	323	
4201	34569	A	4242	3	1855	

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4202	34570	A	4243	2	964	LLKHGVSLYIQDKEGLSALDLV MKDRPTHVVFKNTDPTDVYTW GDNTNFTLGHGSQNSKHHPEL VDLFSRSGIYIKQVVLCKFHSVF LSQKGQVYTWGHGPG\GRLGT WEMNRHAWVPRLVGRD*MVII VSPSWPAAKDHTVVLTEDGCV YTFGLNIFHQLGIIPPPSSCNVPR QGLHNRQNRRYPPVPGSAGPTS MEPSKIRPTGLKFSLTTQQQSEI DLGCSSLCWDYRREPLRLAYW FIKKDIAKDTDEETRRHGVSLYI QDKEGLSALDLVMKDRPTHVV FKNTGSLQFQSIPSCRESQILSEK QGDLFREEPMFGS
4203	34571	A	4244	1	725	FRVDPRVRKHFGLFYAMGIVL MMEGVLSAC*HVCPNYSNFQF DTSFMYMIAGLCMLKLYQTRH PDINASAYSAYASFAVVIMVTV LGVVFGKNDVWFWVIFSAIHV LASLALSTQIYYMGRFKIDLGIF RRAAMVFYTDCIQQCSRPLYM DRMVLLVVGNLVNWSFALFGL IYRPRDFASYMLGIFICNLLLYL AFYIIMKLRSS*KVLPVPLFCIV ATAGMWAC\ALYFFFQNLSSW
4204	34572	A	4245	1	833	MKPVWVATLLWMLLLVPRLG AARKGSPEEASFYYGTFPLGFS WGVGSSAYQTEGAWDQDGKG PSIWDVFTHSGKGKVLGNETA DVACDGYYKVQEDIILLRELHV NHYRFSLSWPRLLPTGIRAEQV NKKGIEFYSDLIDALLSSNITPIV TLHHWDLPQLLQVKYGGWQN VSMANYFRDYANLCFEAFGDR VKHWITFSDPRAMAEKGYETG HHAPGLKLRGTGLYKAAHHI/ KAHTL*VCFHAADKGIPETEKK RRLNWTYSSTWLGRFHNHGRG
4205	34573	A	4246	1	672	GTQNAVNG/VIIFLSWGDAVKS FWIYRGGRKREGPLFHA*Q\FLI YTIIIRAVGSIINYVIANYKLKFI TPGVIDFICTSLIAGILTIKLFLLI NQFEKQQIKKGRDITSARIMSRI IKITIIVGLVLLYGEHFGMSLSG LLTFGGIGGLAVGMAGKDILSN FFSGIMLYFDRPFSIGDWIRSPD RNIEGTVAEIGWRITKITTFDNR PLYVPNSLFSSISVENPG

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4206	34574	A	4247	1	347	PLRP\GQPGPGGAGT/RALRAPP LPSSSELCYGPGQPGRWPRCPQ FPSLPPHSS*LLHTGHWPCTLGY CFIPILRAAPPLPCKCASPVL\SC TYPLPAAPSLPVLVHTSIKCFCF HLQ
4207	34575	A	4248	43	446	VLPAVPRPGQ/PPCVPAPVQAPE PPRPSPGWSQATGSPGPAGAAP SWR\GLPAVPGHTAGVLGPGPP GQRQPGPGGAGTQLCGPHLFL RLLNVAYGPGQPAL/RNVPLQT APALTPSPQHLLCPFLSTHLLNA SVFIC
4208	34576	A	4249	1	1521	RIPESRLPTTAFVQAPWARSGSS GLRRWEKHAGQQVGWWARGP GVRGRQAAGGGAAALTCRGG AGSAVRSCAGLPSLASGSAGCR LHPSYSFGFKVGS/PTVPAALSS *STS/RGREHGGVTVVPVMTQN PRS\PDGPARVEDCEAIA*GTG WL\QQGIGTRPPGTGLGRAR\G APAVPQWNPV\KSCQGPGHPNR LPSHGPSSGEAGRGW/RGLQITP QL/PEVTHRRVLPGDHPATEA\G GFGTG*PGLPGRVPGPGVGGTY QAKALTPLGPVGLLAPASCAQC LQQSADGPGATGHL*ELAESQC RRQPTG\PPGQLAVSGWATVPG VPAAPRPFGPAQQPA/SVPTPSY WA/GSPGAAAWPESHRR*ACD WAW**VLPAVPRPGQ/PPCVPA PVQ\PQSHRGPAHDGARLY*GL PQAEQLHPGGGLPAVPGHTAG VLGPGPPGQRQPGPGGAGTQL CGPHLFLCFLNVAYGPGQPGR WPRCPQFPFLPPILSWNIFGVGT QKKKKKNQSFLKKKKKK
4209	34577	A	4250	167	582	RSLGLAVTEMVPWVRTMGQK LKQRLRLDVGREICRQYPLFCF LLLCLSAASLLLNR*RRSAEPGR RL/SL/LKVQTPGPCCLTVRRPRS CGTGDQWGERAPQRSGLGEHG GASRPEAQAGGVGLIASFPEAS SPELPFSHP

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4210	34578	A	4251	402	1465	DLILSHPTAWFTIKYKPKQLGL QELFPQGHSCAVCGKVKCKRH RPSLLLENYQPWLDLKISSKVE\ ESLSKDLELVLENFVYPWYRD VTDDESFVDELRITLRFFASVLI RRIHKVDIPSIYNQETIKSSNESI *KWIVKARQKVKNTEFLQQAA LEEYGPELHVALRSRRDELHYL RKLTELLFPYILPPKATDCRSLT LLIREILSGSVFLPSLDFLADPDT VNHLLIIFIDDSPAEKATEPASTL VPFLQKFAEPRNKKPSVLKLEL KQIREQQDLLFRFMNFLKQEGA VHVL\QFCLTVEEFNDRILRPEL SNG*NAVSS/WKNCRRFIKHTV WMKVLTKLDLIPSLVEEIPR
4211	34579	A	4252	1	1232	FPGRRFRLVVRLRGAEAASERQ VYSVTMKLLLLHPAFQSCLLLT LLGLWRTTPEAHASSPGAPAIS AASFL*DLIHRYGEGDSLTLQQ LKALLNHLDVGVGRGNVSQHV QGHRNPTTCFSSGDLFTAHNF\S EQLRIGSSELHEFCPTILQQLDS RACTSENQENEENEQTEEGRPS AVEVWGFGFLSVSLINLASLLG VLVLPCTEKAFFSRVLTYFIALS IGTLLSNALFQLIPERSYKNKAQ VDSLPTFLAQAGMLLWRVRIR RRVVDPIRESWMLPFTKIPLWG YGLLCVTVISLCSLLGASVVPF MKKTFYKRLLLYFIALAIGTLY SNALFQLIPENRRKWWQPVHN TFGGSTAWHTDKSIEQSIDTLFD EVKKESEKETPSLQIGDLGPQES LKTFNNTNSPHH
4212	34580	A	4253	3	924	VGACTAAARPLPIPQLQPILHHR GEKSQLWAHSGSSWGFLAVAA VPPSHLCPPLQSRGWKRPP/PLA SAGVLPGCCCCACLVSPSLAQP AG\LGPKPAAPLGPGPWVSVAP CSRPGPCPGTRSPA/P*GHPAMG R\GVHEPRVGPAPPEKAIITETG AGLAERRGQGLGGGSSFRSAEP QGCRSLGPQSPGGDPAHTILRPP SQNGDCAEMHACRLHPAILGT HGTGGLAAQSHAPRALLPSCPS SQQPADGWCSLHLCLPGLLLAP RIHGPSTREGGPGHGTPGPTNP ASSGATRGTRRVRPSVPRSPTL

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4213	34581	A	4254	1	318	VADPVGAARAGGQPLAGRVW PRAGGGHSPRVLGAAGPGPHV CTLRLPGTAIRTEPGAPLACAR AWPGSSPAG/PECLPTSC*P*EG QEPSSHVASLPWGPGVGETQ
4214	34582	A	4255	1	718	FFFFFFSFLCHLYWVSPTPGPHG KLANMANWAPWPS*GLSKLVG KHSCPAG*LPGHARAQASGAP G/ISPDSSAREA*ECT/PCGPGPA APSTRGECPPPSSRPHS/SQQDP GRCSFAPAVPQDAGGQGHWCC APATGHSAPRGCPPARAAPTGS ATPAPPPAACAASSLSMVSAPS R*TTGIASSGTSIPETKHQGTPG TAPAGT/GPGGSTGPKA/PGPAP AHPTRLAGTSGHTAPPTCPPAV
4215	34583	A	4256	702	1026	RSGRTQRAAGVSGSALHQVQS WP\HLKISADQRAGLLF*EHPFP PSASSGCLDVSISSYPVGSD*FIN GMARANGRWKTFTGLHSGKPL GFSDAFCQHHNLIILCWKTW
4216	34584	A	4257	170	1049	RGSGCSAELVPSSRWRPGSRAG AAAGTETPG*PRVYVPAGNGE AGGPGAAWARRAAALPGTAA GPPRPAARPGAAPARGGPAPGA PAQALPR/TPTWPAAR*AQRAP SPPSWGS\AQPGHPGDLAAGVG RGAGGGHSRRGRHHHVRSLAD LLQLPGAAEGAGDRGHLPGPD/ GERS*AASSFSAAGRAAGTASC CSAGGTPPSPCTILSTSSSSLAH VASSS/RRRAEGDTKVS/RGRAE GQDSETGREPGVLHRGSGRTQ RAAGVSGS/RSAPSPVVATTSRS LLTSVQGCFSENILSP
4217	34585	A	4258	178	556	QSPQEHFHPECGRRDILCQVRQ EIRWPNPGEVHHLGLEICPVWI LQLHLALRTRAPEHPLQVHRPG GGAV*RGVPPPLRLLQACDGPE VPAAGRPRPARSSPGQWPP*/PA AVAPPVTERPPTPSAA

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4218	34586	A	4259	5	1044	TGRILDGWHWAKELRLDCPLG DSRRPPFSRVSTEGSPAFLALRL PNVTAGS*EVSMLASTETPLVIT RPSPG\GHDPGPAPRGAAASPA GSPAP*QKSPRPLSAAAPPLLAS DPAPPRAAAPPADTESSVQPPA APHAGPWT\PSAPGPLDVHSPPP \PSRGPFVQSSAEPHNRPSPGAT RPRP\PPRGAAASPAGSPAP*QK SPRPLSAAAPPLLASDPAPPRAA APPADTESSVQPPAAPHAGPWT LERSWAP*RSLPTPIPVADPLCR APLSHRYP*GDCQRSGLCHTSP GRASHLPGPGAHKRTPHACWL PLECHRRSPHP*THPSG*PGPSP QSFFPEFLGSGP
4219	34587	A	4260	2	576	CLVNSTTRRSFQLRLVPVPKFQ PPHMTVR*LFNFGRQLTATTFS/ LRKSYAVREAYELQNCPDPPPF QNGYMINSDYSVGQSVSFECYP GYILIGHPVLTCQHGINRNWNY PFPRCDAPCGYNVTSQNGTIYS PGFPDEYPILKDCIWLITVPPGH GVYINFTLLHTEAVNDHIAVW YENLSSQNICDCDQQF
4220	34588	A	4261	1	837	MWAGNAWRAALSGVPCGRSA QSVLAQLRGILEGELEGIRGAG TWKSERVITSRQGPHIHVDGVS GGILNLTSVRFIRGTQSIHKNLE AKIARFHQREDAILYPSCCDAN AGLFEVLLRPEDAVLSDELNCA SIIHGICLCKAHKYHYCHLDVA YLETKLQEAQKHRLFLVATDG AFSMDGDIVPLQKICRLASRYG ALVFVDECHATGFLGLTGQGT DELLGVMGQVTIINSTLGKALG GASGGYTTGPGPLVSLL/RAQP YLFSNSLPPAVVGCTSKAL

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4221	34589	A	4262	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
4222	34590	A	4263	1	1989	
4223	34591	A	4264	1	1104	
4224	34592	A	4265	1	879	
4225	34593	A	4266	1	1659	
4226	34594	B	4267	1	1500	
4227	34595	B	4268	1	1962	
4228	34596	B	4269	1	1716	
4229	34597	A	4270	1	1152	
4230	34598	A	4271	1	4752	
4231	34599	A	4272	1	2790	
4232	34600	A	4273	1	3477	

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4233	34601	A	4274	1	1007	MLDASCHRTSDSKFFSFGVQTG FLTPELAHLVGPCDRDHNSSPA REQNWTENEFDELTEVGFRKW VITNSSELKEHVLTQSKEAKNL EKRAIKQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVSAQNL LKLISKFSKVSGYKINVQKSQA LLYTNNR\SQIMSELPFTIAMKR IKYLGIQLTRDVKDLFKDNYKP LLKEIREDTNKWKNIPCSWLGR INIMKMAILPKAIYRFNAIPIKLL *TFFTELEKTTLNFIWNQKRARI AKTILSKKNKAGGITLPDFKLY HKATVTKTAWYWYQNRYIDQ WNRTEASEITPHIYNHLIFDKPE
4234	34602	A	4275	737	2460	RIKYLRIQLTRDVKDLFKENYK SLLNEIKEDTNKWKNIPCSWIG RMNIIKMAI/LPKVIYRFNVIPIK LPMTFFSELEKSTLKFIWNQKR ARIAKTILSQKNKAGGIMLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTEPSEMTPHIYNHLIFD KPDKNKQWGKDSLFNKWCWE NWLAIGRQLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLG NTIQDISMGKDFMSKTPKAMA TKAKMDKWDLIKLKSFCTAKE TTIRVNRQPTEWEKNFAIYSSD KGLISRIYKQLKQIYKKKTNNPI KKWAKDMNRHFSKEDVYAAN RHMKKCSSSLAIREMQIKTIMIY HLTPVTMAIIKKSGNNRCWRG CGEMGTLLYCWWDCKLVQPL WKTLWQFLRDLELGIPFDPAIP LLGIYPKDYKSCCYKDTCTPKL ARDDQIHILKQHRRKELETRQK QYRAWYEINPFHSVWPVTAGK SPRHQLPVWVHNPQTSPYLQL QTRDGEESNENNFGSTILASDFF AEIDKLSILQIHMEMEGTQNSQ NNLDKKKTKMEDLHFSISKLLH SYSIQDNVISA
4235	34603	A	4276	3	355	RQPVHLVHELPQQSWGICLNSS EQHGALQHSSLHL/RMCSEPWS SADPQ*R*TCRNL*LPVRGPPRR TDLFSVSSKSTLKEWPLLLMIL AELGSYLILSGRREESYFTSLVL ISIGDC
4236	34604	B	4277	78	791	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4237	34605	A	4278	1	3395	MIISIDTENAFEKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVMARVIRQEKEIK GIQLGKEEVKLSLFVDDMIVYL ENPIVSAQNLLKLISNLSKVSGY KINVQKSQAFSYTNNRQTESQI MNGLPFTTASKRIKYLGIQLTR DVKELFKENYKPLLNEKKVDT NKWKNIPCSWIGRIN\ILKMAIL P/KELEKTTLKFIWNQKRACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEII\PHIYNHLIFDKPDKN KKWGMGSLFNKWCWENWLAI CRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI DMGKDFMSKTPKAMATKAKID KWDLTKLRSFCTAKETTIRVNR QPKEWEKIFAIYSSDKGLISRIY KELKRIYK/KKNNPIKKWAKD MNRYF*KEDIYAANRHMKKCS SSLAIREMQIKTTMR/YHLTPVR MAIIKKSGNNRWEMNNENTWT QEGEHHTLG/HC/WWKARRSRS CLTWMAAGKKRMRKTLQMT
4238	34606	B	4279	1	2011	

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4239	34607	A	4280	1	2661	MTMNFVADSHTGRNPLASAAG AKTGLRPLPRPCGARVWNPPD AGGGGVGSLKTSTPLGPLSAAN SPVHQGSVPQTRARGGGTLFQE VVTSRTLAFRNSLSAFTEVTSG TVSGRKGGRSTHLAGRRVSGG EGSRKAAAAALAAVAAAPGPV RRCSSQSCFSSSGSSHYSARTSP VRVRPRRSLSSRSAAGNRAEAT ESAMEKTLETVPLERKKREKEQ FRKLFIGGLSFETTEESLRNYYE QWGKLTDCVVMRDPASKRSRG FGFVTFSSMAEVDAAMAARPH SIDGRVVEPKRAVAREESGKPG AHVTVKKLFVGGIKEDTEEHHL RDYFEEYGKIDTIEIITDRQSGK KRGFGFVTFDDHDPVDKIVLQK YHTINGHNAEVRKALSRQEMQ EVQSSRSGRGDGYGSGRGFGD GYNGYGGGPGGGNFGGSPGYG GGRGGYGGGGPGYGNQGGGY GGGYDNYGGGNYGSGNYNDF GNYNQQPSNYGPMKSGNFGGS RNMGGPYGGGIWKNTSITERK KSRKLDLIQSKKGSRTKEAPQP PVASLCMHLGHWSRLMVSPGA QLTGKNSHGLSVSSVRKSNVGP RRLCAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTD RPHPFLSRPKPPTQISLVLPLKT DGALERMPQQL/HIASS/GAKVP NPSTQTPPVLLAFFYPFNLPP*N
4240	34608	A	4281	1	908	MRKVKGKNRQSFKCLPPPSGA LQAHGAAAPHGSLLTLHLHLV PVSSAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCED RPHPFLSWPTWISLALLLKTDG ALERMPQQLPSLHPSQGTQSIH PDPSSTSSFLLPFQPPTLKRAAFP CPPSIVNPAVWDTSTPSVAEHH TPIRITLKEPTQFLSQKQYPIPQA ALVGLQPIISHLLASHLLRPTDS PFNTPILPVKKPNGTYRLVQDL RLINQAVLPLVQE/DYSVLLYLP LNVTPGLPPATAFSYPPSPGPVA RARLASRLHSHAA

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4241	34609	A	4282	1	915	MPNYVTFTDTKQLISDTPNNQV PMNRASMAFDAKCLTGCRFDD AIVQFDMTYWPFTVVNDAGRP KVQVEYERDKKLLPIGGVFYGS DKDEGNCKSLPWEDCYQCCET SQNVQDFLFLDVTPLSLDIKTA DGVMAVLIKCDATIPTRQTQTF TTYSDKPSM/LIAKDKNLLRKFE LTGVPPAHHGAHQIEVTFDINA KGILNV\TLTDDKGHLSKEDIEP MVQETEKYKAEDEKQRDKVSS KNSLDPYVFNMKATAEDEKLQ VKINNEHKQKILSKCHEIINWL DKNQTAEKEEFEHAQQELEKSS
4242	34610	A	4283	1	994	MHQTKKGNQWHFGMKAHIGV DAKSGLTHSLVTTRPNEHDLNQ LGNLLHGEEQFVSADAGYQGA PQREELAEVDVDWLIAERPGK VRTLKQHPRKNKTAINIEYMKA SIRARVEHPFRIIKRQFGFVKAR YKGLLKNDNQLAMLFTLANLF RADQMIHCTRGEGLITTKIPKAP DNGSYCLPSKNDDSEEEDPEMS PMVVTKMKEIAEAYLGKTVTN AVLTVPAYFNDSQRQAT/KKDA RTIAGLNGLRISNEPTAAAIAYG LNQKVGTERNVLIFDLGGSITPR IRTPETGSDDAIKSILEQAKKEIE SQKGGECDPCRQSLRPPGPAAN
4243	34611	A	4284	3	677	
4244	34612	A	4285	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRLLARAEKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLV\CRKMGVP YCIIKGKARLGRLVHRKTCTTV AFTQVN
4245	34613	A	4286	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
4246	34614	C	4287	62	217	

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4247	34615	A	4288	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRAILYKRLKVPPAINQFTQAL DRQTATQLLKLAHKYRPETKQ EKKQRLLARAEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVDPIELVVFLPA L\CRKMGVP\YCIIKGKARLGRL VHRKTCTT\VAFTQVNSEDKG\ ALAKLVEAIRTNYNDRYDEIRR HWGGNDLRPK\SVARIAKLEKA KAKELATKLG
4248	34616	B	4289	1	273	
4249	34617	A	4290	1	441	
4250	34618	B	4291	47	482	
4251	34619	A	4292	1	762	
4252	34620	A	4293	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
4253	34621	A	4294	1	1674	
4254	34622	A	4295	1	506	KYHTVNGHNCEVRKALSKQEI ASASCSQRGRSGSGNFGGDRG GGFGGNDNFGRGGNFSGHGGF GGSCCGGGYGGSGDGYNGFGN DASNFGGGGS/YNEFG/NYNNQ SSHFGPLS/GGNFGGRSS/SPLGG APASTYVKGPNSQRTQNEGWF EG*APWRGDGGARGNKGGGA

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4255	34623	A	4296	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCEGWIEEER DESRKSETIFKDLFKVPVLKETI YYKFYGPPVYQIETVYFMALSP PKSKQFDKTKQNNNNKKTHQF VIVFFKTDEHLSARGRRRRSIVK VSLLPAVIGLKSKFLKKPDQLR KLFI\GG\LSFETT\DESLEEPFSR QWGKRYTDSVVMRDPNTKRSR G\FGFVTYAT\VEEVDAA\MNA RPHKVEWKELLEPKRA\VSRED SQRPGCPH*LVKKIFVGGIKEDT \EEHHLRDYFEQYGKIEVIEIMT D\RGSGKKRGFAF\VTFD\DHD\S VDKIVI\QKYHTVNG\HN\CEV* KSPVKSKKMASASSKPKEGRSG FWETFGGGSWEVGFGGN\DNF GRG\GNFSWSVVAFGGSRG\GG GYG\GSGDG\YNGFGNDG\SNF G\GGG\SYNDFG\NYNNQ\SSNF GPMKGG\NFG\GRSSGPYG\GGG QYF\AKPR\NQGGYGGSSSS\SN
4256	34624	A	4297	1	920	DPGDTPNTASAPNCRSGKGRSS SPEHIPPLEKLEDSMQTNPSTNP EPGRLAEWLDPEERQQSLQFGL QEATSIGKGGQYYIKGTPHGTK ESEQQPSALDLPSDRAYPNEKE PENQLWRLVIKLIKEAPEKGAY LNVIKAVYDKPTNGEKLRAFPL RTGTKHRCPLSPLLFNILLEVLA RAIRQEKEIKSIQIGKEEVKLSLF ADDIIIYLESPKYSSRKLQELIKE FSKVSRYEINVHKSVALLYT\NS NQAENQIKNSASFTIAAKNKIK YLGIYLTKDAKDGYKENYKTL MKEIIDDKNKQKYIP
4257	34625	A	4298	1	1194	
4258	34626	A	4299	3	1834	
4259	34627	A	4300	285	502	
4260	34628	B	4301	77	1306	
4261	34629	A	4302	1	354	
4262	34630	A	4303	1	1182	
4263	34631	B	4304	1	1995	
4264	34632	B	4305	1	1518	

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4265	34633	A	4306	1	918	MCPVGPWTHPVVISPVSECIVGI DILGSWQNLHIGSLTDITMVHYI DDMMLIGSSEQEVANSLDLLV RHLHARGCKINPTKIQGTSTSV KFLEFQWCGVCQDIPSKWVLE QKALQQVQAAVQAALPLEPYD PADPMVLEVSVADGVAVWSL WQAPIARIHGSRNQGVEVEVSP LTNIPSDPLAKFLFPAPSTLCSA GLELLVPEGGTLLPGNTTMIPL NWKLRLVPGYFGLLLALSPQA KNGVTVLAEVIDPDYQDEITLL FHNGGGEEYARNTGDPLRHLL VLPSPMIKVNGK\LQHPNPGRT
4266	34634	B	4307	1	1599	
4267	34635	B	4308	1	1569	
4268	34636	A	4309	3	422	
4269	34637	A	4310	1	1089	
4270	34638	A	4311	2	549	LKMTAMQRPMEKRMMNREIIL KERLSLTGIDIKILKKRSIMKVE SHRGEQISVSSLALQRIKYLGIQI TRDVKDLFKENYKPLLNKLKE DTNKWRNVPCPRVGRISIVKM AILPK/ILKKKTTLKFIWNQKRA HIAKTILSKKNKAGGITLPDFKL YYKAT/KTAWCWYQNRDTDQ WNRTKPSEI

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4271	34639	A	4312	371	3036	LIAYQPKKVQDQMDSQPNSTR VLEVLARAIRQEKEIKGIQLGK/ EEVKLSMFADDITAYLENPIVS APNLLKLISNFSK/VSGYKINVQ KSQAFLYTNKRQTE\QIMSELPF TVASKRIKYLGIKLRRDVKDLF KENYKPLLNEIKEDTNKWKNIP CSWIGRINIVKMTILPKVIYRFN AIPIKLPMTFFAELEKTTLKFIW NQKRAHIAKTILSQKNKAGGIM LPDFKLYYKATVTKTAWYWY QNRDIDQWNRIEPSEIIPHICKH LIFDKPDKNKKWGKDSLFNKW CWENWLAICRKLHLDPFLTPYT KINSRWIKDLNVRHKTIKTLEE NLGNTIQDIGMGKDFMTKTPK AMATKAKIDKWDLIKLKSFCT AKETTIRVNRQPTEWEKIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHMKKCSSSLAIRETLYNDR RIGKLTQTCDETAFQPHVCTISR PMLSSPYRSSLTEKWSQDFSKP PYPFLFHKGYLNPREQDKEVLT RAIRQEKERKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNPLK VVSNFSKVSGYKISVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLRIQLTRDVKDLFKENCKP LLNEIEEDTNKWKNIPCSWIGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTVLEKTTLKFIWNQKRAH
4272	34640	B	4313	1	1995	
4273	34641	A	4314	3	549	
4274	34642	A	4315	3	614	EAYGQTECTGGCTFTLPGDWT S\GQFINILEMCLELSPCKSFSAD SARYVLGHVGVPLACNYVKLE DVADMNYFTVNNEGEVCIKGT NVFKGYLKDPEKTQEAL\DSDG WLHTGDIGRWLPDIENHNRLIV CTLTNTSWRSHKIIVLKTYQKA DDTKTPKETTFQNIMNLFLKEK RATAVLIRGGVGETSTDLSKKK PAKLLANF
4275	34643	A	4316	1	478	MKLDLHLSPYTKINSRWIKDLN LRPETIKILEDIIRKTLLDIGLGK DFMIKNPKVNATKTKINKWDLI KLK\NFCTAKEISSREIREPTEW EKIFANSASDKGLISRIYKELKQ IRSTLQLLFGISELPASLFLGFGA IMKSKKASLNTSTAILRQLIW

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4276	34644	A	4317	1	1125	MCHGIGAQIIPSHQTVQLDITAF LKTVKKNKHKFYPAFIHILARL MNAHPEFRMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYYTQGDKVLMP LAIGGPLESPDRDGGPLESTNR DASPESWSCRKSTPRLVAWVS AAKVFIRDKLMERRNRRTGRT EKARIWEVTDRTVRTWIGEAV AAAAADGGGFRVDLARRSIRK DRNARSQNPVHTEGDMNMNIK KIVKQATVLTFTTAFLAGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKVGDN SID\SWKNAGRVF
4277	34645	B	4318	1	1374	
4278	34646	A	4319	1	1293	
4279	34647	A	4320	1	1278	
4280	34648	A	4321	1	1254	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGV\N GYYCEES\LFNKA\YYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDGINSNDIYML GYVSNSLTGPYKPLNKTGLVLQ MGLDPNDVTFTYSHFAVPQAK GNNVVITSYMTNRGFFEDKKA TFAPSFLMNIKGNKTSVVKNSIL EQGQLTVN
4281	34649	A	4322	1	726	
4282	34650	A	4323	1	1050	

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4283	34651	A	4324	1	1185	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YT\LKKVMKPLITSN/TVPQAKG NNVVITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QGQLTVN
4284	34652	B	4325	1	867	
4285	34653	A	4326	1	495	
4286	34654	A	4327	3	1394	GDMNMNIKKIVKQATVLTFTT A/LLAGGATQAFAKENNQKAY KETYGVSHITRHDMLQIPKQQQ NEKYQVPQFDQSTIKNIESAKG LDVWDSWPLQNADGTVAEYN GYHVVFALAGSPKDADDTSIY MFYQKVGDNSIDSWKNAGRVF KDSDKFDANDPILKDQTQEWS GSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDTLKI NGVEDHKTIFDGDGKTYQNVQ QFIDEGNYTGDPLEAETAVINH KKRKNSPRIVQSNDLTEAAYSL SRDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAMRLY ESLCQYRKPDGSGIVSLKIDWII ERYQLPQSYQRTPDFRRRFLQV CVNEING
4287	34655	B	4328	9	1004	
4288	34656	A	4329	1	768	
4289	34657	A	4330	1	1308	
4290	34658	B	4331	58	753	
4291	34659	B	4332	1	409	
4292	34660	B	4333	1	921	
4293	34661	A	4334	1	1026	
4294	34662	B	4335	1	945	

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4295	34663	A	4336	1	528	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFY/Q KDQTQEWS\GSATFTSDGKIRLF YTDYSGKHYGKQSLDTA\Q*NV VKSG
4296	34664	A	4337	1	1701	
4297	34665	B	4338	97	1449	
4298	34666	A	4339	1	1581	
4299	34667	B	4340	1	1539	
4300	34668	A	4341	87	1078	SLPNLDNAAICSSSSSPTRTR*SL SEGATQ\AFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNSIDSWKNAGRVFKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSLGTLQGFPAPAWLALAHP VHPLKHKSGGSNRLSAAIWGIK RKPAR
4301	34669	A	4342	1	1344	
4302	34670	A	4343	1	1713	
4303	34671	A	4344	3	1918	
4304	34672	A	4345	254	1118	RPPAFAKK*PKAYKET/YGVSHI TRHDMLQIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGK IRLFYTDYSGKHYGKQSLTTAQ VNVSKSDDTLKINGVEDHKTIF DGDGKTYQNVQQFIDEGNYTS GDNHTLRDPHYVGGTSWEPGV FSVSCVFFGQQEGV/HG*DEFLD FSYWFQGG*ICLYQKAS*QNTT SYKRYTGS

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4305	34673	A	4346	1	1952	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVFQDHTGTEEHPQPQ\ERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIAYLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHLPDLCSPSQDAQTTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTV
4306	34674	A	4347	1	1029	
4307	34675	A	4348	276	1248	CVWLGCRGYYPKAYKETY\GV SHITRHDMLQIPKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQQLLQLVQFQEVDTDFDFPE EDKKEEFEECLEKFFSTGPARPP TKEKVKRRVLIEPGMPLNHIEY CNHEIMGKNVYYKHRWVAEH YFLLMQYDELQKICYNEFVPSV IFLRYKSPGEAAGTCHLKQRRW VMPEAAAPVGTGSRYPLTGQL
4308	34676	A	4349	1	242	MNSIQIPKQQQNEKYQVPQFDQ STIKYIESPKELDVWDSWPLQN ADGTVAEYNGYHVAFALAG/S PKDADDTSIYMFYQKI
4309	34677	B	4350	1	2198	

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4310	34678	A	4351	1	2796	
4311	34679	A	4352	2047	3531	
4312	34680	A	4353	1	3336	
4313	34681	A	4354	1	1409	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGRDVKFTLEVLRGD SVEKTSRVWSGNERDQELLTE DALDDLIPSFLLTGQQTPAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQK\AYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDGY LLEPDGGALQNFQRYTGIQHVH RIGMAERMWCDRNRERHTVSS SGGNRLPNPGPDRSVRHFPDPR FLCPSCATVTPLHELIANKYLSG KIGAKKLRKLLIKHVD
4314	34682	A	4355	1	2316	
4315	34683	A	4356	93	924	AQTDAAEKSVSIAQLFQACLSIF SSGDV/AGGATQAFAKENNQK AYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTS IYMFYQKVGDNSIDSWKNAGR VFKDSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSNDT LKINGVGKYKTIFDGDGKTYQT VQQFIDEGNYTSGGHHTL\KDP SYNPPLDLSGGNSGYQSQET

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4316	34684	A	4357	1	3118	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTL\RDP\HYVENKG HKYLGFETNTGTENGYQGEESL FNKAYYGGGTNFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGSDESPND FGNRHLHKERLAVYRWHASFI CSGNTMPIVLVDWSDIREQKRL MVLRASVALHGRSVTLYEKAF PLSEQCSKKAHDQFLADLASIL PSNTTPLIVSDAGFKVPWYKSV EKLGWYWLSRVRGKVQYADL GAENWKPISNLHDMSSSHSKTL GYKRLTKSNPISCQILLYKSRSK GRKNQRSTRTHCHHPSPKIYSA SAKEPWVLATNLPVEIRTPKQL VNIYSKRMQIEETFRDLKSPAY GLGLRHSRTSSSERFDIMLLIAL MLQLTCWLAGVHAQKQ
4317	34685	A	4358	1	1326	
4318	34686	A	4359	2140	4390	
4319	34687	B	4360	1	7271	
4320	34688	A	4361	1	1729	
4321	34689	A	4362	5118	5687	
4322	34690	B	4363	1	4726	
4323	34691	B	4364	1	3688	
4324	34692	A	4365	1	1401	
4325	34693	A	4366	1	1932	
4326	34694	A	4367	1	1407	
4327	34695	A	4368	1	1491	
4328	34696	B	4369	1	855	

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4329	34697	A	4370	137	1014	ASEGKQMLRDFVTTRSALKELL KRALNMARNNQYQPLQKHAK L*RPSML*RNCIN*QPGRDT/TN KKENFRPISLMNIDAKILNKILA NRIQQHIKKLIHNDQVGFIPGM QGWFNIHKSINIIHHIKRTNDKN HMIISIDAEKAFNKIQQPFMLKT LNKLGIDGTYLKIIRAIYDRPTA NVILNGQKLEAFPFKTGTRQGC PLSPLLFNIVLKVLARAIRQETEI KGIQLAKEEVKLSLFADDMIVY LENPIISAQNLLKLISNFSK/VSG YKINVQKSQAFLYTINRQTESQI
4330	34698	A	4371	3	1234	
4331	34699	A	4372	1	2850	MGMGPAKPGMGGNLLVCWLQ RPWEKRSIWAEVYRSSRYSHS WLPLSRKGCDFSGTCRQTLSIL TQPLRQWGLEGIKKPNSWIISEE SVSNGGPPLLIPRQTASGVDLQ QTPTDLQLRVLTVRRKTNKQK GIASTSTKRTSTPKPHLYVTIIK DQSYIKPQRWGKNIAEKLKILKI RVALSLQRNAAPHQQWNKAG RRMSLMSSQKKASEVIESQMN EIKGEEKFREKRVKRNEQSLQEI WDYVKRPDLRLIGVPD
4332	34700	B	4373	16	701	
4333	34701	B	4374	1	3743	
4334	34702	A	4375	227	686	KVMLAEYPVFAQLTLTLPPSSA SWEPSRGPGPRGIRGSCPEWLA SGPG\KAAPGAGVPPPAASFPDP PPRLRAPALAVSRGLRRELPSG LDWTHCLRTLPSLIVQILQQAA LLGLPPAYSDQLQRAGQLHFYS GLIKISLVLTTRLSFWGTTE
4335	34703	A	4376	216	644	VTYSKEKECGEVADSVAKTAL EKDGAPRTGDPRPNLGADPPRS LVSSAGPQAVRPVKPARQFPPQ PPRYSQGPARAAGEEGRGMRPP GAGRRLPGPPLPGPEASHSGQL PLM/PPGPGPRLGSQEPVSLSRY LQTQARMPGPRP

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4336	34704	A	4377	18	1023	QIQHSPLVSPLPSLPPQPLVAEE EPPVA/PWPRRLLPATSTSH/PSH PLTEPVPPT\SGRGCCLWTKRQ QKMCRTTYTSVGRK/CTFPIDS GALRLSDGEMRALQTPTGPQST VEGHTHLQSL/PHHDRVTATPG TEPGLRAAGNRRIFYPGP/VTSQ VQPQLLCGYGNASRTPAALTPG PAPPTQASLPNCGICPHLQMGR PTSPC/PPEGGHPSSSLYISLSPPP PSAPALRLPPPLP\SAPTAPAL/P/ PAAPSAPALRLLRPLPCCSFRPR PAAPSAPAPRLLPPLLVCSFRPC PAAPSAPAGLLLPPLLCCSGLSP RLCCPHSSCSSDPPRLQRKADSS
4337	34705	B	4378	1	984	
4338	34706	A	4379	332	847	VKLLLQDKEICILCQKTVYPME CLVADKQNFHKSCF\RCHHCNS KLSLGNYASLHGQIYCKPHFKP TFQNPKGNYDEGFGHKA\HKD RWNWQKPKADSVDFIPNEEPN MCKNIAENTLVPGDRNEHLDA GNSEGQRNDLRKLGERGKLKV IWPPSKEIPKKTLPFEEELKMSK
4339	34707	A	4380	305	505	GNLERMLNLGMVKQQKLPAIM KTQVLML*AINVPAKPLFPQSG GAVRTTHGGKSRLKETGATSD TE
4340	34708	A	4381	56	260	IVKTQSIDG/MGNLRITEKGLKL EGDS/EFLQPLYAKEIQSRPGLG TQEQSCQTLSSCSSRGQQQHAE
4341	34709	A	4382	137	920	
4342	34710	A	4383	532	1680	LLTTRTSFRSENHRHVGLLLVM TDNTRDKEYFGDESKRENEEKT VEKSIGEKQATLTTHANIITIRH CVKPEPDFSDHLNLLLGRADIT GEEMAAQRSSVEKLANGNIAL VDSLRSRSLEEGDSDPHKRLSG AQDIKTTVEEVIADVVEIARELE LEVEPEDVTEFLQAHEKTLTDV ELFLINEQIKWFLEMKSTPRED AVIIAETITKVLEYDINLVTKQQ QGMRQLTPILKEVLLWVKCHQ TALHATEKPFIKGRINPCGKIHT CLNLRNCGQLLIREEEEEDKEE EEQYEEKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEDEEEEDKE DEEEDKEKEEEEDNKEEEEEED KEKEEEEDKE\EKEDKEEEEDK

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4343	34711	A	4384	3	495	EDTGTFRIY\ESAGAVKKARGF LEFVEDFIQVSKNLIGKVIGKNG KVIQEIVDKSDMVPVRIEGDSE NKLPREDKDDRDSRHQRDSRR CPGGRCRSVSGRRGRGGPRGG KSSISSVPKDPDSNPYSVLDN/T ESDQTADTDASKSHHSTNRHTR SRRRRTDEDAVL
4344	34712	A	4385	1	550	TESERKDELSDWSLAGEDDRDS RHQRDSRRRPGGRGRSVSGGR GRGGPRGGKSSISSVLKDPDSN PYSLLDNTESDQTADTDASESH HSTNRRRRSRRRRTDEDAVLM DGMT\ESDTASVNENGL\AKDV IEEHGPSEKAINGPT\SASG\DDIS KLQRTPGERKRLIP*KKENTQE AAVLNGVS
4345	34713	A	4386	1	2063	MAELTVEVRGSNGAFYKGFIK DVHEDSLTVVFENNWQPERQV PFNEVRLPPPPDIKKEISEGDEV EVYSRANDQEPCGWWLAKVR MMKGEFYVIEYAACDATYNEI VTFERLRPVNQNKTVKKNTFFK CTVDVPEDLREACANENAHKD FKKAVGACRIFYHPETTQLMIL SASEATVKRVNILSDMHLRSIR TKLMLMSRNEEATKHLECTKQ LAAAFHEEFVVREDLMGLAIGT HGSNIQQARKVPGVTAIELDED TGTFRIYGESADAVKKARGFLE FVEDFIQVPRNLVGKVIGKNGK VIQEIVDKSGVVRVRIEGDNEN KLPREDGMVPFVFVGTKESIGN VQVLLEYHIAYLKEVEQLRME RLQIDEQLRQIGMGFRPSSTRGP EKEKGYATDESTVSSVQGSRSY SGRGRGRRGPNYTSGYGTNSEL SNPSETESERKDELSDWSLAGE DDRDSRHQRDSRRRPGGRGRS VSGGRGRGGPRGGKSSISSVQY RSNIHNCSTLKRIFLASDMNIVL KDPDSNPYSLLDNTESDQTADT DASESHHSTNRRRRSRRRRTDE DAVLMDGMTESDTASVNENGL DDSEKKPQRRNRSRRRRFRGQ AE\DRQPAIDFIYKEVEKVVSL WQAKDVIEEHGPSEKAINGPTS ASGDDISKLQRTPGEEKINTLKE

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4346	34714	A	4387	1	1882	CGSNMADVTVEVRGSNGAFYK GFIKDVHEDSLTVVFENNWQPE RQVPFNEVRLPPPPDIKKEISEG DEVEVYSRANDQEPCGWWLA KVRMMKGEFYVIEYAACDATY NEIVTFERLRPVNQNKTVKKNT FFKCTVDVPEDLREACANENA HKDFKKAVGACRIFYHPETTQL MILSASEATVKRVNILSDMHLR SIRTKLMLMSRNEEATKHLECT KQLAAAFHEEFVVREDLMGLA IGTHGSNIQQARKVPGVTAIEL DEDTGTFRIYGESADAVKKAR GFLEFVEDFIQVPRNLVGKVIG KNGKVIQEIVDKSGVVRVRIEG DNENKLPREDGMVPFVFVGTK ESIGNVQVLLEYHIAYLKEVEQ LRMERLQIDEQLRQIGSRSYSG RGRGRRGPNYTSGYGTNSELSN PSETESERKDELSDWSLAGEDN RDSRHQRDSRRRPGGRGRSVSG GRGRGGPR\GGKSSISSVLKDPD SNPYSLLDNT\ESDQTADTDASE SHHSTNRRRR/SIRRRRTD\EDA VLMNGMTESDTASVNENGLVT VADYISRAESQSRQRNLPRETL AKNKKEMAKDVIEEHGPSEKAI NGPTSASGDDISKLQRTPGEEKI NTLKEENTQEAAVLNGVS
4347	34715	A	4388	2	421	PRVRDSDTEDDSEAEHFESFIHP TAMMFTSTINLLQTLCLSAGVH AEIMQSEATKTLCGLL\KSSPNR LVYREQHRSWCTLGFVQSIALT LQVCGALSSLQWITLLMKVVE GHAPFTATSLQRQILAVHLLQA VLPSWDK
4348	34716	A	4389	269	417	DLNCKVGSCFEVYSS*KQGIN*I KLGDSKT*P*LSGPTSENLKNSS LAE
4349	34717	A	4390	1	516	
4350	34718	C	4391	1	1527	

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4351	34719	A	4392	200	1267	TFSKASRGGNPHSMTKAPSDFR KARQTGIPGCSQLGSRYSLEPE QSALRLVCIQKLQESSTTCEDFF CPLCGRAWAVSTPLTDSPSPGH QPAVK*LGLVPFSDTHHPLPFQ VLSTDDTSSSSSCSSSCSASSSSP /SLLLLLLFLLLLLLLLMLLLKL FLLLLLFLL/RPPASPPLLPPALS PPL/HCSSSPSAPPASPPPAPPPPP APPPSPPPAPPPSAPSSPAPLPPA PASPPFSCSSSSCSSSCSSSSFSSC SSLSSSAQAEGSLRAPRESSPSL DPSAPQRVKVVPPQAGSGHRA GGALENRPRGKKPWLHFRPGL RSRLPARSLRSRPAPTRWRLRSS GRFTGAATATATART
4352	34720	A	4393	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAKSQGCSRN ARHQKARSMPLQDQHLALAIL LELAVQRGTLSQMLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLLQTFQSIICSKDTPPSEGN MHLLSGPLSPSESFLRESFFTVQ NCRNNEEVTLICKADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFCVGQYLEVR LYALSDAEDGRG\TL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTPASKSR\CSHRWALG DHSQAFLQAIADNNIQDHNVKT HQEQGRSYKEVCTPVIERLRFL SNELRPAVGNDLSIISEFKLLSSL PRWRRIAQKIIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIAIKSPKTITSENP LGPSLGSIPQARFLLMMLSMLT LQHSANNLDLLLNSGTLALTQT ALRLIGPSCDNVEEDMNASAQ GVSATVLEATRKETAPVHLPVS GPELAATMKIGTRVMRGVDW KWGDQDGPPPGLGRVIGELGE DGWIRVQWGTGSTNSYRMGK EGKYDLKLAELPAAAQPSAEDS DTEDDSASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFPAASL QRQRWVAVSLPHALVKSGTVP

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4353	34721	A	4394	266	1110	WARGGCARNALASGNAIQGGK CNPGLFPPSPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFPAASL QRQLCPE/HTSCPVLKDFCKSVI TDVACSSLISTLLVFWGGLLHT HKEASESWREAKSTSYVAAAR ENEEDAKAEPPTPGIKPSDLVRL IHYQENSMGETAPMIQIISHWV PPTTHGIYGSTIQDEIRVGVSYP GHTDARGFQLLLVSGDFSIPYW SLSSAYTSVNSSFVESLQSNLLK GILLPATIMTDPRTTGHQ
4354	34722	A	4395	1	734	MVQLSGKRILNSPYLELRCHQN MDHLGWVIKKSLNRSEVSWVP GLEFPWGPKPFREVIAGPLLRN NGQSLESSSLEGSHVGVYFSAH WCPPCRSLTRVLVESYRKIKEA GQNF\EIIFVSADRSEESFKQYFS EMPWLAVPYTDEARRSRLNRL YGIQAHLFLTANAEDFDTTVQV NKIILITYRQNENSLSSLKTGET EAQGRLQGSPSNVRGHDPDRH AIPLSVNRWNPSKSSPSPAVWS
4355	34723	A	4396	195	1071	LHEFDSSRDLTSGLGGARTHRR LGGPSDAPRGLPAPPPAPPVRPG /PRSPGPSAGTAR/DAPRPSVQM RAQRPARGSTKDLIETCCAAGQ QWAIDNDECLEIPESGTEDNVC RTAQRHCCVSYLQEKSCMAGV LGAKEGETCGAEDNDSCGISLY KASLTCGLQGRCLNPQQASMG LFSYDVQSSKKINRSIQEKLGG HGVCAATPGGGMRNCGRLRRS GQRRGGTDRCEAVLTGLFTRA LIREQMGDPHPLDHTGQLAKPL EVEKTPARWKYLDTNGEKEEP ELRTQCPSLYED
4356	34724	A	4397	1	520	MMGEKAEKPDTKEKKPKAKK ADAGGKRNCRYSRSAMYSRKT TSRKKYSAAKSKVEKKKKFLA TVTKPVGVDKNSGTQVVKLHK MPRYYPTEDVPLKLLSHG/KKK PFSQHR/RRVVFLKQLV/SGTGP LVLNQVPLRRTHQKFVIATSTKI GSSNVKIAKRLTGAYFKKVWK PKHQE
4357	34725	C	4398	67	243	

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4358	34726	A	4399	1	333	QRSCIENILRAC/VGLPPQNHML LEHKM\DAKRVGPVAATYPML NKKGPVPAATNGCTGDANGHL QEEPPMPTT*GPGHTVSRLFLPA APHDPTLKAPTNNSAATQPSKN KKK
4359	34727	A	4400	587	1013	GAASAGRGPGPRAPGLWGRGP AAAGASLVPTDHVHLSYNHLG NNDGENLSAP/SQFRSKEVSKS NVVDD/MVQSNPVLYTPGEEPD HATRCWPHPSAGPSAADRAVP ARPAGAPATEPHAPGTQNGAP GPSLKRVGPVAATYPI
4360	34728	A	4401	2	334	
4361	34729	B	4402	257	975	
4362	34730	A	4403	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRLLARAEKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLV\CRKMGVP YCIIKGKARLGRLVHRKTCTTV AFTQVN
4363	34731	C	4404	62	217	
4364	34732	A	4405	2	69	
4365	34733	A	4406	1	951	GTRPKMPKGKKAKGKKVAPAP AVVKKQEGFRKKW*IPWFEKR P\KNFGIGQDIQPQKRPPPLL*K WPRQYQACSGQRAILYKR\LKV PPAMKPVSPRALD\RQT\ATQLA *AVAHKVQTQRQKQEKKQRL\ LARADEEGCLAKGDVPNERDP PVPSSQEFNPVSPPLVKEQEKLK LVVNWHTDV\DPHPSLVCLPC/ LCPAPVS*KMGGPFTCIIQGKRA RLWDRLVPQERPCTTCPPFT\QV N\SEDKVRLLAKAGLEAIQGPIY N*PDTMEIRPSLGVGNVLG\PKS VARI\AKARNRHKAKETATHTG LNVTLLSFLYYKNN

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4366	34734	A	4407	1	1392	MPDVSEEQKESVCTGSMMREE ESSRKGKVRTAGAKSSSSDRVP RLNQEEVESLNRPITGAEIVAIIN SLPTKKSPAPDGFTAEFYQRIRI QQPIIRIQQPIKKLIQHDKVGFIP GMQGWFNICKSINVIQHINRTK EKNHMIISIDAEKPFDKIQQCFM LKTLNKLGIDGTYLKIIRAIYHK PTANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IIYLENPTVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRIKHLGIQ LTRDVKDLFKENYKPLLNEIKE DTKKWKNIPCSWAGRISIMKM AILPKVIYRFNAIPIKLPMTFFTE LEKTTLKFIRNQKRAHIAKSILS QKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQCTRTQP \SEITPHIYNYLIF
4367	34735	A	4408	1	1947	MALRRLSHDVSGALLLANGES TGNSGGSSGSSPSGGATSGSSQ TSISGDVVEACCSVLSMVCADP VYKVYVAAL\QCMLLVTLEDPS SHFTRMRRRLM/AYADEVEIAE AIQLGVEDTLDGQQDSF\CRHL FPTTIWKPQRTVP/LECTIHLEKT GKGLCATKLSASSEDISERLASI SVGPSSSTTTTTTTEQPKPMVQ TKGRPHSQCLNSSPLSHHSQLM FPALSTPSSSTPSVPAGTATDVS KHRLQGFIPCRIPSASPQTQRKF SLQFHRNCPENKDSDKLSPVFT QSRPLPSSNIHRPKPSRPTPGNTS KQGDPSKNSMTLDLNSSSKCD DSFGCSSNSS/NCCYT\SDETVFT PVEEKCRLDVNTELNSSIEDLLE ASMPSSDTTVTFKSEVAVLSPE KAENDDTYKDDVNHNQKCKE KMEAEEEEALAIAMAMSASQD ALPIVPQLQVENGEDIIIIQQDM TFFRHIIPPIQWIYKKESANLLID STGQRLRIADFGAAARLASKGT GAGEFQGQLLGTIAFMAPEVLR GQQYGRSCDVWSVGCAIIEMA CAKPPWNAEKHSNHLALIFKKL LDFANTACDGDKESEVEDVET DSGNSPEDLRKEIMIGLQYQAEI PPYLGEYDGNEKDSPQPKKMT GVQNAKEVLST

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4368	34736	A	4409	1	4485	
4369	34737	A	4410	2	927	IDHMIGHKASLNKFKKIEIISSTL SGHNGIKLEINSKRDLQNHANT RK\LNNLLLNEHWVKNEIKMEI LKFFELNDHNDTTYQNLWDTA KATF\LLRGKFTALNAYIKKTER AQTDILRSHVKELEKQEQTKPK PSRRKEITKIREELNEMETNKK KIQKINETKSRFFEQINKIDRSLA RLAKKRREKIQITSIRNKTGDTT TDTTEIQKIIQGYYEHLYAHKLE NLEEMDKFLEKYNPPSLNQEEL DTLNRTITSNKIEMVIKKLPTKK KSPGPNGFTAEFYQTFK\EELVP ILSILVHKTEKEGTLP
4370	34738	A	4411	405	517	
4371	34739	A	4412	1	1197	MEISELNAKLRSQEKEKQNEIIK LQLEKLQHFQEEKNKEIAILRN TIRDLEQRLSVGKDSHLKRENE QLKISADLIKEKLKSHEQEYKN NIAKLVSEMKIKEEGYKKEISK LYQDMQRKGRIKVTCEWTCSE RKTEGREPGPVREPTGRSQSAE NEGSKTLAEINTKGTQSPAERIN KIDRLLARLTNKRREKVQISSIR NKTGDIRTDTTEKQKFMQGYH EHLYMHKLENLKEMDKFLEIY SPPRLKREDIETLSRPITISDIEM KNLKIPPKLPELINKFSKVSRYK INVHKLVALLYANSDQTDNQIK NSTHFTIVAKK\YLGIYLTKDM KDLHKENSK/PLLKEIIDDTIKW KHIPCSWMSTTNIVKMTILPKTI YKFNAIIIKIPPSFFAERKKQS
4372	34740	A	4413	1	190	MIQRKRASIGAPCAWVRKKEE EEEEEEEEEEEEEEEEEEEE\K KKKKKKKERTTWLWGNPLT
4373	34741	A	4414	303	429	
4374	34742	A	4415	123	252	
4375	34743	A	4416	1	156	
4376	34744	A	4417	3	351	EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEE\KEEEEEEEEEEEGEEEE LGRLHGGSGKVRGLGFTENQQ GSTNRQHQREDNRKSKQKKIN NTKPEATESLIVNGITITAPA
4377	34745	A	4418	1	192	
4378	34746	A	4419	3	259	
4379	34747	A	4420	1	279	
4380	34748	B	4421	1	708	
4381	34749	A	4422	3	269	

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4382	34750	A	4423	1	322	MAGKQGRSEGASSWRLSSVLQ LNSQYFLQGAQQCTFLAATAW KKRKEEEEEEEEEEEEEEEEE EEEEEEEEEEEE\KKKKKKKK KKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKK KKKKKKENPFSCF
4383	34751	B	4424	327	674	
4384	34752	A	4425	494	960	TRFYDHALHLIHRKGSTTVRSP PPLYFIGESKASALLAISLRWSG RSQPRSSVNQIRKAWGFRPRKG TEE/DERSGCPSDALESDDPMA YIHFTAEGEVTFKSILFVPTSAP RGLFDEYGSKKSDYIKLYVRRV FITDDFHDMMPKYLNFVKGVV
4385	34753	A	4426	1	2539	VGGPRGWRCEDPNPGVGGGGG SCDRRGLETHRPHAMRALWVL GLCCVLLTFGSVRADDEVDVD GTVEEDLGKSREGSRTDDEVV QREEEAIQLDGLNASQIRELRE KSEKFAFQAEVNRMMKLIINSL YKNKEIFLRELISNASDALDKIR LISLTDENALSGNEELTVKIKCD KEKNLLHVTDTGVGMTREELV KNLGTIAKSGTSEFLNKMTEAQ EDGQSTSELIGQFGVGFYSAFL VADKVIVTSKHNNDTQHIWES DSNEFSVIADPRGNTLGRGTTIT LVLKEEASDYLELDTIKNLVKK YSQFINFPIYVWSSKTETVEEPM EEEEAAKEEKEESDDEAAVEEE EEEKKPKT\KKVEKTVWDWEL MNDIKPIWQRPSKEVEEDEYKA FYKSFSKESDDPMAYIHFTAEG EVTFK\SILFVPTSAPRG\LFD\DY GSKK\SDYIKLYV\RR\VFITD\DF HDMMPKYLNFVKGVVDSDDL PLNVSRETLQQHKLLKVIRKKL VP*NRWDMIKKI/SLDDKYNDT FW\KEFGYQHSSLVVIEGPLRIR TRLAKLLR\FQSSHHPTD\ITSLD QYVERMKEKQDKIYFMAGSSK KEAESSPFVERLLKKGYEVIYL TEPVDEYCIQALPEFDGKRFQN VAKEGVKFDESEKTKESREAVE KEFEPLLNWMKDKALKDKIEK AVVSQRLTESPCALVASQYGW

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4386	34754	A	4427	2	622	PARAALGILTSHQSGFLKTSTSK ITSTAWKNKDITMQSTKQYAC LHDLTNKGIGEEIDNEHPWTKP VSSENFTSPYVWMLDAEDLA DIEDTVEWRHRNVESLCVMET ASNFSCSTSGCFSKDIVGLRTS ACWQQHCASPAFAYCGHSFCC TGTALRTMSSLPESSAMW*KKP ARTRLPRGKDLIYFGSEKSDQE TGTLLLPVSS
4387	34755	A	4428	2	1421	QHCSQKDTAELLRGLSLWNHA EERQKFFKYSVDEKSDKEAEVS EHSTGITHLPPEVMLSIFSYLNP QELCRCSQVSMKWSQLTKTGS LWKHLYPVHWARGDWYSGPA TELDTEPDDEWVKNRKDESR AFHEWDEDADIDESEESAEESI AISIAQMEKRLLHGLIHNVLPY VGTSVKTLVLAYSSAVSSKMV RQILELCPNLEHLDLTQTDISDS AFDSWSWLGCCQSLRHLDLSG CEKITDVALEKISRALGNSGHL HQSGFLKTSTSKITSTAWKNKD ITMQSTKQYACLHDLTNKGIGE EIDNEHPWTKPVSSENFTSPYV WMLDAEDLADIEDTVEWRHR NVESLCVMETASNFSCSTSGCF NHRPWSQNEYEQLNYAKQLKE RLEAFTRDFLPHMKEEEEVFQP MLMEYFTYEELKDIKKKVIAQ HCSQKDTAELLRGLSLWNHAE ERQKFFKYSVDEKSDKEAEVS
4388	34756	B	4429	70	348	
4389	34757	A	4430	2	371	
4390	34758	A	4431	1	907	MGHRINIVCKIDAPCARQTRTF HPVVKTVEDCGRYPSVIEFGKY EIQTWYSSPYPQEYARNLAKEG KMGEREMSFVQQLQPMSGRCS LFRELSSCTYLLNTQPP/AVSIH FLAVWIILLVDGNMSKIYCQNL CLLAKLFLDHKTLYYDVEPFLF YVLTKNDEKGCHLVGYFSKWT VLQGQWQVQGIAHFSRALTYLI CFSFPQEKLCQQKYNVSCIMIM PQHQRQGFGRFLIDFISFPRLTIG ASFTQLRKQSMSNSTEIPLLGD NGKSSPTFHWQSLTSSPNAHFS LEAQLSILGHLFQSP

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4391	34759	A	4432	1	3468	MGKKQNRKTGNSKNQSASPPP KERSSSPATEQSWMENDFDELR EEGFRLSNYSELPEDIQTKGKE VENFEKNLEECITRITNKRNFKP TKIKRDKEGHYIMVKGSIQQEE LTILNIYAPTGAPRFIKQVLSDR QRDLDFHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHSKSTEYRFFSAPH HTYSKIDHLLGSKAFLSKCKRT EIITNYLSDHSAIKLELRIKNLTQ NRSTTWKLNN
4392	34760	A	4433	3	1900	FNKCMTLKFRLKNFSRINKIDTP LARLIKKKREKNRIDTIKNDKG DITSNPTEIQSTIREYYKHLYTN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGSEIMAIINSLPT KKSPGPDGFTAKFYQRYKEELV PFLLKLFQSIEKEGILPNSFYEAS IILIPKPGRDTTKNENFRPISLMN IDAKILNKILANRIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHISRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLG\IKYLGI QLTRDVKDLFKERS/YEPLLNEI KEDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRALIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITLHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGM GKDYMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNN
4393	34761	A	4434	2	1932	

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4394	34762	A	4435	1	2571	MKAEIKMFFETNENKDTTYQN LWNTFKAMCRGKFIALNAHKR KQERSNTDTLTSQLKELKKQEQ THSKPSRRQEITKIRAEMKEIET QKTLQKIKESRTWFFEKINKIDR LLARLTKKKREKNQIDAIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGSEIEAIINSLP T/KKCPGPDGFTAEFYRRKRG\I LPNSFYEASIILIPKPGTDTTKKE NFRPISLMNIDVKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSINIIQHINRAKDKNH MIISIDAEKAFDKIQQCFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IILNGQKLEVFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGNEEVKLSLFADDMIVYL ENPIISAPNLLKLINNFSKGSAY KIKVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAILIKLPMTFFTELEKST LKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNGTEPSEIM PHIYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLHVRPKTI KTLENLGNTIQDIGMGKDFMSK

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4395	34763	A	4436	1	1965	MTLESEQTFVYAVTATQTGAK EGTRMSKSNVAGQQGDSGEKA LQKTYQKILREKESALEAKYQA MERAATFEHDRDKVKRQFKIF RETKENEIQDLLRAKRELESKL QRLQAQGIQVFDPGESDSDDNC TDVTAAGTQCEYWTGGALGSE PSIGSMIQLQQSFRGPEFAHSSID VEGPFANVNRDDWDIAVASLL QVTPLFSHSLWSNTVRCYLIYT DETQPEMDLFLKDYSPKLKRM CETMGYFFHAVYFPIDVENQYL TVRKWEIEKSSLVILFIHLTLPRI KYLGIQLTRDVKDLFKENYKPL LNEIKEDTNKWKNILCSWTGR NNVMKMATLPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR AHIAKTILSEKNKAGGIMLPDF KLYFKATVTKAAWYWCQNRD IDQWNRTEASEITPHIYNHLIFD KPDKNKKWGKDSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLG NAIQDIGMGKDFMTKTPKAMA TKAKIDKWDLIKLKSFCMAKET PIGVNRQLTEWEKIFAIYPSDKG LISRIYKELKQTYKKKTNNPIEK LAKEMNRHLSKEDIYAANRHK KKCSSSLVIREMQIKTT/MRYHL TPVRMAIIKKSGNNRCWRGCG
4396	34764	A	4437	300	476	PDLSLWLPLTFFPSFQLW*I*QL CVLELLFSRSIFVAFSVFPEFES WPALLGWGSSPG

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4397	34765	A	4438	413	1689	QKLYKPERIKYLGIQLTRDVKD LFKENY/KLNEIKEDTNKRKNIP CSWVGRINILKMAILQKVIYRF NAIPIELPITFFTKLEKTTLRFIW NKKRVHIAKSIPSKKNKAGGIM LPDFKLYYKATITKTAWYLYQ NRDIDQWNRTEALGITPHIYNH LIFDKPDKNKQRGKDSLFNKW CWENWLVICRKLKLDAFLTPY TKINSRWIKDLNIRPKTIKTLEE NLGNTIQGIGMGKDFMTKTPK AMATKAKIDKRDLIKLKSFCTA KETNIRVNRQPIEWEKIFAIYRS DKGLISRIYKELKQIYKKKTNN SIKKWAKDMNRHFSKEDIYAA NRHEKKWSPSLVTREMQIKTIM RYHLTPVRIMTIKMSGNNRCW RGYGEIGMLLHCWWECKLVQ ALWKTVWRFLKDLELEIPFDPV IPLLGIYPKDYT
4398	34766	A	4439	3	2404	
4399	34767	A	4440	1	1572	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKSMA RELHDTCTSFNSRFDQVEERVS AIEDQTNEINNGENGTKLENTL QDIIQENFPNLARQANIQIQEIRR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKVLEVLARAI SQEKEIKCTQLGKEEVKLSLFA DDMIVCLENPVVSDHNVLKLIS NFSKVSVYKINVQKSHAFLYTN NRQTESQIMSELPFTITTKRIKY LGIQLTRAVKDFFKEKYKPLLN EIKKDTNKWKNIPCSCIGRINIM KMAIVPKVIYGFNAIPIKLPRTF FTELEKTTLKFIWKKKGAKTILS IKNKAGGIMLPDFKLYYKATVT KIAWYWYQNRYINQRNRTETS EITSHIYNHLIFDKPDKNKKWG KDSLFNKWCWENWL
4400	34768	B	4441	1	1558	

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4401	34769	A	4442	837	4329	TWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YTFF/LAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
4402	34770	A	4443	1	816	MRRDYPVKAFTSRKREQHVQK VPSKKSRQVQRTERRFLETTPD LLYQKEKDLLLISSSKKQPRPGI ERHYMMTQGSIHQEDVAILK/V YTSNKRASKYIQQ/TLLEIKGKI/ AHPQIVGDFNTPTSTIDRTIRQQI SIEFYDTIKQWDLTDTCRTGHPI TEYIFCSGAHLTFTKINHIQGPK RILKRFKRIEIIECVLVLKGCQA KNRKKEEDLQTYWMLNIYGPH YRSGSYAAIHRQETICSGQLSQ ALRDRFAMNAKLLLSLAAHLW VIKLDFM
4403	34771	A	4444	87	307	
4404	34772	A	4445	1	534	MEESRGAKPPPALLPGDATLPP GSLGSARHPPEP/RPVPGP/PPHQ TCPGPSACSSRRPEPRSSPGSPA RAPPAPPPPAAPAPRCEPPLWLL LRVPCPGRSGWSWMTT*I/SERP VQKRARSGPQPRLPPCLLPLSPP TAPDRATAVAT\PPVLGPMSSW SPRRAGGPTRPCTALQALSIPA
4405	34773	A	4446	164	660	YPSGRRLREPADVADAWDGME ESRGAKPPPALLPGDATLPP\AP SGQLGTRPSPPSSRPSPHQTCPG PSACSSRRPEPRSSPGSPARAPP APPPPAAPAPRA/SPRRPLPAPRS ASVPAFSAPPSQWPEVGPSPCA LRRAMPRGPGPPPEPRLVAEPG EDAAPTAGR
4406	34774	A	4447	1	417	

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4407	34775	A	4448	1	1802	MSYPADDYESEAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIPEVIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVYEIQDIYENSWTKLTERFFK NTPWPEAEAIAPQVGNDAVFLI LYKELYYRHIYAKVSGGPSLEQ RFESYYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSVLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLLRLHSLL GDYYQAIKVLENIELNKKSMYS RVPECQVTTYYYVGFAYLMMR RYQDAIRVFANILLYIQRTKSM FQRTTYKYEMINKQNEQMHAL LAIALTMYPMRIDESIHLQLREK YG\DKMLRMQKGDPQVYEELF SYSCPKFL\SPVVPNYDNVHPN YHKE\PFLQ\QLKGVF**SSSQQ AQLS/TPIRSFLKLYT\TMP\VAK LAGFPGPSQSQEF\RIPGFFVFKQ QDERTSVWTQRVFSAPGW*NF SQASEVDF\YI\DKDMI\HIADTK VA\RRYG\DFFIRQI\HKF\EELNR TLKEGWGQRPWMIFHTHFREP GFECIIGQGSVFC

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4408	34776	A	4449	1	1722	MNIKAKILNKILANRIQQHIKKL IHHDHVSFIPRMQGWFNIHKPIN VIHHINRTNDKNHMIISIDAEKA FDKIQHPFTLKTLNKLDDMTVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINVVKMAILP KVIYRFNAIPIKLPMTFFTELEK TTLKFIWNQKRARIAKSI\LSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTE\PSEI MPHIYNHLTFDKPDKNKQWGK DSLFNKWCWENWLAICRKLKL DPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNTVQDIGMCKD FMTKTPKAMATKAKIDKWDLI KLKSFCTSKETIIRVNRQPTEWE KMFAIYPSDEGLISRICKE/LFKQ IYKKKNHPIKKWAKDMNRHFS KEDIYVANKHMKKSLSSLVIRE MQIKTTMRHHLTPVRMTIIKKS GNNRFWRGCGETGMLLHCWW ECKLVQPL*KIVW*FLKDLESEI PSDSAIPLGGIHPKAYKSFYY
4409	34777	A	4450	1050	1147	PGEWHGQGSPRCWR*PLPQRC GHLLSCRWRTP
4410	34778	A	4451	1	614	MEELVDEGLVKALGVSNFSHF QIEKLLNKPGLKYKPVTNQNSL GTMQNRAGFPRDEDCLLLQVE CHPYLTQEKLIQYCHSKGITVT AYSPLGSPDRPWAKPEDPSLLE DPKIKEIAAKHKKTAAQVLIRF HIQRNVIVIPKSVTPARIVENIQN TEHYKYCGLCVGPNLEKNLYP VDRM/WKNSCGQFVL*ISSHLE DYPFNAEY
4411	34779	A	4452	2	240	WMELESLSHFQIEKLLN/KPGL KYKPVTNQVNSIQFKGSILEEGI VNMGDDSSMHVSAPEDPPVGQ DVEAEDSDTDDPDPV
4412	34780	A	4453	1	1019	
4413	34781	A	4454	1	2028	

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4414	34782	A	4455	3	1045	DFTSENFSAAWYLIENHSNTSF EQLKMAVTNLKRQANKKSEGS LAYVKGGLSTFLEAQDALSAIH QKLEADGTEKVEGSMTQKLEN VLNRASNTADTLFQ/EKVLGRK DKADST\RNALNVL\QRFKFLFN LPLNIERNIQKGDYDVVINDYE K\AKSLFG\KTEVQVF\KKYYAE V\EPRVEALRELLL\DKLLETPST LHDQKRYIRYLSDLHASGDPA WQCIGAQHKWILQLMHSCKEG YVKDLKGKDFSSNVFQFSGSAL RRVPDTVRVLDSQFSRSALRSV PDTVQVLDSQFSGSALRRVPDT VRVLDGQFSRSALRSVPDTVRV LDKCHCSPAKVVMNAVTIFTG
4415	34783	A	4456	1	440	MQRNLARAFSPGIKKIKMMCL GNSEKDWPKFRGVGEDAGLLA ARECGALLVIRHLINAVRAIVP NKSNNEIILVLQHFDNCVDK\TV QAFMEGSASEVLKEWTVTGKK KLLLQGEEELARLPFITGGSGSC YSSSTLAVEEECRVLA
4416	34784	A	4457	1	276	MEDEMEGLTEAGFRRWVTTNS AELKEHVLTQCKEAKNLDKRL EELLSRITSLERDISDQME/RELC EAYTSINSQINQAEERISEFEDH LAEI
4417	34785	A	4458	3	361	EMVHRKKKAVHRTATADDKK LQFSLKKLEVNNVSGIEEVNMF TNQGTVIHFN\AEMPANSFTITG HAETKQLMEMLPSILNQLGAH CLTSLRRLAEALPKQSVNGKAP LATGEDDDEVPA
4418	34786	A	4459	1	475	
4419	34787	A	4460	57	820	EDGSGGGKFPEGARQGGTGQR RRRKAMRRTGAPAQADSRGRG RARGGCPGGEATLSQPPPRGGT RGQEPQMKETIMNQEKTRHTC RAQ\VRIGGKGTARRKKKVVH RGAAS/ADDKKLQF\SLKK\LGV NNISGIE\EVNM\FTN\QGTSGST FNNP*KFQGISWPANTFHHLQG HAEDKGS*QEMLAQHLKPSLG ADSLTSLRRLAEALPKQSVDGK APLATGEDDDDE\VPDLV\ENF* *RLPRNEANLNLSQLLKIKP
4420	34788	A	4461	1	1527	

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4421	34789	A	4462	8	327	LIWQLTFTKTIKS/CEEYGKIVST KAILDKNTNQCKGMCKGIRTL KSCLCYLINGSSIVEVQKRLAY AGTLEPSLVHQVYSELSYYKLP GTQVVRIIAEVLRMQDSSE
4422	34790	A	4463	2	573	WMEGREKWRGRRKDGRKEGR KEGRKERRREREKGRERK/GKE RKGKERKGKERKGKERKGRER KGTEGKGTEGKGKERKGKEGK GKERKGKERKGKERKGKEGKG KEQKGKERKGKERKGKERKGK ERKGKERKGKEEKGRERKGKE GKGRERKGKEGGKEEGRKERR KEGRKEGKKFSNNGMVEEMQ
4423	34791	B	4464	1	1344	
4424	34792	A	4465	3	373	
4425	34793	A	4466	1	3864	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN
4426	34794	A	4467	3	415	
4427	34795	A	4468	396	676	LCFPYAERPDLQFLC*DLCARSP YLLQAQKYLQEF*AIPHLDQQT EPPDPSVSFYLLDCTLNCTAQH KTC*KKSIGL*EQNQQTLSSIPY SHT
4428	34796	A	4469	1	858	MEWEDNLPLELGRTVAKLLSD HSQTPLGIQMFLLFSLSLRKSPL VCLSYLFNFRFTLESEVQHLSG AITLTAWPKIPFLGIREAKSPRS ENTRLATILEAGHRHLGTSVSK DHPVTFWRPRRDLQSDLKQIKI DLGKFSDNPDGYIDVLQELGQS FDLTWRDIMLLLNQTLTPNERS ATITAAREFGDLWYISQVVAAV AGLVSEAVKIIQG\LTVWT/SHD VNGILTAKGDLWLSDNHLLKY QALLLEGPVLRLRTCATLNPAT FLPDNEEKIEHNCQQVIAQTYA
4429	34797	A	4470	918	1939	

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4430	34798	A	4471	3	2693	PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGVLGQ PVTRYFFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAII HLNIGEGTPICRLLFEEGISPEV WATEGQYGQAKNAHFVQVKL KDSTSFPYQRQYPLRPEAQQRL QKIVKDLKAQGLVKPYSSPCNT PILGVQKPKRQWRLVQDLRIIN EAVFPLYPAIPSPYTLLSQIPEEA EWFTVLDLKDAFFCIPVHPDSQ FLFAFEDPSNPTSQLTWTVLPQ GFRDSPHLFGQALAQDLSQFSY LDTPVLQCMDDLLLAARSETLC HQATQALLNFLTTCGYKVSKP KAQLCSQQVKCLGLKLSKVTR ALSEERIQPILAYPYPKTLKQLR GFLGITGFCRIWIPRYGKIARPL YTLIKETQKANTHLVRWTPEAE AAFHALKKALMQAPVLSLLTG QDFSSYVTKNKQTKKKK\T*IA LRVLALV*GTSLQPVAYLSKKT DVVAKGWPHCLWVMAAIAVLI SKAVKMIQ*RDLTVWTSHDVN GILTAKGDLWLSDNHLLKYQA LLLEGPMLRLCTCAALNLDTFL PHNEEKIEHNCQQVIAQTYATR GDHLEVPLTDPNPNLYTDGRSF VEKGLQKVGYAVVSDNGILES NPLTPGTSAQLAELIALTWALE LGEGKRVNIYTDSKYAYLVLH AHAVIWREREFLTSEGTPIKHQ
4431	34799	C	4472	11	1639	
4432	34800	A	4473	95	2539	
4433	34801	A	4474	345	768	PRGARSTRCLPVERR\CDGLQD CGDGSDEAGCPDLACGRRLGSF YGSFASPDLFGAARGPSDIHCT WLVDTQDSRRVLLQLELRLGY DDYVQVYEGLGERGDRLLQTL SYRSNHRPVSLEAAQGRLTVA YHARARSHPLMNE
4434	34802	A	4475	47	563	RLRFAVFTGAFHALSFLLSFVV LCCTYLKGLKVARFHCKRIDV/ MHHADARAAGGPAPQCAGTLS \EEQKRRRQRATKKISTFIGTFL VCFAPYVITRLVELFSTVPIGSH WGVLSKCLAYSKAASDPFVYS LLRHQYRKSCKEILNRLLHRRSI HSSGLTGDSHSQNILPVSE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4435	34803	A	4476	1	332	ERGRQEMSAKLRPPAEPPCVPA RISP*RPS*RQ*MERRCPPWRCS PMPC/CFFREHALQVRCGPTSA DCGRDPLFSPHPKPLPHPVPDIG WVATAGAQRSSSPVPSSLFVW
4436	34804	A	4477	297	943	TGSWGGGGADQLRPALTTALM PPDNRFGENTPAAPANGHCAP\ EPDITLVQDHSELPIGAAATMA HEIGHSLGLSHDPDGCCVEAAA ESGGCVMAAAT/GVRGHPFPRV FS/SCSRRQLRAFFRKGGGACLS NAPD/TRTPGAAALCGNGFVEA GEECYCVS\GQECRDLCCFAHN CSLRPGAQCAHGDCCVRCLVR/ CMEGSGSHQLPRLVPGGDSAEI LM
4437	34805	A	4478	1	836	MGPLTFRDVKIEFSLEEWQCLD TAPGNLYRDVMLENYRNLVFL VMCSHFAQDVWPEHSIKDSFQ KVILRTYGKYGHENLQLRKDH KSVDACKVYKGGYNGLNQCLT TTDSKIFQCDKYVKVFHKFPNV NRNKIRHTGKKPFKCKNRGKSF CMLSQLTQHKKIHTREYSYKCE ECGKAFNWSSTLTKHKIIHTGE KPYKCEECGKAFNRSSNLTKH KIIHTGEKPYKCEECG\KAFNRS STLTKHKRIHTEEKPYKCEECG KAFNQFSILNKHKRIHMGR
4438	34806	A	4479	1	588	MLGKVQQQEQTIAKDLVVTKY KMCGGT/DIANRVLRSLVEASS S\GGQDYILKEGDLVKIDLGVH VDGFIANVTHTFVVDVAQGTQ VTGRKGDVIKAAQLCVEAALC LVKPGNQNIQVREAWSKVALS FNCMPIEGMLSHQLKQHVIDGE KNIIQNPTDQQKKDHEKAEFEV HEVYAADVLVSSGEGKAKDAG
4439	34807	A	4480	85	561	LSHCLPLQTTEVGGFGNLLGY WIACSIGCVLSTGMLSHQLKQH VIDGEKTIIQNPTDQQKKDHEK AEFEVHEVYAVDVLVSSGEGK VRRVPELAKRGD*ECSPDQMLL KLLFQAKDAGQRTTIYKRDPSK QYGLKMKTSRAFFSEVERRFD AMPFTLRY

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4440	34808	A	4481	1	1408	GTSAPQPARSQLLALACLPAPL LARAFARPLLEDRGDSDHSLW LGRETEAAAAQGKRGCSGGSR KMSGEDEQQEQTIVD/DSLVVT KYKMGGDIANRVLRSLVEASSS GVSVLSLCEKGDAMIMEETGKI FKKEKEMKKGIAFPTSIS\VNNC VCHFSP/L*KSDQDYILKEGDLV KIDLGVH\VDGFIANVAHTFVV DVAQGTQVTGRK\ADVIKAAH L\CAEAA\LRLVKPGNQNTQVT\ EAWNKVAHSF\NCTPI\EGMLSH SLKQHVIDGEKP*FQNPTDKQK\ RAHEKADFEVH\DVYAVEGLV KPQERARPKDAGQRTTIYKRDP SKQYGLKMKTSRAFFSEVERRF DAMPFTLRAFEDEKKARMGV\ VECAKHEL/VWQPFNVLYSGRE GDFVCPVLNFTVL\LMPNGPML ITSGPFEPDLYKSQMEVQ\DAEL KALLQSSASRKTQKKKKKKAS KTAENATSGETLEENEAGD
4441	34809	A	4482	3	190	
4442	34810	B	4483	1	588	
4443	34811	A	4484	1	1312	MSSKGSVVLAYSGGLDTSCILV WLKEQGYDVIAYLANIGQKED FEEARKKALKLGAKKVFIEDVS REFVEEFIWPAIQSSALYEDRYL LGTFF\ARPCIARKQVEI\AQREG AKYVSHGATGKGNDQVRFELS CYSLAP\QIKVIAPWRMPEFYNR FKGRNDLMEYAK\QHGIPIPVTP KNPWSMDENLMHISYEAGILE NPKNQAPPGLYTKTQDPAKAP NTPDILEIEF\KKGVPVEGGPTF KDG\TTHQTFL\ELF\MYLNEVA GKHGVGPYLTSWENRFHWELK SRGILRRPQAG\TILYHAHLDIE AFTMGGDRAQIPNQGLGFEFVE LGVYRFSGTAPECELVGPCLRQ SPQERVEGKSAGVPSLKGPRCT SLGPEVPHCSLYNE\ELVKHGT CQGDYE\PN*LPPGFIQTSISLKA EGNYHRLPRAKVTAQIRPRVQ
4444	34812	B	4485	47	482	

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4445	34813	A	4486	2328	3435	KTTTLEDNLGNTIQDIGPGKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKRVNKHDESLRS HYE*WGMLTDCVVMRDPNTK RSRGCGFVTYATVEEVDAATN ARPHKVDGKVVEPKRTVSRED SQRPGAHLTVKKIFVGGIKEDT GGFAFVTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQRGRSGRGGGFGGNENFG CGGNFSGHGGFGGSHDGGGYG GSGDGYNGFGNDGGYPGGGPG YSGGSRGYGSGGQGCGNQDSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSYNDFGNYNNQY SNFGPMKGGNF/GGRRSGP*GD GGQYFAKPPNHSGYGGSSSSSS
4446	34814	A	4487	1	762	
4447	34815	A	4488	3	333	
4448	34816	A	4489	1	1676	MRDPNTKRSRGFGFVTYATVE EVDAAMNTTPHKVDGRVVEPK RAVSREDSQRPGAHLTVKKIFV GGIKEDTEEHHLRDYFEQYGKI EVIEIMTDRGSGKKRGFAFVTF DDHDSVDKIVIQKYHTVKGHN CEVRKALPKQEMASASSSQRG RRGSGNFGGGRGDGFGGNDNF GRGGNFSGRGGFGGSCGGGGY GGSGDGYNGFGNDGSNF*G\GG SYNDSGNYNNQSSKFEPMKGG NFGGRSSGPYGGGGQYFAKPQ NQAARCVAARWLFRTEARLVF LQKFPPWAVVEVVTVIVAAPA AATATTRDGGGCSRNCNIPEVF PELLGCPNRRGPPGGVREKQQQ TNSKSTRRQEITKTIAELKEIETR KTLQKINESRSWFYEKINKVDR LLDRLIKKKREKSQIDAIKNDIG DIVTDPAEIQTTIKEYYKRLYAN ELENLEEMDKFLATYSLHSLNQ EEVESLNKPVTSSEVEAVTNSL PTKKSPGPDGFTVLLEVLAPAIR QEKEIKHIPIGREEVKLSLFADD VIVYLENPIVSAQNLLKLISNFS

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4449	34817	A	4490	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCEGWIEEER DESRKSETIFKDLFKVPVLKETI YYKFYGPPVYQIETVYFMALSP PKSKQFDKTKQNNNNKKTHQF VIVFFKTDEHLSARGRRRRSIVK VSLLPAVIGLKSKFLKKPDQLR KLF\IGGLSFETTDESLRSHFEQ WGTLTDCVVMRDPNTKRSRGF GFVTYAT\VEEVDAAMNARPH KVD\GRVV\EPKRAVSREDSQRP GAHI/TLVKKIFVGGIKEDTEEH HLRDDYFEEIILNSMEKIEV\IEI MT\DRGSGKKRGFAF\VTFDDH DSVDKIVI\QKYHT/VGNGHNCE V\RKALSKQEDG*VLHPAQRG\ RSGSGKLLVVGRGRWFSVGMD NFG\RGGNFSWSVVAFGGT\RG\ GGGYGWQWGMAYNGFGNDG\ SNFGGGG\SYNDFG\NYNNQ\SS NFGPMKGGNFG\GRSSGPYG\G GGQYF\AKPR\NQGGYGGSSSS\
4450	34818	A	4491	134	612	TVLNSMSVILAISTLLKIITGELL QSFGDGLLWNLVIGIRGIDGLSP KVRKVLQLLRLRQIFN/GTFVK LIKVTVNMLRTVEPYIAWGYPN LKSVNELIYKHGYGKISKKRIA LTDNVLIARSLGKYGIICMEDLI YEIYTVGKRFKEANNFLWPFKL
4451	34819	A	4492	1	1983	
4452	34820	A	4493	1	1527	
4453	34821	B	4494	1	2211	
4454	34822	A	4495	1	2478	
4455	34823	A	4496	2	1544	
4456	34824	B	4497	1	2151	
4457	34825	A	4498	1	744	
4458	34826	B	4499	1	2172	

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4459	34827	A	4500	1	2535	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAYLGV LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAEKAFDKIQQHF MLKTLSKLGIDGTYLKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSDQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNYLFFDNPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NIRPKTIKTLEENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLKSFCTGKETTIRVNRQPT
4460	34828	B	4501	1	1785	
4461	34829	A	4502	1	1415	
4462	34830	B	4503	1	3262	
4463	34831	A	4504	1	278	

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4464	34832	A	4505	3	2528	ENKDTTYQNLWDAFKA\VCRG KFIALNAHKRKQEKSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIDTQKTLQKINESRS WFFERINKIDRPLARLIKKKREK NQTDTIKNCKGDITTDPTEIQTT IREYYKHLYANKLENLEEMDK FLNTYTLPRLNQEEVESLNRPIT GAEIVAIISSLPT/K/KSPGPDGFT AEFYQRYKEE/LEKEGILPNSFY EASIILIPKPGRDATKKENFRPIS LMNIDAKILNKILAKRIQQHIKK LIHHDQVGFIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KAFDKIQQRFLLKTLNKLGIDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNTQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKDDTNKWKNIPCS WVGRINIVKMAILPKLPMTFFT ELEK\TTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEIMPPIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGL GKDFMSKTPKAMATKAKIDK
4465	34833	B	4506	1	5401	
4466	34834	A	4507	1	5271	MNIDAKILNKILPNQIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIILIDAEK SFDKIQQPFMLKTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLE VFTLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKQISNFSKISGYKINVQKSQA FLYTNNRQTESQIMSEIPFTIAL KRIKYLGIQLTRDVKDLFKENY
4467	34835	B	4508	924	3423	
4468	34836	A	4509	525	673	RDSWGTCPVSGAGKVDWPPSS *HHR*HQQWCCGMPHQLSTKE NISIKDHLTKEKRKGGAV*RII

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4469	34837	A	4510	25	1766	GTCQFAAMNVVFAVKQYISKM IEDSGPGMKVLLMDKETTGIVS MVYTQSEILQKEVYLFERIDSQ NREIMKHLKAICFLRPTKENVD YIIQELRRPKYTIYFIYFSNVI\SK SDVEVIGLKLIEQEVVAEVQEF YGDYIAVNPHLFSLNILGCCQG RNWDPAQLSRTTQGLTALLLSL KKCPMIRYQLSSEAAKRLAECV KQVITKEYELFEFRRTEVPPLLL ILDRLDDAITPLLNQWTYQAM VHELLGINNNRIDLSRVPGISKD LREVVLSAENDEFYANNMYLN FAEIGSNIKNLMEDFQKKKPKE QQKLESIGS\MKA\FVENYPQFK KMSGTVSKHVTVVGELSRLVS ERNLLEVSEVEQELACQNDHSS ALQNIKRLLQNPKVTEFDAARL \VMLYALHYERHSSNSLPGLM MDLRNKGVSEKYRKLVSAVVE YGGKRVRGSDLFSPKDAVAITK QFLKGLKGVGNV\YTQLQPF\L H\ETLDHLIKGRLKENLYPYLGP STLRDRPQDIIVFVIGGATYEEA LTVYNLNRTTPGVRIVLGGTTV HNTKSFLEEVLASGLHSRSKES
4470	34838	A	4511	1	1335	MAPVTMMGYRSGKMGILADV QLQVGPPGPWLHLVVIAPVPEC ITGIGIFSSWGSPDVGPLLYDIR AIMWGSLAPAENTWILGNNHR RFLAQLKPRVIMQDFSNVISKS DVKSLAEADEQEVVAEVQQVI TKEYELFEFRRTEVPPLLLILDR CDDAITPLLNQWTYQAMVHEL LGINNNRIDLSRVPGISKDLREV \VSSAEIDEFYANNMYLNFAEIG SNIKNLMEDFQKKKPKEQQKL ESIADMKAFVENYPQFKKMSG\ TVSK\HVTVVG\ELSRL\VSERN LAGRFSEVEARNWAC\QNDHS\ SALQNIKRLLQNPKVTEFDAAR LVML\YA\LHYERHSSNSLP\GL\ MMDLRN\KGVFWRKYSKARVL AVVEYGGKRVRGSDLFSPKDA VAITKQFLKGLKQQEIVNCVLA AANVYIKQLPLSIQPSASLNGCI SLEKKPLVSTQRN
4471	34839	A	4512	1	816	
4472	34840	A	4513	26	257	
4473	34841	A	4514	56	236	

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4474	34842	A	4515	170	373	HSPRGSTASF/CEVSETKNPPIPD TPATREAEGLRSRLAVYSTRDS PCVACSGSYTQAQGSLGRKFQ DP
4475	34843	A	4516	262	358	
4476	34844	A	4517	2298	2556	NHKNPRRKPRQYHSGHRHGQG LHD*NTKSNGTKSNGNKSQN* Q\WDLINLKSFCTAKETTIRVNR QPTEWEKIFTIYPSDKGLISRI
4477	34845	A	4518	801	944	DQEPTNSRHILATQMGPSPITKQ SNPGV**KECGFSCSPRVWRYL VS
4478	34846	B	4519	85	660	
4479	34847	A	4520	693	827	
4480	34848	A	4521	272	339	
4481	34849	C	4522	532	2754	
4482	34850	B	4523	1	519	
4483	34851	B	4524	266	935	
4484	34852	A	4525	1	1584	
4485	34853	A	4526	1	723	GALPNGDRGRRKSRFALYKRP KANGVKPSTVHVISTPQASKAI SCKGQHSISYTLSRNQTVVVEY THDKDTDMFQVGRSTESPIDFV VTDTISGSQNTDEAQITQSTISR FACRIVCDRNEPYTARIFAAGF DSSKNIFLGEKAAKWKNPDGH MDGLTTNGVLVMHPRGGFTEE SQPGVWREISVCGDVYTLRETR SAQQRGKLGLQTGDMAENT/T VHALPSNCMVWRRSQTRQQIS
4486	34854	A	4527	1	335	
4487	34855	A	4528	328	871	DCGGGRARTAIFAGAARAADN KKCAGARRALGRARGCSATAR PRRRRRRPRGLAPPRPARPPPG GMSYKPNLAAHMPAAALNAA GSVHSPSTSMATSSQYRQLLSD YGPPSLGYTQGTGNSQVPQSKY AELLAIIEELGKEIRPTYAGSKSS \MERL\KRGIIHARGLVRECLAE TERNARS
4488	34856	A	4529	1	653	MAGPAESSPQGAHPNSPFALQH HSSLTVKPLHRQNVIQHQVAG QENRRGHQAGSSTSPQPLEALK RPNLRAPFHSQSRRILIPPAGNP TPGAAAPADPSTQRRDRWGCA LPMPRVAAGSAHHQQAGPTAA AQHRTPVALFSPPLSLVYGQQQ RKESETPTVPTPPARARGWTET GVEHVPAYNRTRAPEKCDI/SV PSPHSSPDAETSHPRHISPCPG

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4489	34857	A	4530	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
4490	34858	A	4531	1	2073	MKPCAHSWNAELSRNIIRHSFN LVMVAASQVAVSQLLGSYEILL LVSIELMFCFGLGYFFIPMQEW PNTYGERVFVDVESSVFKWNH KCLHKTEAERDYTKKRLKLCG HKPGNAVGQQKLEEARNRFFT RAPGGSAALPTLRFQPSDTDFR LLASRTILTFETKNPSELAERLR SVCGNQSNAYARLLEYRLNAL RGLWNAQRQLALEEQHERESS GDEETLALLKRQGLLQQPEQAP FTSRMGLLLVFPLIQSQSRTDPS LCNITAEVLLNCLRDCQPLSLT KEPADCLNGIETLLCSWLEETS DTGRHIPHKQKENAAAALVAL ACARGFVYCRNEELEPGWVAF GSGSLLHRPVSFDNKPHSLFQVI DQNTLQVCQVVPMPANHLPIG STMSTVHLSSDGTYFYWIWSPA SLNEKTPKGHSVFMDIFELVTL KGKKAKGKKVAPAPAVVKKQ EAKKVVNSLFEKR\DIQPKRELT YFVKW/PRYVRLQQQRAILYKQ LKVPPAINQFTQALNCQTVTQL LKLAHKYRPETKQEKKQRLLA QAEKKAAGKGGVPTKRPPALR AGVNTITTLVENKKAQLVVIAH DVDSIELVVFLPALCCKMGVPY CIIKGKARLGRLVHRKTCTTVA FTQVNLEDKGALAKLVEGIRTN DNDRYDEICCHWGGNILGPKS VACIAKLEKAKAKELATKLG
4491	34859	A	4532	1	2565	
4492	34860	A	4533	1	644	MPKGKKAKEKKVAPAPAVVK KQEAKKVVNPLFEKRPKNFGT GQDIQPKRDLTHFVKWPCYIRL QQQRTILYKWLKVPPEINQFTQ APDSQTATLLLKLAH/KYRPET NQEKKQRLLARAKKKAAGKG DIP\TKSPPVLRAGVNTITTLVE NKKAQLVVIAHDVDPIKLVVFL PVLCHK/MGVPYCIIKGKARLG HLVHRKTCTTVTFTQVNSEDK

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4493	34861	A	4534	1	931	KSIQKGLKMCLSSSLLPPSKMP KGKKAKGKKVAPAPAVVKKQ EAKKVVNPLFEKRP\KNFGIGQ DIQP\KRDFTRFVKWPRLLSGC MR\KRAILYKAG*KLPPA\INQF HPGPWDPANKLLQLL*AWAHK \YRP\ETKAKRKKQRL\LARA\E KKAA\GKGDVPNERDPPV\LRA\ GVNTVTHLWWRNKKAPAWVV IATRRWIPFEL\VVFLPAL\CREK WGSPYCIIKGKARLGR\LVH\RR PCT\TVGFHTR*NSKDKRRLLA* AGLEAIRTQFTIDQIRWRSGRH\ WG\GNVLG\PKSVARIRQASKR QRLKELATKLG
4494	34862	A	4535	3	227	
4495	34863	A	4536	1	338	
4496	34864	A	4537	1	352	
4497	34865	A	4538	2	368	
4498	34866	A	4539	3	468	
4499	34867	A	4540	2	790	PRGRNRRRKTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PDVVSLLEQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELDCFSLPRDTTLVHYI DDIMLIGSSVQEVENKLDLLVK DKLLHLAPPTTKEEVQHMVGL FGFWRQHIPHLGVLHQPIYRVI RKAA/SFEWGPEQEKALQQVQ AAVGGKQSENNLGHQRSPGLW
4500	34868	B	4541	179	1219	
4501	34869	A	4542	1706	2517	THLLVPGMQPLTWQMPFSPFLS ISPTRSNLPSAATPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLATVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGIPHSIA SDQARIHRSRNQEVEVEVAPLT ITPSDPLAKFLLSVPVTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPPGHFGLLLTLSQEAKNG VTVLAGVIDLDYQDEISLLLHN GGKKEYARNTGDPLGRLLVLP CPVIKINGKLQQPNPGGTTNGS DPSGMKV

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4502	34870	A	4543	3	367	DLWPFTRVTVH/WGKANDQTF QGLLDTGSELTLIPGYPKRHCC PPVKVRVYGGQTDGSWRMTV GYHKLNQVVTPIAAAVPDVVS LLEQINTTPAIKWVVHSSIPSSN GSGVYVIRLEQVLKAQ
4503	34871	A	4544	2	541	
4504	34872	B	4545	1	681	
4505	34873	A	4546	2	1091	PRGRNRRRKTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PDVVSLLEQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELDCFSLPRDTTLVHYI DDIMLIGSIKFLGVQWCGACRD IPSKDPADPMVLEVSVADRDAV WSIWQALIDESQQRPLGFWSKS LPSSADNYSPFERQLLAYYWAL VETERSTMGHQVTMLPELPVM NWVLSDPSSHK/ANGLAGWSG TGKKHDWKIGDKEIWRRGMW MDLSEWSK/D/VKIFVSHVSAH QRVTSAEEEFNNQVDRMTRSM DTTQPLYPTTPVIAQWAHE
4506	34874	A	4547	1	1236	
4507	34875	A	4548	1	1467	GEKGNDQTFRKLLDTGSELMLI PLRVVIPTTSLFNSPIWPVQKTD GSGRMRVDYHKLNQVMTPTA AAVPDVVSLFEPINTFLGTWYA AIDLANALFSIPVCKAHQKQFA FSWQGQQYTFTVLPQRYINCLA LCHNLIQRDLDHFLLPQGITLV HYIDSGPFIK*PEAASFEWGPEQ EKALQQVQAAVQAALSIGPYD PADPMVLEVSVADGDAVWSL WQAPKGESQWRPLGFWSKALP SSTDNYSSSDVQLYTDSWAVA SSLAG*SGTWKKHDWKIGDKEI WGRGMWMDLSEWSKTGKIFV SHVNAHQLVTSAEEDFNNQVD RMTRSVDTTQPLSPATPVVAQ WAHEQSGHGGRNEGYAWTQQ HGLPLTKADLTTATAECPICQQ QRPTLRPRYGTTSQGDQPATC WQVDYIEPLPSWKRQRFLLTGI NTHSGYGFAYPPCNASAKTTIH GLIACLIHCHGIPHSIASLYRER GTHFTDKEVQQWAHAH

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4508	34876	A	4549	2	1602	NLSPILPQDLWPFTRVTVHWGK GNDQTFQGLQDTGSELMLIPGD PKRHCSPPVKVGSYGGQVINGV LAQVRLTVGTVGPRTHPVVISP VPECIIDIDILNSWQNPHIDSLTG RVKAIMVGKAKWKPFEPLLPIK IVNQKQYRIPGGIAEISATIKDL KDAGVVIPITLPFNSPFWPVKKT DGSWRMKVVYCKLNQVVTPIT AAVPDV/VVSLLEQINTSPGTW YAAIDLANAIFSIPVHKAHQKQ FAFSWQGHQNTFTVFTILLHIH KVGHAQQHSIIKWKWYIHDGA RAGSEGTSKLNEEVPQMPMVT TSAALPSLPRPAPMASWGVLY DQLTEEEKTRAWFTDGSARYA GTTQKWTAAALQPLSRTSLKG SGEGKSSQWAELQAVHLVVHF SWKDKWPDVRLYIDSWAVAN GLAGWSGTWKKHDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI

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4509	34877	A	4550	1	1891	MLSSTQNAGGSYQRVRGALDT QEWKWGEVSPRTLNVDGRAL VSVANTHGTDRPAYTLNPQSR DQRSGVITLGYKRPLEREDLFE LKESDSFCTACPIFEKQWRKEV LRNQERQKVKALNKLDEALCP GIILTQSTDSNANLFQKQPHRHT QTSGRWQIIIFCEHSSDFGWNG YGYAVALLVVVFLQTLILQQY QRFNMLTSAKVKTAVNGLIYK KLGWSGKVSWLILHDVGHGIM EGYIAWGKGSDVRITWEKKST EMRTRPAQKMALLLSNVSRQK FSTGEIINLMSATHGLDSKPQSP LVCPFSNPNGRISPLARAGLAD HYRVTHLQILKLYAWEPSYKN KIIKIRDQELEFQKSARYLTVFS MLTLTCIPFLTKISLGRLEDFLN TEELLPQSIETNYTGDHAIGFTD ASFSWDKTGMPVLKESIRIRIEQ VLNQLSLFETVDYPGSVAYVSQ QAWIQNCILQENILFGSIMKKEF YEQVLEACALLPDLEQLPKGD QTEIGERAVNISGGQQHRVSLA RAVYSGADVYLLDDPLSAIDV HVGKQLFEKVIGSLGLLKNRTH ILVTHNLTLLPQMNLIVVMKSG RIAQMGIYQELLCKTKNLTN\FT KSSVNKKKVGEWEESGRGS
4510	34878	A	4551	2	542	LTSAKVKTAVNGLIYKKVSLAT LCVYFLLDERIILTAPKVFTSMS LFNILRIPLFELPSVISAVVQTKI SLGRLEDFLNTEELLPQSIETNY TGDHAIGFTDASFSWDKTGMP VL/NRGSEAYVSQQAWIQNCIL QENILFGSIMKKEFYEQVLEAC ALLPDLEQLPKGDQTEIGERVR
4511	34879	A	4552	1	667	IETNYTGDHAIGFTDASFSWDK TGMPVLKESSVAYVSQQAWIQ NCILQENILFGSIMKKEFYEQVL EACALLPDLEQLPKGDQTEIGE R/GKETAVNISGGQQHRVSLAR AVYSGADVYLLDDPLSAIDVH VGKQLFEKVIGSLGLLKNRTSH SVCHYTLLAVPHLLEVQILTGN FIQSLGFNYHEYANNSNAYIVN LDLFPGFQTCVYKLLSPIRCLIC
4512	34880	A	4553	201	336	QQTPGKAVHAPFIADQSLT*EL VSVFPQFQLFPYRR*DSHSGKS
4513	34881	A	4554	3	515	

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4514	34882	A	4555	1	852	MPCTTSGLDKVPTSKKALTRY GYGSLTLDFSGSIIPCKMCLSPS TRIVRPSQPRGTEDPDETGDTEF VNSDESFLLEGTASPSPVVAVSP PRPMLPSAFPPLSEDINPVLPEA TVLASPEVVAKQTHVDSPRKPL STFLFASRPVTKLKSRQTPGGE VDSVTCEEKTDGPWRKTVDYC KLNQVVTPIAALVPDMVSLLV QINTSSDTSYAAIDLAKAFFSIP VYKAHQKQFIFSWQAQQYTFT VLPQGYIISPALCHNLIRR/DLD HFLLPQDITLVHYIDDIRL
4515	34883	B	4556	288	327	
4516	34884	A	4557	51	598	LFGGCHTSGGLAVRVPRMPRG SRSRTSRMAPS\ASRAPLK*ELE PRQAQVAQPPA\AAPPSAVGSS\ AAAPRQPG/LFMAQMATTAAG VA\VGFCCGGHTLGHGI\TGGLS VGGKLIA*ALRRP*HQFNQGSF RGTQAKHSKQQPALPLLWRIKT SFREVVPPEPRVTIQGFCGGFPM RLLETVPDL
4517	34885	A	4558	1	10434	MTVIRSGIAYILHLKSYDVNIQT GSNACNQPTHPNGDCSHFCFPV PNFQRVCGCPYGMRLASNHLT CEGDPTNEPPTEQCGLFSFPCK NGRCVPNYYLCDGVDDCHDNS DEQLCGTLNNTCSSSAFTCGHG ECIPAHWRCDKRNDCVDGSDE HNCPTHAPASCLDTQYTCDNH QCISKNWVCDTDNDCGDGSDE KNCILNCTASQFKCASGDKCIG VTNRCDGVFDCSDNSDEAGCP TRPPGMCHSDEFQCQEDG
4518	34886	A	4559	24	849	ATGRCCCGLAPGFPLCWVLYP GGRGSA\CPEPHVLRTGSPLQRE QRTNGRTDLSSLLPNLNFDSPP RCKHKNQLAITLRKRIRKLATS LFSSTIFRISGTSVIISAPGAGLPL PALFPTRCQPKFSRSIDPTGKAV QTADIRLSARATLWLGGSIEESP VLCSTLRLLLRRLPPPLTWTSPN RPTQPCTAQTQTNQSVGIAAPS AIRVIYPESVVLNAVIYLPGDPE VSGLPRAFKRRFSVEVRLDCGT FKLLLVYCTHPGDKKVNTCKT GALVAF
4519	34887	C	4560	192	449	
4520	34888	A	4561	1	786	
4521	34889	A	4562	3	14073	

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4522	34890	B	4563	58	1282	
4523	34891	B	4564	1	684	
4524	34892	A	4565	1	1356	MGRKYTLKWEFEEGFTEKKEL KKVTSEGYITPVEIYDYRQYCY ALQRPIATTQIDDVRDGHTTRL AKLEKQEQTHSKASRRQEIIKIR AEPKEIETQKTLQKINESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDKGDITTNPTEIQTTIRE YYKHLYANKLENLEEMDKFLH TYILPRLNQEEVESLNRPITGSEI EAIINSLPTKKSPGPDGFTADFY Q\MLEVLARAIMQEKEIKGIQL GKEEVKLSLFADYMIVYLENAI ISAQNLLKLI/SNFSKVSGYKINV QKSQAFLYINNRQTESQIMSER PFTIASKRIKYLGIQLTRDVKNL FKENYKPLLNEIKEDTNKWKKI PCSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI WNQKRACITKSILSQKNKAGGI MLPEFKLY/YQGSSTQTAWYW
4525	34893	A	4566	1	1102	MANCDINRKDEKGGKEKKDRS KSKSLMDTLKRQLSAKQKPKG KAGKPSGSSADEDTFSSSSAPIV FKAVRAQRPIR/STSLRSHHCSP MPWPLRPTNSEETCIKME\PSPP LNGVRKDFHDLQSETACQEQA NSLKSSASQNGDLYLRLDEHVP VVIGLLPQDYIQYTVPLDEGMC PLEGSSSYCLDSSSTMEVSVVPS QVGGRSFPEDESQADQNLVVA PEIFVDQSMNGLLTGTTGVMLQ SPRVGPHHVPPLSPLLPPMQNN QIQRNFSGLTGTEAHMAESMLC HLNFDFNSAPGVARVYVSVQSS GPMVVTSLTEELKR\LAKQGWL WPPLKSVRRCVLARRSLYTKQL NQEEGTELNLGSSCLLC
4526	34894	A	4567	364	661	PFHFTCFSCKVYFADPGSAARS VPGSPSAVCAQCILCTGHCAVC PGLGEHHSSGRTLMKTKLHSK KLKPCYLLC*SKN*KTQGGSPK S*NVNKYLVTLI
4527	34895	A	4568	53	470	CISIIILPGPSAKTLSPVLSLSSPY TASFQPTFVRTFSHQTTYLSLGS VPVAQLKCSAGQQRGELLCRR GVWGSWISVSHFTEIATLPAAC LEDGE\DFNLGGILDSSKYL*SIQ KTNTHRIVDGKVVSETNITDVL

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4528	34896	A	4569	1	1635	MGWTCKILFLVAAATGAHFLV QLVQSGAEVKKPGASVKVSCK ASGYTFTYCYLHWREPVSFICG RCILLTLLLGDCLWGEGAWTQ GDVLQPSDRASFLAMGVNTTG QQVGDLSGDFPNSVGKACKCR EFHTLTPLAHTSSTTHETFPGMS HIALELSQGSSLLQCLEAQTQG QRQELTVSANEQPESRGHGCVL LCETQSEGKSVRAQAQTSLKGS QKRLGGARTLCTGLSPGQRKQ ERSKIDTLTSQLKELEKQEQTYS KASRRQEITKIRAELKEIETQKT LQKINESRSWFFEKIYKIDRPLA RLIKKKREKNQIDAIKNGKGDI TTDPTEIQTTLRQYYKHLYANK LENLEGMDKFLDAYTLPRLNQ EEVESLNRPITGPEIEAIIN/STPT KKSPGPDRFTAEFYQ\RSDVLA RAIRQKKEIKCIQLGKEEVKLSL FADDMIVYLEIPIISAQNLLKLIS NFSKVSGYKISVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTKDVKDLFKDNCKPLLN EIKEDTNKWKNIPCS
4529	34897	B	4570	1	429	
4530	34898	A	4571	1	897	MDLNYTLEQMDLTDIYRTFHPT TTEYTFYSTGHGTFSKTDDVIG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLLNECWVKNKMKMEIKKLF ELNDNNDTTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKNKNHMIISIDAEKAFDKIQH PFMIKTLSKISIRGTYLNLIKDIY DKPTANIMLNGEKLKAFTLRTG T\RMNQGCPLPSLLFNI/VLEVL ARAIRQEKEIKGIQIGKEEVKVS LFADYVIVYFENPTDSSRKLLEL IKEFSSFWIQD
4531	34899	A	4572	1	1461	
4532	34900	A	4573	49	365	
4533	34901	A	4574	45	534	VCHLEPGERCGPSRGCRAVGV QTEKMQTAGALFISPALIRCCT RGLIRPVSASFLNSPVNSSKQPS YSNFPLQVARREFQTSVVSRDI DTAAKFIG\AGSATVGVADSGA GIGAVFGSLIIVYARKLSLKQQL LFYAILGF\ALSEGM\GLFCLMV AFLILFAM

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4534	34902	A	4575	98	624	DWYSRSHPKELWEGSKKKSIN HSACSLQAHGGPISTSLNPHSKP RGRVSPPPGKRQQECRARPGRS PELAGPPPANVQETSQKNACAS RLSEPPGEGP\EPAAHPQPHRGS SSGPCSRGGYRQPLFPGPAASG VPASGSV/RSRIPGAPQGVALAR RGPQGSPSPAPRFFPATERQS
4535	34903	B	4576	1	604	
4536	34904	A	4577	3	331	LAPAPSAAWRTGLKALTPSST WMLCASE\HHVGSGCVGDHLA GCRQEKTLPCQR\YCVFCRRRR ARSLQAQCGFSLTPALELLPVPF LKLLCPGPPRRRRICRILPGAGL
4537	34905	A	4578	1	871	
4538	34906	A	4579	3	510	GPPSRVDDFVAAAAAAVAPVV LYACPRHSPIPPWSIRGRRVVVT GFGPFGEHTVNANWIAVQELE KLGLGDSVDLHVYEIPVEYQTV QRLIPALWEKHSPQL\VVHVGV SGMATTVTLEKCGHNKGYKGL DNCRFCPGSQCCVEDGPESIDSI IDMDAVCKRVTTLGQCI
4539	34907	A	4580	1	285	MAPGALPALGEEEGPGASGLSA ELGHLSAGSRAFRETSVDSALD TPFPAGTFVRLEFKLRQTE\SGR RKDWKKPKCKVQPERRKQKCL TCVKLEC
4540	34908	B	4581	1	228	
4541	34909	A	4582	1	697	MGLERPVDRVMWLPGALWNS AVVSAPVGEEWALAGTGNQGL QDIQGMHCPEEGISQIHGRDHR NAKDSHTGVWCSCTLGIISTIIIR PKCRFSIDRSDSDYLPTSSCRRD PGGAEPCQDRPRVEQLCSVLAN RSGPLAKCHWYESPVSYTQVC VSDLCQYGTGNRMLCTMLEAY VQLCALRCALPARVASQPGMQ LRVACPANSYYDSCGPPFPATC ASLNSSAPCTLQCTVSCFCLEGF ALEAG\SSVPHACCGCHLQGRY I/APGPWPSATGMRAPCPTRRC VSLTSASMARATACCAPCWRP TSNSAPCAARCLPAWRASLGCS YVWRVQPTATMTPVGHPSRPP VLASTPPRPAPSSAQ
4542	34910	B	4583	1	208	
4543	34911	A	4584	2	230	

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4544	34912	A	4585	106	669	GCGCVLLPGGVGAPGHSPEGP VPPRDARQLRTCGLAGTLHLST SCGHPTGAWRGALGSQWNGH NPVQDHLQEAQPWFLEFDRG* RCFWRMATSFPRYPTWDDY*R LPCCRCLPQCKKPAETTGCLPIS GEKTHGGVGDLLGEAPARLRQ WASQRQPATDLPA*ASRGRPA* GKDTHRACVAGEAAQDA
4545	34913	A	4586	2	597	TPKGGIRLGLAKLGCPTAWINP YGRGMPLAHSVLSSGARVLVV DPDLRESLEEILPKLQAENIRCF YLSHTSPTPGVGALGAALDAAP SHPVPADLRAGITWRSPALFIYT SGTTGLPKPAILTHERVLQMSK MLALSGATADDVV\YTEVLPLY HVMGLVVGILGCLDLGTSLAS YGLRVYFILWSVLGPSRRTLCL
4546	34914	A	4587	9	573	EEEERKKKKK\KKKEEEEGEEE GGGMGEKKKKEEEEEGEEEGE KEREKER\EKERKKKKEERKEK ERERKKKRERKKEKERERKEG EGERERKSTECTSSSYI/IKKLVV KQPQAAPSGEIPEEGIAVLGGDS SMPVIVPEDLPVGQDVEVEDSD INDPDSLILVSSQAGGGGVITAY CNLEHLGSSDPPT
4547	34915	A	4588	1	297	
4548	34916	A	4589	114	752	DGSAAPRATSDSFTYTVCVSEF PVDDFMELGRSIPDTQL/DAVIE SQKANQCAVLIYT/SGTTGIPKG VMLSHDNITWIAGAVTKDFK/P TDKHETVVSYLPLSHI/AAQMM DIWVPIKIGAL/IYFAQADALKV RLSKDLGSDFILLGSPVGLRPST KRLPVLSKLGHTYRRVVWVEE SSGPHTISNQNNYRLQGPMMK LKRHFVAQKYKKQIDHMYH
4549	34917	A	4590	1	837	MVTQKLPNAQENLKHAERQAA GCCPGRSHIFQHVGPGASESLR GEGCSTHPEAQGAQERCEQWK KDQHWCLASHTDVTQQWGRH IVQEGGTHRGPSAVLSLRTALD EG/ARGGCSHPITAQLPLQLRHL PRPPPAPAR\PSPAPPAATSPPT\P PPAPAR\SSPAPPAATSPPTASSG ACAALPQLPLQLRHLPRPPPAP AR\SSPAPPAAMSPP\RPPAPARP RLRRSTACATALRPGERGSAAA QPGARSETSFCRLG/AAAAVLD PAFISSQALACPVVGVI

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4550	34918	A	4591	3	377	
4551	34919	B	4592	1	1632	
4552	34920	A	4593	1	1224	MDGTNRFYLYVWETERQQDV EHVARCILCYDKCRPDPECPAG TPGPQEVDVDLVFVVDSSYGV DADVYRGSLSLADAALEDLEV AEQPGASHRGARVALVTHTTP NF\GRGFHLTTYGNRKQMQRH VREASARPLQGTAPPGHALEW TLENVLLAAPRPRKAQVLFAIV ASETSSWDREKLWTLSLEAKC KGITLFVLALGPGVGTHELAEL AELVSAPSEQHLLRLQGVSEPE VNYAQGFTRAFLNLLKSEQSPG TGAPWVEWGEGFTEPGIWACR WTNQYPPPELTEECGGLHRGD TVLQLVTPVNRFMYAAKENSL KRKTKANFHLAVELELDESYFR AYYEGTLYEVSALPLQRSNELL QKWSLFHGSNGRRVSGSHPEV ALQQGGTGLPAVLVWQLWRQ
4553	34921	A	4594	266	556	HKVQQICYRLRLVSQILFSINQT LAERQIVTFTVYPDTERDRETR NLADLKQIKIDLGKFSDNPDGY IDILRGLRQSFDLTW\RDIMLLL NQTLAPN
4554	34922	B	4595	1	735	
4555	34923	A	4596	70	624	PTAMVEEGIAAGGVMDVNTAV QEVLKTALIHDGLARGIREAAK ALDKYVYQSQYCGFLQPDQKL ATQGKKGMGVHGVKRKSS*M ASVLPGNLRKRRQAH\LCVLAS NCDEPMYVKLVEALCAEHQIN LIKVDDNKKLGEWVGL\CKIDR EGKPRKVVGCSCVVVKDYGKE SQAKDVIEEYFKCKK
4556	34924	A	4597	145	682	SWRNRTVSNGSAVSASSVHLCF AECKALCGERILTDGSDVSRPTI AAGGVTDVNTALQEV\LKTALI HDGLAR\GISRTWPKAL\DKRQ AH\LCVLASNC\DEPMYV\KL\V EALCAEHQINLI\KV\DDNQET* EKWV\GLCKI\DREG\KPRE*WL VGS*CSSLRTIGKESQAKDVIEE YFKCKK
4557	34925	A	4598	252	590	RSLDLVWWQLSGGLAGSAKPK PCTPVKQSTVMSFPSHKEQYFL MDGKKK/YDKESEKYYSILEKH LNLSAKKKESHLQENSSGPSVS TKLINLFSKRLLCAFLPAQLTPY SFCS

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4558	34926	A	4599	1	1662	
4559	34927	A	4600	4430	4904	LIKGTRCLGRRPSFAYSRSNI*A *S*P/EGTSAQLAELLALTLALE LGNGKRINVYTDSKYAYLILHD HAAIWKERAFLTSGGTPIKYHK EIMELLHTVQKPKEVAVLHCQS HQKESSPLEDTTTAGPLLHPYP AGSSPERSSPSSQQLLGDLFRGII
4560	34928	A	4601	1	2630	MEQANHPVRLINVVCKDTLKKI VQQETSCPLTHVHYAEAITGRC TAPEDKGSLDQKPPTDDPTGCP WQVPAHVITLTETWVCLTIEGQ EIDFLLDTGVQKPNGQWRLVQ DLIPIKEAVIPLYPVVPNPYTLIS QIPEKAEWFMALDLKDAFFCIS LHSDSQFLFAFEDPTNHTSKITR TVLPQGFRDSPPLFGQALAQDL GHFSSPGTLVFQYVDDLILATSS EASCQQATLDLLNFLANQGKV VPNLWGKLPLNTTRKSWSYCT QCKNPRRWQSYTAKAIKKQLA EAGPVTAILLLLIFGPCIFNLLIK FVSSRIEAIMLQMVLQMEPQMS STNNFYQGPLDRCTDPLSGLES SPRCSEAPCLMSQWTGDIEYDL LLPPIPHQTTLCDLQNLKGIFSR YHRKWYGEILALLTPTANVCG HSQVPHACSIYHDPVTWNPQG LLPKSLYGVTKWGDKEHFEWG SQQQRAFYELK\KKLMSAPALG LPDLTKLFTLHVSDREKKMAV RVLTQTMGPWLGPVAYLSKQL DGVSKSWPPCLRALAATALLA REVDKLTLGQNLNIKAPHAVV TLMNTKGHHWLMNARITRYQS LLCDKPHITIEVCNTLNPTTLLL VSESPVEHNCVEVLDSVYSSRP NLRDHPWTSVDWELYVDGSSF INPQGESVWGIIQGKRPIKLWG KRRKVSARDLAIIGGSVEAPKL
4561	34929	A	4602	1	506	FLALTSRFLFVLLNEETRSHLEK SLCWKVSPHIKMDLLQWIQSK AQSDGSTLQQGSLEFFSCLYEIQ EEEFIQQALSHFQVIVVSNIASK MEHMV\SSFCLKRCRSAQVLHL YGATYSADGEDRARCSAGAHT LLVQLPERTVLLDAYSEHLAAA LCTNPNLIELSLYR
4562	34930	A	4603	3	381	
4563	34931	A	4604	3	483	
4564	34932	A	4605	3	410	

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4565	34933	A	4606	2	249	SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
4566	34934	A	4607	2	481	LAPLVKEIHDNFGMGEGLMTT GHAITATHKTADGPSGKLWRD\ GRGAHQNIIPASTGAAKAVGK VMPELNGKLTGVAFRVPTANV SVVDLTCRRQKPAKYDDIGKV VRQAPEGPLKGILGYTEHQVVS SDFNSDTHSSTFDAGAGIALND HFATLSPPPH
4567	34935	B	4608	79	278	
4568	34936	A	4609	2	1201	PSTACRNSARACSTVSRIFFCVA SRATSLRTPMGKVKVGVNGFG RIGRLVTRAAFNSGKVDIVAIN DPFIDLNYMVYMFQYDSTHGK FHGTVKAENGKLVINGNPITIFQ ER\YPSKINWG\DAGAEYVLEST GAFTTMENAGAHLQGGAKRVI ISAPSA\D\APMFVMGVNHEKY DNSLKIISNA\SCTTNCL\APL\A KVIHDNFG\IV\EGLMTTVH\AIT\ ATQKTV\DGPSGK\LWALMGPR GFFQEHQSLPFTGGC/ARVVGQ GSSPELERGKLTWAWAFRCPQ LPKRVNGWDL\TCRL\EKPCPK YD*HQGRVVKAGRRKGPLQGA ILGLQLSNPGGSPSGLSTSDNPL LPPFDAWGLAFALQRTHFCSKL IFLGIDNGILGYSNQGGWDLHG PPWPTWAFQGS
4569	34937	A	4610	61	226	WRIMPTKKVMITMGRTTQRRM LES/SQQFWPCHLH*KLVPSCLQ LGCLVFHFRRER
4570	34938	A	4611	153	495	QHAAECKAHAGLPGLPLPARK LASRHGAPRWRQSGVGPGGKV ENYGRRRL\PGTRHPQSLSHKP AKKIDVARVTFDLYKLNPQDFI GCLNMKATFYDTYSLSYDLHC CGAKRIMK
4571	34939	A	4612	1	643	
4572	34940	A	4613	286	698	ESDNNLTQGTSI*QGTRHPQSLF PLSPAKKI*CGPVLTFLTCYKLN PQGLSLGCLNIEGRFFMDYVIPF PIDLALLLGAKRIMKG\TLHWA LFSMQTTGPRA/VFTSCYLQQL LDATEDGHPPKGKASSLIPTCL KILQ
4573	34941	A	4614	59	294	
4574	34942	A	4615	1	2253	

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4575	34943	A	4616	2	197	LARSGMGFYRRGLLGEVKGRV EGNRMWHVIVRTSPNHRYTFT LKTHPSVVPGSIAFSLPQ\RPWS
4576	34944	A	4617	302	441	
4577	34945	A	4618	944	1257	RLPFSPRSVGPTPQAPRLLCNG WRQLPTTFFTELEKTTLKFIWN QKRALIAKTI/LKPKNKAGGITL PDFKLYYKATVTKTARFLLYK VSQIDNTDLFDPVKIKFE
4578	34946	A	4619	1	1370	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSM NVIQHINRTKDKNHMIISIDAEK AFDKIQQPFMLNTLNKLGIDGM YLKIIRAIYDKPTANIILNGQKL EAFPSKHGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIIYLENPIVSAQN LLKLIGNFSKVSEYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SIRIKYLGI*\LTRGVKDLFRENY KPLLNKIKEDTNKWKNIPCSWV GRN\NIMKMAIL\PKVIYRFNAIP IKLPMTFFTELEK\TTLKFIWNQ KRARIAKSILRQKNKAGGITLP DFKLYYKATVTKGAWFQHHK HTLIKEPLLDSVFSPNRPDHGK KQDKQPQTKNIANASADSKNT QQMNGFVTGAATSFIPKDRTAS SLCGCTGRRRQSVAKYLRIRPHI NVPSFTYYK
4579	34947	A	4620	2	671	WHQNLALTRASGSFHS/WEEG KGGADMSHEICVANLQVYVRS TDFDRTLMSAEANLAGLFPPNE VQHFNPNISWQPIPVHTVPITED RLLKFPLGPCPRYEQLQNETRQ TPEYQNRSIQNAQFLNMVANET GLTNVTLETIWNVYDTLSCEAP SPPWGRKPPLERLWPRPRELTC PLRYT\QTHGLLLPPWASPQTV QRLSQLKDFSFLFLFGIHEQVQ KARLQG

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4580	34948	A	4621	1	1923	DSVAFEDVAVNFTQEEWALLG PCQKNLYEDVMQETIRNLDCG HETEFVEYENLRDPMNMPLHT TDGPHKCKICGKGFDCPSSLKS HERTHTGEKLYECKQCGKALS HSSSFRRHMTMHTGDGPHKCK ICGKAFVYPSVFQRHEKTHTAE KPYKCKQCGKAYRISSSLRRHE TTHTGEKPYKCKCGKAFIDFYS FQNHKTTHAGEKPYECKECGK AFSCFQYLSQHRRTHTGEKPYE CNTCKKAFSHFGNLKVHERIHS GEKPYECKECGKAFSWLTCFLR HERIHMREKPYECQQCGKAFT HSRFLQGHERIHTGEKPYECKE CRKAFSWLTCLLQHERIHTREK PYEGKQCGKAFTHSRFLQGHE RTHTAKKLCECLSTVSARKSVD LIIASYPLFLNLFSTPKTLRNCSY RRHERMHTGEKPYECKQCSKA LPDSSSYIRHERTHTGEKPYTCK QCGKAFSVSSSLRRHETTHSAE KPYECKQCGKTFHHLGSFQIHM KRHTGDRPHKCKICGKGFDRPT LVRYHERISTGEKPHECKQCGK AFDHLGSFQRHMIRHTRDGPH KCKICGKGFDCSSTLQSHERTH TGEKKLYECKQCGKALSHSSSF RRHMTMHTGDGPHK\CKICGK
4581	34949	A	4622	1	256	MGKGSFKYAWALYKQKAECE RGVTIDTSLWKFETSKCYVTI\K DFIKNIITGTSQQGQTASVAAFC ILSSCPASWKNQVSHRLGG
4582	34950	A	4623	173	717	SINAVASTRRTIEKFEKEAAEM GKGSFKYAWVLDKLKAERERG ITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQADCAVLIV AAG\VGEFEA\SICQNG\QTREH ALLAYT\LGVK\QL-ICRVNKMD STEPPYSQKRYEEIVKEVSTYIK KIGYNPDTRAFVP\ISGLNGDH MLEPKC
4583	34951	A	4624	3	525	GCPSGPGHRCVAGHGAPGAVC RHVPTAWPGYSRCSPGPGPRGV EAVGHQRHRAPETHSTPAADR HRRGLPGS\KSDSAMEPSPSPAP QAQPPKPVPKPRTVFGGLSGPA TTQRPGLSPALGGPGVSRSPEPS PRPPPLPTSSSEQSSALNTVEMM PNSIYFGLDSRGRAQAAQDK

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4584	34952	A	4625	2	448	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFTCQSGDFTRPTA
4585	34953	A	4626	1	751	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAGV*FFFKQKIFRA LSTG\EKGFG\YKGFPAFHRIIPG FMCQGW*LSHRHNGTGWQVH LMGRNFEDE\NFILKAYGVLGS LSMAKCLDPTKIGSPVFPSCTA KT\EWL\DGQALWCFGK\VKKG LNIVEAMERF\GSRNGKTS\KKI TIADCGQLE
4586	34954	A	4627	3	615	PECIIGIDILSSGQNPHIGSLTGR VRAIMVGKAKRKPLELPLPRKI LNQKQYRIAGGIEEISATIKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALGLLLGFGGN*TFDY
4587	34955	A	4628	3	354	DSWA\VANGLA\GWS\GTWKK HDWKI\NDNEIWGK\SMWIDLS EWSKTVKIFVSHESAHHIT*KSS AEEDFNNQVDRMIHSVDTTRPL SPATPVIAQWTHEQSGHGGRD GGYTWAQQHGL

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4588	34956	A	4629	281	1529	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLTAMGVI GSHGARGQVVALNRQRQGDL QPFTRVTVHWGKG/NMQIFGGL LDTGSELTLIPGDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKQYHIL GGTVEISATIKDLKDTEAVTPTT SPFNSPIWPVQKTDGSWRMTV DYCKLNQVVTPIAAAVPDVVS LLEQINTSPGTWFEWSPK\KAL QQVQAAVQAALPFGPYDPADP MVLEVSVADRDAIWSLWNAAI GESQRRPLGFWSKALLSSADNY SPFERQLLASYWALVETERLTV GHQVTLRPELPIMNWVLSDPSS HKVSGAQQRSIIKLKWYIHDW
4589	34957	A	4630	453	719	ARGSKHTGLIAQWAHEQSGHG GRAGGYAWAQQHGLPLTKAD LP\AMATAECPICQQQRPTLSPR YGTIPW/WAWDAPGGRGCWRL QKAGE
4590	34958	C	4631	122	325	
4591	34959	A	4632	1	346	MAGEKVEKPDTKEKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGGDKNGGTQVF\ QIITYSSYTQKVQLPKSTLKQRQ GPCPQGAL
4592	34960	A	4633	115	905	EAFQTLHFCCLGLRQGTKRMA GEKVEKPDTKEKKP\EAKKVDA \GGKVKKGNIKA\KKPKKG\RPH \CSRNPVLCSEGFGRYSRS\AMY SRKAI\YQEGSTFSPLKSKVEKK KKEKVLATVTKPVGGDKNGGT RVVKLRKMPRYYPTEDVPRKL LSHGKK\PFSQ\HVRKLRASITP\ GTIL\IILTGRHRGK\RVVFLK\QL AKLAYLLC*LGPLVLNRVPLRR THQKFCHLPLSTKIDISNVKIPK HLTDAYFKKKKLRKPRHQEGEI
4593	34961	A	4634	2	350	FVALAAVLCRQCLPRAWVCRR AGQGSGRHYRAAICAELKKPLT IEEVAP/DPVGPHEVRVDVHFC GVNFGDILICRDQYQERPHLPFT PGPVADSRKGLPIRSCCPPYNL WHCDFCS

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4594	34962	A	4635	1	556	MGLKLNTHMDQTRGSLSGDTL EGSPSKRAKIILKRGGFRGILGG VGVQERRTGQRPALPCHDLRR AEVVPDHRRGGPRPVGPHEDL WQIPEKVSLQEAAVLPITYGTE SFALEHRARTQPGEIVLVTAAA GATGLAVMWQQISSGQGNIAA AGSDEKCKLAM\EKGAQSSVN YSQGSLKDSATDQ
4595	34963	A	4636	1	142	
4596	34964	A	4637	2	368	
4597	34965	A	4638	2	504	HKVGHAQHHSFITWKWYTRD WSRAGPEGT\GVPYDQLTEEEK TRAWFTDGSARYAGTIRRWTA AALQPLSRTSLKESGEGKSSQW AEVRAVHLVVHFTWKEK*PDV RLYTDSWAVANGLAGWSGTW KKHDWKIDDNEIWGRGMWIDL SEWSKTVKIFVSHESAHHIT
4598	34966	A	4639	182	840	RTAVKGNLPTTPVI/SQWAHEQ SGHGGRDSGYTWAQQHGLLIT KADLAMTTAECLISQQQRPRLS LQYSSIPWGNQPATWWQIDYIR PLPSWKGQSQDSQDRSRNQGV KVKVAPLTITPSDTTAKFLLHV PAALHSAGVDVLVPEGGMLPP GGTTTIPLNWKLRLPPGHFGLLI PLSQQAKKRVTVLAGVIDLDC QDEISLLLYNRDAKELYRYTAH
4599	34967	A	4640	3	283	SRVSCSPPPLSPPPPLSPPPPLSPP PLLSPPPPPLSPPPSPPPPVSLPPP PPVFSFPSSCP/PPFPPPLLPPLPPP PPLSPPPPPPPWSPSPPI
4600	34968	A	4641	1	531	MGSSHCTQPGMLAAAVGQAVP GTDTGADSVSLSASCCHQHAIH CAQAIRAKGHLQAHTELPSAPT QPPSCARQCPKSGGDLGGRELY NNHEIRSGKHIGVCISFANNRLF VVSIPKSKTKEQILEEFIKVTGS YWVLGLSFDFRKWPV/GQCCQ SFHGRLRATPARRAERRDARSF AL

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4601	34969	A	4642	115	2405	ATAEGSGSSGVKERGAGIRKAE RRRTEASGGGGGRGRRRSWRR AGAEGVSEADARGRGGKGREG KGGSRGGARAHRERARRRVEL DRVCCQRRELRPPFYNSSTRAG HREQRARVSRNPIPSDRISPPQP NGEISGNMATEHVNGNGTEEP MDTTSAVIHSENFQTLLDAGLP QKVAEKLDEIYVAGLVAHSDL DERAIEALKEFNEDGALAVLQQ FKDSDLSHVQNKSAFLCGVMK TYRQREKQGTKVADSSKGPDE AKIKALLERTGYTLDVTTGQRK YGGPPPDSVYSGQQPSVGTEIF VGKIPRDLFEDELVPLFEKAGPI WDLRLMMDPLTGLNRGYAFV TFCTKEAAQEAVKLYNNHEIRS GKHIGVCISVANN\RLFVGSIPK SKTKEQILEEFSKVTEGLTDVIL YHQPDDKKKNRGFCFLEYEDH KTAAQ\ARRRFN*VGKVQGFG GNVGTVEWADPIEDPDPEVMA KVK\VLFVRNLANTVTEEILEK AFSQF\GKLERVKKLKDYAFIHF DERDGAVKAMEEMNGKDLEG ENIEIVFAKPPDQKRKERKAQR QAAKNQMYDDYYYYGPPHMP PPTRGRGRGGRGGYGYPPDYY GYEDYYDYYGYDYHNYRGGY EDPYYGYEDFQVGARGRGGRG ARGAAPSRGRGAAPPRGRAGY SQRGGPGSARGVRGARGGAQQ
4602	34970	A	4643	2	369	
4603	34971	A	4644	1	1002	MNAGCGQTHDCAYRQKRPED VNEEGRLEQRNRKRQDEWGPR DKPASSGYKAGTLDVENWNRA GEGLKHAHQKGLKVDSSAFCT CSLIRTVLMPLSPYYSAGQQAE SKNLKESVVPPTASIENKKQER EDKNWPILPPPVAETSVPPPSVA GIETPIQRILRSAAIAGEPSGPCA FPISVRPDSNNPQQFIHEHTPLEF KLLNELKTSVVNIGVQSPFTLG LPESAFGAMRLLPFDVKHWAR TCLSASAYLTWNLNGQEMCTD QVRQNRAAGHGDIAEDMLLGN GP/YFRPGTSNGTKRAWATIPEE GVPVQSFLPFMEGSQEPSAQFL ARLREAV
4604	34972	B	4645	1	575	

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4605	34973	A	4646	1	776	VVLMRNLMSGTIFSMLANISML GSLVIIIQYITQEIPDPSRVPLVA SWKTYPLFFGTAIFSFESIGVDL PLENEMKNARHFPPILTLGMPI VTTLDIGMAALGYLRFGD\DTK GSIILSLPICWYLHGLSGEGPSQ SFSERETKAQVIVPRSEVNVPRR PVSEHSGRGEQLCGLSCRLYQS VKLLYIAGILCTYALQFYVPAEI IIPFAISRVSTRWALPLDLSIRLV MVCLTSAPMTRSTPFCKYSTRG RRRWLEIPV
4606	34974	A	4647	1	1294	MGKDFMSKTPKAMATKTKIDK WDLIKRKSFCTAKETTIIVNRQP TEWEKIFATYSSHKELISRIYTE LKQIYKKKTNNPINKWAKDMN RHFSKEDIYASKKHMKKCSSSL AIREMQIKTTMRYHLTPVRMEII KKSGNNRQPIVGPCDNSVILLY KILANRIQQHIKKLIHHDQVGFI PGMQGWFNTCKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLGIDGMYLKIIIAIYD RPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGSQLGKEEVNLSLFADN MIVYLENPIISAQNLPKLINNFS KVSVCKINVQKPQAFLYTNNR QTESQIMSELPFTIASKRIKYLVI QLTRDVKDLFKENYKPLLNE/I K/EDTNKWKNIPCSWVGRINIV KMAILSK
4607	34975	A	4648	2	711	WNRRRPCIAKTIL/SQKNKAGGI TLPDFKVYCKSTVTKTAWYWY QNRHIDRWSRTETSEITPHIYNH QIVDKPHKNKQWGKDLLFSKW CWENWVAICRKLKLNLFLTRY TKINSRWIKDLHEKLKTIKTLEE NLGNTIQDIGIGKDFMTKMPKA IATKAKIDKWDLIKLKSFCTAK ETIIRVNKQPTEWENISAIYPSD RSLISRIYKE\LKNIYKRLDAVA HTCNPITLKGQGRWIT
4608	34976	A	4649	1	576	
4609	34977	A	4650	1	771	

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4610	34978	A	4651	1	887	FPEDSEPISISHGNYTKQYPVFV GHKPGRNTTQRHRLDIQMIMIM NGTLYIAARDHIYTVDIDTSHTE EIYCSKKTAWEILDRPMVATCR MKGKHKDE\CHNFIKVLLKKN DDALFVCGTNAFNPSCRNYKM DTLEPFGDEFSGMARCPYDAK HANVALFADGKLYSATVTDFL AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDYIYFF FREIAVEYNTMGKLLGLHHELL RRTQDYGHKAGCPESCLLSVRR CPPPQSKAHRESVEELIKGCRR HAGFCACGHITT
4611	34979	A	4652	1	2890	MVLLKVDPGLWGSSLRVLLKA DPPYGTQAHAERHGRALAGGL GVGEQSQSLDLLRMSHTYGAL FLPRAAVSSWCASVRIRKIKKSP LLDGAPLLYEPDTWLGKWSSS WTLVFTHPFSAALTHSALTARS DTGSLTLSPDGKLYSATVTDFL AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDYIYFF FREIAVEYNTMGKVVFPRVAQ VCKNDMGGSQRVLEKQWTSFL KARLNCSVPGDSHFYFNI
4612	34980	A	4653	1	480	MEGVEEKEKVPAVPETLKKKQ GNFAELKIK\PKMAFVLRIRGVS GVSPKVRKVLQLLRLHQIFSGT FVKLN/KASVNMLRIVEPYIAW GYPNLKSVNELIYKRGYGKINK KRIALTDNTLIVPSLGKYGILCM EDLIHEIYTVGKHFKEANNLLW PFKLSSP
4613	34981	A	4654	3	279	
4614	34982	B	4655	119	177	
4615	34983	A	4656	157	359	HQRCRK**TKLEG*TCRKIEVN TDYIKP*E*EFWMIYYISIYLTSI CSSICNENILQLENREKSRNT

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4616	34984	A	4657	65	900	GLAFPPILQKESPHPCLWILFTSP VALSTSRPPCVISSAALCPRRHG FLPPRLLAPLAAAFCPRPRCFLP LPPRLFAPAPVDFCPRRCGFLPL PPRVFAVSCPRRRGLLPPLLFAP SAAAFCGFLAPSPWLFAAFGTR CRGFLGLLVPAAAAFFPRRLRF FLPRLFSPAAAVTFCHPCFLPPP PRLSVPAAASFCRRGFQQEIRTV EIRGSGTRVGLQHQTGHLPRGP SSLPAELHA*ARVSPLEASPPSC TR/WMQQPEDLGPALTLGRICG VGACWEL
4617	34985	A	4658	927	1157	ARRSTAPVDCK*LQP*AQAAL WVLVWDHEAARQPEGVVQPA PGLWPSSRRWRKFQAPGSSGV CHPGALQACPEELS
4618	34986	A	4659	1	563	MKLVAVFDKQDLHHGGDDISA SSMHTQSPERFTSASELGTNNV SAFSV\YQAASEIEVTSSVLHAS SQKGLSSQHLGFGAPQAGGGSF RHLAPQRKEVLEEYFKYDPEH KLIFRFVRTLFKAMRLTAEFAIE ITHGGRDVERATGLVNKIHRQG CGDSFCNIGGNAKPYVCCGKE YVSSSKHQNGIAI
4619	34987	A	4660	1	681	MGKYAEALRSQQKAVLMSVR VMGIEHPNTIQENMHLALHCFT SRQLSLALSLLQGAHYLM/LLV LGE/DHPEVA/LLDNIRRVLHRV MEYDLSLCFLDNALAVSTKYQ GPKALKVALGHHLITSVYESKA EF\RSALQHQKEGLAAH/TSLGE DQEKTKESSEYLKCLTQLAVAL RRAMHEIYRNGSSNNIPPLNFT APSMASVLEQFKGINGILFIPLS QKDLESLKAEVAQ
4620	34988	A	4661	2	443	VWQSGGDSITSKTNIITCVNCY LYTCIDSSFNQYHSILIVRARQD IWLPVALHRPWESSPFIHVINNI LQKILKRSTQFIFTLIAIIMGLIA VTVIAATAGVALRQSIQTVHFV DKWQKNSTRMWNS/QRIDQKL ANQINDLRQTVIW
4621	34989	A	4662	2	377	FAFTWTDPDTHQAQQITWALL PQGFADSPHYFSQAQISSSSITY LGIILHENTRALPADHV*LISQT PISSTKQQLLSFLGMVRYFCLWI PSFTILTKPLY*FTKANLADPTD PKSFPHSSFRSL

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4622	34990	A	4663	1	1095	MAKAVLSKKNKTGSTTLPDFKI YYKDIVTEEPGIETLRHTSSTKF SKGLPSRESFSEKQNKTTTHLH PGEINSFIAHTKPAWRSLHTDA HEIWCRDSDQVNSPGRSIPCPPA LCSMRKIHLRPLVLRPASPRNIS PILNPLHLIAALLPNPKPPFRPPL VSPDLNPQVKDISTPSWATDHV HLTVSLKPYHPYPAQCQYPIPQ HALKGLKPVITRLLQHGLLKPI NSPYNSHILPVLKPDKPYRLVV QDLRLINHIVLLPIHPMVPNPYT LLSSIPASTTHYSVLDLKHAFFT IPLHPSSQPLFAFTWTDPDTHQA QQIT*AVQPQSFTDSPHYLNQA QISSSSVTYLGIILIKAHVLSLPIV
4623	34991	A	4664	655	2417	KKRESMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGRQGWF NICKSINVIQHINRAKDKNHMII SIDAEKAFDKIQQLFMLKTLNK LGIDGTYFKIIRAIYDKPTANIIL NGKKLEAFPLKTGTRQGCPLSP LLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDANKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRAHITKAILSQKNKA RGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTQPSEITP HIYNYLIFDKPDKNKQWGKGS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNVRPKT TKTLEENLGITIQDIGMGMDFM SKTPKAMATKDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK \FSQPTHLTKG*YPESTMNSNKF TRKKQTTPSKSGRR\NEQTLLK RGHLCSQKTHEKMLTITGHQR NANQNHNEIPSHTC

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4624	34992	A	4665	1	234	MQNQEKFGELISEWAPYGRPRP QIAVGDHHISVYDGEVNWRMS SLQASAAGKDYANRGTEWGEE PSQMLRHELLSGEMCVSRNRG QPLANSERRSEALSPVTPKKLIP ADGHKSDPGRTWMKLETIILSK LTQEQKTKHHMFSLISG*FAEN DGFQLHPCPS\GSLLWPSAGISF FGVTGLRASDLLSLLARGCPRF LDTHISPLSSS
4625	34993	B	4666	1	2553	
4626	34994	A	4667	33	272	
4627	34995	A	4668	1	3045	
4628	34996	A	4669	1	334	
4629	34997	A	4670	159	245	FPIVASPWLLC*LMSFAGTWVK LETIILSKLSHGQKTKHRMFSLI DTVVVGSDDFPLLRVPGCCASS LNAAHTSVNIKLELT
4630	34998	A	4671	122	359	TANLKNGRKFL*PIHLTKG*YPE STKNVNKFTRKKQTTPSKSGQK I*TNTSQKKTFMQPTGT*KNAH HHWSSEKCKSKP
4631	34999	A	4672	2	66	RLVYADTCFSTIKLKAEDASTS ENMRCLVFCACDSLLRMIVSSF IRVPTKDMYSSFFMAA*YLLQY HQVKSRRCFYE
4632	35000	A	4673	519	899	SALVCHTCSNWQVHLGDSVFY RSEEQPLEPLPFSYLSSLFPGLHP DPVSSGSQQPS*MPHTDASVTS SHGLGGLAGRNSCIYPCCAPAL CADYLWGSPDLFLLLSFQHKG NVGVGLAHSPQFQQGN
4633	35001	A	4674	1	278	
4634	35002	A	4675	158	592	GYYWRPSFQSLRENNECQRKS NSVNAGCLNCDHCVLGIYQQH *QNYFSFDIHYFLSETGRKVSSS I/AYFTIGETEALSGKVVPYWQQ AAGQGCTLHLLLPQTRLFPGKG RRQPGLLREF
4635	35003	A	4676	302	721	
4636	35004	B	4677	1	871	
4637	35005	B	4678	1	559	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4638	35006	A	4679	3	2386	RVATMAPHRPAPALLCALSLAL CALSLPVRAATASRGASQAGAP QGRVPEARPNSMVVEHPEFLK AGKEPGLQIWRVEKFDLVPVPT NLYGDFFTGDAYVILKTVQLRN GNLQYDLHYWLGNECSQDESG AAAIFTVQLDDYLNGRAVQHR EVQGFELAP\FLGYFKSG\LK\Y KKGGVASGFKHVV\PNEVVVQ RLFQ\VKGRRVVRATEVPVSWE SFNNG\DCFIL\DLGN\NI\HQWC GS\NSNRYERLKATQVS\KGIRY NERSGRA\RVHVSEEGTEPEA\M LQVLGPR\VALPAGTEDTAKED AAN\RKLAKLYKVSNGAGTM\ YVSLWAD\ENEFTQGA\LKSED CFILDHGKDGKIFVWK\GKHAN TEERKAALKTASGFHSPRWDY PKQIQVSVPFLEGG\ETPLFKQV FKNWRDPDQTDGLGLSYLSSHI ANVERVPFDAATLHTSTAMAA QHGMDDDGTGQKQIWRIEGSN KVPVDPATYGQFYGGDSYIILY NYRHGGRQGQIIYNWQGAQST QDEVAASAILTAQLDEELGGTP VQSRVVQGKEPAHLMSLFGGK PMIIYKGGTSREGGQTAPASTR LFQVRANSAGATRAVEVLPKA GALNSNDAFVLKTPSAAYLWV GTGASEAEKTGAQELLRVLRA QPVQVAEGSEPDGFWEALGGK AAYRTSPRLKDKKMDAHPPRL
4639	35007	A	4680	1894	2161	MFGLPNARAATSTAPFASHSLC LCFRILLLLGPGINLANPRNHLV LHQKFSILGRHFSL\ATEEPCISL ALAPSKRWECNSSS*RYENN
4640	35008	A	4681	1	1803	
4641	35009	A	4682	1	501	MTFQCVVNTHYLTYPRPQRFL YLVVVRPSCASWIMFVLIDRGY VFSYFPQSYGGFGSRILSKPIEV QVGGRSVVAQMWSNKCGQYS DLASLGCISR/YSAGSVYYYPSY HHQH/NPVQVQKLQKELQRYL TR/KIGFEAVMRIRCTKAKPTRH RHYGELEISITIIRAIGK
4642	35010	A	4683	350	623	

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4643	35011	A	4684	1	3252	PPGPERSRLGLGVSLHQRSCPK CIAVFTRVSEPRIQFPASRILPSS NTSKDFDPVSGQSNYGGSQGS GQTLNRPPVASNPVTPSLHSGP APRMPLPASQNPATTPMPSSSF LPEANLPPPLNWQYNYPSTASQ TNHCPRASSQPTVSGNTSLTTN HQYVSSGYPSLQNSFIKSGPSVP PLVNPPLPTTFQPGAPHGPPPAG GPPPVRALTPLTSSYRDVPQPLF NSAVNQEGITSNTNNGSMVVH SSYDEIEGGG
4644	35012	B	4685	51	236	
4645	35013	A	4686	1004	1405	
4646	35014	A	4687	1	771	
4647	35015	A	4688	1	405	SENVDDVSVMMG/TPANKALL DTTGFWHD/DFNNATPNDICVA IRSE/AADAGIAQAIMQQLEEA/ LKQQA/LDRNLNVMMFSDNVT LE/DEIQLK/TRAREKGLLV/MG PDCGTSMIAGTPLAFA/NVMPE GNIGVIGASGTGFRR
4648	35016	B	4689	1	1656	
4649	35017	A	4690	1657	2259	LPQPQPATPWPSAPTPRFASPAA AMATLWSGTCRIRLWSGSSRA TRTAPAALIFPITALGSGQGAW TTRCAAGTCGRAASCSSMTSA/ AQIFSPCHCPNQDWLAVGMESS NVEILHVGKPEKYQLHLHESCV LSLKFAPCGRWFVSTGKDNLL NAWRTPYGASIFQSKESSSVLS CDISRNNKYIVTGSGDKKATVY EVVY

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4650	35018	A	4691	62	1371	QNQSTISVMLRSAMTTTMAAD LITAI/MGQRKQHIDTGFWHDD FNNATPNDICVAIRSEAADAGI AQAIMQQLEEALKQLAQGSGS SQALTQVRRWDSACQKLPDAN LALISVAGEYAAELANQALDR NLNVMMFSDNVTLEDEIQLKT RAREKGLLVMGPDCGTSMIAG TPLAFANVMPEGNIGVIGASGT GIQELCSQIALAGEGITHAIGLG GRDLSREVGGISALTALEMLSA DEKSEVLAFVSKPPAEAVRLKI VNAMKATGKPTVALFLGYTPA VARDEN/VWFGSSLDEA\SLAG CFSVRARSPLTRIDGMMILGMF GGCFAASLWANNVKLRMPRSR IRIMQAIIGGIIAGFGARLAMGC NLAAFFTGIPQFSLHAWFFANP LLIGQTLEDPHEYIDYLDKEFPL YQLVECVVSLNYSYHWECTEI
4651	35019	A	4692	1	1125	MEAEVDKLELMFQKAESDLDY IQYRLEYEIKTNHPDSASEKNPV TLLKELSVIKSQYQTLYARFKP VAVEQKETKSRICAGMTKTMN VIQKLQKQTDLDLSPLTKEEKT AAEQFKSHSFGMWPCKLKYRQ NKKKKKKLSQNRSTTWKLNNL LLNDYWIQNEMKAEIKMFFET NENKDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLAL QLKELEEQEQTHSKASRRQEIT KIRAELKEIETQKNLQKINESRS CFFEKINKMDRLLARLIKKKRE KNQIDAIKNDKGGITNDPTEIQT TIREYYKHLYANKLENLEEMD KFLDTYNLPRLNQEEVESLNRPI TGSEIEARINSLPT\KKSPGPDGF
4652	35020	A	4693	2	421	GRVGGRVGKIRT*LN*IETKKY KR*NETKSWFFEKIKMDRPLAR LTKKRIKEIQITSLRNETGNIITD TTEIHKIIQG*SSSSSSSSSSSSSSS SS\FSSSSSSSSSSSSSSDTFKRPIT GIKIEMVF*KLPTKKSRISL

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4653	35021	A	4694	1	654	MEYYAAIKNNTFMSFAATWM KLEAIILSKLTKEQKTKRHMFSL VSTLELGALTALVRCGRWRRQ CDDEAMACVTQGRPLARLTKK RREKIQITSLRNETGDITTDTTEI QKIIQGYDEHTYAHKVENLEG MDKLLEKYNPPRLNQEELGTL NRPITSYEMEMIIKKL/PNEKSP GPDGFTAEFYQTFKEELVPILLA LFHKTEKEGILPNSFYEASITL
4654	35022	A	4695	1	786	MPPSLAYKNPRPQQADTQVA/T MSRGVHWRKKMQAAGPREDV KRSTQAEEHTDRHQHTSR\HQL LLMRIFEMGWKKPSPFQEESIPI ALSGRDILARAKNGTGKSSAHD IPLLKRLDLKKDTIQTIVIVPTG GPALQVSQICIQVSKHMGGVK VVMTTGGTNSGDDVLRLDDTV HMVIAAPGRILNLIKKGVAKLE ETYLRHIGRPGHFGHFGLAINLI TYGDHFNLKGIEEQLGKEIKPIP SNIDKSLHVAEFHSKAVENEKP
4655	35023	B	4696	1	501	
4656	35024	A	4697	2	573	YSACFFLFSIAMGILLTVPPSFWI PTSFSAFLGFFSSFSLLVLHQPD FSFVLGLWRIISLLVLKIVEGSS NQGMQMASRSWEWPSSSRKM ATSVRTLPEP/GPSGCRAPSAFPF RKEAGADPSGCPGGRQVPLVAI GRGGALEPQRWELRAPGSAGR LPREGGRTFPGAQSPAGAQSPA GKQSPPGAQSPLH
4657	35025	A	4698	2	346	PPINISVPHC*PFGG/EPLEILIPAP ERSSHVLSQSPVRTHSSAVHQS VGASLNCGDKQPPNFSGSKIFF LIYLHLMTGQVRGSSVLCHPNT GIQKEGGTVNEIPIAIEKRKKHA
4658	35026	B	4699	1	468	
4659	35027	A	4700	2	284	ETGEFTQLKELNIQGNCWTLLL PELGNLYLTGQKKVCKVENSP WVTPIAGQFQLDVSCVSECVCS ETYEYLYGQHMQ\ANP\EPPKH NNHKSGKD
4660	35028	A	4701	5	189	
4661	35029	A	4702	38	190	

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4662	35030	A	4703	2	882	WPSVSSG/PSSAVSFSSFDPGVA SCTSSSASGIQRPMASEVPCASG IPIKKIGHRGVDSSGETTYRKTT SSALKCAIQLCITHTVGSLDPTP ERHVLIEPLIELSSSGADGSLLH VSIHDEFIIKTVQHKQAEFLQKL IPGYHIDLNQNSWTLLPKFYGL CCVKAGGKNTQIAVMKNLLLR LNSEGERILLCIGITDILQSYRFV KKLEHSWKALVCDGDTVSVHR PGFYTERFQCFMCNTAFKKIPA RTLTTPNAGKDVEQQELSSLLM GMRSGTATVEDSLVVSYKTKH
4663	35031	A	4704	2	410	
4664	35032	A	4705	2	728	
4665	35033	A	4706	1	1208	MKMEKVNTSWLLPPSSISVLIR RGAGSMVLLLQSQRQYIFEYDS SDRLLAVTMPSVARHSMSTHTS IGYIRNIYNPPESNASVIFDYSD DGRILKTSFLGTGRQVFYKYGK LSKLSEIVYDSTAVTFGYDETT GVLKMVNLQSGGFSCTIRYRKI GPLVDKQIYRFSEEGMVNARFD YTYHDNSFRIASIKPVISETPLPV DLYRYDEISGKVEHFIIITTAEM TLSKHFDTHGRIKEVLA/YEMF RSLMYWMTVQYDSMGRVIKR ELKLGPYANTTKYTYDYDGDG QLQSVACNDRPTWRYSYELNG NLHLLNPGNSVRLMPLRYDLR DRITRLGDVQY/KIDDDGYLCQ RGSDIFEYNFNGAPTKTLSQAS GILQSLQGLHEVHRNPACSDFA
4666	35034	A	4707	1	663	MMLLLLALLGAGLLGASLLTS WHAPARNKIPRAQKWREEPDL DPKPILELPLAELAQQLRTEELS LESILCSYLKQALKVHQEVNCL MDFLGECEEELQALKKLKKSE RGLLYGVPMSLKDTYDSMFLE KPATKDGVIMKVLKAQGAIPFV KTNIPLTLLRSLKRASWALNAA TPIYGQMLSPLNLKKTCGGSS/G GDHGGWPHGPGRGEPGAVPCK

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4667	35035	A	4708	2	624	SDARLHKDDTDICFSKTLNSCK VPQIRYASVERLLERLTDLRFLS IDFLNTFLHTYRIFTTAAVVLGK LSDIYKRPFTSIPV\RRARKLSLT SPLNSKIGALDLTTSSSPTTTTQ SPAASPPPHTGQIPLDLSRGLSS PEQSPGTQPEVSGSSPHSTAQSK IWSLVWKQYWLMAPSHALKT CHAARLARTFVTSSSATKVHCA ISLK
4668	35036	A	4709	1	195	
4669	35037	A	4710	1	1845	MAEAEPGRPGERGGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPKDKEEIVICDRASVKE FKEEISRRFKAQQDQLVLILSGK ILKDGDTLNQHGIKDGLTVHLV IKTPQKAQDPAAATASSPSTPDP ASAPSTTPASPTTPTQPSTSDSA SSDAGSGSRRSSGGGPSPGTGE GSPSATASILSGFGGILGLGSLG LGSANFMELQQQMQRQLMSNP EMLLQIMENPLVQDMMSNPDL MRHMIIAKPQMQQLMERNPEIS HMLNNPELMRQTMELARNPAV MQEMMRNQDRALSNLESIPGG YNALRRMYTDIQEPMFSAARE QFGNNPFSSLAGNSDSSSSQPLR TENREPLRNP/WSPSPPTSQAPG SGGEGTGGSGTSQP\GSGMFNS PEMQALLQQISENPQLMQNVIS APYMRSMMQTLAQNPDFAAQ MMVNVPLFAGNPQLQEQLRLQ LPVFLQQMQNPESLSILTNPRA MQALLQIQQGLQTLQTEAPGL VPSLVSFGMSRTPAPSAGSNAG STPEAPTSSPATPATSSPTGASST QQQLMQQMIQLLAGSGNSQVQ TSEVRFQQQLEQLNSMGFINRE ANLQALIATGGDINAAIERLLGS
4670	35038	C	4711	59	464	

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4671	35039	A	4712	1	1902	MAEAEPGRPGERGGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPKDKEEIVICDRASVKE FKEEISRRFKAQQDQLVLILSGK ILKDGDTLNQHGIKDGLTVHLV IKTPQKAQDPAAATASSPSTPDP ASAPSTTPASPTTPTQPSTSDSA SSDAGSGSRRSSGGGPSPGTGE GSPSATASILSGFGGILGLGSLG LGSANFMELQQQMQRQLMSNP EMLLQIMENPLVQDMMSNPDL MRHMIIAKPQMQQLMERNPEIS HMLNNPELMRQTMELARNPAV MQEMMRNQDRALSNLESIPGG YNALRRMYTDIQEPMFSAARE QFGNNPFSSLAGNSDSSSSQPLR TENREPLPNPWSPSPPTSQAPGS GGEGTGGSGTSQVHPTVLNPFG INAASLRSGMFNSPEMQALLQQ ISENPQLMQNVISAPYMRSMM QTLAQNPDFAAQMMVNVPLFA G\NPQLQEQLRLQLPVFLQQMQ NPESLSILTNPRAMQALLQIQQ GLQTLQTEAPGLVPSLVSFGMS RTPAPSAGSNAGVYPPRPPLPHP ATPSHIFSNRG/SPAPQQQLMQQ MI\QLLAGSGNSQVQTPEVRFQ Q\QLEQLNSMGFINREANLQALI ATGGDINAAIERLLGSQLS
4672	35040	B	4713	309	527	

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4673	35041	A	4714	1111	2506	KKDQRETRNQKGLGFLRDRPQ WVSGKMKQECLQ/HWNAMAI NNHRAVAIFPKRRHGREDGLLS NLPTFGSYAPLRRVSNEFIASAV QRILLERRALPHGNCKLGGLTP QFMNRKNALVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRIKYLGIQ LTRDVKDLFKENYKPLLNEIKE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTFFTE LEKTTLKFIWNQKRARIAKSILS QKNKAGGITLPDFKLHYKATV TKTAWYWFQNTDIDQWNRTEP SEIMPHIYNYLIFDNPEKNKQW GTDFLFNKWCWENWLAICRKL KLDPFLTPYTKIKSRWIKDINVR PKTIKALEENLGNTIQDIGMGK DFMSETPKAMTTKVKIDKWDL IKLKSF
4674	35042	A	4715	3	372	SVGVALRPWKRE/RAASERRSS SGGGGGGGGGGGGGGGSGS GQ/HAPAAPAGGIEAVNMASAS YHISNLLGVLAAAALAVTQALP \PPSAVAGSFSAPKSPAHRSAGL PIPAEPLSSPLLQPPPP
4675	35043	A	4716	1	1008	
4676	35044	A	4717	1	2619	
4677	35045	A	4718	449	801	VLLLSSMSRRKCQSLYVDLLM KKETE*SMEKEKLTMHPLSCTH I*PRPQAPEADKQMRR*TEEQN CRMMWQKKEKEHLNAKRSLA GSGWRDQPLDGKAPGEDHLPIP SPFQLPIHPI
4678	35046	A	4719	1	1255	
4679	35047	A	4720	2	843	CLHGFGYRIRDSELQKIHRAAV KGDAAGVERCLARRSGDLDAL NK/TAQIAGAQPREEACTVILLE HGTNPNLKDIYRNTALHYAVY SESTSLAEKLHFHGANIEALDK VLSISFLSKILMSSLKTCGRDAE DYTISHHLTKIQQQILERKKKIL KKEKRGKASESEFLNSLGGPTL DKKIRNVEISDESAVSILHELCV DSLPALDDEVLSVATKCVPEKV SEPLCRPSHEKGNRIVNGKGEG SEECLCPAAHRLRCGERLYLPP RLGCERLCLATTPSEK
4680	35048	A	4721	295	1050	

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4681	35049	B	4722	306	554	
4682	35050	A	4723	2	7973	
4683	35051	A	4724	2	316	
4684	35052	A	4725	81	228	DPPLCLGLL\LHRASIVQKRIIYF QDEGSLTKKLCEQGKTLKHSQ QMFFK
4685	35053	A	4726	1	1043	MELEWKVNVKVNSQDTNHHG SLQLARGEAAAVKFGRMSKKQ RDSLYAEVQKHQQRLQEQRQQ QSGEAEALARVYSSSISNGLSN LNNETSGTYANGHVIDLPKSEG YYNVDSGQPSPDQSGLDMT\GI KQIKQEPIYDLTSVPNLFTY\SSF NN\GQLAPGIT\MTEIEIVAAEKF PLIYKQSFLLTVLSFGGGGSVIC GPTFAKVSSSRRFIHHGDKIQPS INALGWTFMEETPQIFKCRTNT HGKELEHDLPEHSSGQGSTRRK SSCLRRDNNPMLLSGGRFYEKI HNFITGTFDVRKMEHAEGKTSD LVHVGFQAIKMPSSLKQEASNG LIKLEEASGARMKTGHIK
4686	35054	A	4727	467	584	
4687	35055	A	4728	1	1794	
4688	35056	A	4729	110	1797	PSQQEPGSGTSCLRYCWTAQTL PSVTMKLWVSALLMAWFGVLS CVQAEFFTSIGHMTDLIYAEKE LVQSLKEYILVEEAKLSKIKSW ANKMEALTSKSAADAEGYLAH PVNAYKLVKRLNTDWPALEDL VLQDSAAGFIANLSVQRQFFPT DEDEIGAAKALMRLQDTYRLD PGTISRGELPGTKYQAMLSVDD CFGMGRSAYNEGDYYHTVLW MEQVLKQLDAGEEATTTKSQV LDYLSYAVFQLGDLHRALELTR R\LLSLDPSHERAGGN/LCRYFE QLLEEEREKT\LTNQTEA\ELTTP EGIYERPVDYLPERDVYESLCR GEGVKLTPRRQKRLFCRYHHG NRAPQLLIAPFKEEDEWDSPHI VRYYDVMSDEEIERIKEIAKPK LARATVRDPKTGVLTVASYRV SKSSWLEEDDDPVVARVNRRM QHITGLTVKTAELLQVANYGV GGQYEPHFDFSRNDERDTFKHL GTGNRVATFLNYMSDVEAGGA TVFPDLGAAIWPKKGTAVFWY NLLRSGEGDYRTRHAACPVLV GCKWVSNKWFHERGQEFLRPC
4689	35057	B	4730	1	2433	

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4690	35058	A	4731	425	1079	PMGTSFLYECANFQSVSLGDPQ EPSCLCGGQPQGAAGGSSGSED ALLCLWDLQARKWKFEMSYTS GNIRGSSFCQFKSSFLVYFKALL KFRELFAQFKSFMGEKKLSLAP PMSDSSGDGIIRKIDYASCKRSG \SSIRALPKTYQQP/EVLNDTWV SFPSWSEDSTFVSSKKTPYEEQL HRCEDERFEEMKTAGFASFGER SKTGVPNLRVTDWYRLVAC
4691	35059	A	4732	3	425	GASSEEAEGASEGP\GAPGGWG APGSQGAQEGGDLQEAEESQE GGDPRKPRSPRKVERHRKAGA PGRDLGRPSLTVLL\NHCVLQR LRKIYHSSIKPLEQSYKYNELRQ HEITGQRCPCCEEPKPQHQERA LFVVVSENRNI
4692	35060	B	4733	1	1056	
4693	35061	A	4734	171	511	LLSVRHVVRNTQETANDVQVW /LDREGGSKJ\NTGVCFLDHMLD QIATAVSRME\INVKGDLYIDD HHTV\EDTGL\ALGEALKIAPGD KPGICRFGFVLP\MDECL\ACAL DISGGPH
4694	35062	A	4735	563	763	
4695	35063	A	4736	365	1644	RTSQMSSSAWRQQNRARPSSAI LPSSLSLGHPALPQFSQRMPAT ASQLPGMVGVLEGYGQTAASP GSVSSCSPACSSCCLGCWWPSS WPSCRLHPHLGRPIAHCLPE/VL TTTTTTPTITTSQAAGTPKGQQE SGVSPSPQSTCGGLLSGPRGFFS SPNYPDPYPPNTHCVWHIQVAT DHAIQLKIEALSIESVASCLFDR LELSPEPEGPLLRVCGRVPPPTL NTNASHLLVVFVSDSSVEGFGF HAWYQAMAPGRGSCAHDEFR CDQLICLLPDSVCDGFANCADG SDETNCSAKFSGCGGNLTGLQG TFSTPSYLQQYPHQLLCTWHIS VPAGHSIELQFHNFSLEAQDEC KFDYVEVYETSSSGAFSLLGRF CGAEPPPHLVSSHHELAVLFRT DHGISSGGFSATYLAFNATERL CLVESTSS
4696	35064	A	4737	1	154	

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4697	35065	A	4738	1	700	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVLIRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTA\LGGILKKKGHHE AEI\KPRGTVSNATKHKIPVKVT WRSSPECII\QVLQSKHPGDF\GA \DAQGAMKQGPGSCFRKDNWP PTYKELGLSRAKPLAGFPTPNPS WAPGFKRERGLISV
4698	35066	A	4739	1	154	
4699	35067	A	4740	1	617	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVLIRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTA\LGGILKKKGHHE AEI\KPRGTVSNATKHKIPVKVT WRSSPECI\IQVLQSKHPGDF\GA \DAQGAM\NKALE\LFRKD\MAS NYKELGFQG
4700	35068	C	4741	46	522	
4701	35069	A	4742	78	617	TKELLHSKRNCHQSEQATYKM GENFCNLLI*QSANIQNLQRT*T NLQEKNKQPHQKVGEGYEQTL LNRRSLCSQKTHEKILIITGHQR NANQNHNEIPSHTS*NGNH*KV RKQQVSYKLL*MRPRRTRQVT Q*RREPETSLAKETPGNPTNTN AKFKTRGARISHYSSGNGERLP RTVC
4702	35070	B	4743	1	6477	
4703	35071	A	4744	1	623	MSSDISEVEDKNEFLTEQLSKP QIKFNTLKDKFLKTRDTL\RKKS LALETVHNNLSQTQQQIKEMK EMYENAEAKENNSTGKWSCVE ERICQLQHENPCIEQQLDDVHQ KECLPSRKEKFKSEPPAFLSGN QVKSSSCSLQTLFPPDDLILYLE NPKDSTKKLLELINKFRVTGYK IKLQKSVAFLNDKNEQSKEENQ ECNPIYNNYK
4704	35072	A	4745	2	3272	
4705	35073	A	4746	1	579	
4706	35074	A	4747	3	510	

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4707	35075	A	4748	1	1261	MEAVDTFLVFNALNFLLTSQTT GCSSSCDPGHGLGQGSGNRFPI AAASARTAEEAKWFFSNKDYS NVLQLPDPKKTEYHIHEKRFSD SRILCYYPEFGKVEEIILTAMKH DWFGKHRKDDKIEKTGKIKIQE SFTSEEERIRMKQEQERIQAKTR EFRE\RQARERDYAEIQDFHRTF GCDDELMYGGVSSYEGSMALN ARPQSPREGHMMDA\LYAQVK KPRNSKPSPVDSKGKVLGEADP VYPRRNPGTEGNASSLPSVSFSE SPPVRAAFAGYHYVAFPWLQK LMSGTSGKDPEKEADLARVVT LRVVTLRIETHVKTLAFTAALL QQLACIDVGMDKQNDVYTYN KILLSFKRKEILTHTTTRMSLED IILSEINQWQEDKYRFGLYEVA QVVKLIETESKVVVSRDGGRG
4708	35076	A	4749	10	2051	
4709	35077	A	4750	2	2118	
4710	35078	A	4751	1	658	MWNSKTLAAFRPCPKDPLNFE LERDNLAYLAEEIPKQQSIQYIT WMILKAFSHMHLQRDNLKLEL MFKRKAKHKGLKNLHPDHVIE KKNLFSAEKFKPAAEIYISNEEP NVNSQDNGKKCLQGMSEIFAA APAITDNTSDKTTLIKVSSWPYI ADRRCPLVNVTREDSPSEDPVF LRTLGKGDWFGEKALQGWGL\ KGIHHVSAQEPVCLLLPFMTPR
4711	35079	B	4752	1	471	
4712	35080	A	4753	315	407	
4713	35081	A	4754	411	1042	
4714	35082	A	4755	1	423	
4715	35083	C	4756	202	321	
4716	35084	A	4757	5	413	CFFFFFFETESHFVTQAGVQWR DLGSLQSPPPGFTPFS/SPQPPKE PGPQAPATTPGQSFAFLVEMGF HHVSQ\EVSIS*PRDPPASASQS AGTTGVSHRAWTFCFLRQSLA LSPDWSAVARSQLTATSASWV QVSRR
4717	35085	C	4758	150	491	

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4718	35086	A	4759	1	548	GIAFCLNLIKTLKLPNFKSCVIL LGLLLLYDV/FFVFITPFITKNGE SIMVELAAGPFGNNEKNDGNL VEATGQPSAPHEKLPVVIRVPK LIYFSVMSVCLMPVSILGFGDII VPGLLIAYCRRFDVQTGSSYIY YVSSTVAYAIGMILTFVVLVLM KKGQPALLYLVPCTLITASVVA
4719	35087	B	4760	642	1985	
4720	35088	A	4761	39	252	
4721	35089	A	4762	1	783	
4722	35090	C	4763	218	358	
4723	35091	B	4764	372	374	
4724	35092	B	4765	129	1036	
4725	35093	A	4766	1211	1983	SQSCLLLQEDFAPIAGEQEAEQ HQEDLRALLRASLQGQCSRQP GTRLHGSAPWPGEAQNRSRPLP GDSPSLDRYRGI/SDAVGKSRSG DIGSSLRVEAGDKRTQASPERQ PHCGAHDAQDISGGREIFKPRQ LPGSAIWSIKVGHGSGFPGKRR PRGAGLSGRGGRGRSKLKSGIG AVVLPGVSTADISSNKDDEENS VLDMVVLFSSSDKFTLN/QVCG SFGQGAEGRLLACSQCGQCYH PYCVSIKMDACSSSELKY
4726	35094	A	4767	1	603	MANFNDCVLDKEKVCIAAKFIT HAPAGEFNEVFSDIRLLCNNDS LLRERAARAFAHYNMDQFTPV KMEGCEDQTIIACIESHECQPKN FWNGRWRSEWKFTITPPTAQV VGVLKIQVHYYEDGSVQLVSH KDVQDSLTVSNDAQTAKEFIKII ENAENEYQTAISENCQTMSDTT FKVLRRQLPVTRTKIDWNKI\LS YNI
4727	35095	A	4768	1	867	MADFDDRVSDEEKVRIAAKFIT HAPPGEFNEVFNDVRLLLNND NLLREGAAHAFAQYNMDQFH AVK\IEGYEDQVLITEHG\DLGN SRVLDPRNKISF\KFDHLRKEAS DPQPEEADGGLKSWRESCDSA LRAYVKDHYSNGFCTVYAKTI DGQQTIIACIESHQ\FQPKNFWN GR\WRSEWKVP\ITPPSAQ\VVG VLKIQVHYYEDGNVQLVSHKD VQDSLTVSNEAQT\AKEFI\KIIE NAENEYQTAICGNYQTMSDTT FKALRRQLPVTRTKIDWNKILS YKIGKEMQNA

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4728	35096	A	4769	2	690	WPSGSASRPRHLRAPEPV\GKA GKNKGAGLTPA/AGTSGCAGR AESRGPPTGSHGSEPSRGSKGL CGRGTRSLPERGAEVLPHLPAQ TSPQLGSQGAWP/RHPRKPFRP AARAGTQPPGFVPSTPALLKVL YRSAHTQHSGRAAPEPSRLALG PTLQQKRHMGHRRNLTFSSTY NKKCGFGWAVEMRFSALLDVT TTPSRVAFWGSRGPPLGMERQL QLLSGYSPDGWLSTSM
4729	35097	A	4770	1	590	MDTRIGTTDTGTYGKVEGARR MRLKKLPIEYYAYYLDDEIICTS NPCEFPGYGIEREYPCETSGPLE LTVQEDQGEEPQREELTRKKTS KVCRGSPLAWATGVKPCLKKK RRRRKEERRKKKEEGEGEGEEE EEEEEEEEEEEEEEEEEEEEE EE/EEEEEEEEEEEEEEEEEEE EEEEEESDPCTSWNTSQP
4730	35098	A	4771	1	288	
4731	35099	A	4772	1	237	MRSSVIGPRSHIPSQRKSGIQEE EEEEEQEEEEEEEEE/EEEEEEE EEEEEEEEEKGLLDQEAARHLV LPAATQCKPKM
4732	35100	A	4773	1	794	MASHSSPMGSQYYYGFPGPDS AMHALNTVVSEKDLTLDLSGL VARNKRCGPHSYSLNTHLLHA CLRLPTQRENTTLKTFIPQGWEI HTDQVEREAECQPGRLKICVHD TAQELPLASTARNALLGRNLCP FRQSSTTQMPDEIPISLDDRMRP PSLKKKK/VVGEEEEEEE\EKEK EEEEEE/DEGEEEEEEEEEEEE EEEEEEEEEEGGGGGVGEEEEE EEGEGEGGGGEEDEEE*EEEEE EQKKKEKKKKEQEEGGGEGG
4733	35101	A	4774	115	341	
4734	35102	A	4775	1	651	
4735	35103	A	4776	189	618	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAELSGNNSISF\HHE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEDLLYNFI YIIFSKMPTKVPSLWDSKLGAE QAAPEENNKKEQQEEYQGKSF SFLNLTECWP
4736	35104	A	4777	1	414	

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4737	35105	A	4778	189	692	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAELSGNNSISF\HHE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEDLLYNF IYIIFSKMPTKAMSISSMFKFAT KIRMTVTPNPKCCWIPVFPAYL STSKAAKCMHHTAHHGQEKSD HCISPSPIPAP
4738	35106	A	4779	2	3815	
4739	35107	A	4780	957	1493	KNRNYNKLSLRPQCNPTRTQD* ETHSKPLNYMETEQPSPE*LLG T*RNEGRHKAVL*NQ*EKRHNI PESLGHI/AKQCVEGNL*H*MPT RESRKDLKLTP*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQELVF*KDQ QN**TASKTNKEEKREESNRRN KKC
4740	35108	A	4781	1	4962	
4741	35109	A	4782	2421	3011	NQACQPGQAGAARAGQCFPRV AQRPGPGPAGMALAHPDLYLC HSAGDQCR*DEEADPPEGQAPT HFQVHPAGGLHLLDRLAAPQH QAGTQGQGQPGRHH*PAARSS PVEPPSTGSPSRPTTTMWPSCSR RQGGLGPGL*CVQQPHLLDAP GTLPVLGALVCRLQPWRCLPL GGGGGVGGSQRPPGGGGGNG GRNWG
4742	35110	A	4783	1	932	MRTPKSSIKPSLGEEKENYRGS LKETAPSLQKEWAEQSSKSQET VGVKGITRHFQVSTLLERREDR KSKEPPLLIPRQTVSGVDLQQTP TDLQLSVLTVRRKTNKQKGHP HQKPICTSPSSNTKVKNLEKQL DEWLTRITNAEKSSKDRMELKT KARELHDECTSLSSRCDQLEER VSVTEDEMNEMKRGEKFREKR IKRNEQSLQEIWDYVKRPNLCL IGVPESDGENGTKLENTLQDIIQ ENFPNLARQANIQIQEI/RENAT KILLEKSNSKTHNCQIHQS*NEG KNVKGSQRERSGYPQREAHQT
4743	35111	A	4784	477	638	LLCCGFELPLLARRSLIV*SLLLS THQSHSPSSFVPLLVRSCIPLEEE RRSDF
4744	35112	B	4785	1	1509	

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4745	35113	A	4786	3	832	ERHHPPPQAGPHPPRRRKERNT HRQPTPQPHGA/WKISVPQTTN KGISSSITSTQRNQPQATTVEKA HNESTRTPEEPKGAVRGTR*KK KKTSRDTPPQTP*EKSSSATRNK AGGKDSDKRERKATEDQTTPS KRRKLHPMAKKLKTLKKN*MN G*LE*PMQRSP*RT*WS*KPRHE NYVMNAQASVTDAINWKKGPP PRPTTNDAKIVTRPTHPTCSHH RPPRKPPRTHPTPTPTQNKISQ* NGYTPPRGKRVREDRCKPPQAP TSAPRAAKQRQS
4746	35114	B	4787	1580	4673	
4747	35115	A	4788	1	462	MKLEHQEAQRRSGQGREKRR WPEGKAGPGCEGAWILCPESQ DDSKQEGDNNMIVVSRNAVRS VKAEFQGDNLENWESCSEAIIV QGRDNGVPHKAHGLGTEEEGT VLKISERQNWLDLVDFILLGGD LFHENKPSRKTLHTCLELLRKY CMGDRPVQFEILSDQSVNFGFR KLTNRKDIHTKNPSVRHHHQRP KVDETIKMGKTQSRKTRNSKN QSTSPPPKERSSSPAIEQSWMEN DFDELKEEGFRRSNYSELKEEV RTNGKEVKNLEKKLDKWITRIT NAEKSLKDLMELKTIAQELRDE CTSLSNQCDQLEERVSVMEDQ MNEMKREEKFREKRIKRNEQS LQEIWDYVKRPNLCLIGVPESD GENGTKLENTLQDIIQVNFPNL ARQANIQIQEIQRMPQRYSLRR ETPRHIIVRFTKVEMKEKMLRT AREKGLECSGAGLAHCKLWLL GPSDPPDCSSVSPVLRVHLVLPS SLPHSVGTPFLGSVSIPPSVPRFP DRVFHPYPYTHYCDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLCQY

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4748	35116	A	4789	1314	2221	KNRNYNKLSLRPQCNPTRTQD* ETHSKPLNYMETEQPSPE*LLG T*RNEGRHKAVL*NQ*EKRHNI PESLGHI/AKQCVEGNL*H*MPT RESRKDLKLTP*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQELVF*KDQ QN**TASKT/IQRRKERRIK*TQ* KMLKEDITTDPTEIKTIIREYYK HLYAHNLENLEEMDKFLDTYT LPRLNQEEAESLNRPITNSEIET VINSLKEKAQDQKDLQLNSTRA LFTIAKAWNQPKCPSMTDEIK/I NVEHIHHGILCSHQKE
4749	35117	A	4790	2	2260	TKDKNHMIISIDGGKAFDKIQQ PFMLKTLNKLGIDGTYLKRIRAI FDKPTANIILNGQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLARVI RQEKEIKGIQFGKEEVKLSLFA DDMTVYLENPIFSAQNLLKLIS NFSNVSGYKINVQKSQAFLYTN NSQIMSELPFTIATKRITYLGIQL ARDVKDLFKENYKPLLNEIKED TNKWKNIPCSQIGRILWPYCPR QEDENFNSLLQNGDILNSSTEE KFKAHDKKDFNLPEYDLNVEE RLVLIEKSVDSTATADDTHKLD HINMNLNKLITNDTFQPEIMERS KTQDIVLGTSFLSINSKEETEHL ENGNKYPNLESVNKVNGHSEE TSQSPNRTEPHDSDCSVDLGISK STEDLSPQKSGPVGSVVKSHSIT NMEIGGLKIYDILSDNGPQQPST TVKITSAVDGKNIVRSKSATLL YDQPLQVFTGSSSSSDLISGTKA IFKFDSNHNPEEPNIIRGPTSGPQ SAPQI\YGPPQYNIQYSSSAAVK DTLWHSKQNPQIDHASFPPQLL PRSESTENQSYAKHSANMNFSN HNNVRANTAYHLHQRLGPARH GEMWAISPNDRLIPAVTRSTIQR QSSVSSTASVNLGDPGSTRRAQ IPEGDYLSYREFHSAGRTPPMM PGSQRPLSARTYSIDGPNASRPQ SARPSINEIPERTMSVSDFNYSR TSPSKRPNARVGSEHSLLDPPG
4750	35118	A	4791	1516	1729	ILAPHSLLACRVSAERSAVSPM GFPLWVTQPFSLAALN/DFFLHF NFG/RI*QLCVLELLFSRSIVVAF SEFP

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4751	35119	A	4792	3	1426	RRYDELQNSSGRDGKPRAMAV TRSTSSTSSGSNSNVLVPVSWK RPQYSQKRAKEKLVHVLSLCG QEVGLSKNPSVIFSSCGDLDLLE HQTSLVSSEDGAREQENMDDT NSEQQFRVFRDFDFLDVELEDG EELQGESMDNFNWGVRRRSLD SLDKCDMQILEERQLSGSTPSL NKMHHEDFDESSEEEDLTASQI LEHSDLIMTLSPSEETNPMELLT TACDSTPPEPHSFNTRMSSFDAS LPDMNNLQISEGSKA\EAVREE EDTTVHEDDLSSSINELPAAFEC SDSFSLDMTEGEEKGNRALDQF TLASFGEGDRGVSPPPSPFFSAI LAAFQPAACDDAEEAWRSHIN QLMCDSDGSCAVYTFHVFSSLF KNIQKRFCFLTCDAASYLGDNL RGIGSKFVSSSQMLTSCS\LDKL KFSVLELQEYLDTYNNRKEATL SWLANCKATFAGGSRDGVITC QPGDSEEKVIKAC
4752	35120	C	4793	60	164	
4753	35121	B	4794	44	2547	
4754	35122	A	4795	401	9546	PRADITTCDRRITPGTCSRPLPV LPASLYAADMASQQDSGFFEISI KYLLKSWSNTSPVGNGYIKPPV PPASGTHREKGPPTMLPINVDP DSKPGEYVLKSLFVNFTTQAER KIRIIMAEPLEKPLTKSLQRGED PQFDQVISSMSSLSEYCLPSILRT LFDWYKRQNGIEDESHEYRPRT SNKSKSDEQQRDYLMERRDLAI DFIFSLVLIEVLKQIPLHPVIDSLI HDVINLAFKHFKYKEGYLGPNT GNMHI
4755	35123	A	4796	2	6107	GERKPKIDLFRTCVAAIPRLLPD GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHHTLL DSSLKLLLQLLTQWKLVIQTQG KVYEQANKIRNSEARDLELDV GVDVDVGVDVDADVDVDVDL GVDVDVGVDVDADVDVDVD MGVDVDVDRIYGFGCKCGCDR DVDRVVDVDVDIDVDVDVDM DVNIDVDVGLGAGVDVDMDV HIDMDMDVDIGSDNILQSALRR

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4756	35124	A	4797	3	565	MLPGHLFCLAKAGKEEQEEKG QIITRKTITPQNIPGPGAHITATH RGRCTVATKFSGGLCKEPNRLT WY/GPPLKGAHGGR/GPSSRVPS FPAAGQPPIGGALHGAGSRGLA RTRAQLGGPPGGELRGT/SGNG DGQGPDGDSRKSGSPLRPSHL/P DPAAVAGAPVSGHLQTPGHHA GRRQQAGPRGAGLP
4757	35125	A	4798	1	417	
4758	35126	A	4799	1	1069	MPRPPVPANALGARGEAVRLQ LQGEELRLQE\ESVRLHQINIYL SDRISLHRRLPVRWNPLCKEKK YDYDNLPRTS\VTKAFYNEAWS TLLRTVYSVLETSPDILLEEVIL VDDYSDREHLKERLANELSGLP KVRLIRANKREG\LVRARLLGA SAARGDVLTFLDCHCECHEGW LEPLLQRIHEEESAVVCPVTDVI DWNTFEYLGNSGEPQIGGFDW RLVF\RWHTVPERERIRMQSPV DVIRSPTMAGGLFAVSKKYFEY LGSYDTGMEVWGGENLEFSFRI WQCGGVLETHPCSHVGHVFPK QAPYSRNKALANSVRAAEVW MDEFKELYYHRNPRARLGLAC DECSIKAGWWL
4759	35127	A	4800	1	1152	MHNSDGIEVMRQQKAEIGRVG GLEGIQLGVTEVIVNGARMLES YNCKAELGATGLVNYQISVKC SNQFKLEVYLLNAENKVVDNQ AGTQGQLKVLGTNLWWPYLM HEHPAYLYSWEGRPDGAQAVG ALTPGTLAV\EVWLTAQKSLGP/ SDFYTLPVGLRTVAVTESQFLIS GKPFYFHGVNKHEDADIQGKG FNWPLLVKDFNLLCWLGANTF CTSHYPYTEEMLQICYRYGIVVI DECPAPSGHT\GPSVPSLLARW QLFNNVSMHHHMWVVEEPVL RDKNHPAMVMWSLAKEPASFL ESAGYSFKSLTMEQTARVLDLD TGEAVLQYRSLPRGAHKTLGK KRKISSYNVDLTSCQLAKEKCL KGPSSFLQSRQERMNSELRDN
4760	35128	A	4801	293	535	
4761	35129	A	4802	94	686	
4762	35130	B	4803	1	2187	

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4763	35131	A	4804	596	1789	MFHVIERPYECKECGKNFRSGY QLTLHQRFHT\GIHKGGKPYEC KECKKTFTLYRNLTRHQNIHTG EKLFECKQCGKTYTTGSKLFQH QKTHTGEKPYECKECGKAFSL YGYLKQHQKIHTGMKHFECKE CKKTFTLYRNLTRHQNIHTGKK LFECQECGKAYSTGSNLIQHRK THTGEKPYKCKECGKTFSLHG YLNQHQKIHTGVKPYECKKIHT GGKPYECKECGKAFSRASNLV QHERIHTGEKPYVCKQCGKTFR YGSALKAHQRIHRSIKVNQWL DSPRHKSINCDPMSPRTRKTRE RSHVSGRSLCQRLLGQGAQLRE FKQPPRNRFRRVCGLVARNTFP RGLRGRRASRRNAAASRLEDA VAELLKARCSALGGSGLPEGLS
4764	35132	A	4805	2	489	CQGEGAKWEQGMTGRRWVVG PPASSTPPHS/HFWLLVLSRGLV GIGEASYSTIAPTIIGDLFTKNTR TLMLSVFYFAIPLGSGLGYITGS SVKQAAGDWHCALRESFLQLV RLLKVTHLLQQLQLLYPTNGK RQDTNHTRSQCAHYLPHLDFQ VALCAYAVLQC
4765	35133	A	4806	1	327	
4766	35134	A	4807	899	1219	ANRKASTMRWYVRPFCSGLST LSREKLYPLRMLRMRASTGPLS GALGMYSTASPRLMFSGCSISS AR*LFRSSAVTMPPAAWMSFTI WAVRLPL*KAWAPSMASVS
4767	35135	A	4808	2152	2633	SRLDCGQGLVNGSCDYHHGCT GDTPRRPEWHRSLAHCMSPVD SLPGCAVSGSSDPWEVSWLWQ Q/VDRCDNREE/VMW*QRLGFP SPTVSFPQRAVSASKPLQ*APS WISLHSTLSQCRASDLRGRHTV PEVVYEWSPCALPTHREHPNAI MEGWPPPQAWWA
4768	35136	A	4809	2	387	SNASVILEGEDLRFSCSVRMAG RLQGRFSVIWQLVDRQNRRSDI MWLDR\DGTVQPGSSYWERSSF GSVQMEQVQPNSFSLGIFNSRK EDEGQYECHVTEWVRVVDGE WQIVGERRASTPISIIALGE

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4769	35137	A	4810	46	3753	EIRSWEKRKRLVLCLLEAADM KCFFPVLSCLAVLGVVSAQRQV TVQEGPLYRTEGSHITIWCNVS GYQGPSEQNFQWSIYLPSSPER EVQIVSTMDSSFPYAIYTQRVR GGKIFIERVQGNSTLLHITDLQA RDAGEYECHTPSTDKQYFGSYS AKMNLVVIPDSLQTTAMPQTL HRVEQDPLELTCEVASETIQHS HLSVAWLRQKVGEKPVEVISLS RDFMLHSSSEYAQRQSLGEVRL DKLGRTTFRLTIFH
4770	35138	A	4811	1	3728	MKCFFPVLSCLAVLGVVSAQR QVTVQEGPLYRTEGSHITIWCN VSGYQGPSEQNFQWSIYLPSSP EREVQIVSTMDSSFPYAIYTQR VRGGKIFIERVQGNSTLLHITDL QARDAGEYECHTPSTDKQYFG SYSAKMNLVVIPDSLQTTAMPQ TLHRVEQDPLELTCEVASETIQ HSHLSVAWLRQKVGEKPVEVIS LSRDFMLHSSSEYAQRQSLGEV RLDKLGRTTFRLTIFHLQPSDQ GEFYCEAAEWIQDP
4771	35139	A	4812	897	1217	ANRKASTMRWYVRPFCSGLST LSREKLYPLRMLRMRASTGPLS GALGMYSTASPRLMFSGCSISS AR*LFRSSAVTMPPAAWMSFTI WAVRLPL*KAWAPSMASVS

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4772	35140	A	4813	1	1507	MWNSKINHDHDDQFLKTYYVL ESSISVGVASNASVILEGDDLRF SCSVRMAGRPQGRFSVIWQLV DRQNCRSNIMWLDRDGTVQPG SSYWERSSFGSVQMEQVQPNSF SLGIFNSRKEDEGQYECHVTEW VRVVDGEWQIVGERRASTPISII ALEMGFAVTAISRTPGVTYSDS FDLQCIIKPHYPAQVPVSVTWR FQPVGTVEFHDLVTFTRDGGV QWGDRSSSFRTRTATEKAESSN NVRLIISRASDTEAGKYQCVAE LWWKNYNNTWTQLAERTSNL LVIRVLQPDRMGVSARALRGEP SPSQMPQACCHGNTGALVIGIN EPESLPCLQTVTKLQVSKSKRT LTLVENKPIQLNCSVKSQTSQN SHFAVLWYVHKPSDANGKLIL KTTHNSAFEYGTYVEEEGLRAR LQFERHVSGDLFSLTVQRAEWL LSPNYAWYKLAEEVSGRTEVT VKQPGGSLGLGC\SVSGWAAEP VCTQGPRPCSWNTPLALTAAC
4773	35141	A	4814	1	627	
4774	35142	A	4815	166	435	
4775	35143	B	4816	1	240	
4776	35144	A	4817	1	288	VVPASSPGAASEPRRRRRCLQP EKSVSPGSGGGHRDPPKARPPR PPSAPKP*RPRPFS*LARSLCFPA AGCAYGVGVGGAGGGRAGLR QPVPAVAE
4777	35145	A	4818	206	1041	VSVGSAPSDMPAAATRW/CNSR CQHGQRLSAR/PVAGPGT/RTSS FPWLAPRNVVVPGSLEMPGTA GPQRGSHSSPQGSSALLSFS/CV HNVESKEPVCLLLPSMASRLLT PRGTCRPVPGCLQHPLSLPPVL VGTQSPSQAPKSAKRPSPQPQL GWLQLHPGGSGLCLLPAPAGS MECAALESVPSQLGIGAPGPCW AQAGVQGWSNVATSSPSGPSA QGQPRAPPCLVCGPAQCGTSGS RSRATGLRPSCLECQVWWSPQ CGANPGDTTSSQDAGTRCSKV
4778	35146	A	4819	2	487	

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4779	35147	A	4820	152	758	RGARGPEWDGQLDGPGSQMC GMASAPRLRRSGVRAAAGHPV QQPRLLDGLSLTDESDSCVSFEP PSHPSSSSGPVTALSRGWNFLK AFPLMGETQERER/VLTHFSRR YCQCNPD/AQPSEDGIH/TLTCA LMLLNTDLHGHVIGEVTGETN RTDKQQNRTEQSKRQANADKH NEHANNEQQHEHDKDNDTRTR DTEMRHAKRDNA
4780	35148	A	4821	100	220	
4781	35149	A	4822	100	1588	CLKISTGYTGSMAEEASGNLTI MAEGEGEAGTSTHGQSRRKRE KEEVLHPFKQPDLVRSHYRENS KEEICPHDSVTSCQTPPPTLGITI RHEIAASICHVADTAGVAGDA MMRKTDLIPPFIGLTLQGGRSA DMGNQKKWRKGSENLATLVA MASERFHWQYSGNSTIQPKQK QHGMITRLVTAPVCPGLVQPSL CAVGLRNIMSLSSHTCALQNTK QAWEGYDDCHSQRVSQPGEN MTKLSFLNLLNQMPSWGEGKM VPADFSGSCWEGTGTGSPAGSQ VSFLNRHNDGQLAGDSPGLPPP PCPRGLQGAEQRSALRRHKAD VHRDQWLVISFSKKLRTSARK WYEAGPFSGVPRVLPAAAQGG TDFPFSPSEEPFQPSPFSMVQAH TVRSKPQFHFPAAGENCLNRSE LSRNQGLQARVGPLAIMSSDPS GDFVLYTPTILGFVGLEVLVSR EGTFLWRYSTCP\LNYKLWLPP GYLGLLVPKDQKVRAVFLGM
4782	35150	A	4823	1329	1881	AHLEAAGWSSSVQPGPSPRVLG RAEEHGQQSGRAKEIGHKIPKE TFDELTAELETISSK\CLYLAKK NQVIQQELLSMKEVQQKCKKL EEVNKILEQEVVNLKTHEKNM VEFGDVEECKLQLEERAGQEIE KLEEINLQRACLSAKKVRAEGE LEPRRHHNHTLGFTEGPWGLM SVITGAYDLIR
4783	35151	A	4824	176	308	LGNLTSPFFN*KHRSTKGFTTLS TVALLLTGHVGIKTSNCHPGY

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4784	35152	A	4825	1467	1890	DWFDELTAELETISSK\CLYLAK KNQVIQQELLSMKEVQQKCKK LEEVNKILEQEVVNLKTHEKN MVEFGDVEECKLQLEERAGQEI EKLEEINLQRACLSAKKVRAEG ELEPRRHHNHTLGFTEGPWGL MSVITGAYDLIR
4785	35153	B	4826	1	753	
4786	35154	A	4827	225	410	
4787	35155	A	4828	225	410	
4788	35156	A	4829	225	411	
4789	35157	A	4830	141	1001	GGVRGVQQKETCAFKVLESIG KLG\LALSVAGGAENSALYNVD AGHRAVIFDRFRGEQDIVVGEG THFLIPWVQK/PPIIFDCRSRPRN\ VPVITGSKDLQNVNITLRILF\RP VASQLPRIFTSIGEDYDERVLPSI TT\ENLKSVVAPFDAGELITQRE LVSRQV\SDDL\TERAATFGLIL DDVSLTHLTFGKEFTEAVEAKQ VAQQEAQRARFVVEKAEQQKK AAIISAEGDSKAAELIANSLATA GDGLIELRKLEAAEDIAYQLSR SRNITYLPTG\QSVLLQLPQ
4790	35158	A	4831	194	453	QPLPEPLELRPKAL*LTPSQIFSA *RLKTAARLPRKPWAVLPQGFT DTPPHFSQAQISSSSVTYLSIILV KTHVLCSPEFHRTGVV
4791	35159	A	4832	1	86	PCESYLEHL*WSCRLLRRLGSV SLQLLS
4792	35160	C	4833	191	263	
4793	35161	B	4834	1	741	
4794	35162	A	4835	3	96	
4795	35163	A	4836	1	301	QEQQKMNTLQGPVSFKDVAVD FTQEEWRQLDPDEKITYGDVM LENYSHLVSLAYEVATSCTSEIL KPSNLPKSFFFSH*QDMISPSQT SSLSWSRERSCG
4796	35164	A	4837	3	273	VLHFISAGNTFAHQQEHSPRKG PNNLSKRKLLPAV\GPRVFHGE DRHL/LFSTRKE*ARSLCYVQG GVQAPAAAFCSLLSLWGWAGC AFWC

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4797	35165	A	4838	3062	3688	RSVTRAPPRSTFPLAQAPSPRSH HIREPTPSPHLGPLRGSHRGPPS RPLPPALAALSLLETLQPRLLHP HLHL\LHDQGRACVRAYAHPS YLWRCHALGVWVES/ARLRPS ALPPAHSPPLAAPLLSSSVQPPA PALEPPPRPPAAGAAARCLAAQ HHHPSRLGVRQPPLAVGALGST WPPQAPAPPPELSALEQDRVGA QPPPPPSQGA
4798	35166	A	4839	1	197	
4799	35167	C	4840	26	358	
4800	35168	A	4841	84	433	PASAPLGLSATVSACFQEQQKM NTLQGPVSFKDVAVDFTQEEW RQLDPDEKITYGDVMLENYSH LVSLAYEVATSCTSEILKPSNLP KSFFFSH*QDMISPSQTSSLSWS RERSCG
4801	35169	A	4842	1	372	VQWLFMQICLGGKHQQLRHQG VQEKMLPLEGS*VIEAGSPTLIG ETLSLEIINYIIGAGLESVHTHKS RQLGGWTRPGSHFQQVLIPAHT PMNLEPSQLSLEPRLVPAQQSL PSAPTPSKALSQ
4802	35170	B	4843	7	267	
4803	35171	B	4844	213	3895	
4804	35172	C	4845	141	359	

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4805	35173	A	4846	831	3017	RRRLHYSGSTRPWRTRAMLPR TLSLRPHLSLSLHLPLPCLLLHL\ LPTHLPPGPKHQPTVREL/ARRC RLPRACHPAQNLLEQQPLRPSH LQRH/LSLLPPLGLSQSGPPG/LA PQPLL*LQTPDHFAGADPCSIHG TSH*HQGTSNPSGRDGYQTPSH ICP\SPAPKQSFLFGTQNTSPSSP AAPAASSAPPMFKPIFTAPPKSE KEGPTPPGPSVTATAPSSSSLPT TTSTTAPTFQPVFSSMGPPASVP LPAPFFKQTTTPATAPTTTAPLF TGLASATSAVAPITSASPSTDSA SKPAFGFGINSVSSSSVSTTTST ATAASQPFLFGAPQASAASFTP AMGSIFQFGKPPALPTTTTVTTF SQSLHTAVPTATSSSAADFSGF GSTLATSAPATSSQPTLTFSNTS TPTFNIPFGSSAKSPLPSYPGAN PQPAFGAAEGQPPGAAKPALAP SFGSSFTFGNSAAPAPATAPTPA PASTIKIVPAHVPTPIQPTFGGAT HSAFGLKATASAFGAPASSQPA FGGSTAVFSFGAATSSGFGATT QTASSGSSSSVFGSTTPSPFTFG GSAAPAGSGSFGINVATPGSSA TTGAFSFGAGQSGSTATSTPFT GGLGQNALGTTGQSTPFAFNV GSTTESKPVFGGTATPTFGQNT PAPGVGTSGSSLSFGASSAPAQ GFVGVAPFGNTFAHQQEHSPR KGPNNLSKRKLLPAVRAQGPPR
4806	35174	A	4847	9	935	IPCFGCAMPMYQTRRQENDLR TASIAV*RRKQQDDH*KQRRW QNIQRKGPKRYIVIAGNSQSHQ PMIFSMLRKLPKVTCRDVLPEIR AICIEEIGCWMQSYSTSFLTDSY LKYIGWTLHDKHREVRVKCVK ALKGLYGNRDLTARLELFTGRF KDWMVSMIMDREYSVAVEAV\ RLLILILK\NMEGVLMDVDCES VYPI\V*ASN*ALASAVGEFLYW KLFYPECEIRTMGGREQRQSPG AQRTFFQLLLSFFVESKSHFVTQ GGGSGQFSAHRNLCLPGSGNFH VSASRVAGIAGAPPHTWLIYVF
4807	35175	A	4848	1	1749	
4808	35176	B	4849	282	1227	

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4809	35177	A	4850	221	907	FEDSFNRGVKKKAAKRPLKTTP VAKYPKKGSQAVHRHSRKQSE PPANDIFNAAKAAKSDMQHRE VRVKCVKALKGLYGNRDLTAR LELFTGRFKDWM\VSMIMDRE YSVAVEAVRLLILILKNMEGVL MDVDCESVYPIVLFYPECEIRT MGGREQRQSPGAQRTFFQLLLS FFVESKLHDHAAYLVDNLWDC AGTQLKDWEGLTSLLLEKDQS TCHMEPGPGTFHLLG
4810	35178	B	4851	1	2361	
4811	35179	B	4852	1	878	
4812	35180	A	4853	1	313	MPHTPRCLFRPQASCLVHFLEQ QNKLLETKLQFFQNRECCKSNL EPLFEGY\TLRREAECMEANSG RLASELNHVQEVLEGYKKKYE EEVALKATAENEFVALKK
4813	35181	A	4854	188	354	
4814	35182	A	4855	405	647	LPLISDQVSYSPPLMSKSLASLY QESY*TILARIPLPLISPFVNSLST DLFILLIGNTSIAIFAEFGVSAISL PSCNSLE
4815	35183	A	4856	1	585	MSSGEGKRTWLGSLWGGVRVP VPPPICGLRVAVTSAGTSSFSLA PKPTRIRGERGKGQGRG/SSGN GGRGRAGASAGGSRGEVVSVA NDGRWRGRGRGVGCPRSSKRE DNRFAKHGRASGKAWEPHPPS QALRALFGPIRRRGRAAETRIV YWIKDRQLTNRDSTILELQKVL KTCCAQSMKIFCCLWNFVYKQ
4816	35184	C	4857	12	468	
4817	35185	A	4858	1	1156	MAFRKKIITAGCIDHVLSVSDS QQMQANLTQRTEAEIRKQTQIA PTFPAHSLPDKYLGFALLNRKII GTFLVFNMCKRNHEDKNEAFT VLREKKVFNLEFCTLQNYSSEV KEKERQRFSDKQTLREFATRKP ALKEMLKVLQRYKERKHIRKR NVKYSADHTTDHTANQADPNQ QEPHVPGHAPDNKTIRQKQNQ HKDNTTRKHNQMTSDTSRTNT KVSGQPRGKQTRRRHERQQKA RERGQHRQK/RDAQTREHTQR QRQARAEE\QVIENKREEKRTS ERTNDSTRREGTRRPRRTEKGE RQEEGDRATATHRKDHDRQQP HGAPHCSRSSRHGAPTGPLYCC SPLPGTPSCTICTVQYGRLWPH MATEQLNMAGPNQDFQDVVW

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4818	35186	A	4859	1	1580	MAPALLLLLLASGAAACPLPCV CQNLSESLSTLCAHRGLLFVPP NVDRRTVELRLADNFIQALGPP DFRNMTGLVDLTLSRNAITRIG ARAFGDLESLRSLHLDGNQAG GAGHPRALRGPVNLQHLILSGN QLGRIAPGAFDDFLESLEDLDLS YNNLRQVPWAGIGAMPALHTL NLDHNLIDALPPGA\FAQLGQLS RLDLTSNRLATLAPDPLFSRGR DAEASPAPLVLSFSGNPLHCNC ELLWLRRLARPDDLETCASPPG LAGRYFWAVPEGEFSCEPPLIA RHTQRLWVLEGQRATLRCRAL GDPAPTMHWVGPDDRLVGNSS RARAFPNGTLEIGVTGAGDAG GYTCIATNPAGEATARVELRVL ALPHGGNSSAEGGRPGPRTSPP PLALLPRYNSSEDETLIYRIVPA SSHHFLLKHLVPGADYDLCLLA LSPAAGPSDLTATRLLGCAHFS TLPASPLCHALQAHVLGGTLTV AVGGVLVAALLVFTVALLVRG RGAGNGRLPLKLSHVQSQTNA
4819	35187	A	4860	2	403	
4820	35188	A	4861	87	442	PVFPWHPYSKDQKEESQSVLVI WQKTAGGGWSTWWILSFSPET EKVVKK/AHVDTL*NEMWDVT K*TAFKIPSCT*HQQHP*SFFRK SESQVIVFAGQGVKIH*YILLHS NVIHYMNEI
4821	35189	A	4862	2	651	EFIKQWDADKFEHIQTLEGHHQ EIWCLAVSPSGDYVVSSSHDKS LRLWERTREPLILEEEREMERE AEYEESVAKEDQPA\VPGEIQG D\SYFT*KKTIETVK\AAERIMEA FELYREETAKMKEHKAICKAA GKEVPLPSNPILMAYGSISPSAY VLEIFKGIKSSELEESLLVLPFSY VPDILKLFNEFIQLGSDVELICR CLFFLLRIHFGQITS

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4822	35190	A	4863	1	703	MGLTKQYLRYVASAVFGVIGS QKGNIVFVTLRGEKGRYVAVP ACEHVFIWDLRKGEKGLKQEV TCLCPSPDGLHLAVGYEDGSIRI FSLLSGEGNVTFNGHKAAITTL KYDQLGGRLASGSK/RQPGGIV FTESILAYSSACQDKQNHYWGS SQ*CADFVIQLRQYCCSFSCS*F H*NMEQVYTAVYSHNDL*ICTL LILCTW**TGSHRNKAPKTMFP RCTEGLDRGNRPATHS
4823	35191	B	4864	1	2616	
4824	35192	A	4865	3	674	PECTGRTLRSASQQHDTFYILA CELNSLADDAQR\YDVP\NSCL YPPDLPWRPVMQAKKKELARR DDIEDGDSMISSATSDTGSAKR KSKKNIRKQRMKILFNVVLEAR EPGSGRRLCDLFMVKPSKKDYP DYYIIILEPMDLKIIEHNIRNDKY AGEEGMIEDMKLMFRNARHYN EEGSQVYNDAHILEKLLKEKRK ELGPLPDDDDMASPKLKLSKA ASHFII
4825	35193	A	4866	3	425	
4826	35194	A	4867	1	1115	LCSVPTLCLASSHLVSNLSTFKQ \TSSFIRHVVATLLGLYLALFCF GWYALHFLVQSGISYCIMIIIGV ENMHNYCFVFALGYLTVCQVT RVYIFDYGQYSADFSGPMMIIT QKITSLACEIHDGMFRKDEELT SSQRDLAVRRMPSLLEYLSYNC NFMGILAGPLCSYKDYITFIEGR SYHITQSGENGKEETQYERTEP SPNTAVVQKLLVCGLALLFHLT ICTTLPVEYNIDEHFQATASWPT KIIYLYISLLAARPKYYFAWTLG TAPRKWSPCPGPQCIQLRAADP SGPEPLLMLSSQERQPKAKPPK EAHADIAGTPREGEKTRTGGPG KAFLRDPGASSSVELSRTQLWV LTPPPIAKAPCECLQ
4827	35195	B	4868	218	656	
4828	35196	A	4869	1	180	
4829	35197	A	4870	12	199	GLFPLEPGANGI*GC/SGRIRAQ RWLPGRPKFTGESFIR*PPRVAK ESGQLIWFGCVPTQISS

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4830	35198	A	4871	1	5058	MKLRGVSLAAGLFLLALSLWG QPAEAAACYGCSPGSKCDCSGI KGEKGERGFPGLEGHPGLPGFP GPEGPPGPRGQKGDDGIPGPPG PKGIRGPPGLPGFPGTPGLPGMP GHDGAPGPQGIPGCNGTKGER GFPGSPGFPGLQGPPGPPGIPGM KGEPGSIIMSSLPGPKGNPGYPG PPGIQGLPGPTGIPGPIGPPGPPG LMGPPGPPGLPGPKGNMGLNF QGPKGEKGEQGLQGPPGPPGQI SEQKRPIDVEF
4831	35199	A	4872	3	1646	EDEGRAKGHHTWQQTRENESQ AKGETPYKTIRFRETYYHKNSM GETTPMIQLSPTGSLPQHVGIM GATIQDKIWVTPGLPGFPGTPG LPVKRGFPGSPGFPGLQGPPVIP GPTGIPGPIGPPGPPGLMVTPGP PGLPGPKVNMGLNFQGPKGEK VKQGLQGPPGPPGQISEQKRPID VEFQKGDQVIPGDRGPPGPPGI RGPPVTPGGEKGEKGEQGEPG KRVKPGKDGENGQPGIPVMPG DPGYPGEPGRDG/EKGNAVMG PPGPPGFPGERGQKGDEGPPGIS IPGPPGLDGQPGAPGLPGPPGPA GPHIPPSNKGDTCFNCIGTGISG PPGQPGLPGLPGPPG\IPGAPGA PGFPGSKGEPGDILTFPGMKGD KGELGSPGAPGLPGLPGTPGQD GLPGLPGPKGEPVRITFKGERGP PGNPGLPGLPGNIGPMGPPGFG PPGPVGEKGIQGVAGNPGQPGI PGNKGDPGQTITQPGKPGLPGN PGRDGDVGLPGIPGLPGQPGLP GIPGSKGEPGIPGIGLPGPPGPK
4832	35200	A	4873	110	256	CSGTYRCYSF/HSRDPYLWSAPS DPLE/LVVTGPARQYYTKGNLV RIASGL
4833	35201	A	4874	2	2888	LSDPCSSRWDERSLSQRSRSWS YNGYYSDLSTARHSGHHKKRR KEKKVKHKKKGKKQKHCRRH KQTKKRRILIPSDIESSKSSTRR MKSSCDRERSSRSSSLSSHHSSK RDWSKSDKDVQSSLTHSSRDSY RSKSHSQSYSRGSSRSRTASKSS SHSRSRSKSRSSSKSGHRKRAS KSPRKTASQLSENKPVKTEPLR ATMAQNENVVVQPVVAENIPV IPLSDSPPPSRWKPGQKPWKPS YERIQEMKAKTTHL

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4834	35202	A	4875	350	986	LWGGGSARLLRLPRGPCLPPAS PSSPSSSSELS*SCSLGPSSSSSS SSSCSLCPSSSSSSSSP*LPPSSSS SSSRPLPPPSSSSSSSSSSSSSSSS SECLCSPSSRPRTTVAGLGPAPG FPSGPVDTCSVWLLRFTSTMIW DCSLRL*VPEPPSSSSNSSPPSSL HKLAGGPPASSTPPSFSSLKKG WAGPMVAGTVPPAVPAPSSTR TE
4835	35203	A	4876	1	496	SQSYS\RGSSRSRTASKSSSHSRS RSKSRSSSKSAVLASTARCAGS RKQCVPLPIRLCQLQSRSLQPS MVPWRWGLTGPRGIALPPAAR PGPLHEAPRWGPPPRRAPRPWP PGARPGRRRRRAAASPAPSSCG PRASGAAGGGRGAPIGARASA GAAVWTPISTT
4836	35204	A	4877	3	4578	TLAVFVPTLAGFSVALGGPAW GRRRRSVSGVGVWLQWQCFLF CSRGPAQAGGQPALAATSVAM GAQDRPQCHFDIEINREPVGRI MFQLFSDICPKTCKNFLCLCSG EKGLGKTTGKKLCYKGSTFHR VVKNFMIQGGDFSEGNGKGGE SIYGGYFKDENFILKHDRAFLLS MANRGKHTNGSQFFITTKPAPH LDGVHVVFGLVISGFEVIEQIEN LKTDAASRPYADVRVIDCGVL ATKSIKDVFEKKRKKPT
4837	35205	A	4878	1	1689	

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4838	35206	A	4879	1	1604	MGISCPGSSKMLNSRALPVLKL TQGALRDCKERANYTNFNIYK AVESQGKFVCVLYNGQQSPEY VMIPCTSVSPTGQEVPEDRGMR MVMKNKPNKPSKMQSLKSSKH LTNSVIVIAVGIFFSVTLQARDP QLDDAIEQLRGVCIRAWEKITS GGEQYPSFSAIKQGPKEPYIDFI ARLQESLKKMIADSAAQDIVLQ LLAFDNANPDCQAALRPIRGKA HLVDCIKACDDIGDGSSNGKAS YFGSKSKVFQTSYTSAQKAELV AVIEVLTAFDMPINVISDSSYM VYSTQLIENAQLRFHTDEQLMT LFTQLQTAFRSTMHPFYITHIRA R\HTPLPGPLTEGNQMADCLVA NAISNARHFHNLTHVNASGLK HRYSITWKEAKNIIQRCPTCQM VHSSSFRGGVNPRGLEPNSLWQ MDVTHIPLFGRLAYVHKRRRIR GGGGGEGEGEGEGEEEEEEE EEEEEEEEEEEEEEEQEQEQEE QEQEEQEQEEQEQEERRRKDTE ELSYSLPLNRTQPCWHPDFGLP
4839	35207	A	4880	1	1146	
4840	35208	A	4881	1	1577	MGQVWALVHSTLETFHTDEEE GEYNEVTEQVCLPAKAGSAAV DLCCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQIVTS TSVPWKAKPGDHIAQLLIVPKK F\EGLKEPLQVERQSSCQGLGY/ PFLMAAIVKPPEPIPLKWLTDKP IWTEQWPLSKEKLEALEDLITQ QLKKGHIAPTFSPWNSPVFIIKK KSAEQDCEWFVFTILAVNNLQL KPAKRFHWKVLPQGPNQQPIWI PSRYLKPYHKPDAKEEIPEGSQ GFPVAAMSRLTLRRTPTVTSNT HRTQPPTWGQIEKLPQMAEENL RKAGQPVTISNWILPRITKFKPI EGAENVFTDGSSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIIQRCPTCQVMLSAAE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKISGGNCGPHPHPRLQPCPD

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4841	35209	A	4882	1	420	MTNISTTLKDLKDAGMIDPIKS TFNL/PIWIPQKPDGSWKTTANN /R/KLNQATISIAAIVLDVASLPG KARSYHGFSSHAGRVIDSNNQK DIEGCTYILNVAGKNMFGIQLR RSVIFPCPNLMYTDNCSSHGPR GPSDYDSDP
4842	35210	A	4883	213	687	PEHILPGAQEGPSC/PLEPELE/V *NMSSWNTLSESCKMHGDLKY LFVITAKDQQ/VSIAAST/*GFC WNQ*VSASPSQAPGMPLVLGR RLWQGSRLGGLSISLSDDCHGA HNHSFKRVTTTLQVFSWTVPQ AEPAMDCIHTA/DSPRQRLP*QA HESVAEVIIT
4843	35211	A	4884	1	648	MSSWNPLPESFKKHGYLLYLFV ITAKDQQ/VSITASTWGFYWNH\ SQGKNPEQMEASQKPVAGLWA WWLNISLSAASHGAQNHPFKR VTTTLQSQGWNKDLWIMRELL CNNRPEQLLQETATIKAPIAPAD PWSQEVIYNFCKAVSSVSCMPF NIHFNSNIPPESSGDWRMQQPC KVEQSILGAQRGGGGCRPGSLR ELFPCLLAEPNMEEEVAALRA
4844	35212	A	4885	3	597	GTLEPAAEWSVLLGV\HSQDGP LDGAHTRAVAAIVVPANYSQV ELGADLALLRLASPASLGPAV WPVCLPRASHRFVHGTACWAT GWGDVQEADPLPLPWVLQEVE LRLLGEATCQCLYSQPGPFNLT LQILPGMLCAGYPEGRRDTCQP SPEPGPMCIS/VSHIQRLRDAVS HTWQRGTEPARLGSWERRQRQ QQQGPV
4845	35213	B	4886	387	552	
4846	35214	A	4887	20	612	
4847	35215	A	4888	792	959	TGLSSSQNPKATKSIPWHNRLL PNVDSQVQQNSQAIIYTN*GNS ESQYPFSKMDT
4848	35216	A	4889	268	500	
4849	35217	A	4890	1	529	
4850	35218	B	4891	259	1672	
4851	35219	A	4892	480	657	
4852	35220	A	4893	2	377	WCDFSSSLHRSVQALRTFCVTL SGAFVRDCTTVLSSTTCEPSTD V/CWAMNIVTSVLLLYGSEEEA FWLLVALC\ERMLPDYYNTRV VVIRTYDQRYEQCVDLYDGLP TTLFTTDDWHVWPDLTGLP

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4853	35221	A	4894	1	251	TEARKAAAVMPKTAVLAAERP KKAWGVLIPKKSTKRTPKAFA GGGCW/TKVGWSKVAKKVPKP EASKPKKAAPKTRRYKSTLKTK
4854	35222	A	4895	283	427	PSVSKESPLNSPASQAGSATFAT TPLTPPK/PAATSSVAAAALLPA LPR
4855	35223	A	4896	111	1095	SRGWSRLPVPCCAPALLSPWAV NGIRRRGAGDGTRRGGSGCAG AHSAGLVASGPESWIPGPVPPG AEPPRRGDSGLARCPAPGHPSR ASPQRPAEGFDALAAPSRVPGD SRQLSRNNTRSRCEGRGGKTPP AWAGVHRHGPPPAAPPGRARV HGHRLRGGLGPGGGKRGLPGC CPRAADPRGRP/GETSRSGERGP PGRSAPLSLQPRHRTGLET/RQP SPLARSRPGLGPRPSARRPSRPA PPPPPPELHRGAPQRGRVASQT RPGARARPAADTHSSLKSPASQ AGSAAFATAPLTPQKPQLRAP WQPLHSFRPCRGVTSRLRTAPP
4856	35224	B	4897	243	452	
4857	35225	A	4898	3	353	RRYLSPKYIKMFVLDEADEMLS RGFKDQIYDIFQKLNSNTQVVL LSATMPSDVLEVTKKFMRDPIR ILVKKEELTLEGIRQFYINVERE EWKLDTLCD\LSAMHGDMDQK ERDVIMR
4858	35226	A	4899	3	410	NLQEWKLDTLCDLYETLTITQA VIFINTRRKVDWLTEKMHARDF TVSAMVCLPAASLLWVCPSEV SYLKPGFLEPRCLPGLLHICFLF QHGDMDQKERDVIMREFRSGS SRVLITTDLLVSRGN**QRQKG GSKVI
4859	35227	A	4900	1	235	MLSYVLEVTKKFMRDPIWILVK KEELILESIHQFCINVEQEKWKL DTLRDLYETLTITQA\VIFTNTR RKCCSKVREI
4860	35228	A	4901	3	48	NSNVEREEWKLDTLCDLYETL TITQAVIFINTRRKVDWLTEKM HARDFTVSAMHGDMDQKERD VIMREFRSGSSRVLITTDLLVSR GN**QRGTRGVEAGHTM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4861	35229	A	4902	2	879	AQFPTRLDLKATQALVLAPTRE LAQHIQKVVMALGDYMGASC HACIGGTNVRAEVQKLQMEAP HIIVGTPGRVFDMLNRRYLSPK YIKMFVLDEADEMLSRGFKDQI YDIFQKLNSNTQVVLLSATMPS DVLEVTKKFMRDPIRILVKKEE LTLEGIRQFYINVEREEWKLDT LCDLYETLTITQAVIFINTRRKV DWLTEKMHARDFTVSAMHGD MDQKERDVIMREFRSGSSRVLI TTDLLARGIDVQQVSLVINYDL PTNR\ENYIHRIGRGGRFGRKGV AINMVTEEDK
4862	35230	A	4903	1	1764	MASLEEGIYSLKINSKRSSYNS MNPQFTAGSEGQNETEEPNKFQ SRKGRPQDSGSSLSLSVLQEILG DDIPKVKEEAVISSQSDLGECPY CGERPARNATIFAPQKEKESAP EMSSSCDKRVTVNPPEKFSEGR PKTQNTLICEKCSQPSNFLDDY NPHVIIQKRLSNQSRVICEKSSP PLNVPDNYNSHSVIQKHKEKM AIERPSSGSDWSDVGGTTVIFSE EKPFSLCLPVVSEPPYYATDYT TFPPHYSPWHDYTSSWFSSTKS SCYPSLGSSSNTLQAGKSSCSSS SRSNNNIFQGERSSHQSFLSDYS TSFPVSSENTSRDLKMTEEGRS KNSSLFYYSRNVEAEAKEERVY QEETLGHPYGGRASSFPPRTIW QPEQPGFIDTHCHLDLLYSRLPF KGTFTKFRKIYSNTFPKEFQGCI SCFCNPQNLSDNLWEDQLKDD LVWGVFGCRPHFAHYYNNYQE RSILKALRHPKAVAFGEMGLD YSSKCTTHIPEQQKVFKRLLRL AVSLK\KPMMIHCREADEDLLG ILKKYVPSDHKMYQHCFTGSYP VIKPLLSCFPNLYVGFMAILTYS SAEQARETVKK

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4863	35231	A	4904	125	820	VLAPNYHITFRNLSSVSSPVTSA EPVLQAGQARELSFSSLHPASPL LVPSTPALTLHAFNALVLFPSFP LEKAAKRERPKSKIQITARVGK MRRTWSPHTTISAGGSVNGAST LKNSLVWEAKPADTTNPTPPTT HPNPGPTPPTNTNRHPPPHHPLT NTPAPPHQPPATTP/SPQTQTPN YCPNTDHTTPTHDTPNPVPPTR RTPPNRTGKRTNTSQNYRLVSP APKIHWEA
4864	35232	A	4905	407	757	
4865	35233	A	4906	5	426	GKTSTKSQNASSPPKDHNSSPA REQN/WIENEFNELTEVGFRRIT SLEKNINDLMELKNTARELREA YTSINSQINQVEERISEIEDQLNE IKHEDKIREKRMKRNQQSLQEI WDYVKRPNLRLIGVPESDIENG TKLENTL
4866	35234	A	4907	1	2267	MTGQFQDVVREEARPLPNRIM RLRFNHFATECSWDHLYVYDG DSIYAPLVAAFRCEVENRYQGN PLRGTCYYTLLIDYQFTFSLSQE DDRYYTAINFVATPDEETPPIRG RQTAHTGELQLTSGGYPSGMK LPEEGTGERNRITINKKDVHTET PSKGHQHQRPKVDKSTKIKKN QRKKAENSKNKNASSSPEDHN SSPAREQNWMENEFDELTEVG FRRWVITNSSKLKKHVLTQCKE AKNLEKRLGQLLTRITSLEKNV KELMELKNKAQELCEAYTSINS QIDQAEESISEIEDQLNEIKHED KIREKR\IKRNKQSLQEIWDYVK RPNLRLIGVPESDGENGTKLEN TLQDIVQDNFPSLARQANIQIQE ILKTPQRYFSRRATPRNIIITFTK VEIKGKMLRAVREKDHSAIKLE LRIKKLTQNCTTMWKLNNLLL NEYWVHNEIKAEINKFFETNEK KDTTYQDLWDTAKAVFKGKFI ALNAHRRKWERSRIDTLTSQLK ELEKQEQTNSKASKRQEITKIR AELKEIETQKTLQKINESRSWFF EKINKIDRLLARPIKKKREKNQI DTIKNDKGDITTEPTEMQTTIRE YYKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPTTSSE IEAIINSLPTKKSPGPDGFTAKL YQRYKEEVVPLLLKLFQTVGK EGPLPNSFYWANIILIPKPGRHT

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4867	35235	C	4908	605	760	
4868	35236	A	4909	94	400	
4869	35237	A	4910	1	1538	MPIQMQYPQYKLVENKTQPPVI YQYWPPADLQYRPPPEVKYRP QVVCPVPNSTAPYQQPTAVVF NPTAPPSGQGIIAQNTDLVEWF FLPHSTIKTFTLYLDQMATLIGQ ARLRIIKLCESDSDKIIVPLNKEQ VRQAFINSGAWQIGLADFVGII DNHYPKTKIFQFLKLTTWILPKI TRHKPLENALTVFTDGSSNGKA AYTRPKERLIETQYHWAQRAE LVAVITVL\QDFNQSINIVSDSA YVVQATKDVETALIKYSIDDQL NQLFNMLQQTVRKRNFPFYVT HIRAHTNLPEPLTKANEQVDLL VSSAFLEAQELHALTHVNATGL KNKFDITWKQAKNIVQHYTQC QIPHLPTQEAGVNPREQHFTGK KNSPHEGKLIWWKDKKNKTW EIGKVITWERGFACVSQGENQL PGWIPTRNLKFYNEPLGDAKKS ASAETKNPQLSIIDSPGKAPGCL MPTTQNWLVEVPTVSATSKFT YHMVYPPAPKRQRPARTGHND DGSFVKKGDM
4870	35238	A	4911	1	759	FRMVIRCLPQRELDCDRGNWT ATSAELTGIKWRRYNFGGHGD CGPIISVPAQDDPILLSFIRCLQA NLLCVWRRDV*PDC*ELWIFW WGDEPNLVGV\YIMNCRLWKK DSGKMAFPMNVGRC/FFKAIHN LLERCLMDKNFVRIGKWFVRP YEKDEKPVNKSEHLSCAF\TFFL \HGESNVCTSVEIAQHQPIYLIN EEHIHMAQSSPAPFQVLVSPYG LNGTLTGQAYKMSDPATRKLIE EWQYFYPMVLKKKKK
4871	35239	A	4912	1	539	MRHPCDGNSLYFDHISVNMLA VMLYYGFGRVSIGKTGLRGVQ RHLWPLPLDASSTKTVSSSHSD KGEIFSPFPCSLINCNNFEMRNT TKCLMDKNFVRIGKWFVRPYE KDEKPVNKRVTSQEIWLFDEY\ GVSLPCFAVERCALLPLCLLPR LMISISSTSRQPQYISRRGLKAKI SWVV
4872	35240	A	4913	198	620	

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4873	35241	A	4914	63	1267	RNRILRMEFFDWFWAFWSWLL NMIRSQNAKDSSSNSMENTDSP WCELFRELCKINALDVPDSLLV RGNEFSASVHNTFDHMWRTKE RYEAGWLLLSSADRVMKENDE LRDSVSWLQKQILSLKSAKIAL SGSLISYRERAEIVEKQTQTLIM RVADLQQKGYINSPALCHNLIW RDLDHFSFPYDITLFHYIDDIML IGSSEQEVANTLDILKGQRFVLT VIDTYSRYWFASPECNASA/KT TIHGFTECIIHYHGIPHSIASYQG THFMAEEPGW\SKNQGVEVTPF TITPSDPVATFLLPVPMTLRSAG LEVLVPEGGTLPPGDTTMIPLN WMLRLPPGHFGLLLPLSQQAK KGVTVLAVVIDPDYQDEISLLF HNGAIISDGNGVILIGLLQWFST
4874	35242	A	4915	2	2210	
4875	35243	A	4916	1	2036	MDTFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRYKEELVPFLLQLF QSIEKEGILPNSFYEASIILIPKPG RETTKKENFRPISLMNIDAKIVN KILAKRIQQHIKKLIHHDQVGFI PGMQGWLNTCKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLKKLGTDGTYFKIVRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPFLFNIVLEVLARAIR QKEIKGIQLGKEEVILSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKTNVQKSQAFLYTNNI QTGSQIMSDLPFTIASKRIKYLG IQLTRDMKDLFKNYKPLLTEM/ KTKKWKNIPCS/WELEKTTLKFI /WNRKRARIAKSILSQKNKAGG ITLPDFKLYYKATVTKTAWYW DQNRDIDQWNRTEPSEITPHIY NYLIFDKPEKNKQWGKESLFN KWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNLRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATQAKIDKWELIKLKSFCT AKETIIRVNRQPTKWEKIFTTYS SDKGLISRIYNELKQIYKKKKQP HQKDFAYHFTVFVFYFGAFLLE AAATSLHDLHCNTTITG/HATPE **PV*HKRSSLTITYLCRSG*IIW WCDPHTHS
4876	35244	A	4917	1	1359	

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4877	35245	B	4918	1	948	
4878	35246	A	4919	1	981	
4879	35247	A	4920	1	3747	
4880	35248	A	4921	1	1875	
4881	35249	A	4922	1	2238	
4882	35250	A	4923	1	3924	
4883	35251	A	4924	1	1068	
4884	35252	B	4925	62	389	
4885	35253	B	4926	1	3663	
4886	35254	A	4927	1	1474	MAVSTTVRVDMPCCAVMLYC WGRSGKEQQPDEALKGKGFTV CFEGLRFGQKPGSYFSLDQIGH VEIQMITPPWRGTTLSTKRGGR KRGKTESDREHNLAPPKGRDTP KKEGAHVRGGPLSGTPPTEKK GKARSPRYGDTHRGEGLNKTH RAPQNFSESPEPTINKIDRPLAR LIKKKREKNQIDTIKNDKGDITT NPTEIQTTIREYYKHLYANKLE NLEETDKFLDTYTLPRLNQEEV ESLNRPITGSEIEAIINSLP\TKKS\ PGTDGFTAKFYQRYKEELVPFL LKLFQSIEKEGILPNSFYEASIILI PKPGRDTQKKENFRPISLMNID AKIVSKILANRIQVHIKKLIHHD QVGFIPGMQGCVGSSARAIGQE KEIKGIQLGKEEAKLSLFADDTI ECLENPIVSAQNLFKLISNFSKV SGYKIHVPKSVSFLYTNNIQAES QIKNAIPFTIASKRIKYLGIQLTL EVKELYNKNYKTLLKEIRDE
4887	35255	A	4928	419	1002	CYQRWKVLKKSSGPLARL/IKK REKNQIDAIKNDKGDITTDPTEI QTTIREYYKHLYINKLENLEET DKFLDTYTLPRLNQEEVESLNR PITGSEIEAIINSLQTKKSPGPDG FTAKLYQRYKEELVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RIRIAKSILSQKNKAGGITLPDF KLYYKATVTKTAWYW

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4888	35256	A	4929	1	2502	MFFETNENKDTTYQNLWDTFK AVCRGKFIALNTHKRKQERSKI DTLTSQLKEPEKQEQTHSKASR RQEITKIRAELKEIETQKTLQKIL QKINESRSWFFEEINKIDRLLAR LIKKKREKNQIDAIKNDKGDITT DRTEIQTTIREYYKHLYANKLE NLEEMDKFLDTYNLPRLNQEE VESL\HRLITGSEIEAIINSLPTKK SPGPDGFTAKFYQRYKEELVPF LLKLFQSIEKEGILPNSFYEANII LIPKPGTDTTKKENFRPISLMNI DVKILNKILANRIQQQIKKLIHH DQVGFIPGMQGWFNIHKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQPFMLKSLNKLVLEVLAR AIRQEKEMKGIQLGKEEVKLSL FADDMIVYLENPIISAQDLLKLI SNFSKVSGYEINVQKSQASLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL NEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAILIKLPM TFFTELEK\TTLKFIRNQKRACIA KSILSKKE\KAGGIMLPEFKL*Y KATVTKTVWYWCQNRYIDQW NRTEPSEIIPHIYNHLIFDKPDKN KKWGKDSLFNKWCWEHWLAI CRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLAGHLGNTIRDI GLGKDFMTKTPKAMATKAKID KWDLIKLKSFCTAKETAIRVNR
4889	35257	A	4930	1	4187	MGDFNTPLSTLDRSMRQKVNK DSQELNSALHQADLTDICRTLH PKSTEYTFFAAPHHTYSKIDHIV GSKALFSKCKRTEIITNCLSDHS AIKLELRIKKLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVY RGKFIAFKAVCRGKFIALNAQN RKQERSKIDTLTSQLKELEKQE QTHSKASRRQEITKIRAELKEIE TQKTLQK\ISESRSWFFEKTNKI DRPLARLIKKKR

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4890	35258	A	4931	1	1818	MSSRGPCTLETLINPSPSVADDI PHLRPKPVYITTTRDNENIYSTK IPYMAARVVFIKWIVTFFLEKK YLTATQNTKNGVDVLPKIIQTV GGGAVQERAPELDGGGPTEQD KSHSNSSTLSDRRLSNSSLCSIE EEHRMVYEMVQRILLSTRGYV NFVNEVFHQAFLLPSCEIAVTR KVVQVYRKWILQDKPVFMEEP DRKDVAQEDAEKLGFSETDSK EASSESSGHKRSSSWGTH\NSFT SAMSRGCVTEEG/TIQMLKAGV QALLQPVLCVFPLIPLPPLCNQA ARPAVVSIPLGDLLPWLSVLGG PADQWHLSYLKPEGSSAYACIL EALESAGKGLWKVSAVGRKP WTRGRSDRKGTVGHQVQFLFF KDEGRVDSRILTLMVAWIRPN\ LCVYISRELWDDFLGVLS\SLTE WEELINEWANIMDSLTAVLAR TVYGVEMTNLPLDKLSEQKEK KQRGKGCVLDPQKGTTVGRSF SLSWRSHPDVTEPMRFRSATTS GAPGVEKARNIVRQKATAKRS QSISNCVHLSEALPATKSVPLLL HTLYKNKALKAALGQPVGKAD QLVVAGSPSVCCVEDQWGRSN LEAMVLWLYCIPPDGDVLYL
4891	35259	C	4932	96	278	
4892	35260	A	4933	1	261	KLRLPPGHFGLLLLLSQQAKKG VTVLAGVIDPDYHNEISLLLHN GGKKKTRPAEMLAEGKGNTE WVGEEVSHQYQL*PHDQLQKR
4893	35261	C	4934	36	385	
4894	35262	A	4935	1	2349	
4895	35263	A	4936	207	561	QLAEPPHWIPGTRKDAQCLVGL FGFWRQHIPHLGGLLWPIYRVT QKAASFEWGPE*EKALQQIQPS VQAALPLGP*DLADPMVLEVS MADRCAGWSLWQAPIGELQQ KPLGFWSKALP

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4896	35264	A	4937	1	1375	MSTTQLDTMGAESLCNMETVQ VEDEGIQKLKEIRMVEWITPFRP THPSCEGPEDIPLTNALQNTFVR AAPASLKSPVVALLLSPVGYRT HAVVISPVPECRFGIDILSSWQN PHIGSLAGRAHQKQFVGSWQG QQYAFTVLPQGHINSLALCHNL IWRDLDHFLLSQGITLVHYTDD IMLIGSNLADPMVLEVSMADRC AGWSLWQAPIGELQQKPLGFW SKALPSSADNYSPFERQFFACY WALVETECLPTGHQLTMQPEL PIMNWVLSDPSSHKWVHGQSG HGGRDSGYSWTQQHGLPLTKG DLSMTTAECQIFQQQRPILSPRY GTIPWGDQPATWRQKWQRFVL TGIDTYSRYEFAYPACHASTKT TIHGLMEFLIHHHGIPHSIASDQ GTHLMAKEVRQWAHAHGIHW SYHVPHHPEVAGLIERWNE\GL LKSQLQHQLVNRLRRELQCWL
4897	35265	A	4938	1	324	INCLRNCKTYQA/RKPLWFYNT SLKFFLNKP/MLADVVFEIQGTT VPAHRAILV/ARCEVMAAMFN AGIFQAMCLLICAE/MYQVSRL QHICELFII/TQLQSMPSRELASM NL

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4898	35266	A	4939	108	2304	VAAAYPPPASPPWSPARSLAGA APAPLCVGPAAVEAREGDAAG DERIAGELAARGPREAVSRCFS PSRRPALGFEIMSIHIVALGNEG DTFHQDNRPSGLIRTYLGRSPL VSGDESSLLLNAASTVARPVFT EYQASAFGNVKLVVHDCPVW DIFDSDWYTSRNLIGGADIIVIK YNVNDKFSFHEVKDNYIPVIKR ALNSVPVIIAAVGTRQNEELPCT CPLCTSDRGSCVSTTEGIQLAKE LGATYLELHSLDDFYIGKYFGG VLEYFMIQALNQKTSEKMKKR KMSNSFHGIRPPQLEQPEKMPV LKAEASHYNSDLNNLLFCCQC VDVVFYNPDLKKVVEAHKIVL CAVSHVFMLLFNVKSPTDIQDS SIIRTTQDLFAINRDTAFPGASH ESSGNPPLRVIVKDALFCSCLSD ILRFIYSGAFQWEELEEDIRKKL KDSGDVSNVIEKVKCILKTPGKI NCLRNCKTYQARKPLWFYNTS LKFFLNKPMLADVVF\EIQGYG QCPAHRAIL\VAPCEVM\AAMF NGNLHGKAKSVLIPVYGVSKET FLSFLEYLYTDSCCPA\GIFQAM CLLICAEMYQVSRLQHICELFII TQLQSMPSRGTGHPWNLDIS/V DLL*KGPSFHHSWIAFSTWAYF HFHCYLTYLIFQFKRPGIFRDLF S/EGRNGSFLFGKRHRWGPSNM LLGRQLAGITGKYYFTSPGNVG
4899	35267	B	4940	1	3117	
4900	35268	A	4941	1	1162	MRVCARACVRTRTRMCVYAH TCVCVRTYAYVRVRVRVHVRA RVRVCAYARTRVRNSLSILPFIQ LTLATPIHHIHQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLIRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPLALLLAFLCSTSPGF GDPDGLGVIAYQDTVRPNAAT AISELNALAVKGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTL\MTGLWLAVLADTGATV LVTANALRLLRRR

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4901	35269	A	4942	1889	3387	QWAIKQFKHAEKENPYLFGGG HLRAIFR*SGFQ*RQLHTMHWG AS/QQAEHP/LAQPSTRAQLRTPI P/TADS/QRALVGSGMKPRLNG ERVLICAAGKHPADAFTGLINE LESAGQTVVLVVRNDDVLGVI ALQDTLRADAATAISELNALGV KGVILTGDNPRAAAAIAGELGL EFKAGLLPEDKVKAVTELNQH APLAMVGDGINDAPAMKAAAI GIAMGSGTDVALETADAALTH NHLRGLVQMIELARATHANIRQ NITIALGLKGIFLVTTLLGMTGL WLAVLADTGATVLFFPRLFEAR NSQVGNGETNQTRFRLCAAPG GTFIADFTAGTGRRARPRRNRR RVVVSFDFHQNMRRFLMEIVA ARFVVSKVAAHFRTFHYGGVIF ISRENVIWRGFESIFDHLEQRFR LLFTIDNPVGVKNFVAAVLGVR LGKHIQFDVVRVTTKLCESILQI VNFIFRQSQAKTQVSVDQRLTA LPQQINAGNRSRLMVGKQLLCI
4902	35270	B	4943	1	2104	
4903	35271	C	4944	1	1215	
4904	35272	A	4945	3	268	YEFNRPYPEIQRSGIS\KLLEPLL FAATSDSQLSKTEISSIKINSETV PVYQLRYNGNNALMFATYQD KMLVFSSTDMLFKDDQQDTEA
4905	35273	B	4946	1	1725	
4906	35274	A	4947	1	1437	
4907	35275	A	4948	2	736	QCPYPYIAATGRILVVTHLICLA PQIVENQVTYPLTTTMLSVPGA KTVRGFSQFGDSYVYVIFEDGT DPYWARSRVLEYLNQVQGMLP AGVSAELGPDATGVGWIYEYA LVDRSGKHDLADLRSLQDWIL KYELETIPCVSEVASVGGVVKE YQVVIDPQRLAQYGISLAEVKS ALDASNQEAGGS\SI\ELAEAEY MGGTCSAHGRALSRGVLWCRF SAIVRGPPRGMFCGAGAAPNLI
4908	35276	A	4949	531	632	
4909	35277	A	4950	532	609	

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4910	35278	A	4951	1	525	LGVEATA\IGDFGK\AAEKLPVP\ VELAQACAHAVMKSGIDLAVS YCMQVNHGFAQPLEFLLGGLD KVPVLLVFINGVATPLPGFQRT RMLGEAIGRFTSTPQYAGDTVN DEDISNTIRALFATGNFEDVRVL RDGELRKFPTCESDDNFRPVTF SVNYVIRHDWVGIRRVVPENE
4911	35279	A	4952	1	2769	
4912	35280	A	4953	1	681	
4913	35281	A	4954	1	1230	
4914	35282	A	4955	1	774	MLRTSDRPPYQYPKRCIPLSVL EVLRCARRWSLRPYKQLARAYI /ERYRHDR\DIEREKRGRLNQEI RGLVEQTNASLLNENANKDSK AHERGDIHYHDLDYSPFFPMFN CMLIDLKGMLTQGFKMGNAEI EPPKSISTATAVTAQIIGSVHIYG GTTINRIDEVLAPFVTASYNKH RKTAEEWNIPDAAGYANSRTIK ECYDAFQSLEYEVNTLHTANV EGLTGDDGIAVEALKKNSQKPR MSASHNCELVSLRGRQYT
4915	35283	A	4956	1	1278	
4916	35284	A	4957	461	1002	SLSTKGYAAAKWCSTACAGS/T LLLIVLLWVFIPKGFFPGQDNGI IQGTLQAPQSISFANMAQLQRQ VADVILQDPAVQSLTSFVGVDG TNPSLNSARLQINLKPLDERDD RVQKVIARLHTAVDKVPGVDL FLQPTQDLTIDTQGSRTQYQFT LHATSLDALNTWVPQLMEKI\Q QLPKLS
4917	35285	A	4958	1	291	MNPVDRPLLDIGLTRLEFLRISG KGLA\GLTIAPALLSLLGCKQED IDSGTVGLINTPKGVLVTQRAR CTGCHRCEISCTNFNDGSVGTF FSRIKPH
4918	35286	A	4959	1	306	MKNFEVLQPLQNSLSGLPLWV SERILQQINQLTHYEPVIGIMGK TGAGKSSLCNALFAGEVSPVSD VAGCTRDPLRFRLQIGEHFMTI VDL\PGVGESGVRD
4919	35287	A	4960	2666	2775	
4920	35288	A	4961	9	308	GDLDGSRHRAFLCHLPVELKTA LMFPVTLTRALMETAY/ATAVS A/NFRTESRGAH/SRFDFPD/RDD ENWL/CHSLYLPESESMTRRSV NMNPKLRPAFPPKIRT
4921	35289	A	4962	1	1132	

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4922	35290	A	4963	1170	1352	RNLPDAAGQSCAGEIRLYRQQT QRSRLQRWLHLACFRRCNLHR RELDATA*QHVRSCRWR
4923	35291	A	4964	1	312	MRKLTALFVASTLALGAANLA HAADTTTAAPADAKPMMHHK GKFGPHQDMMFKDLNLTDAQ KQQIREIMKG\QRDQMKRPPLE ERRAMHDIIASDTFDKVKAEA
4924	35292	A	4965	3	205	KDHIKGVLEAQNSLSTQVSLFF *SFFG*NSNMRNLIQIYRSL/CTK AI*LMNFKRHKNQLVINYLSRS
4925	35293	A	4966	1	915	MTGVATARARGLRRPLSVGQV PPFARLWKGVQTVERHMLANI GTGSQHPGCGFQLINQNSVIVF AAGEVNGFTSGDVQCLKMRSG DMNDIQRRQRLLPDGNKFGEIQ TTIREYYKHLYANKLEDLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIEAVVNSLPTKKSPGPE RLTAEFYQRYKEELVPFLLKLF QTTEKEGLLPNSFYEASVLLIPK PGKDTTKKENFRPISLMNIDVKI LNKILANRIQQHIKKLIHHNQV GFIIGVQGWFNICKSTNVIYHV NRTNDKNH\IISIDTEKAFD
4926	35294	A	4967	1	1338	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4927	35295	A	4968	1	1928	PPLVIHRQTGSGEDLQQTPTDL QLRVLTIRRKTNKQKGHPHQNP ISSRRHEITKIRAELKETETQKTL QKKSMNPRSWFF\ERINKIDRLL ARLIKKKREKNQID\AIKNDK\W DITHRIPTEIETII\REY\YKHLYT NKL\EN\LEEMDKFLDTYTLP\R LN\QEEVESL\HRLITGSEIEAITN SLT\TKKSPGPDGF\T\AEFYQRY KEELVPFLLKLFQSIEKEGILPNS F\YEASIILISKPGRDTTKKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHHQVGFIPGMQGWFNIL KSINVIHHINRTKDKNHMIISIEA EKAFDKIQQPFMLKTLNKLGID GTYLTYLKIIRAVYEKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNVVL\EVLVGAIRQEKEIKG IQLGKEDVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSEVSGYK INVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKT LNQKFSYWFRVNKHYIHQRTFP LKETEFNTIATLYNGASP/RTAP KSTGTNGHQASGLPRF*RIAFCS ALVKSKRKLYQGYLPGQTDRR EEGVSWCPGGP
4928	35296	A	4969	2	237	QPVEDTWLSTPAAPMVDSLIAR VRVMARGNAITLPVCGRDVK/F TLEVLRGDSVEKTSRVW\SGIET YQELVTEDALDDL
4929	35297	A	4970	1	1752	
4930	35298	A	4971	1	723	
4931	35299	A	4972	1	1701	
4932	35300	A	4973	1	1446	
4933	35301	A	4974	1	403	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKG\LALKGLRVLLVEV RHRV
4934	35302	A	4975	1	1374	

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4935	35303	A	4976	1	2259	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLAL/KGLRVLLVEVHKRWS*N DEGYRHCTV***\HPEARKITRR WRIGEAADLVGVSSQAIRDAEK AGRLPHPDMEIRGRVEQR\LVIQ LNKLIICVMCLVRDCDVLKTYF HR*SGLLPIKVAFTKP/HVSVHL AQDLALKGLRVLLVEEPPSAPN LGIGTINVVCAADVLIVPTPAEL FDYTSALQFFDMLRDLLKNVD LKGFEPDVRILLTKYSNSNGSQ SPWMEEQIRDAWGSMVLKNV VRETDEVGKAAPMVDSLIARV GVMARGNAITLPVCGRDVKFT LEVLRGDSVEKTSRCDNLKTCH TSHGSVMAETAVINHKKRKNS PRIVQSNDLTEAAYSLSRDQKR MLYLFVDQIRKSDGTLQEHDGI CEIHVAKYAEIFGLTSAEASKDI RQALKSFAGKEVVFYRPEEDA GDEKGYESFPWFIKRAHSPSRG LYSVHINPYLIPFFIGLQNRFTQF RLSETKEITNPYAMRLYESLCQ YHPLTIEKVMKPLITSNTVTDEI ERANVFKMNGKWYLFTDSRGS KMTIDGINSNDIYMLGYVSNSL TGPYKPLNKTGLVLQMGLDPN
4936	35304	B	4977	1	1744	
4937	35305	A	4978	1	2367	
4938	35306	A	4979	1	1215	
4939	35307	A	4980	1	946	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGQAPCMK\LTMRS SSSSAPSPWML
4940	35308	A	4981	1	1572	

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4941	35309	A	4982	1	1617	
4942	35310	A	4983	1	550	
4943	35311	A	4984	1	3818	
4944	35312	A	4985	607	3777	
4945	35313	A	4986	671	3091	ARCQRVPGRPVPDLLRCLPRAT TPAPSPAPGLVVRRLAAPVPAA APVPAAAPVPAAAPVPAAAPVP AAAPVPAAAPVPVAAPVPVAA PVPAAAPVPAAAPVPAAAPVPA AAPVPAAAPVPVAAPVPAAAP VPRFQSPNQTASTSDSPHIGQLP HQTVPISDSFHTGQSPHRTDSTP DSPHTGQLPHRTVPTPD/ELPHR TVPTPDSFHTRQSPHQTASTPDS PHIGQLPHQTVPISDSFHTRQSP HQTASTQDSPHTGQIPHRTVPT PDSFHTRQSPYRTASTPDSPHIG QLAHRTVPTPDSFHTGQSPHRT DSTPDSPHTRQLPHQTVPISDSF HTGQSPYRTASTPDSPHTRQLP HQTASTPDSPHTRQSPHRTVPT PDSSPHQTVSTPDSPHTRQLPH QTVPTPDSFHTRQSPHQTVPTP DSPHTRQLPHQTASTPDSP\TPD SPHTGQSPHQFPHQTVPTADSP HTRQLPHQTVPTADSPTPDSFH TRHSPHQTASTPDSPHIGQLPHR TVPTPDSFHTRQSPHQTASTPDT PHTRQLPQQTVPTADSPTPDSF HTRQSPHQTVPTPDSPHTRQSP HRTVPTPDSFHTRQYPQRTVPT\ QTASTPGSPHTKQSPHQTVPTP DCPHTGQSPYQTVSTPDSPHTR HSPHQTASTPDSPHIGQLPHQT ASTLDSPHIGRHPRQMAPTPESP HARQLPCQMAPTPDSPTLDGPH
4946	35314	B	4987	1	891	
4947	35315	A	4988	157	1990	
4948	35316	B	4989	1	2157	
4949	35317	A	4990	1	378	MSIKGTYLKVIKAIYDKPTASSI LNGENLKAFLLRTGTRQGCPLY KINVYKSVALLYTTNDQGENQI NNSTPYTTAPRKIKYIGIYLTKE VKDLYKENYKTLLKEVIDDT/R WKHIPCSWMGRINIV
4950	35318	A	4991	1	392	

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4951	35319	A	4992	3	1570	ETDFAFVGQAGVQWCDLSSPQ PLPPWVQAILLPQPPRQGCWSG IPKWSGISEDVQVWKNCKLDL AAATGKNCLGQGEEALLTQMR TGNQREVSDWWEEFVYLRSRN PLMVNSNYYMMDFLYVTPTPL QAARAGNAVHALLLYRHRLNR QEIPPVRGPQWVRDGGVVLWP LGHVGPGRQLTAHGFLQTLLM GMRPLCSAQYEKIFNTTRIPGV QKDYIRHLHDSQHVAVFHRGR FFRMGTHSRNSLLSPRALEQQF QRILDDPSPACPHEEHLAALTA APRGTWAQVRTSLKTQAAEAL EAVEGAAFFVSLDAEPA\GLTL EDPAASLDAYAHALLAGRGHD RWF\DK\SFTLIVFSNGKLGLSV EHSWADCPISGHMWEFTLATE CFQLGYSTDGHCKGHPDPTLPQ PQRLQWALPDHIHSSISLALRG AKILSENVDCHVVPFSLFGKSFI RRCHLSLDSFIQIALQLAHFRDR GQFCLTYESAMTRLFLEGRTET VRSCTREACNFVRAMEDKKKT
4952	35320	A	4993	1	1027	MPAKSPGQDVLGTDNIKIDVFK QTNQKSHTGEKPYECPECGKAF SEKSRLRKHQRTHTGEKPYKC DGCDKAFSAKSGLRIHQRTHTG EKPFECHECGKSFNYKSILIVHQ RTHTGEKPFECNECGKSFSHMS GLRNHRRTHTGERPYKCDECG KAFKLKSGLRKHHRTHTGEKP YKCNQCGKAFGQKS\QLRGHH RIHSGEKP\YKCNHCGEAFSQKS NLRVHHRTHTGEKPYQCEECG KTFRQKSNLRG\HQRTHSGEKP YECNECGKAFSEKSVLRKHQR THT\GEKP\YNCNQCGEAFSQKS NLRVHQRTHTGEKPYKCDKCG RTFSQKSSLREHQKAHPGD
4953	35321	A	4994	154	331	IPAAATCMGSLLGG*ETPGLWA RRSVKSRGLFPGLPSPSRASVRS LLLLPAWAAFLEGIVDTRPTAW RAFPWTLFLSVFCQFLDFPETSL DSQKLSLDTPSF

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4954	35322	A	4995	657	1455	PEPKPAAVAPPPESPLPAGDSEG CLQPGHLL\PASPRLPRPRQAAS LAHRPEKSAPGADCPSGRR\GR PWTCGGLSGPAAAPRPCPLAPA FAPAFLALGAQR\GPGPEQGGH ERQAERPGRRSRRTRAYSARIY LPVAAEWPMGPGPEPGAGGRR RGEVPGPGAQRSPARRRRGGPA AVSSGGRGVGGLRGAVLFQHP EQQQRPVGLAGLGAQQPAHV WRYGPLST/PPALGPPAAARGP\ GRRLFLPFSFSPSAGAPGAASRP SPRRSP
4955	35323	A	4996	1	415	
4956	35324	B	4997	8	211	
4957	35325	A	4998	1	563	MDPNHEEIPDLPEKEFRRVKSK NHMTISIDAEKAFDNIQHRFMI KTLSKIGIQGTHFN\IIKAIYDKP TASIILNGENLKAFPLRTGTSIVL EVLARAIRREKEIKGIQIGKEEV KLLLFADDMIVYLENPKDSYRK LLEQIKEFSKVSRYKINVQKSIA LLYANSDQAENQINNPTSFTIA AKNKIK
4958	35326	A	4999	667	960	
4959	35327	A	5000	317	1157	EFRMDPAIALVLALSLTVPKLT VPDSPLRLYRSFCTSACTSNLV VHFA*KEKWPDV*LYTDSWAV ANGLAGWSGTWKKHDWKIDD NEIWGRGMWIDLSEWSKTVKIF VSHESAHHIT*KSSAEEDFNNQ VDRMIHSVDTTRPLSPATPVITQ WAHEQSGHGDRDGGYAWAQQ HGLPLTKADLAMVTAECPICQQ QRPTLSP*YGTIPRGDQPATWW QVDYIGPLSSWKGQRFVLTGID/ TSGYEFAYPARSSANSTIRGLM ECLIHHHGIPHSIASNQLYS
4960	35328	A	5001	2	15246	

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4961	35329	A	5002	1	951	MALALNRYL/CLAVLPLITKCA PLFAG/TEHRAIMVDSMLHTVY R/LSRGRSLTKAQRDVIED/CLM SLC\RLLRRLVFDVPILNEFA/K MPLKLLTNHYERCWKY/YCLPT GWANFGVTSEEE/LHLTRKLFW GIFDSLAH/KKY/DPELYRMAM PCLCAIAG/ALPPDYVDASYSSK AE/KKATVDAEGNFDPRPVET/L NV/IIPEKLDSFINKFAEYT/HEK WAFDK/DKEIYRWPIKESLKAM I/AWEWTIEKAREDLDPREGYN PQPPDLSAV/TLSRELQAMAEQ LAENYHN/TWGRKKKQELEAK GGGTHPLLVP/YDTLTAKEKAR DREKAQSY
4962	35330	A	5003	273	478	
4963	35331	A	5004	2	622	GAPRSLSEKERQLMGMINQLSS FREQLLHAHYEQKKLAASQIEK QRQHMKLGKQ\QQEQIARQQQ RLIQQQHKINLLQQQIQQLYAA QLAAMQVSPGGKLPGIPQGNL GAAVSPTSIHTDKSTNSPPPKSK TCCLLLWEDEHSASIPEVTNQQI HLHLASSITDHGGKVIWERCLE ESGKGVTGFPDWSPRWGRIPPE GSKEGFTKE
4964	35332	A	5005	3	512	
4965	35333	A	5006	1	642	MHAQTYAHTDTRAQPCTSMEK QVSLKPTEEAHKKERKPQKPG KYICQYCSRPC/AKPSVLQKHIR SHTGYG\CEMYPHGLEMERIPG EEFEEPTEGESTDSEEETSATSG HPAELSPRPKQPLLSSGLYSSGS HSSSHERCSLSQSSTAQSLEDPP PFVEPSSEHPLSHKPEDTHTIKQ KLALRLSERKKHQVIDRLGSGI LAGLSWQLLPQGEAL
4966	35334	A	5007	341	1020	TLNRRQGCCLGSWLTRSNGILL FEISRPTYLPILLILFLVKR/HKL KMSVLNMVVRHDPGSTESAKA KEELIFRCRSRHFRASPLFSQHA AADKHKFQRFLTADMALAVTV YAPTTFPPSSLLLFKQKSNGMH NLIATGHLLLVDPNRMVIKRVV LSDPPFKICTKMAVVCYMFFNR EDVQWFKPVELRTKWSRRGHI QEPSGTHGRMKCSFDRKLKSQ NTELMNLYK

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4967	35335	A	5008	1	847	EKAQALEDLAGFKDPAPGHTE ESMTHDKTTKIPCKSPPELVDT ATSSKKWPRACGQKVEVKEEL LAVGKLTQTSGETTHTNKEPEG EGKGMKAFKQPAKQKLDPENV TGSRRLPRVPKEKAQPLEDLAS FQELSQTPGHTEELANGADSFT SAPKQAPDSGKPLKISRRVLQA PKVEPVGDLVGTR/D/PVKSQSK SNTSLPPLPFKRGCGKDGSVTG TKRPHCMPAPEEIIEELPASKKQ R/VVAPRVRGKSPEPLVIMKRSL RTSAKRIEPAEDLNSNNMKTNN
4968	35336	A	5009	9	1094	IRHEEESMTDDKTTIIPCKSSPEL EDTATSSKRRPRTRAQKVEVKE ELLAVGKLTQTSGESTHTDKEP VGEGK\GTKAFKQPAKRKLDA EDVIGSRRQPRAPKEKAQPLED LASFQELSQTPGHTEELANGAA DSFTSAPKQTPDSGKPLKISRRV LRAPKVEPVGDVVSTRDPVKS QSKSNTSLPPLPFKRGGGKDGS VTGT\KRLRCMPAPEEIVEELPT\ SKKQRV\APRARGKSSEPVVIM K\RSL\RTSAKRIEPAEELNSND MKTNKEEHKLQDSVPENKGISL RSRRQNKTEAEQQITEVFVLAE RIEINRNEKKPMKTSPEMDIQNP DDGARKPIPRDKVTENKRCLRS ARQNESSQP
4969	35337	A	5010	1	459	MAKPWRALCILLRSLDSFLQLS ASLTCFGFMHNTYKNRPWGVL RSSTERSPRKGTAGDMRAGGRF NAPLIGQDLLFKEHFASKALDT CTNIARSAKTQGGPVAAILLLL AFGPCIFNLRVKFVSSRIKAIKL QM/RLTIYRGPLDRPAGPSTGL
4970	35338	B	5011	1	687	
4971	35339	C	5012	194	418	
4972	35340	A	5013	17	396	
4973	35341	A	5014	1	70	

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4974	35342	A	5015	1	994	MGFVKVVKNKAYFKRYQVKF RRRREGKTDYYARKRLVIQDK NKYNTPKYRMIVRVTNRD\IICQ IAYARIEGIMIVCAAYAPELPK\ YGVK\VGLTNYAAA\YCTGLLA GPAGFFHRFGMDKFYEG\QVEV TGDEYNVESIDGQPGCLHPAY WDARPLPRTSPLAIKVFWLP*R GA\VDGGLVLFPPQYPNRFPWL WIPESQGNLNARRYHREGTIHG PRIVAGLHAPTLMEEDEDA\YK KQFVRQYVKNS\VTPD\MMEE MYKKAHAAIR\ENPVYEKKPK KEV\KRKRWNR\PKMSLAQKK DRVAQKKASPL\RAQERAAEKL NQTIFYKDFSDIAN
4975	35343	C	5016	27	308	
4976	35344	C	5017	68	307	
4977	35345	A	5018	388	1485	
4978	35346	A	5019	3	1940	RDRMILLKMEQEIIDFIADNNN HYKKFPQMSSYQRMLVHRVA AYFGLDHNVDQTGKSVIINKTS STRIPEQRFCEHLKDEKGEESQ KRFILKRDNSSIDKEDNQSVCS QESLFVENSRLLEDSNICNETYK KRQLFRGNRDGSGRTSGSRQSS SENELKWSDHQRAWSSTDSDS SNRNLKPAMTKTASFGGITVLT RGDSTSSTRSTGKLSKAGSESSS SAGSSGSLSRTHPPLQSTPLVAG \VAAGSPGCVP\YPENGIGGQVA PSSTSYILLPLEAATGIPPGSILL NPHTGQPFVNPDGTPAIYNPPTS QQPLRSAMVGQSQQQPPQQQP SPQPQQQVQPPQPQMAGPLVT QSIPAKKELNAFRVRNQEQRDT GTLHEGSGKISRMVLGWEPLSP YAPDRDDVATQFGQMTLSRQS SGETPEPPSGPVYPSSLMPQPAQ QPSYVIASTGQQLPTGGFSGSGP PISQQVLQPPPSPQGFVQQPPPA QMPVYYYPSGQYPTSTTQQYR PMAPVQYNAQRSQQMPQAAQ QAVLEVLSPLVSTVMPPKLAVL VMAGFRLRLELSESVLLQALW WSDHLSSFSELLCRLPDVLPEPS LLPLEYDHQKDAQGQDYLTCM VLVTLLLESPTGIQEDDSNEISVI

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4979	35347	A	5020	3	1353	GDAYALVLRVTLYCGKCH\NE VVLAPIFEILSTESIQDQLPYSV MLMSMLAITEGRRSFSVSVENA CSNYVTTVQVKEVNQMHISPN SCNAIHPRDHILEISGTPTHTLQ VEELEDAISQMSQTLLLLIEHDP VSRSPAQLRLDAWLSPHTQNA GHPHALSTLDTKDNLEGTLRRC SLRLSNSISKSPSPSSPKEPLLLS RDISCWESLCCSSTYSKQNFRSC DLIHGEVLGKGFFGQAIKVTHK ATGKVLVMKELMRCDEENQK TFLTEVKVTLPSNLLPPGHDLL QTGAREQTGILKTGGLSVPGGA GHPAACRAGGVGPHCEHAVRP DPRLTPLALAQPPAGGCSTASIA PLFSIPAVSRVFRASRGLAACLE AEQAGRTILTCEVCKLVVGLSL DSQQQLSSVLCGWLCLSCPQL WSLNRHPQHQHHLVEMQNLKS HPRPGETESAL
4980	35348	A	5021	1	588	MEYPDGGSTLDLLEPGPLDETQ IITILREILKGLDYLHSEKKIHRG VKAANVLLSEHCEVKLVDFGM AGQLADTQTKRNTFVGTPFWI APENNPPTLEENYSKPLKEFVE ACLNKELSFRPTAKELLKHKFIL RDTKKTSYLTELIDRYKRWRA KQSQEDSSSEDSNSETDGQDS\G GSDSGDWIFTIQEKDPKNL
4981	35349	A	5022	1	1380	GPRASPPRADRRGPAVPSQEVA VLSAMAHSPVQSGLPGMQNLK ADPEELFTKLEKIGKGSFGEVF KGIDNRTQKVVAIKIIDLEEAED EIEDIQQEITVLSQCDSPYVTKY YGSYLKDTKLWIIMEYLGGGS ALDLLEPGPLDETQIATILREILK GLDYLHSEKKIHRDIKAANVLL SEHGEVKLADFGVAGQLTDTQI KRNTFVGTPFWMV\PEVIKQAG YDSKADIWSLGITAIELARGEPP HSELHPMKVLFLIPKNNPPTLE GNYSKPLKEFVEACLNKEPSFIP TAKELLKHKFILRNAK\KTSYLT ELIDRYK\RWKAEQSHDDSSSE\ DSDAE\TDGQASGGSDSGDWIF TIREKDPKNLENGALQPSDLDR NKMKDIPKRPFSQWLSTIISPLF AELKEKSQ\ACGGELGGPLKEL RGAIYLAEEACPGISDTMVAQL VQRLQRYSLSGGGTSSH

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4982	35350	A	5023	1	346	MAGEKVEKPDTKEKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGGDKNGGTQVF\ QIITYSSYTQKVQLPKSTLKQRQ GPCPQGAL
4983	35351	A	5024	67	599	SAAKSEMAGEKVEKPDTKEKK PEAKKVDAGGKVKKGNLKAK KPKKGKPHCSRNPVLVRGIGRY SRSAMYSRKAMYK\RKYSAAK SKVEKKKKEKVLRNLLQNQVG GDKN\GGTR/VGLNFRKMPRI\Y PTE\DVP\RKLLSHGQKNPFSQH V/REKLRASITPGTILI\ILTGRHR GKRVVFLN
4984	35352	A	5025	101	202	PVPGTSSCTDRYHYKKH**KIN TKLVSKYILNM
4985	35353	A	5026	2	562	LRTVPDLPGRRFRAMRTGQRR* PELPPDMNSLEQAEDLKAFERR LTEYIHCLQPATGRWRMLLIVV SVCTATGAWNWLIDPETQKVS FFTSLWNHPFFTISCITLIGLFFA GIHKRVVAPSIIAARCRTVLAEY NMSCDDTGKLILKPRPHVQ*QS SLIVMGLRIAFLRISDTAKSHKG FLLRLDM

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4986	35354	A	5027	1	2090	MGAVFFMLFSWWITSGHIQLLC TRRRATVSTHQEFVVTVSPFSL GLVVSGCLDADTAMPGSAEEQ FQWQSQDGQKDIEDELTTGLEL VDSCIRSLQESGILDPQDYSTGE RVIHFGKTLGLSSEDYSIMEKG QMVKEVTVTPQVSVLKANETM ASALCGQEGHDDPLLLTVQMS TGNHYIKDNSLFPWVKWPSLLS QSALQLNSKPEGSFQYPASYHS NQTLALGETTPSQLPARGTQAR ATGQSFSQGTTSRAGHLAGPEP APPPPPPPREPFAPSLGSAFHLPD APPAAAAAALYYSSSTLPAPPR GGSPLAAPQGGSPTKLQRGGSA PEGATYAAPRGSSPKQSPSRLA KSYSTSSPINIVVSSAGLSPIRVT SPPTVQSTISSSPIHQLSSTIGTY ATLSPTKRLVHASEQYSKHSQE LYATATLQRPGSLAAGSRASYS SQHGHLGPELRALQSPEHHIDPI YEDRVYQKPPMRSLSQSQGDP LPPAHTGTYRTSTAPSSPGVDS VPLQRTGSQHGPQNAAAATFQ RASYAAGPASNYADPYRQLQY CPSVESPYSKSGPALPPEGTLAR SPSIDSIQKDPSKYPILCDGGNPF CALVYRPSSRERASSL/LKSMCY Q*NRLYPKFRRVLGSGFEGMQ RRFCASKGIKGRFCGSSLEQDC EHGGQHPCYPKLVPTLWNPHQ REGNQKNSERV
4987	35355	A	5028	123	3825	
4988	35356	A	5029	1	593	MQVCSSGGRILRVSGTERQLRR EGGRFCLGRGVRNLREGGALR APFTAPSLTALPPDIVDIKPAN\ MEDLTEVTTASESHPHHCNLFV YSSSKGFLRLCDMRAAALCDK HSKHPCDDIGPIQIIQGHLRTSR GWMIILPALQSTFRCRMDEQNL RAFLAPRLCDFSTSQPQPGSPEQ PVMSGLISPWTKPSRSSVFSM
4989	35357	A	5030	1	894	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4990	35358	A	5031	1	3115	RQICSMASELGARDDGGCTELA KPLYLQYLERALRLDHFLRQTS AIFNRNISSDDSEDGLDDSNPLL PQSGDPLIQVKEEPPNSLLGETS GAGSSGMLNTYSLNGVLQSES KCDKGNLYNFSKLKKSRKWLK SILLSDESSEADSQSEDDDEEEL NLSREELHNMLRLHKYKKLHQ NKYSKDKELQQYQYYSAGLLS TYDPFYEQQRHLLGPKKKKFK EEKKLKAKLKKVKKKRRRDEE LSSEESPRRHHHQTKV
4991	35359	A	5032	1	1522	MVAQASGQTIREAEVGGSLTA QEVEATSILLSDESSEADSQSED DDEEELNLSREELHNMLRLHK YKKLHQNKYSKDKEWMSQLA ALNYYLAGGDEQKLLDLSYSPP QNRQPAMAKAHNNNNNNNNN NNNNHNKNPKRLLDERELLTY STATQSFDTRNTRSFDEDAKES RAAALRAANKSGTGFGESYSL ANPSIRAGEDIPQPTIFNGKLKG YQLKGMNWLANLYEQRLERL RFLQLEQEHTCPQEGRAERLRG QPLKLWALLHFIMPTLFDSHEE FNEWFSKDIESHAENKSAIDET KLKKVKKKRRRDEELSSEESPR RHHHQTKVFAKFSHDAPPPGT KKKHLSIEQLNARRRKVWLSIV KKELPKKTLYTQDAPFHVVITS NQLVVQDVKYFQRVKWQYMV LDEAQALKSSSSLTRSNARYPL VSSQRKIHDQQVTTDKSSKMDP KEEEYIPAKHEMENTKLQFYLS AIGEKQ\VRWKILLQFQCRNRL LLTGTPIQNTMAE
4992	35360	A	5033	1	974	MGFHHVARAGLELLTSGMCCY FAQDLRPEQSIKASLQRIILRKY EKCGHHNLQLKKGYKSVDEYK VHKGSYNGFNQCLTTTQSKIFQ CDKYVKDFHKFSNSNRHMTEK NPFKCKECGKSFCVLSHLTQHK RIHTTVNSYKLEECGKAFNVSS TLSQHMRIHTGQKHYQCGEM\ GIAFNKSSHLNTHKIIHTGEKSY KREECGKAFNISSHLTTHKIIHT GENAYKCKECGKAFNQSSTLT RHKIIHAGEKPYICEHCGRAFN QSSNLTKHKRIHTGDKPYKCEE CGKAFNVSSTLTQHKRIQQQQQ QTIKQTKNLLNNNNKKLWV

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4993	35361	B	5034	22	684	
4994	35362	A	5035	1	1338	
4995	35363	A	5036	1	596	MGMTDMGKSKKKSQGPPSFPP GGAPPPAIGAPAGRERPPGTGD PFNQRPCDNLKTCHTSHGSVM AETAVINHKKRKNSPRIVQSND LTEAAYSLSRDQKRMLYLFVD QIRKSDGTLQEHDGICEIHVAK YAEIFGLTSAEASKDIRQALKSF AGKEVVFYRPGEDAGHEKGYE SFPW/FIKRSPE*RRGKFPFTQM GQD
4996	35364	A	5037	787	1692	
4997	35365	A	5038	289	1338	
4998	35366	A	5039	982	1347	
4999	35367	A	5040	1	780	
5000	35368	B	5041	148	334	
5001	35369	A	5042	2	545	
5002	35370	A	5043	1	732	
5003	35371	A	5044	1	1110	
5004	35372	A	5045	1	1170	
5005	35373	A	5046	1	870	
5006	35374	A	5047	1	1254	
5007	35375	A	5048	614	1236	TARVAAARRRCQCWGSGACGS ALTLPRTSSLTLTETPIVQQTRM VVRCPTASLPSQWRSCPSSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVTDRTVRTWIGEAVAAAAAD GVTFSVPVTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
5008	35376	B	5049	1	1281	
5009	35377	A	5050	2	893	
5010	35378	A	5051	1	1416	
5011	35379	B	5052	49	768	
5012	35380	A	5053	1	792	
5013	35381	C	5054	1	1461	
5014	35382	A	5055	887	1203	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS

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5015	35383	A	5056	740	1431	CCQTLPVFHPPHPSHLGPRPCPP TH/HLPSEHRSLFLEAACHDSDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRHRLHR PQQPSPPLGIPHPSLL\TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
5016	35384	A	5057	1040	1477	
5017	35385	A	5058	1	1422	
5018	35386	B	5059	1	1404	
5019	35387	A	5060	353	870	AWSSPRSRCPLHSRTPSLPRVEG QAHIGPGL/HRYQQGHQDLFIL RSDLPSQVFIRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSVPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
5020	35388	B	5061	1	1612	
5021	35389	A	5062	2	429	WGHWASPRLWWAWGSPGPAG LKPPGTVAASTGFSQWLLYIETI SRTPVELELKNSKVRKDVLS/R GPHSLYLVQDAQLEHAMEIAK VSVQALQAYRAPPPRMEQANP KTPPDANLYKKGPSPSPRRANT TRLGSRATKTIHPDS
5022	35390	A	5063	508	1007	PPLAQKQAVASQSHSPCGGFHR RWFRMRLTGEIMKIITCFKLVP EEQDIVVTPEYTLNFDNADAKI SQFDLNAIEA\ASQLATDDDEIA ALTVGG\SLLQNSKVRKDVLSR GPHSLYLVQDAQLEHALPLDT AKALAAAIEKIGFDLLIWTSSRI QAVALASPLSNT

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5023	35391	A	5064	1	1670	MNIEFFDPPRIVSGLTLNRINIQH PFHLTGIRYCIDERQRTVNDVL QAHAGRVLQQYLPAPATATFR CQSRNRTENPQFLVCQWAGED QITQLLQEQWRVLIVMIFRTHN HMAGPRRWFRMRLTGEIMKIIT CFKLVPEEQDIVVTPEYTLNFD NADAKISQFDLNAIEAASQLAT DDDEIAA\LTVGGSLLQNSKVR KDVLSRGPHSLYLVQDAQLEH ALPLDTAKALAAALEKIGFDLL IFVKGTCLVLLVAFGLVTTHFQ PCLFGVQNGEQETVQILLVGVV GGMERAERIIIPFTLAINNQPTT RLTKTIAQGMPAIIQRNIPNPRIS LQPAPTPRHSANPATMQPHAQ ATPTPKPHTRTYPTRPPHPQRSA TPGTQRTPTPGPQTARDRAPKP DHTRPQTAHTAHHTSNDPQQR HRTRQRHTNKQHPHPAPPRLPT LPQNNKRQKPAESDTRKHHTP HMRQPTAHAETTARNTQAAQH CHTQNTPQANRHATGDRPEHH QARDRTRIDPKPNPDPRTITGHT KGTTYAHKHTPLATHHMTRPT TGHRHGTHH
5024	35392	A	5065	548	924	GLLRPRFSVNSPHFNTWLLSAN SINWR*YGFMPSLLILLL*LNPM GRYSGASLVSRRMASTTLPGHS IAMRQPVCGIFALTRAIISI/AM WDFHVEDFMPERMALNLVLNS AI*LPKIFPARWMKFS
5025	35393	A	5066	33	424	CRFDESFWCDA\HAIFVAPTLY AYDFYADKTLVPLTDALANTW QKQFPLDYGKGRLWGSVAFVI GSALTGKLVTMFDYRVILALLT LGVASMLLGFLIRPTIQPQGASL QQESTGWSAWLALVRQNWRF LA
5026	35394	B	5067	1	265	
5027	35395	A	5068	142	609	CLFRQVSAPHITRVCITRSAATI QTIDLNNLDTGD*LQPAFPPVW LISPGPFHPTPSVTRVPLEKEIRT FAQRLSVLHGINAPEFFDKPLFS SLVLTLRDEGYISDSGDAEPAE TMKVYQLQTNIVIIHKCFKAGF TLAVGNQFLLINKQRASHQN

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5028	35396	A	5069	983	1387	LVWKVIPWRPAWKITLCVLNS CRRACLFAPAT*TANRLQAVC/ WLQSANPSINRGTLEKESRTVA QRLSVLHGINAPEFFDKAVFSSL VLTLRDEGYISDSGDAEPAETM KVYQLLAELITSDVRLTIESATQ GEG
5029	35397	A	5070	1	1815	
5030	35398	C	5071	1	354	
5031	35399	A	5072	1	678	MTDKQQGEKQKQKTEDKTKT KQKQRKNKTDKRRKTKTERNT QRTPERQTNTNQTRTKQ/RRPD TGVTQADTRQDTSARR\LMRQP RSAAAWMAALRGARDPKLITM VPHSKISRSIVRKGLPMTETQRR TETSKNYRPREQQTRNRQQQD PRQQRTVQTHQQEERRETKDN NTHTKPHETLARRHRRHNIHAL AAADLVIEAASEVWKSKKRSL HSWRKFAPTNAIDH
5032	35400	A	5073	93	729	SADPRNRRDTRAAKFTRDAGK TDC*NL*THIETPDPGDRYSRAG SCGPG/PLKRRLNVWKSKKRSL HSWRKFARHKRY*PLTLRQSLY TAIAAEIKNPERVAGLHFFNPAP VMKLVEVVSGLATAAEVVEQL CELTLSWGKQPVRCHSTPGFIV NRVARPYYSEAWRALEEQVAA PEVIDAALRDGAGFPMGPLELT GPDWAGPPFCCHLFGV
5033	35401	A	5074	145	1038	SILRLRQKRKQLTAYDFADNCD KALY*RNHRLIREILALVCAHD RQKK/YLPSLAGFL*LKNEINRL SVRGW/SRRRSFSVR*/PFTNTD RARSHFYQFVIIDELQSLFQSHA DRRNQNNGFVSTGSTHVGQFL TGQAVYSQVVRAAMNTDNLTF VNFCTVTEEQLTAILQTEQRER DRFTLTVRDQYAVLTLTHFTRT YVVVVAEGGVQQTSTGSHGHE LRTEANQTTAWDHVVETYAAF TVWIHVFQVALTFAQRLHYRT LMLFFNVQSHVFIRLLFTTVDFT EDNFRTGYRQFETFTTH

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5034	35402	A	5075	39	4329	YAPATFSAATQPTPKKINNPVP RNSAMHWQTRIQAQANGYWL EREQWLAVGEQWFWRMEWSG PHRAAAGRLCHHHGNDATWH RG*FHLCFRPCV**RIEQPQEGY AIIMETTPPGTGVNFIFVSDPAF DKGYAFDFFCLEPMSHAPDDH HRPEGGDLIALAPGESTTSEMS LRVPVANCAVTTASLDSYYGE AMAIGERAPVALLDFAASARL AVGEALTNIAATQIGDIKRIKLS ANWMAAAGHPGEDAGLYEA
5035	35403	A	5076	1	625	MRASGTDEAVVLVPPIRMTLEQ ALEFIDDDELVEGAAAAFEALE MMGSGRDREI\RYGEGSP\WFDI \VLPCGGGITLTLHKLR\SAQPLL \AVLNRLEQKKPVGLRYDPQAQ SLVCLPTQTRTGWNLNGFEASI THRALRTSRYDGQYYCQGPRT LTIRRTVIMTGSSDPHDTTDSNN DRVLGPSRYDGQYYCQGPRTL TIRRTVIMTGS
5036	35404	A	5077	3	516	ATLSCEVVLENLAASPVVTTLE YTLFDGER\VVHSSAIDHLAIEK LTSASLAFTVEQPQQWSAESPY LYHLVMTLKDANGNVLEVVPQ RVGFRDIKVRDGLFWINNRYV MLHGVNRHDNDHRKRRGVGM DRVEKDLQLMKQHNINSVRNA HYRKRRNKEVRTKKKIESIEEK
5037	35405	A	5078	3	678	ASYYCTRN\DLELVAVCDSRLS QRQALAEKYGNASVWDDPQA MLLAVKPDVVSVCSPNRFHYE HTLMALEAGCHVI\QAREM/CD TARKLGKVLAYDFHHRFALDT QQLREQVTNGVLGEIYVTTAR ALRRCGVPGWGVFTNKELQGG GPLIDIGIHMLDAA\MYVLGFPR /SVEDSLCGTIELHSGCILWLETS FALNIREHAIMNIRFCGDKAGA SVFPAHIYTATQR
5038	35406	A	5079	2	294	YSFMV/PIFGGRRWTVFSTAILI/I PCVWLGIAVQNPNT/PFGIFIVIA LLCGFAGAN/FASSMGNISFFFP KAKQGA\PVFAF/LGVNGVPQA DGSVMSLAMPH
5039	35407	A	5080	1	834	
5040	35408	A	5081	2	135	QYASALVSTAIALLLV\CLAFLY PAAN\SEIHL\GVLSIFWGDPDG

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5041	35409	A	5082	1	324	MQGGYNIHPLIDALDDAKLAPI AAKALSHTLLMFDNFYDVEEK AKRGNEYA\QVMQSWAD/AEW FLNRPALAEKLTVTVFKVTGET NTDDLSPAPDAWSRPDIPLHAL GC
5042	35410	A	5083	1	866	MGLAQAKLLIEAPVNGGRNYN GPKVAKFLVGGASLNDVYLHQ HDKYRYDRYHLIRNREKTH\IM PEWVTQNIMNGRGVNRLDDVN RPKSPEIKNDIRLFRQELRDAAY HFQGDADNDQLSVTPLVGLGK SSLLIK\TIFHRMRWAEQNLSICS SSFNRPAIFVRNIIQLLREGKKV EITVGDKHENDFYIPEDEPFKIIG ALPYLYEINLRRFLSRLQYYVN TDQLVVRVW\KEDDN\TYHL\K GWWGDDKWMVITG\NKLDPR AWRLDLENAILIHDPQLELAPQ REKELE
5043	35411	A	5084	1	3483	VMFFFLPGLLMASWATRTPAIR DILSVSIAEMGGVLFGLSIGSMS GIL/SLGVVSETLWDT*C/HSWS RCPAH*SG**Y*/VLALWLTSPL LFAVGLGVFGASFGSAEVAINV EGAAGEREMNKTGLPMMHGF YSLGTLAGAGVGMALTAFGVP ATVHILLAALVAQIAAWYKAL QEQIPDFIPRAPQRQMIADVAK TLAGEEGRHLAIEAPTGVGKTL SYLIPGIAIAREEQKTLVVSTAN VALQDQIYSKDLP
5044	35412	A	5085	1	848	MLVGKVVVSEGASFRTHGAVD TSKAYVSLENSGWTIIADITTTN QNTLLNLANLAMSDANVIMMD EPVTRSSVTASAENFITLTTNTL SGNGNFYMRTDMANHQSDQL NVTGQATAGDSLTLVTTGGGD AAFTLGNAGRVFDIGTYEYTLL DNGNHSWSLAENRAQITPSTTD VLNMAAAQPLVFDAELDTVRE RL\GSVKGVSYDTAMWSSAINT RNNVTTDAGLRAQAIKTVHHR QNRLIHFSLNGSTFNVYRHFRR TKTCPKDAETNGKEQGRCQPE CQT
5045	35413	B	5086	75	1777	

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5046	35414	A	5087	1	860	MKAPGLPADQQFFADLFSGLV LNPQLLGRVWFASQPASLPVGS LCIDFPRLDIVLRGEYGNLLEAK QQRLVEGEMLFIPARAANLPVN NKPVMLLSLVFAPTWLGLSFY DSRTTSLLHPARQIQLP\SLQRG EGEAMLS\ALTLFSRSPLEQNIIQ PLVLSLLHLCGSVVNMPPGNSQ PRGDFLYHSICTWVQDNYAQP LTRESVAQFFNITPNHLSKLFAQ HGTMRFIEYVRWVRMAKARMI LQKYHLSIHEVAQRCGFPDSDY FCRVFRRQFGLTPGEYSARFQG
5047	35415	C	5088	86	601	
5048	35416	A	5089	1	870	
5049	35417	A	5090	305	625	VAPGDRHAFPLAPSGLSPELTLP QTQCCAQATVQGLEGTRSWSQ SGTSSLSPWSHTSLRRRRKEEG EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEE/EEEGEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEAKTQ
5050	35418	B	5091	1	552	
5051	35419	A	5092	2810	3117	LTLNSHMAPALIPILAMSAPMT PMKN/LSQVHAQGLVIRDLPLIA SNFRNTEDLSSYLKRHNIVAIA DIDTRKHAACAVPNTLVARGL RKHLKRVAAPQHWIAG

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5052	35420	A	5093	2	1902	LKYPMKRVGKRGEGKFERISW DEALDTISDNLRRILKDYGNEA VHVLYGTGVDGGNITNSNVPY RLMNSCGGFLSRYGSYSTAQIS AAMSYMFGANDGNSPDDIANT KLVVMFGNNPAETRMSGGGVT YYVEQARERSNARMIVIDPRYN DTAAGREDEWLPIRPGTDGAL ACAIAWVLITENMVDQPFLDK YCVGYDEKTLPANAPRNAHYK AYILGEGPDGIAKTPEWAAKIT SIPAEKIIQLAREIGSAKPAYICQ GWGPQRHSNGEQTSRAIAMLS VLTGNVGINGGNSGVREGATG SAVGEVVFNTSMTGYQEILTD\ LPI\PSNRYS\SYP\ILAMSAPMTP MKN/LSQVHAQGLVIRDLPLIAS \NFRNTEDLSSYLKRHNIVAIA\ DIDTRKLTRLLREKGAQNGCIIA GDNPDAALALEKARAFPGLNG MDLAKEVTTAEAYSWTQGSW TLTGGLPEAKKEDELPFHVVAY DFGAKRNILRMLVDRGCRLTIV PAQTSAEDVLKMNPDGIFLSNG PGDPAPCDYAITAIQKFLETDVP VFGICLGHQLLALASDVEKNVV MITAQNHGFAVDEATLPANLR VTHKS\LFDRYVTGHSSHR*TG\ FSFQRHPEASPGPHDA\AP\LFD
5053	35421	A	5094	8	456	
5054	35422	A	5095	377	1228	KQARGRLCPAKPQGWSCPRPW QPTFC/GQCDLKVRPGVIGDHF GALKFDCPTGFRTCLGRITPLFL PSSPIWNGCIFPIPVPGGDCGEG VQIRSLSCMVHSGSISHAAGRV EDALCGEMPFQDSILKQLCSVP CPGDCHLTEWSEWSTCELTCID GRSFETVGRQSRSRTFIIQSFEN QDSCPQQVLETRPCTGGCSPQA RPAAIRQCIPACRKPFSYCTQGG VCGCEKGYTEIMKSNGFLDYC MKVPGSEDKKADVKNLSGKNR PVNSKIHDIFKGWSLQPLDP
5055	35423	A	5096	1	519	

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5056	35424	A	5097	1	743	MCPAIDAVLVYVNRKWTNLSD PMPVGQMGTVKYVLMSAPATT ASYIQLDFSPVVQQQKGKTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVNI QDTMIGELPPQTTKTLARFIPEV AVAYPKSKPLTTQIKIKKPPKV AMKTGKSLLHLHSTLEMFAAR WRRKAPMSLFLLEEHFNLKGQ HSLHENQLQMATSLDRRGN/YT GFITSYLEEAYIPVVNDVLQVG LPLPDFLAMNY
5057	35425	A	5098	2327	3435	KTTTLEDNLGNTIQDIGPGKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKRVNKQDESLRS HYE*WGMLTDCVVMRDPNTK RSRGCGFVTYATVEEVDAATN ARPHKVDGKVVEPKRTVSRED SQRPGAHLTVKKIFVGGIKEDT EGFAFVTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQRGRSGRGGGFGGNENFG CGGNFSGHGGFGGSHDGGGYG GSGDGYNGFGNDGGYPGGGPG YSGGSRGYGSGGQGCGNQDSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSYNDFGNYNNQY SNFGPMKGGNF/GGRRSGP*GD GGQYFAKPPNHSGYGGSSSSSS
5058	35426	A	5099	1	636	MRDPNTKRSRGFGFVTCATVE EVDAAMNARPCKVVGRTVEPK RAVSREDSQRPEDTEELHLRDY FEQYGKIEVIEIMTDQGSGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGSGNFGGGRGGGF GGNDNFGRGGNFSGHGGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVNYNNQSSHFGPM
5059	35427	A	5100	1	3622	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCLRVDGQQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAAATSNVHMVKKISI TERSCDGAAEMKWEDQNIGD

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5060	35428	A	5101	1	782	MRRRLQLDSLLHPPSCFSSTLK CGKAAAAACDSSDQIQERLQT GHLPCEASHTICPPNHHSQSTLR PPLPPP\HNHTLSHHHSSANSLN RNSLTNRRSQIHAPAPAPNDLA TTPESVQLQDSWVLNSNVPLET RFWCCQRFLVFPGLQLQHLTLS LPVWSHGALPVSLCIFTWLSSH KDTSHFGLRVHLLSLPLEAKYS FYPGCPVLEPAPNPLKGPWCLW GVGTFRRYCTTFLFNESEPKDL VGEKFKSDRLCREAHLQE
5061	35429	A	5102	3	1864	
5062	35430	B	5103	1	525	
5063	35431	A	5104	2	351	RPAVGAEKSNPSKRHRDRL\NA E\LDHLASLLPFPPDIISKLDKLS VLRLSVSYLRVKSFFQVKRQRR EIHGRNCQKKRNQNLKDRGWQ WQMPKMWMTTRANEGPCRSG GPEHWTPRP
5064	35432	A	5105	1	375	RPLQKQRPAVGAEKSNPSKRHR DRLNAELDHL\ASLLPFPPDIISK LDKLSVLRLSVSYLGVKSFFQG QGLAVADAEDVDDHTGERRP MSFRRPRALDTQALRRTQFGLH LLMVNIAGLIATDRL
5065	35433	A	5106	407	910	NVTPAHYDEQQNFFAQIKGYIR CILFPPDQFECLYPYPVHHPCYR QSQV*LDNPDYERFPNFQNVVG YETVVGPGDVLYIPMYWWHHI ESLLNGGITITVNFWYKGAPTP KRIEYPLKAHNKVAIMKNIEKM LGEALGNPQEVGPLLNTMIKGP IQLACQGSRPPAR
5066	35434	A	5107	237	908	HEKPGRQRETRSQNHHHHHHH HHHHQEKIRIQTFTERP*EDTER SDCPQAKKRSPRRNQPC*HLDF ELPAARAATQPVNSGARAGRA GATVPRHTATLLLLHQRRDYA GGSLCDIDRAPDAKQGGKS*ES ETDSRFWKGTVC*DHTAGWVH GRPTTPHHSSPDSRNGGFQLHQ QIALAAGWREGASRPKQEPLQP GPEQGQRRGRREPVQGKAPSG HQSWPAE

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5067	35435	A	5108	57	873	SGLCTAAFHHQMEVVHT*SVSS RS*R\PTTPVIAQWAHEQSGHG GRHGGYAWTQQHGLPLTKAD LAMATAECPICQQQKPTLSPRY GTIPQGDQPATWWQVDYIGPL ASRKGQRYGFAYLARNVSAKT TIHGLMECLIHHHGIPHIIASDQ GTHFVAKEVRQWAHAHGIHW FHHVAYHPEAGGLTEWWNGL LKSQLQRQLGDNTLQDWGKVP QKAMYALIQCPIYGIVSPIARIH RSRNQGVKVEMAPFTITPSDPL AKCLLPVLVTLRSAGL
5068	35436	A	5109	1	311	QITMQPELPIMNWVLSVPSSHK MGHAQQH\QEVAQMPRVSTPA TLPSLPQPALMAPWTVPYDQL MEEEKARARYAGTIQKWTAAA LQPLSRTSLKDSGEGTSKW
5069	35437	A	5110	3	591	DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLTM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEEKSSQW
5070	35438	A	5111	1	582	
5071	35439	A	5112	1	635	

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5072	35440	A	5113	2	1538	FFPIGFWRQHIPRLSVLLQHIY* VT*KAASFEWGPKQEKAL*QV QAVVQVALPLGPYDPADPMLL EVSVADKDAGCSLWQAPIGES QWRSLGFRSKALPSSADNYSSF ERQLLACYWALVETECLTLGH QVTI*PELPIMNWVLSDPSSHKV GHEQQHSIIKWRWYICDWAVV GRESTTNGLAGWSETWKKHH WEMGEKQIWGRSMWMELSEW SKTVKIFVSYVSAHQCVTSTEE DFNNQWDGMTCSVDTTHPLSL TTSVIAKWAHEQSDHGGRYGG YAGAQQHGLPLTKADLAMTTA ECPICQQQRPSLSPQYGTISQGD QPATWWQVDYIGPLPSWKGQR FVLTVIDTYSGYGFAYPEHNTS AKTTVNGPMECLIHRHGIPHGI ASDQGTRFTAKEVWQWAHAH GIHWFYYVPHHPEAAGLIGWW NGLLKSQLQCQLGDNTLQGWG KVLQKAVCALNQHPIYGTVSP VARIHGSRNQGVEVEVAPFIITS SDRLAKFLLPVSSTSCSAGL
5073	35441	A	5114	488	966	ILVGSKGQSVCPGPSSSGTRGSS SPGVAVSNKAAATVGPQ*VTQ QEGGPGSRQRTRAGSPELVPAG PSAVEGEEGSWTPGGPQVPRKR SAAPSRQR*HWLRCTPA*QRRG DWPRAAGRCHAARPPAAGSRA PTKISARPTRISRLGPRAASKAQ RLQRL
5074	35442	A	5115	197	421	KLKATMNSFHKS*SCALVSTRP CSPRGDPRATLTTIPALVEPPCG TQDPKMAAEAPQRPGKRLGRN LLTRRRPT
5075	35443	A	5116	3	5649	LLEKLRQRIHDKAVALERAIDE KFSALEEKEKELRQLRLAVRER DHDLERLRDVLSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ WLKEEMETKFSRWQKEQESIIQ QLQTSLHDRNKEVEDLSATLLC KLGPGQSEIAEELCQRLQRKER MLQDLLSDRNKQVLEHEMEIQ GLLQSVSTREQESQAAAEKLVQ ALMERNSELQALRQYLGGRDS LMSQAPISNQQAEVTPTGRLGK QTDQGSMQIPSRDDST
5076	35444	A	5117	2	157	YLGRHLCLFSEHEEHSSRKEMV LVEGLCSEQGRRG*TLASSSER KPLENER

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5077	35445	A	5118	248	621	TDEPSLLSHTFCPKGALLSACSG ACPLSSGTQAGMPPSTEALQPC RGLTVPHQ/LG*RPQGMLWWK ALAADWSVEWQKGRRGLGKA LSVTSRTGRLLCR*GSAEAAAS PLAASPRRSSRALGAGIP
5078	35446	A	5119	2	157	YLGRHLCLFSEHEEHSSRKEMV LVEGLCSEQGRRG*TLASSSER KPLENER
5079	35447	B	5120	125	994	
5080	35448	A	5121	1	550	RRYRPRRVQDPGGPAEAERGPP RRLLNARVHVCRAEASERAPGP CGRVSAHVERARDPRLE*QLED KAAPRQDFTQQLRGPEKQHRM VWQEKEDMHKQLVEASETLKS QAKELKDAHQQQKLALQEFLE LNELMAELYSQKQKVWDKEEE MEVAMQKADMMWQEI*RSKK LRKRMLFSQMRWL
5081	35449	A	5122	135	638	GSFPGPAPLGQTLVTLGLAWQS SGWILRGWLVPPRAKCSPRGQ ALAICLSLRGLGARSTWAETRP QGPRGSLASLCPAHMDLSIWKT GDGGPRSAFSKVHQGSLNTFG VDTAARRLSQARTAPSPSV\SAP SSAAAPASAGPPPAPGAPPTPA QALRPAPPSPRPAER
5082	35450	A	5123	193	610	VGELLPFRFKISLRPFLALCLSSL GPCRQPHSGSVPA*NPLLGPRA KSSPHSGCGLAPFAIPELLRRLP LEGSAHCPAPEGAASPPTSWDS ADPPCRETSIFAPPRVVLTPGPS APQASPSQPLLFLTPRWDRLPES VL
5083	35451	A	5124	2446	2630	VGFFFFFWWGERGTGSYSVTQ ARVQ*YDLGSLQLLPPSFKGFS CLSLPGSWYYRHGPPRLG
5084	35452	A	5125	3	710	EDGDWDQRRGGEAGDQDQRR GGEDEDQDQRRGGEDGNRDQ KRDGENGDWDWKREDENKDQ DEKREGEDGNQDQRRGGEDGD QDQRRGGEDGNQDQRRGGKD GDQDQGRGGEDGDQDQGREG EDGDQEQRRRGEDGE*DQRRG GEDGGQDQKRGGEDGNQDWS REGEDRD*HWRRGGEVGE*DQ RRGGEDGE*GQRRGSEDGDWD RSRGGEDGDQDQRSVGHLCHS QGPPASGCVS

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5085	35453	A	5126	506	882	RCSGQGGFDGNKGTKALPTISA DTTRCWRTLRVTQMTCRFRRF KAFFIGIMSCGRTGRILFPPCSS MSWIPCRAKNS*GNVISQSPSK NR/WQIMMVIQLLNFYLPGDFV SFRIMLKGNWEVTRTRG
5086	35454	A	5127	107	1327	ERRKRAVGGFDLVLGEQPSDKI FR*VIV*GLALWLPLSKSFVIPP AELAINPSAKCKTDMTVMEDA VEVR*VWLQD*GLDSLEVLLDS FGPVRDCSKDNGGCSKNFRCIS DRKLDSTGCVVGLPCKLVVDS SGCYDRHIGVDCSDGFNGGCE QLCLQQMAPFPDDPTLYNILMF CG*VELPARPLDGRSCQLITETC PEGSDCGESRELPMNQTLFGEM FFGYNNHSKEVAAGQVLKGTF R*TSYT*N*YQQLPDGLVVATV PLENQCLEEISEPTPDPDFLTGE CAFSTLFGYPVLQHWKVRSVM YHIKLNQVAISQGEHCCRLSCD GATSRADFVALLDQFGNHYIQE AIYGFEESCSIWYPNKQVQRRL WLEYEDISKGEWHACWQILSTF PWIVISLHNCLP
5087	35455	A	5128	3	23	FYSAFLVADKVIVTSKHNNDTQ HIWESDSNEFSVIADPRGNTLG RGTTIT*VSIPPSL

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5088	35456	A	5129	1	2462	MRALWVLGLCCVLLTFGSVRA DDEVDVDGTVEEDLGKSREGS RTDDEVVQREEEAIQLDGLNAS QIRELREKSEKFAFQAEVNRM MKLIIHSLL*NKGIFLERLISNSS C\ALDRLSLISLTDENALSVNE* LTVN\IKCDKEKNLLHVQHTGV GMT\REELVKN\LGTIAQIWDQ ASFLNKMP*SHRKMGPVNLPEL IGPVWVSGFLFPPSLVADKVIVT SKHKQPIPQHIWGVWTPNGIFL *LLDPRGKHS*DRGNRQFTLCP *KEEASDLPWNLDTIKNLRQKN IHSFIKLFLIYVW\SSKTETV*GA PWGEEEAAKEEKEESDDEAA\V EEEEEEKKPKTKKVEKTVWDW ELMNDIKPIWQRPSKEVEEDEY KAFYKSFSKESDDPMAYIHFTA EGEVTFKSILFVPTSAPRGLFDE YGSKKSDYIKLYVRRVFITDDF HDMMPKYLNFVKGVVDSDDL PLNVSRETLQQHKLLKVIRKKL VRKTLDMIKKIADDKYNDTFW KEFGTNIKLGVIEDHSNRTRLA KLLRFQSSHHPTDITSLDQYVE RMKEKQDKIYFMAGSSRKEAE SSPFVERLLKKGYEVIYLTEPVD EYCIQALPEFDGKRFQNVAKEG VKFDESEKTKESREAVEKEFEP LLNWMKDKALKDKIEKAVVSQ RLTESPCALVASQYGWSGNME RIMKAQAYQTGKDISTNYYAS
5089	35457	A	5130	45	416	RWGLAMFPSLDNKSETLSQKK KKKDLCPHISFEMDLTTADAR WVQDAATRLLATTRCPPNSRG SR**ISWRAGCCPGGWAGPHW GHDGCL*PSCVSSS
5090	35458	A	5131	3	477	GRLPRHRGGEPGAAQPAGRQP RGGAAATAAGAPRAGGGAAA GNARRCREAAARDPHHGEGSG PEPSQCEGAAHQRAGRAQGD* GGSGATGEGGRRGHDSHNPLG RVRGSTLPPS**N*VGL*VPSWP QCGPAHPPGQHPALQEIHQRLP LESGGHRVV

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5091	35459	A	5132	3	446	RTGSWGWSASQQRHRKDRGL DSAGSGWVSHILPVPAPPPADA RPSASRWRRQGSHPLPGRTECP SVQPLCLPPPAGHHRNHSIASPS QTPPPRSLPGSQDKSLFLPRDRR TGEGEGHMN*APLSAPGTSCRS GGSTSWLPEILGPTQ
5092	35460	A	5133	352	588	DIFKVGGCFLFKRLRCQQRFFL LIFSSSTQSA*RVSNGPYH*EIK MAVYYGELRKNGLIQESCDNIQ PRQGSFNMDSMQ
5093	35461	C	5134	13	144	
5094	35462	A	5135	587	1078	LSQRFPLSSRIKLQRLSLQNGIP QIKELDYLFRTNSNQINFNLLSH RVRARPPAPPGRPNPSPGPDRPP EPPARAGSSRRGPGEPPRRQPQ RRFRRRGPDRPGRLSRGL*RRR ARPASPQPRQHHSRGPAGRPGV APRRPAGLAAAAERLTARGAA ASPAIPRA
5095	35463	A	5136	44	455	HLRNRTR/PSQITPHIYNHLIFDK /PLFNIWWWENWLAICRKLKLD PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP
5096	35464	A	5137	101	861	LIGYQPKMSRTRRIHSRILPERIK YLGSQLIRDVKDLLKENYKPLL NEIKEDTNKWKNIPCSWIGRISI VKMAIL/PQAICGKLKLDPFLTP YTKINSRWIKDLNVGPTTIKTLE ENLGNTIQAIGMGEDFMTKTPK AMATKAKIDKWDLIKLKSFCT AKETTIRVNRQPTEWENIFTIYP SDKGLISRIYKELNQIYKKK\TR NPIKK*VRDMNRHFSKEDIYAA HRHMKKCSSLLDIREMQIKTTM RYHLTPI
5097	35465	A	5138	3	314	LKSFCMAKETTIRVNR*PTEWE NIFAIYPSEKGLIYRIYNEATNK DLVRRSGPLKTPKKKSQLTVLN LVTFKRTPALSEEKESAQVLWQ FKKPECVLTSKRVH

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5098	35466	A	5139	1	1278	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPEMQGWVNICKSI NIIQHINRTKDKNHMIISIDAEK AFDKIQQRFMLKTLNKLGIDGT YLKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIMQEKEIKGIQLGKE EVKLSLFADDMIVYLENPIVSA RNLLKLISNFSKVSGYKINVQK SQTFLHTNNRQRESQIMSELPFT IASKRIKYLEIQLTRDVKDLFKE NYKPLLN
5099	35467	A	5140	1	430	GGVFFLRTPTDCCGMLQGAAG STGFYASEARPRGPACSLDRGS SSLLSWGLHQDPLFPAAKQHRR EAGRADQNSPRPRLSTG*QTPT L*RRPAAATGRRRAQPPRATSV SAPASPPCPRARPPHHARPPRVL ACQP*ATAPGP
5100	35468	A	5141	1	346	
5101	35469	A	5142	3	1336	
5102	35470	A	5143	5	283	
5103	35471	A	5144	1	1368	
5104	35472	B	5145	1	838	
5105	35473	A	5146	1	962	
5106	35474	A	5147	19	87	
5107	35475	A	5148	41	831	GLQNPKHQSSQLVDLKMKKSL LQCMFQYLIVLQ*YLK*YLGTQ LTRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWIGRINIVKMA ILPKDPTTAQLSPRGSTAQKGH WRPCPLPPRGVPRSPRGPTSHP HHDPCPGGAPVRNTGSERWQR KLRSGPKSDWAGRAQAPSLGE GGAKNGKSHPGSHRAFSLPRAP RRLGPGSQPGRFRGFLKQARGR AGEGHSAILLAPESPNAQVSNV TSATYRSNLSGLPRPCSVVLLG

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5108	35476	A	5149	1	2233	MKAEIKTFFETNENKDTTYQNL WDAFKAVCRGKFTALNAHKR KQERSKIDTLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QKALQKINESRSWCFEKIHKID RPLARLIKKKREKNQIDAIKND KGDITTDPTEIQTTIREYYKHLY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGSEIVAIINSL PTKNSPGPDGFTAEFYQRYKEE LRIKYLGIQLTRDVKDL\FKENY KPLLNEIK\EDTNKWKNIPCSW VGRINIVKMAILAQGNL*IYKFN AISIKLPFTFFIGL/EKNLTFKFIW \NQKRS\RIAKSILSQKNKAG\GI TLPDFQTITYKATVTKTA\WYW YQNRDIDQWNRTEPSEITPHIYT ILI\F\DKPEKNKHGGKASL\FIK W\CW\ENWLA\ICRKLKLDPFLT PYTTINSRWIKDLNLRCQIIKTL EENLDNTIQDTDIGKDFMTKTP KAMATKAKIDKWDLIKLKSFC TAKETTIRVNRQPIEREKIFAIYP SDKGLISKIYKELKQIYKKKNK QPHQKVGEGYEQILLKRRHLCS QQTHESMAHHHWPCREMQINT TMRYHLTPVRMAIIKKSGNNRC WRGCGEIGTLLHCWWDCKLV QPLWKSVWRFLRDLELEIPFDP AIPLLGIYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTM IDWIKKMWHIYTMEYYAAIKID
5109	35477	A	5150	1390	3491	DLLTRTACAVPGWGCSSRATC QARGWRLLSSPPHPSGVQPLLC HLPYPPSPFSLLSNLTPFLRAFPR SLETS*KWART/WPGAVAHAC NPSSLGGRGRWIT*GREFETNL TNMEKPCLY
5110	35478	A	5151	310	445	YLTKIWPGAVAHTCNPSTLGGR GGWIT*GQEFETSLANMVKPHL Y
5111	35479	A	5152	44	1132	PQVIHPPRAPKLLELQEPPRWIH DLNQDTPSALCQH*RTC*HRAE GVSWFKSWIHLGGSCNSSSLGA RGGWIT*GQEFETSLTNMAKPH
5112	35480	C	5153	183	323	
5113	35481	B	5154	504	2474	
5114	35482	C	5155	66	269	
5115	35483	B	5156	2414	3096	

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5116	35484	A	5157	9	239	HHHYCQHHHHHHHHHHHHH LPAPCRNLRV*PVCFRYKLWFH YGKQHLLFLDFLLSHSEWCEM VSHCGFDLHFSDD
5117	35485	A	5158	3	387	TDTKPLSCSSCPPRGKKPVSHR DQ*RRWGRRCRGEPGTEACWS AGALQF*KPRSRGGRTSKMTSG PSAEKGGG*AGRKPGRRHFGRR VLRHSCVLPVARELWGRHGPC GWRQKNVPWKWSELLPVVAP
5118	35486	A	5159	1	277	MPPPPPPSESPGPGPVGSRLPPG PAVTGNEKELRGNP*VGLAPPR PRFRASRREGVTGKVHRPNRLQ LRAPPKG*SDQRGQNVPPSEAK SLC
5119	35487	A	5160	1	3285	
5120	35488	A	5161	3	194	IPLSLQSKEVGQQLQDDLMKVL NELYSVNQMGCLAL*QAEGSSI WQLAAIVHQQQN*TPSWGQ
5121	35489	A	5162	520	844	VQAPGKCHAQMPAPAAPVPLG RSRNPGRLASAVPVSSLLRFLPF LQPIPPSDILPLSFEAVPSSPAAE SGLHPCTRRRKRARPSC*VPGL LLSPQPHPPPHVWRKGIL
5122	35490	A	5163	1	794	FRGFLDRGDCAALPCTYPHSPC SH*GGNCLPSLLTRPCVKA*PQ MSGRKSSMRRWRRQSRLTAGT SS*TPTSSTMC*ALVGSSTWNC MLQAGSTAPGAGTPGSRPTWS SSSTCSWTAPSGRARCACASSS SCAMSAARRGWTSPACWRRTS RAWWTTSSPACASSATASVAA STASTWPAARTTGGTAESSARP ARRASCTGSPARSCWRRRRPPT PSPGRPAPPSRRTRRAQAGTSA LSPGACFGPRSCC*SSTCSSLSV APY
5123	35491	A	5164	3	57	RIGQGVPVVHS*VEGGPNVISIV LEYLRDTPPVPVVVCDGSGRAS DILAFGHKYSEEGG*VKVFLWC THKWKEDPM
5124	35492	A	5165	1	1326	
5125	35493	A	5166	2	337	YSVTMTPGKLRTLCEIDWPALE VGWSSEGSLDRSLV*KVLCPEL VPSGGFLVSLTSRMKPQTLTGS VKVLKDGMSGVCSFRCSDVSR VSSFWWVRGLAGWSTTLLRKL
5126	35494	C	5167	339	548	

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5127	35495	A	5168	3	413	SQAFLPAASRRERPPEPVDPKA TDPRSGTRRLPPRLPCQWTTPE HSHTSQLNLSRAFPKEPNPAAT Q*NPSGASPRERPHARAQEDRN GEC*EGNGSRPDLEEEASTPRA SPTPSD*PLWLHPPRPLVLETPL LQL
5128	35496	A	5169	3	479	FLHSTHIYWAHSMHELLKTAV VSISGQCTSLNTESGIWGGVPE NAR/CPPAEGTVPASLQPRDPPR LPGSH/ASLPSASPPSRHVTWPP EP/EAAGPKPS*IRCRWPPAGAT TKANPKESGRLVESMLPLPKSR SAPVTFSAFACSGLPERVHEVF RVGKLR
5129	35497	A	5170	81	329	QSVSSPSWFPQFPVQVQKVPCY QVYRGDLVV*KHVAPPPSLPSS FSGHVRHDCFPFAFHDDRKFPE ASPAMLPVSSLGPHYL
5130	35498	A	5171	335	467	MPSTPTARKPESPEALARVESIA CLPSPAP\PHECSPQASEETG
5131	35499	A	5172	1	2424	
5132	35500	A	5173	2	304	CLTKNTSATREKQVTELHRRSK LQPEPAKTKALQTVIE*KDITLC *VKEHLYIVACWALRLHLVFLP TKAGISPALMKVSYPGKPLTLK QLGRLVILQEQ
5133	35501	A	5174	44	286	GVQNGVEELILVRRMQKSPGP GEMESGSLEKEPLGTQTGPVPS EGTE*TQGPPRTPSLQTQGPQRT PSLQTQGPPNTPSL*TQGPLRTL SLQTQGPPNTPSLQTQGPPRTPS LQTQGPQRTPSLQTQGPPNTPS
5134	35502	A	5175	206	384	KRVFAHQADGRARSGFISSAGP GSQAGPGQGTG*QREDVEAAG QPGSTAEGVRT*SDPG
5135	35503	A	5176	270	818	RNERKPSQRTAVGLGAGQLQP GQPGVQSEEPGPLEAGCAAGV LPGPAEQDREGIYSK*KRVFAH QADGRARSGFISSAGPGSQAGP GQGTG*QREDVEAAGQPGSTA EGVRT*SDPGSSHPAAAAFYEN IQDGEALGRCGAKRTATAAP*Q RG*EGF*AGPTAAEKNEEGPPP VFSLFNSHL
5136	35504	A	5177	122	436	LTSLFSAISTKAKVSPLCSARAC SPSPAARAALGSPGFTC*GAGV APTPVPVAAPAPATAPATAVAA AATTTVVSAAMFTRRATRAAA ATGAWGFVAGAPWPLQT

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5137	35505	A	5178	20	1341	MRRCVAAPLAHRW*QKLGLPG CTPTVCSFLSPQPPPRARSSSAT LSSGAPRRAATPQPQTTPPSSVQ PCAATPCARGGRPAPAGVTWP TTRPSMA*RTS*ASTTAPRMAP PRSHACARSHRPETARSARTAP RSAITRRAFTSTRPPPTTRTVAS SGTHTSGLSPTASRLARCRAPG RSSTIIT*TCRSPTRLCCPAQRPL PPASSPSSSRTSRSVWTRRCTRL RWTSSRPPSWMALRTVGTSTGP TA*RSLRRCQASTWRSRPSTSA PPSWCARWAAT*PLPSACQRK WSMLWRTGTARVSTSACGAAP STSRSTSRPSTPMLRAPVPAGW QPPALHPQPPRPSHTRQPWPSA RRSCRWRTCTTRPASSTSSPRA T*TSHWPPTTRWRMSRCSTPTK TNCTCMRGLGTCQAGRLRGCP WPPGPSWAPWSRSWPCSLCSA
5138	35506	A	5179	47	598	ASGPASIVVLRQQFIKFFLDEICS LEERVWCRKLCLLYILWKEPR AVQAKSRCSDIRRELYRPVSLA GLSGDFLRAGRYSAHTVNGAW SAWTSWSQWA**SRGLLLALH NMLKIIIAFCSLQVATRIQSTFIS SWHLSPSLLGSRSFSLYMSFGS VLCPLFISHDTSSYSTKSFQSFSC LGVW
5139	35507	A	5180	236	690	LQNWSYLAEQCWNGGFIYLIM LRRFKHKAHSTYNGNSSNSSEP GETPTL*LGDRTAKKGKRTRKF GVISRPPANKAPEESKGSAGCE VSSDPSTELENGPDPELGNGHV FQLENGPDSLKEVAGPHLERSE VDRGTEHRIPKTDAPLTTSN
5140	35508	A	5181	2	480	WPFWAMVQRPSSAILCGPATLP PNCRGACCARCRATGALSAYP AIHRPATRPPAPPAPGPLTSPPPL SVQNSNPDPLPSARPSPGPAAPR HARHSPSELPALTLSARGSSAL CTKLKVEAAA*SCSASAWNWR LLPRNHVDSRCQPEPDGARARD GRGP
5141	35509	A	5182	3	153	
5142	35510	A	5183	3	239	
5143	35511	A	5184	1	394	
5144	35512	A	5185	1	435	
5145	35513	B	5186	84	2068	

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5146	35514	A	5187	149	832	DAGLSWREATRPGAPLHRPGC QDASTQMTRPGDPGSSALFPLP SP*PEREELPMSSRRSPKPELPG EACSRRPPTRPRPRTATRGPPLN GRLPRARLPVSAGAGALGGGR CRRRVAPRRVTPRLATRPSGVA PRGSG*AATTKLSLAFGVTPLA LTPWSRTPFRKREERPPF*YPRP ATPEASPAHVENFRSNQTRYTS AE*SGQQLERPSIAEISAQATVE PRSTI
5147	35515	A	5188	45	312	AEAQGGAEAEGHGGGGGPAPS QGCPARAAGARGWQPAPSPQK P\TPSDTTPPP\RTQPPVTQPCHP VTQPPVTQPPVTQPRHPMKIPPP G
5148	35516	A	5189	15	549	PRHKEPESQAPGRRAPQAAAY QQAASPAR*QGGSCSRCPPG*A VEAAPAP*GQALGCVSQGPA*V GPTRSPHPTAGLSRPHGPPSVRS TGWSPSSRPLQAQEAPWPVAPT HIPPPLDPGQPHSCGLGAGCQP RAPAARAGHP*EGAGPPPPPWP SASAPPCASAQPVLWLRFPRET KT
5149	35517	A	5190	1	2445	
5150	35518	A	5191	1	708	FSEGRNRFLNVGPTRFSTSRQTL MWIPDSFFSSLLSGRISTLRDET GAIFIDRDPAAFAPILNFLRTKE LDLRGVSINVLRHEAEFYGITPL EKIKMEYCFSVCMYS*QVCFE MFLVRRLLLCEELERSSCGSVL FHGYLPPPGIPSRKINNTVRSAD SRNGLNSTEGEARGNGTQPVLS GTGEETVRLANTIDSKYVAND DWLIFQYVDEEDLMNAIKDFSS VTKERTTFTDTHL
5151	35519	A	5192	31	330	YGGTATVQRWAESRHVPFPPS QEQNANKICSVCQEEKDSADSY GEIPWWQGPERCWPVRLMLAT LGDYKWVLTGIGTDS*LGFTIPT DHANAFSAKEIPQ

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5152	35520	A	5193	1	734	MISEVIVIQMLFLHAFSKVFSAL IKNNKKPLQDAQIKWKAISGLS GGMRRSECNRERDQVTRTQCR DISQK\RGPGD*GMATSKNGAM A*QLGPGCQGDASTGNAEFGES AHAWSGGGRVPGVTGPDREEV GRSWQGTSCGGGTSGCGRLQ* DGVASRGRW/DPARPREQRAG VRQLAAPLGGP*SRRPWEPPGG SSCGRYLFAISSWSGVTVAQEG QRKRGSGK*RTERSGPGLGRRL PPLLLTV
5153	35521	A	5194	3	449	EGQRSSSPATALSSSGPPSLKM ATSKNGAMA*QLGPGCQGDAS TGNAEFGESAHAWSGGGRVPG VTGPDREEVGRSWQGTSCGGG TSGCGRLQ*DGVASRGRWDRR DRASSGRESGSWLHHSGARSLG APGSRPVEAPAAGSEAKTPG
5154	35522	A	5195	606	841	CTVGFALPVFY*GFSH*CSSGIL V*NSRFLLCLCQALVSG*CWPH KMS*GGFPLLLLTGIVSEGMVP ASLCISGRIQL
5155	35523	A	5196	620	930	IPFISFSCLIALARTSNTMLNRSG ERGHPCLVPVFKGNASSFCPFS MILAVGLS*IALIILKYVPSIPNL LRVFSMKGC*ILSKAFSASIEIIM WFLSLALFI
5156	35524	C	5197	1	819	
5157	35525	A	5198	591	815	
5158	35526	A	5199	187	387	FFKTICFMRVRVKRPPNRLCVS NMAVYFTWVQAGLHCESYPEH L*WSCRLPRRLGGVRL*PLEGE
5159	35527	A	5200	1	1197	
5160	35528	A	5201	119	375	ILDISPLSDE*IAKIFSHSVGCLFT LMVVSLAVQKLFSLIISHLSILA FVAIAFGVLDVK/CLVHAYVLN GIA*VFF*GFYGFRSNI
5161	35529	B	5202	1	1053	
5162	35530	A	5203	2	157	
5163	35531	A	5204	12	176	
5164	35532	A	5205	2	223	QTVLEDRSPRARWIF*G**GTIC SIPIPSFWWFSSNLSHSFVCRSPP SSSPGGLPMCTCVSKFPWAVW PFSRY
5165	35533	A	5206	61	308	

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5166	35534	A	5207	487	898	DFAEVAYQLGISSGVCRTTDFH EPRMLLSDRSSGSFVTII\SVFLS FSSLKCL*SPLVHDALHQAFHP GKSRLRFLGSMACCMSKFTCPP TLSTVPSSTPFSFSCSLIKTRSAT LLKLWSISLRFRLHSWSSAFRV
5167	35535	A	5208	9	191	IPQHIYPPKTKPGRI*ISE*TNNR L*NCGNDQ*LINQKESRTRWIH SRILPKTNREPNHE
5168	35536	A	5209	1	1989	
5169	35537	B	5210	1	1488	
5170	35538	A	5211	929	1209	IPFISFSCPIALARTSNTMLNRIC ERGHPCLVPVFKGNASSFCPFS MILAVGLS*IALIILRYVPSILNL FRVFSMKGC*TLSKAFSVSIEII
5171	35539	A	5212	242	642	FSLKRSFTSLVSWIPRYFILFEAI VNGSSLMIWLSVCLLLMYRNA CDFFPLILYPETLLKLLISSSSLY LW*NSAVNLSGPGLFLVGRLLII ASISEPAIGLFRDSPSSWFSLGR VYVSRNLSISSRFSSLFV
5172	35540	A	5213	747	885	
5173	35541	B	5214	115	1267	
5174	35542	A	5215	209	322	
5175	35543	B	5216	1	3321	
5176	35544	A	5217	390	655	CLFPVHYPRLHAMMHQMKNP VLVLGIGGFILGILGVIGGPVSLF KGS*KLLGLIETGKISLDHPVPG GTPTKMALYEHFMNTKEFGIE
5177	35545	A	5218	3	221	
5178	35546	A	5219	798	914	FVFLWDRW*YPLYHFLLCLFDS SLFFSLLVLLAVYQFC
5179	35547	A	5220	12	460	YLCMLHEVLVLCFSVPSGHFSF SLN*LF*LAVPVTFYQG\LSFLA QA*ASQVDFRQLCWQQEFQAS GS*LAGLHGSGIH*ARPLGSWL QLPFQESEWFCLSGVPGATVVS /CTF**SPF*LV*DGISLWF*FAFL *WPVMMSIFFMCLLAA
5180	35548	A	5221	3	508	AERNGSRQGVGAGAGDHEVLQ LLPDKWKQKILCPVQLLRGAW SNYYSPDANRQP*VQGNAHLF AECWPHGEDSQPTVPTSQGRM LAGPARHLPHPHVPSPSGSLRG SDSEDTH*GTVAGSGCLHCLAP GHLHPGWPPSRVLPIPDRSVHQ GPGRKAPPTPPRVTPLFT

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5181	35549	A	5222	584	1052	LRKAAASGSFVFVAPDPNTDTG SSQCSESESGSRGCSMGHQRSL QHHYHHHHHHHHQHHHHHHH HLDTGWRGE*SRHSAGLCPPSQ RRLHSCQTSPSCSPPSGHRCI*LT GIEAA*CHSL*PYQKDACHHFE EHSPPP*RPPHLPRHHLHPQPSS
5182	35550	A	5223	1614	2308	LRKAAASGSFVFVAPDPNTDTG SSQCSESESGSRGCSMGHQRSL QHHYHHHHHHHHQHHHHHHH HLDTGWRGE*SRHSAGLCPPSQ RRLHSCQTSPSCSPPSGHRCI*LT GIEAA*/WS*PLTLSKRCVSPLR RAQSSSVTSSTSAQASSAPPEKK *L*PERPYSSPHPASVADLQMC LPLNRITGQTNRPLHRAILLRW MRSCNLLTCTVLSNVSFSFSELS YSRNTMCRG
5183	35551	A	5224	3	407	SVGLILPSSLQHHYHHHHHHHH QHHHHHHHHLHQRKLAPPLC* ADLPTCAPHQGIRPFGGFPQTS GSPGLPVYAEEQGTERLSLQGT GCGCQAGLLCWGPPVASTSVG FSLESSVSPEQVPLSPGPAGTDA
5184	35552	A	5225	1	1287	
5185	35553	A	5226	3	1315	STMALLHSGRVLPGIAAAFHPG LAAAASARASSWWTHVEMGPP DPILGVTEAFKRDTNSKKMNLG VGAYRDDNGKPYVLPSVRKAE AQIAAKNLDKEYLPIGGLAEFC KASAELALGENSEVLKSGRFVT VQTISGTGALRIGASFLQRFFKF SRDVFLPKPTWGNHTPIFRDAG MQLQGYRYYDPKTCGFDFTGA VEDISKIPEQSVLLLHACAHNPT GVDPRPEQWKEIATVVKKRNL FAFFDMAYQGFASGDGDKDA WAVRHFIEQGINVCLCQSYAK NMGLYGERVGAFTMVCKDAD EAKRVESQLKILIRPMYSNPPLN GARIAAAILNTPDLRKQWLQEV KGMADRI\IGHAGLQLVSNLQG REG\STH\NWATHSPTKLGMFC FHRG*KLEQVERLIKEFSIYMTK DGRISVAGVTSSNVGYLAHAIH
5186	35554	B	5227	57	386	
5187	35555	A	5228	1485	1883	
5188	35556	B	5229	117	641	
5189	35557	C	5230	1	552	
5190	35558	B	5231	250	378	

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5191	35559	A	5232	3	1117	TPDPGQGCSEGGIVHETRPSPQP LCQGSCAVGCSPLGLLR*RMM ALGKIPPGHRGPAFLPAVESAH VVPGLPGLTRETLPAPLGPHRPP QPPQGPLSTAPPAPLVSPLGPHV PGLPGPPPGCPSPLPLRPCPPPS WLRPHRPVQPWWGT*GSGWRP RCRPGAAGRNPGLPRACCRGL CRGPH*RPGGPRPGHSGPRTSS WGRTMGNRPRPSASAG**PRHR R*TSAERPGSPPQQSASRTGGRS PLSHPGSWWGVMGPPGLWAG APSMWG*GPGSRVAGGSGRRP TSPRPPHYPPHPPGTWPSGAQS GRR*QAQTPGAATEG*GGWGL PPKPWCPQDQFLGVQDWVLPP NGARVGGTWAWKRESVLVPG
5192	35560	C	5233	229	522	
5193	35561	A	5234	1	972	MTAEYYKLKQVVTPIAAAVPD VVSLLEQINISLCTWYAVIDLG NACFYIPVHKAHQKQFAISRHG QQYTFTVLLQ/RRDLDLFSLPQ DITL\VHYVDGIMLIGSSEQEVA STLDLLVRHLHARGWEINLTKI QGLATSVKFLGVQWYGACRDI PSKVKDKLLHLAPPTTKKEAQH LAASFEWGPEQKGLQQVQVAV QAALPLGLYDPADPMVLEVSV ADRDAVWSLWQAPIGESQWRP LGFQNKALPSADNYSPFERQLL ACYWALVETEATPVITQRAHE QSGHGGRDGGYAWAQQHGLP LNKADLAVATAKCPISQQQRPI
5194	35562	A	5235	3	246	
5195	35563	A	5236	3	841	
5196	35564	A	5237	1	746	RDLDLFSLPQDITL\VHYVDGIM LIGSSEQEVASTLDLLVRHLHA RGWEINLTKIQGLATSVKFLGV QWYGACRDIPSKVKDKLLHLA PPTTKKEAQHLAASFEWGPEQ KGLQQVQVAVQAALPLGLYDP ADPMVLEVSVADRDAVWSLW QAPIGESQWRPLGFQNKALPSA DNYSPFERQLLACYWALVETE ATPVITQRAHEQSGHGGRDGG YAWAQQHGLPLNKADLAVAT AKCPISQQQRPILSS
5197	35565	A	5238	1	483	
5198	35566	A	5239	1	1908	
5199	35567	B	5240	1	2718	

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5200	35568	A	5241	522	693	LDFFLVFLQQFLPRPSSSEI*MLP GFPAAAYGPVAAAAVAAARGS GRKVYGTGDSQA
5201	35569	A	5242	1	225	MGRNQSRKAENSKHESTYSPP KDHSSSQAMEQSWTENGFEKL GFRRKEALYYLDLTASCQSQEL FQKWVSLCCPD*S*TYSPPKDH SSSQAMEQSWTENGFEKLGFR RKEALYYLDLTASCQSQELFQK WVSLCCPD
5202	35570	A	5243	1	1129	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDRNRERHTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSVMAETAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYK\SL CQYRAFVNGGGEEKARGKPIL CRYGVGM

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5203	35571	A	5244	1	1753	MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELHDEQMAALYRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISHLHIHAEDTFLPFY LGKKDDVTYAIKPTCWPGLDII PSCLALHGIEIELMGKFDEGKLP TDPHLMLGLAIETVAHDYDVIV IDSAPNLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDIKGFEPDVRILLTKYSNS NGSQSPWMEEQIRDAWGSMVL KNVVRETDEVGKAVINHKKGK NSPRMVQSNDLTKAAYSLSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSLAGKEVVFYRPE EDAGDEKGYESFPWFIKQSEE/P QSGNFYTDTLGMAEFRRGGLR ATAGPRLSRTRDCQGTEKVHG KTVFDKTVP/WVPKRLKSPSCK NRWP*KMQKLSVCTASSPGQQ LSTVRVTQREICFPVVRREVLLL IGTLTQTRKGQISVRA
5204	35572	A	5245	337	1977	

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5205	35573	A	5246	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIG\LQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCLALHRIETEL MGKFDEGKLPTDPHLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK
5206	35574	A	5247	1	1383	
5207	35575	A	5248	1	1731	
5208	35576	B	5249	1	1290	
5209	35577	B	5250	1	3345	
5210	35578	A	5251	1	1959	
5211	35579	A	5252	3	2356	
5212	35580	B	5253	334	1710	

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5213	35581	A	5254	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPV NVSKSDDTLKINGVEDHKTIFD GDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSAKK RDAELANGALGIIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPLYESLCQYS
5214	35582	B	5255	1	1452	
5215	35583	A	5256	1	1323	
5216	35584	A	5257	1	1557	
5217	35585	A	5258	1	2259	
5218	35586	A	5259	1	2418	
5219	35587	A	5260	1	1218	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKERNQNISRYISNRLAR RECHDSPEEGTGNTRSKERLQG RLPSRGLTESQEHLLDTRKQFW FEDFKDGLGPILKCDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLSAS NYQRMPDFRRRFLQV\CVMEIN KQTSMRLSYI
5220	35588	A	5261	1	2028	
5221	35589	B	5262	1	1653	
5222	35590	A	5263	1	1446	
5223	35591	A	5264	1	1788	
5224	35592	A	5265	22	1893	

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5225	35593	A	5266	1	2144	MEKKITGYTTVDISQWHRKEHF EAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARL MNAHPEFRMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYYTQGDKVLMP LAIQFFDMLRDLLKNVDLKGFE PDVRILLTKYSNSNGSQSPWME EQIRDAWGSMVLKNVVRETDE VGKDTGVRSKISGVIKMPMGV AVVNCCTYGSDYRVWLASWM MSQWLHYPEWYRKENKHKFY PAFIHILARLMNAHPEFRMAMK DGELVIWDSVHPCYTVFHEQTE TFSSLWSEYHDDFRQFLHIYSQ DVACYGENLAYFPKGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYYTQGDKVLMP LAIQFFDMLRDLLKNVDLKGFE PDVRILLTKYSNSNGSQSPWME EQIRDAWGSMVLKNVVRETDE VGKGQIRMGTELEFFRLSETKEI TNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRM PDFRRRFLQCDNLKTCHTSHGS VMAETAVINHMKRKNSPRIVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASMDIQHAL KSFSGKEVVFYRPEEDAGDEK/ GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFLLSE
5226	35594	A	5267	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYNV VFALAGSPEDADDTSIYMFYQK CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRK\PDGSGIVSLK/ID WIIKRSQLPQSAFYQPFMGLRR ESFYFRWERRTLGPLKSFSVKR GTEAGKFRLAALLVRL
5227	35595	A	5268	1	1395	

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5228	35596	A	5269	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KIRRKNGPVSATFTSDGKIRLFY TDYSGKHYGKQSLTTAQCDNL KTCHTSHGSVMAETAVINHKK RKNSPRIVQSNDLTEAAYSLSR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSL/KIDW/IIE/ RYQLPKVPSPEARKITRRWRI\V KQRI*LGFLLRLSEMPRKQGDY RTRIWKFEDGLSNVLVIQLNKLI ICVMCLVRDCDVLKTYFHR
5229	35597	B	5270	1	1668	
5230	35598	A	5271	1458	2675	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRSQNDF*RR GI
5231	35599	B	5272	1	1317	
5232	35600	A	5273	1	987	
5233	35601	A	5274	1	571	
5234	35602	A	5275	1	4161	
5235	35603	A	5276	1	1228	
5236	35604	A	5277	387	3466	
5237	35605	A	5278	1	6721	
5238	35606	A	5279	1	1651	
5239	35607	A	5280	5082	5879	
5240	35608	A	5281	1	231	NHLAVRRLTELSGGQRQRAFL AMVLAQNTPVVLLDEPTTYLDI NHQVDLMRLMGELRTQGKTV VD*VRDLNQVSRYC
5241	35609	A	5282	1	303	CLRILCPYPYIPLTEKTLA*PAL YTLELTADMAETCKQFLPEFSL TFSFQRGWEKETEYAEVLERNF ERDRQLTYTAHGPHKADLRIQE SGVPYNEILVTL

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5242	35610	A	5283	1	273	TNSSVGPGDRLL*QTAAPHRGK LKVFFGACAGVGKTWAMLAE AQRLRAQGLDIVVGVVETHGR KDTAAMLEGLAVLPLKRQAYR GRHISEF
5243	35611	A	5284	66	1200	HILPAGHPTLRHSLFPHQQGRSS VQSALGAASGNGLKLVGRFEW GPSRRARSGYPDATGYDQ\PKPI SAAVKEFFGSSQLSQFMDQNNP LSEITHKRRISALGPGGLTRERA GFEVRDVHPTHYGRVCPIETPE GPNIGLINSLSVYAQTNEYGFLE TPYRKVTDGVVTDEIHYLSAIE EGNYVIAQANSNLDEEGHFVE DLVTCRSKGESSLFSRDQVDY MDVSTQQVVSVGASLIPFLEHD DANRALMGANMQRQAVPTLR ADKPLVGTGMERAVAVDSGVS GGVVQYVDASRIGIKVTKTRCI RVKQVSTSTTLPLFLMESNPLF WMAVLVSAGILGQWPIGRLAD KFGRLLVLRVQVFVVILGSIAM
5244	35612	B	5285	1	862	
5245	35613	A	5286	1	579	DPRD*RLKVAK*MVTLFGPQFV RELQQRGFDIFLDLKFHDIPNTA AHAVAAAADLGVWMVNVHAS GGARMMTAAREALVPFRPDAP LLIAVPV*RSIKASDLVDLGMTL SPADYAERLAALTQKCGLDGV VCSAQEAVRFKQVFGQEFKLV TPGIRPQGSEAGDQRRIMTPEQ ALSAGVEYMENGRPGTQSVK
5246	35614	A	5287	484	978	GIVRIPHRLADIKCWRAVLYNY THYSYQANLCCANLE*ADLSGS VLDCANLQGVKMLCSNAEGAS LKLCNFEDPSGLKANLEGANLK GVDMEGSQMTGINLRVATLKN AKLKNCNLRGATLAGTDLENC DLSGCDLQEANLRGSNVKGAIF EEMLTPLHMSQSVR
5247	35615	A	5288	3	504	YRLSQSSSKSLVSRSWLNMRFIS SVMFMEPTSSSENRFTSPSCSE MSSSEATLRSFFLGTTSPCRSM VGLQLVKSSQSSSVSSFSSHVRL SQSSSKSKVSRLAGT*EGSEKRS FREEKVPCLRLGLPESTLYAHC SV*SRTHVFSGTSHHSSKVAVG MSIVQMRKL

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5248	35616	A	5289	2	442	HVIWHMPRKTSKCRQLLCSGA SRNADTAARQSTCSSHRPPGKIP SLGPRRVPGCSSVPSSRGEQSTG SPAAPRCGDVTHTEASQEEQP* LRGTHGPASTPEQGTAKAKVR DRRAVVHPGKTGIPSAAG*KGR GRPGEPPGAAVQVE
5249	35617	A	5290	151	1185	YVDQVTHITESPLPSVSYSFAFG SLISAVDPVATIAIFNALHVEED TEKGHVRLTPASPSTFFFFFSTE EKYAPGSCCRKAAVL*LLHISH QLSLDSPSLTVVIYVLKHIDLRK TPSCRHCEI*VGDHTAVLSVLFS PSLGIMAILFSGIVMSHYTPREA SP*SCCLFTVSSHTVCCHPGLRG AIPYALSLHLDLEPMEKRQLIGT TTIVIVLFTILLLGGSTMPLIRLM GLPGGAPRWCQLVAVGPPFLP AQGNTVESEHLSELTEEEYEAH YIRRQDQLSLFN*N*SCLWPSPC LPPPP*TPHTKHPVASPPFHGPA PDALTAWLCLSTQDLHHGRIQ MKTLT
5250	35618	A	5291	5	198	VCGRQQSLEAGL*GAATPFAVF PRPWSAVRVKEYGYTRLHILN GTHIHIQQVSDDQAFAQCHPP
5251	35619	A	5292	137	308	HLERTGPNLPPGARLATRPTTR LPAASPRGRDT\PLPIPISFYSETE AKGEAPYIEPE
5252	35620	A	5293	612	1078	RPPEKKERGRRVRGRRGGGGK RRRRKRKKRKGSKGREDAAAA AAAAQSPRTRAPAPD*ERRPQP APSARAPPRPLLPAPRRSRPAQV PPDSASPWAAAAGLALPPPQCP GGGARPLRLLPQPPAPGGTAR WEPRRPRPAAAPGLLQSPGPLP RQS
5253	35621	A	5294	515	817	LALPHLPSNLLLKGWLKLKA*S RPSRTPSFG*LSQWKHALKRLK PVITCLLQHGFLKPINSPYNSLIL PVLKPDKPYKLVQDLRLINQIV LPIHPMVSQA
5254	35622	A	5295	1	951	
5255	35623	A	5296	1	1077	
5256	35624	B	5297	87	1423	
5257	35625	A	5298	29	234	
5258	35626	B	5299	77	327	
5259	35627	B	5300	1	235	
5260	35628	A	5301	2	2144	
5261	35629	A	5302	1	855	
5262	35630	A	5303	845	1057	

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5263	35631	A	5304	1	933	
5264	35632	A	5305	1	954	
5265	35633	A	5306	1	1603	MEAEKFHQMPSVSRRTRKASG VIQSKSENLRTRGANSHALKRL KPVITRLLQHGLLKPINSPYNSPI LPVLKPDKPYKRFLAFYGWSPR SLIVDSCSKLEQHSTLSRVILVIY KGFCRFRNHHQTGFSPAGANQ RGPLAATLSGPGGEGQSAVACL TGEKKNHPGAQYANRLSPRVG RFINAAGTTGFPTGKRAVSATQ LMDFADFGTTITQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQSSQLS SLRLTLPDRLRSPLDHHGRRAS GNSHSGSPKPPSCLPLISPHLNP QVWDISTPSLATDHMPITIPLKS N\TLTPLNLKCQYPIPQHALKRL KPVITRVLQHGVLKPTNSPYNS PILPVLKPDKPYKLVQDLRLINH IVLLPIHPMVPNPYTLLSSIPPSTI HYSVLDLKHAFFTIPFHPSSQPL LAFTW\TDPDIHQAQQIT\WAVL P\QRFPRTGPHYFNQAQISSSSV TYLGIILIKTYVLSLPIVSD
5266	35634	B	5307	1	874	
5267	35635	A	5308	144	539	
5268	35636	A	5309	1165	1639	PHPAVASRRGRAGPGGLSAPER TPSSELSPLSKGDLRKTHRTFSP Q*GDLRKTHRTFSTR*GDLRKT HRTFCTR*GDLRKTHRTFSTR* GDLRKTHRTFSTR*GDLRKTHR TFSTR*GDLRKTHRTFSTR*GDL RKTHRTFCTR*GDLQKTHRTFS TR*GDLRKTHRTFSTR*GDLRK THRTFSTR*GDLRKTHRTFCTR* GDLRKTHRTFSTR*GDLRKTHR TFCTR*GDLRKTHRNFSTR*GD LRKTHRTFSTR*GDLRKTHRTF CTR*GDLQKTHRTFSTR
5269	35637	A	5310	235	453	SHWPWLCSSTSCSSQRSIVSSG MARGPFLRKRDLLFPPPPPGSH GLELLEIIFHQGISQVHHLLHLQ VWL*NLNVPDSSLPAENEATGP GFVPPPLAPVRGPLFPV\D\ARGP FLRKRDLLFPPPPPG\AM\FGASR DYFPPGDFPGPPPAPFASMAFL N

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5270	35638	A	5311	2	2333	TGRGYCGDHESSFGAMEEPGA TPQPYLGLLLEELRRVVAALPE GMRPDSNLYGFPWELVICAAV VGFFAVLFFLWRSFRSVRSRLY VGREKKLALMLSGLIEEKSKLL EKFSLVQKEYEGYEVESSLKDA SFEKEATEAQSLEATCEKLNRS NSELEDEILCLEKELKEEKSKHS EQDELMADISKRIQSLEDESKSL KSQVAEAKMTFQIFQMNEERL KIAIKDALNENSQLQESQKQLL QEAEVWKEQVSELNKQKVTFE DSKVHAEQVLNDKESHIKTLTE RLLKMKDWAAMLGEDITDDD NLELEMNSESENGAYLDNPPK GALKKLIHAAKLNASLKTLEGE RNQIYIQLSEVDKTKEELTEHIK NLQTQQASLQSENTHFENENQ KLQQKLKVMTELYQENEMKL HRKLTVEENYRLEKEEKLSKV DEKISHATEELETYRKRAKDLE EELERTIHSYQGQIISHEKKAHD NWLAARNAERNLNDLRKENA HNRQKLTETELKFELLEKDPYA LDVPNTAFGRGSRGPGNPLDH QITNERGESSCDRLTDPHRAPS DTGSLSPPWDQDRRMMFPPPG QSYPDSALPPQRQDRFCSNSGR LSGPAELRSFNMPSLDKMDGS MPSEMESSRNDTKDDLGNLNV PDSSFP\AKKEATGPGFVPPPLA PVRGPLFPVDARGPFLRRGPPFP

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5271	35639	A	5312	141	2788	GLRVPLSPSSPRSRLRSGPLRLP GADSGSGPKAVCSPPFIVAPTG RGYCGDHESSFGAMEEPGATP QPYLGLLLEELRRVVAALPEG MRPDSNLYGFPWELVICAAVV GFFAVLFFLWRSFRSVRSRLYV GREKKLALMLSGLIEEKSKLLE KFSLVQKEYEGYEVESSLKDAS FEKEATEAQSLEATCEKLNRSN SELEDEILCLEKELKEEKSKHSE QDELMADISKRIQSLEDESKSL KSQVAEAKMTFQIFPMNEERLK IAIKDALNENSQLQESQKQLLQ EAEVWKEQVSELNKQKVTFED SKVHAEQVLNDKESHIKTLTER LLKMKDWAAMLGEDITDDDN LELEMNSESENGAYLDNPPKG ALKKLIHAAKLNASLKTLEGER NQIYIQLSEVDKTKEELTEHIKN LQTEQASLQSENTHFENENQKL QQKLKVMTELYQENEMKLHR KLTVEENYRLEKEEKLSKVDEK ISHATEELETYRKRAKDLEEEL ERTIHSYQGQIISHEKKAHDNW LAARNAERNLNDLRKENAHNR QKLTETELKFELLEKDPYALDV PNTAFGREHSPYGPSPLGWPSS ETRAFLSPPTLLEGPLTLSPLLP GGGGRGSRGPGNPLDHQITNER GESSCDRLTDPHRALSDTGFLS PPWDQDRRMMFPPPGQSYPDS ALPPQRQDRFCSNSGRLSGPAE
5272	35640	A	5313	217	447	FQRMSGL*GYSPPLGGQPAL*E CQGAADSAGG\RGLDSERSLGR \PAASGPNTALGWQAQPWS*Q AGPELPRAEFLQA
5273	35641	A	5314	3	287	TLRNRHRELRTCLSGPGLGLPT QVSVVAGGCCVCPSSSQSPVPR PPALSAAPWHSHRAGCPPSGGL *PQRPLILWNQPLSNTLLEKELA PPPAH
5274	35642	A	5315	3	468	ALARSPAG*PQSPDGDLCFRHR KGERRPAAPAGQCPAGRQRHV PAAGRDGKPGRAPGADR*AGPI LHLYHLPAPCGGGTPGDSNPRR APAQRSE*CTPPPPQ*RNNRKPS TRAGLLLPS*HVQLSGGLTLCP GDRVS*WPQGVLAAPGPGPCT HL
5275	35643	B	5316	64	288	

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5276	35644	A	5317	73	265	NGRTSRCFSPGKH*EYCSGTFH PLQVVGKIYSNLDKIL*ASRAR WGLCSRKPGYWSCTQPPTSS
5277	35645	A	5318	125	461	
5278	35646	A	5319	298	593	LGVEVEPVTGGDAVIGASHDAF LQVNIESIVPEHSTRCKLLGKFI RIWIKYFRHLVHGGGSAPVSLV TGPVHGDSLLGPVAPEPPRVVE PARQVRAHAVVVAGPLRRGRG LGRHRLRARSG*GMPQSVRGA CGAQGHGPAGEDQRLLPRERG PAGQVQQPGVVPGLQDPEGCL RVQDQ*PGLREQSPHRARDA*S ILSKFE*IFPTTCSGWNVPEQYS QCLPGEKHRDWPR*LHHLL*PA QLPPPVTTSTGHPSAIEGLETPL RSPLTPGPPGKSIIPHHPQSPDCD GTDCAAFPENIIRLRSRKICKRG
5279	35647	A	5320	1124	1835	HSLHFPKFPSFLFLTLITLGLLM AVPPGLITTHQQRQAML*YKPL ARLLEPLISFPSWKSILKEITSQC SICYSTTPQRLFRPPPFPTHQTR GFAPPR/HWQIDITHMPQVRKL KYLLVLVDTGSKKATVVISSLL SDIIPRFGLPTSIQSDNGPAFISQI TQAISLALGIQRTHGLLKTHLT NLSHQLKKDWTILLPLSLLRIQ ACPRNATGLHSDG/VGPKLLPG SPFQLHHTWDSP
5280	35648	A	5321	1	1758	
5281	35649	A	5322	1	1967	
5282	35650	A	5323	76	1908	

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5283	35651	A	5324	524	2144	QSDLSASQHGLFPLATEVRSSG AASCPDSDSICPAPTIAPGRATP PQANCWASEGTLRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLFSNLQGP RSRPVAFLSKQLDLTVLGWPSC LRAAAAAALIVLEALKITNYAQ LTLYSSHNFQNLFSSSHLTHILF CSPGSFSCTHSLLSLPQLPIVPGP DFSPASHIILDTTPDPHDCISLIH LTFTPFPHISFFPAPHPDHA*FIN GSSTRPNRHTPAKAGYAIVQVT SPPLKTSHFLSIVEIYPQGNNFS VFHLLFYYSSGIIQAPLLSLHIKL RDLPPPRTGKSALLNMPRVRKL KYLLVLVDTGSKKATVVISSLL SDIIPRFGLPTSIQSDNGPAFISQI TQAISLALGIQRTHGLLKTHLT NLSHQLKKDWTILLPLSLLRIQ ACPRNATGLHSDGEARSSFQAH HFNFITHGTVPDVFVPILQLLNE DFEDPCLGYLPSPEISICLEPTSW SKDRSCSSGEEGSAGQTVTGDL HKAQTPELDQPASLNCPDL
5284	35652	A	5325	1	420	RTRGGEKE*EEKQRSRR*RIK*E EEEK*RRSRGAGDKG*NERRRR NRGEPVEKEEDDRRRKRQWRR GEEEKRRRGRNCGGGGGEEKE DGRRRRLPCFLLLPSLLVSLLW LVSFLPCVFGFFGAPAVVFARF RGLRAFCRF
5285	35653	A	5326	2	467	
5286	35654	A	5327	269	777	
5287	35655	A	5328	2443	2627	VGFFFFFWWGERGTGSYSVTQ ARVQ*YDLGSLQLLPPSFKGFS CLSLPGSWYYRHGPPRLG
5288	35656	A	5329	57	394	
5289	35657	A	5330	33	311	HNTLPKTKPWFQEPGDEEPQQE EPPTESRDPAPRLPRSP*SADPP WRSQRPQGLTRPPPEPLRPHGS PPAHLSLFCQRSCPGPQERPHPS TM
5290	35658	A	5331	226	406	
5291	35659	B	5332	51	90	
5292	35660	A	5333	1	348	PPSQRV*GWHEMRQGGRQHAQ PVLSQQGLTAGHCHHQHCRRP LACDVRPVVYEKVSRDHGLVS GQHN/PAPESQGQSTSPPRHTGR KQARAGGEKKVTSDPANTAQH NPNTGSRGRP
5293	35661	A	5334	109	380	

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5294	35662	A	5335	448	724	WPSRSALAAGGRTAPTPRSRAG PPAR*RAGRESARGTS*GIRPRS QPARRPCPPAPVGRGLPPGPAR PPPRAAPREPPRCRAAAHTSRP AGS
5295	35663	B	5336	1	1554	
5296	35664	B	5337	99	366	
5297	35665	A	5338	1	714	
5298	35666	C	5339	391	689	
5299	35667	A	5340	2	614	
5300	35668	A	5341	2	461	
5301	35669	B	5342	45	1148	
5302	35670	A	5343	215	849	IKRLPLMKRMWL*LQPESLEIA GILVQ*MIE*QPKKGTNSIPVSK PSP/VVQKPNGQWRQVQDLRLI SDAVIPLYPAVSNPYTLLSQILE EAEWFTVLDLKDAFFCIPLRSD SQFLLAFEDPTDHTSQLTWTVF TQGFMDTPHLFGQSLAQDLGH FSSPGTLVLQYVDDLLLAKQQA TLDLLNFLANQGYKLSKLKAQ LCELLVFSSCARMHS
5303	35671	A	5344	1	1035	MGQVWALVRSTLELFHTDDEE EGEYDEVTEEVTEQVYLPAKA KVAQEEEVHPYPSAPPHYYFEE KEWPDPPDLSFLEDTGRKVVAP VTEQHLERLLSVLFRQEFSRLD ERDDAVEQLRGVCIRAWEKITS GGEQYPSFSAVKQGPKELYADF IAWNLLRQESLKKVISDSAAQD IVLQLLAFGNVNLDCQAALRPI RGKAHLVDYIKACDGIGAKQD SERFAFTIPVVNNLQPAKHFHY FTDGSSNGKASYSGSKGQNQQ PIWILSRHLKPYHEPDAKEEIPG G/CPRTPWLQPCRD*C*GGP*/P VTSNTR*TQPPTWGQIKKLSQM VEENLRKAGQLVTMTVYWN
5304	35672	A	5345	1566	1767	KGGWSQRHSQGACYTCRKSGH WAKECPQPGIPPKPRPICVGPH* KSDCSTHLAANPRAPGTLAQGS L
5305	35673	B	5346	1	3429	
5306	35674	A	5347	1	1776	
5307	35675	A	5348	1	933	

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5308	35676	A	5349	1	1743	MGKVWAVVRSTLELFHTDDEE EGEYNEVTEEITEQVYLPAKAK AVKEREQRGNITATFEPFPFKLL KEFKQAINQYGPGSHFVMGLL KNVAVSSQMIPTDWDALTQAC LTPAQFLQFKTWWAHEASIQA ACNAQAQPQINITTGQLLGVGG WAGLDAQVVMQDDAIEQLRG VCIRAWEKIPLCGEQYASFSAIK QGPKEPYVDFIAWLQESLKKVI ADSAAQDIVLQLSAFDNANPDC QAAL*PIRGNAHLVDYIKACDG IRGNMHKATLLVQAMAGLRVD KGNPLLPGACFNCGKHGHTKQ ERRKKSVSQAARWGKRKTADP EICPKCKKGKYWANQCHSKFD KDGTLISGNAMRAEQDCEWFT FTIPAVNNLQPAKHFHRFTDVS SNGKASYSGSKGGQARVQLFE NASVRATNSDLPQSSLWCRRKT SVSVAVLVSATIPISRVQGPSQV LGQGEKQTNQNVVPNPYTLLS QIPEEAKWFTALDLKDAFFCIPL HSDSQFLFAFEDLTDHTSQLTW TILPQGFRDSPHLFGQALAQDL GHFSSPGTLVLQYVDDLLLATS SEASCQQATLDFLSFLAN
5309	35677	A	5350	1	1085	
5310	35678	A	5351	1	3105	
5311	35679	A	5352	1	5172	
5312	35680	A	5353	41	324	
5313	35681	A	5354	18	270	KLSQVCIDLL*IREGERDMYPG WAKFPSPYSLKGT*PIAQGVLW SFGDFFYC/IPSTLPTPKSWRLFE SPFPESLTPVSLVWWPC
5314	35682	A	5355	80	384	SNNRTEGAWGKCQLMSS/PLTE PQVTLTIDSQEIDFLLDTGAAFS VLISCPEQLSSRSVTI*GILGQPV TRYFSHLLSCNWETLLFSHAFL VMPESPTPLLGR
5315	35683	C	5356	99	317	
5316	35684	A	5357	388	476	KVCPRPCRTSM/LPIRII*KLPQV CLDLL*IIEGEGDMYPG*AKFPS PYCLKGT*PGTIAGSWARGVSA AASPSYSSPSY

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5317	35685	A	5358	254	849	LQPESLEIAGILVQ*MIE*QPKK GTNSIPVSKPSP/GVQKPNGQW RQVQDLRLISDAVIPLYPAVSNP YTLLSQILEEAEWFTVLDLKDA FFCIPLRSDSQFLLAFEDPTDHT SQLTWTVFTQGFMDTPHLFGQ SLAQDLGHFSSPGTLVLQYVDD LLLAKQQATLDLLNFLANQGY KLSKLKAQLCELLVFSSCARMH
5318	35686	A	5359	1	909	
5319	35687	A	5360	153	436	CFCCCVEGNKPRNLQRTTKTPR LSVMSPSSCRGRGIWPNPGTC/R PSPSLI*SRSRQTWRITTPCQQG NKTGQRMNLTN*QEQASEGG* *QTPLS
5320	35688	A	5361	1	1632	
5321	35689	C	5362	1	675	
5322	35690	A	5363	604	1047	SNNRTDNPTSVAYLSKETDVV AKGWPHCLWVVVAVAILVLEA IKIIQGKDFTVWTSHDVNGILG AKGNSWLSDKRLLRYQALLLE GPVLQIHTCVALNPAIFLPEDGE PIKHDYQQIVAQTYVT*EDLLE VPLANPDLNLYTNGSSFV
5323	35691	A	5364	749	1002	QLKKGTNSLLVSKPSPVWIPTG TLTQIMGTGVANIC*PVF*KD*G ELGKMNYAMMSTITQGKEENP AFLKWLWEALRKYTPLSP
5324	35692	B	5365	114	2309	
5325	35693	A	5366	413	1157	
5326	35694	A	5367	105	478	YGHCCYDHRICCFFPATEQKVC PCAAQG*PL*LRGDDPEMSVYI *QLPLYYSSDLLSAANEVQILAF FQGDVSFFPVATTTDTLSVTFN FPFNYQGVNDFDFDFKQFLHSS FDFCFGRVFSNFE
5327	35695	A	5368	531	1087	RLQPPGAPVEDITRPVSAKPRD ADRNSTGCYLV*LQHQRQTES GRQLSGL*GPGCNGVH/ASLYR TSAMFAERFGSYSRRSTTAGIPS LLRLKSTIRRSDRSRRKAQRKR CGQVMPQHRRSIRPLLQPITPSL NRNLHRSPHRSRNRWSRLNRR LKHHLRRSQNRSRSWKKKLHR RVKPMLCNWVR

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5328	35696	A	5369	544	1381	VNPALQVLVVAITPPPSLPSPSCI RVLTRVSNAIAAKPLCLAVCAV VEGGRIRALVAVAAWGAGVTG GPAGLIACGPVSPSVIRGQFRHA GISFFLYAIGGEMVPAVRRQNH TPA*HKRFAKAFQLAHPNAVN AEHFAGGDRHLFSHLNQGCVV KHHVRRDITFIGYRFTQFA
5329	35697	A	5370	81	863	AYGNPVEIAGGARQAGVNFTG VFRPRFSRRWRRISGETCKLWW RRWRSAWASINQTFASWSTLIF RAISNPIIRKPDAPGVMACPRKR CCFTIRLIWRGCAVVWKRSR/E GQLQDIERHKLNAMGAFAEAQ TCRRLVLLNYF/GRRASGAVRE LRYLPRSAETVRRFNRCSDCPF HHWSCESAVWDGLCGGSDSCC GVSRARLFASPVNLPITGEIPER GFHPFCGRTTENGKNHPRNLFI WRSNCSVLPVKVMSLCSSTPCP
5330	35698	B	5371	12	273	
5331	35699	A	5373	145	336	SEEEEEDEEEEEEEEEEEEEEE E*EEGESAIICAKVCISVFPRRK NELNMAITPNTIPKLNHW
5332	35700	A	5374	294	657	VAPGDRHAFHGGGSGLSPELTL PQTQCCAQATVQGLEGTRSWS QSGTSSLSPWSHTSLACPQKEE GEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEAKTQ*KSG QKI*TDSPQKK
5333	35701	A	5375	2	588	SRPGITGSTISYGDPGHGAGPPG ADLGPARSLKPERAAGAQLAA GEARQSGDPGLPGGPGHSLGTA PC*VDKGWGHPVSTVHHQRQP QPGGLRAPGTALLAGTQPSHPA AGPWEPQPQRGVRVLGGRRDS *VGGG*GQHNKALWGPR*PHT EQKPDRKLSRIPLRAAGGEKRG CGCDRAGCLVLGPPQLPAQGL
5334	35702	A	5376	1	445	SLSHRAGGGGGVGGGAVCLFS PPRTKRESAPESPSRVLGHSPVP S*GAPSTRGSVSRILTSGGTHER SNGLTCHRNQAGTGPSALRSGR P*CLSRANPPGSKRSAGPVHEE RT*PCRLSGSAGITQ*DGN*KAG PRVPEAPERGCATC

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5335	35703	A	5377	3	313	QNDEVAFRKLKLIIEDVQGKSY LTNFHGMNLTHDKMCSMVKK WQTVIEAHVDVKTTNGYLLCL FCVGFTKKCNNQIWKTSLF*QQ SNMEDFFVLTTGIISHLHEPFLV VTDYDQ
5336	35704	A	5378	45	764	TSFLTTGGKKGS\KKKVVDPFS KKD/WL*YVKHRAMFNIRNIGK DVGSPRTQGTKIAS\DGLKG\RV FE\VSLADLQNDEVAFRKFKLIT \EDVQGK\NC\LTNFHGMDLTP* QKCCSMVKKM/WQTMI*SSPL MVKTT\DGLLASVCSCVGFTKK \RNNQIRKTSYAQHQQVRQIRK KMMEIMTREVQTNDLKEVVNK LIPDSIGKDIEKACQSIYPLHDVF VRKVKMLKKPKFELGKLMELH GEGS
5337	35705	A	5379	3	501	SSARFVSSSSSGGYGGGYGGVL TASDGLLAGNEKLTMQNLNDR LASYLDKVRALEAAKILSDMRS QYEVMAEQNRKDAEAWFTSRT EELNREVAGHTEQLQMSRSEV TDLRRTLQGLEIELQSQLSMKA ALEDTLAET/EGDVRADSERQN QEYQRLMDIKSRLEQE
5338	35706	A	5380	1	716	AQLKVKFWYWPEAGAGGLRR FKHY\YTPFKDCRDKILGATIKN SRIVLQIDNAGLAADDFRTKFE TEQALRMSV*ADITGLRRVLDE LTLARTDLEMQIEGLKEELAYL KKNHEEEISTLRGQVGGQVSVE VDSAPGTDLAKILSDMRSQYEV MAEQNRKDAEAWFTSRTEELT REVAGHTEQLQMSRSEVTDLR RTLQGLEIELQSQLSRLWGFCC PLEGVFWVEGWEGRDPYPRLF
5339	35707	A	5381	3	832	
5340	35708	B	5382	141	1067	

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5341	35709	A	5383	3	1316	GVAPSVLRLAMTSYSYRQSSAT SSFGGLGGGSVRFGPGVAFRAP SIHGGSGGRGVSVSSARFVSSSS SGAYGGGYGGVLTASDGLLAG NEKLTMQNLNDRLASYLDKVR ALEAANGELEVKIRDWYQKQG PGPSRDYSHYYTTIQ\ELRDKIL GATIENSRIVLQIDNARLAADDF RTKFETEQALRMSVEADINGFR \RVLE*S*TLAQEPNLEDARIEG LKEE\LAYLKKNHEEEISTLKGP KCEAQV\SVEVD\SA\PGTRSSPK ILSDMRS\QYEVMAEQ\NRKD\A EA\WFT\SR\TERIETREVAWPHR SSFQMSQAPRLLDLAAATPQGS *DLSCQSQLEPLKAALGKTPLA ENRKA\RFGNPQLAPYPQALDS AVI*KPQLG/DIVAKLDSSTGRI QEYQ\RL\MDIKFARLEQEIAHP NRSLA/LEGQEDHYNN\LFASK
5342	35710	A	5384	23	279	GCLRGSLERCGTLCKI\SLHEISG PESRVQ\QPLSSREEEEEEEEEEE EEEEEEEEEEEEEEEEEEERKK ECSKAQCKHFPLSEVL
5343	35711	A	5385	1	507	MEKNEKEQEEEEKKEKNSKKK EEEEEEEGGGEEEEEEGEGGEE EEEEEEEEEEEEEEEEEEEEE EEEE/EEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEKKKKKK KKKKKKKKKKKKKKKKKKKK RKKKKKEEEEKVVEEEDEFIWF LGNSLYFPSFSHFAWSQIPSRED EGERRLRVNSMIMDFTSNTNH
5344	35712	A	5386	3	259	
5345	35713	A	5387	53	387	LEEEKEEEKEEEKEEEKEEEEEE KE/DEEGEEGEGGEGEEGEEGE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEMIVLKIIVAKQLF
5346	35714	B	5388	1	1446	
5347	35715	A	5389	3	122	
5348	35716	A	5390	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEKI FLGHRVGI
5349	35717	B	5391	1	1269	
5350	35718	B	5392	44	244	

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5351	35719	A	5393	1	626	EEGEVEEEGEEEEEEEEGEGEE EEEEEGEGEGEGEGEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEQEEEEEEEEEEE EE\EEAAAAAAAASRDSHTSLEL TYWPPCPALRDTLVSNCSLSSL CTSGDSFHW*ETTIPAMSSCSH QHSLHQLGIIPRQILMRMASLM RRIC\EDHPATAEQ**HV*GPPD
5352	35720	A	5394	2	506	
5353	35721	A	5395	1	480	
5354	35722	A	5396	1	492	
5355	35723	A	5397	1	870	
5356	35724	A	5398	111	407	
5357	35725	A	5399	1	651	
5358	35726	B	5400	1	2427	
5359	35727	A	5401	571	966	SPFTNSRLTIFISFSECGQIAEIYI LSQPFMVRIMATEPPIINLQPGN FTLDIVSRDHTTAL*PGRQEQNS VSKKKEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEKKKK
5360	35728	A	5402	1	1674	
5361	35729	A	5403	1	306	
5362	35730	A	5404	2	431	
5363	35731	A	5405	1	585	
5364	35732	A	5406	1	708	
5365	35733	A	5407	3	595	
5366	35734	A	5408	287	659	
5367	35735	A	5409	1	633	
5368	35736	A	5411	3	634	
5369	35737	A	5412	344	481	
5370	35738	A	5413	1	525	
5371	35739	A	5414	1	501	
5372	35740	A	5415	1	461	
5373	35741	A	5416	302	567	MLCCLEISSTRYPKSSLSSSKFH KSLGQGQNAASLFAKT*RESPL LQFPASSSSPSETTSAWTLLFISL SAFLTKAFNKSLGGSKLSH
5374	35742	A	5417	251	844	NLGRGSQTSILDFCAPAGLIPCG SCQGLGLPHSEATARAVYWPL SAMAGVAGTQGTKSLDSSLFA KT*QESPLLRFPTSSSSPSETTSA FILLFISLSEFLSKPFNKSLGGSK LSHIFVSSSEPSKLSQPLHMPIQ ARISSFTSGHTDDSTVLFSVLLK LPLPVPSQAFSLKPGSIVMLLSS WSDNFNIPSISDSDA
5375	35743	A	5418	1	1113	
5376	35744	A	5421	1	337	

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5377	35745	A	5422	2	680	
5378	35746	A	5423	144	373	
5379	35747	A	5424	1	597	
5380	35748	A	5425	3	3319	
5381	35749	A	5426	1	612	
5382	35750	C	5427	46	168	
5383	35751	A	5428	1	663	
5384	35752	A	5429	10	417	IAIMNDTVAIRTRKFMTNRLLE RKQMVIDVLHPGKATVPKTEIL EKLAQMYKTTPDVIFVFGFRTH CGGGKTTGFGMIYDSLDYAEK NEPKHRLARHGLYEKKKTS*K QRQERTNRMKKVRGTAKANV VAG*KPNE
5385	35753	A	5430	67	263	GKTTG\FGMIY\DCLDYAKKNE PKHRRARHGLYEKKKTSRKQR KERKNRMKKVRGTAKANVGA GKK
5386	35754	A	5431	2	537	TPGSTTTTKFPTASTSEDRSPIM ND\TVTIPH*EKFMTQPTYFRGN QMVI\DVLSPPGKGDQCPKHRK FGKKLAQNVPRPTPD\VIFVFWI QNFIFGGGKTT\GF\GMIYGFPGI YAKEKMNPDHRLCKDMGLVL RKEKGPSRKANGKGTARNRIG RKVPGGTGKGPNVGCWAKRR NEVSSS

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5387	35755	A	5432	1	2195	ARGLSMGH*FP/PHFQCALA*M PAPGRGPPPPLPP/CPDAPPACA ATMERPEAGLRVAPRSPVQPGC TSVLPVAKRFNARILWLKRPQR QLWSLWRAQATVSLGGFHVM LSLQVHRINARVKEAWQLPPRF QMMYQKAWVLRQKPAAAVEP SQRNSPRAMLGGNVGLEPPPRV STRALPSGAVGRGLPPSRPKND TATGSLHPELGKAADIQFHPVR AATGASPCKSIGTELPKALGAH VLLQCALDVGHGVEGELWSFK TRQPSDFSIFSPPFPPFYSTKPPLS SWPIPNEPLGTPPRRGRGGAEG LLTSQCSHILNGLCFTGGINSNE CENVSRKKKMSEEFEANTMDS LVDMPFATVDIQDDCGIFFDVW KLRVNCQEILANRHPGRAMRK VVLTKTSWEGESLAVGKLPLK RLVSLDCQLRCLQCECGILIRQ HVVWLERTTGHWHPRSSQSCR LNTTSTALEHCNAFIYNTVCSH KLKDHSHDNGKSSGFLNPVAA PHSCIVMGHLTLLITTSYYTPLT KPDTDPTLKKEGLISQDSSSLEV LLHTDPLGKRGTPDPRVDDDSL GKFPVTNSQARKRILEPDDFLD DLDDEYCEDAPKHRGKGCGSA HKELDASNLEDQDKPYACDIC GKRYKNRPGLSYHYAHSHLAE EGEDKEDSQPPTPVSQRSEEQK SKKGPDGFALPNNYCNFCLGNS
5388	35756	A	5433	1	580	FSPLIHLILSGHSTCFREHRVGG KVTDQQDPKAEEFFLVQNKMK SLPCLLLSTQTRQPSDFSIFSPPF PPFYSTKPPLSSWPVLNELLGTP PRRGGGRAEG/PPHFPVG\GPGR GAPSPPRRGGWPGGGLTPQPPS RTGRLAGRGADPPTSLPDGAA GRAGG*PHHLPPGRGGWPGRG APHFPVGVAGQRRLFIC
5389	35757	A	5434	405	685	KVSHVYFYPHRPRNHPISQFFPH PSRLSIPQNRHCHHGPS/RNEPL GTPPR/PGSWPGRGAPHFPETFN HGRRWKGSRHVFTWPEQERE WGSATHF
5390	35758	A	5435	1	654	
5391	35759	A	5436	1	426	
5392	35760	A	5437	1	548	
5393	35761	A	5438	1	459	
5394	35762	A	5439	1	346	

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5395	35763	A	5440	1	1248	
5396	35764	A	5441	1	1257	
5397	35765	A	5442	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRSLH AKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWIHDEMKAEIKMFF ETNENKDTTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGDI TTDPTEIQTTIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESLNRPITGAEIVAIINSLPTK KSPGPDGFTAEFYQRYKEELHI NRAKDKNHMIISIDAEKAFDKI QQPFMLKTLNKLGIDGTYFKIIR AIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMTVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIPCSWVGRIN IMKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQK\RARI AKAILSQKNEAGGITLP
5398	35766	A	5443	1007	1719	TEPKTKTT*LSQ*MQKKPLTKF NNPSC*KLSIN/IVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLLSNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKHLFKENYKPLLKEIK EDTNKWKNIPCSWV\GRINIVK MAILPKVIYRFNAVPIKLPMTFF TELEKTTLKFIWNQKRACIAKSI LSQKNKAGGITLP
5399	35767	B	5444	1	1020	

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5400	35768	A	5445	1	1576	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNYLIFDKPEKNKQW GKDSLFNKWCWENWLAICRKL KLDPFLTPYTRINSRWIKDLHV RRKTIKTLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLKSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAAKKHMKKCSSSLA IREMQIKTTMRYHLTPVRMAII KKSGNN/R/CAPGTPERQNHSLS WKGS*SQEPSGLAQWIPLPWSP AS*DPLA*NSCCQHSCLKSTWD AQACARKLRTLIKGYRNCQLE
5401	35769	A	5446	1	984	
5402	35770	A	5447	1	1563	
5403	35771	A	5448	1	1449	
5404	35772	B	5449	1	1605	
5405	35773	B	5450	1	1569	
5406	35774	A	5451	1	690	MSELPFTIASKRIKYLGIQLTRD VKDLFKENYNPLLNEIKEDTNE WKNIPCSWVGRINIVKMAILPK ATVTKIAWYWYQNRDIDQWN RTERSEIMPHIYNYLIFKKPEKN KQWGKDSLFDKWCSENWLAIC RKLKLDPFLTPYTKINSRWIKD LNVRPKTIKTLEENLGITIQDIGI GKDFMSKTPKAMATKAKIDK WDLIKLK\FCTAKETTIRVNRQS TKWEIISSLD
5407	35775	A	5452	1	1919	

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5408	35776	A	5453	1	1416	MIILIDAEKAFDKIQQPFMLKTL SKLGTDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILP\R DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFHKWC WENWLAVCRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLKSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL
5409	35777	B	5454	1	810	
5410	35778	B	5455	1	1277	
5411	35779	B	5456	130	1701	
5412	35780	A	5457	1	1395	
5413	35781	A	5458	3	1646	
5414	35782	A	5459	1	759	
5415	35783	A	5460	2821	5781	
5416	35784	B	5461	1	2025	
5417	35785	A	5462	1	3663	
5418	35786	B	5463	1	2265	
5419	35787	A	5464	1	2241	
5420	35788	A	5465	1	2478	
5421	35789	A	5466	1	2067	
5422	35790	A	5467	1	2988	
5423	35791	B	5468	1	2061	
5424	35792	A	5469	1	2141	
5425	35793	A	5470	1	400	
5426	35794	A	5471	2	2507	
5427	35795	A	5472	1	768	
5428	35796	A	5473	1	1527	
5429	35797	A	5474	1	1293	
5430	35798	A	5475	1	1038	
5431	35799	A	5476	1	1572	
5432	35800	A	5477	1	1290	

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5433	35801	A	5478	1	524	MSELPFRIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNK WKNISCSWVGRINIVKMAILPK/ VKHR/FSACLQSLGRSGTTGLE ALAM*PIWPQEVE*VKFPALPS GASSTKGGCVP*QIQVEERLLS WKL*QA*TSW\YQRQRRSDSSL RERK*PKSIQRNVRRLSYYTP
5434	35802	A	5479	2	1547	
5435	35803	A	5480	1	2376	
5436	35804	A	5481	1	1824	
5437	35805	A	5482	1	1071	
5438	35806	B	5483	1	1839	
5439	35807	B	5484	1	1368	
5440	35808	A	5485	1	1884	
5441	35809	A	5486	1	1053	
5442	35810	B	5487	1	2532	
5443	35811	A	5488	1	2373	
5444	35812	A	5489	1	2361	
5445	35813	A	5490	1	2274	
5446	35814	A	5491	1	1686	MASPGPAPTASPKIHSELLTATR EAQRHHPVPRGQDLVTSESFSL SFCFSAAIFIFELLGSNSEGVTDL RLWLCQPAPRCGEWTYNPLEQ CCDDGVILDLNQTRLCGSSCTF WPCFQHCCLESLGSQNQTVVRF KVPGMKPDCKSSPITRICAQAG VQISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASQ RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA LIAKSILSQKNKAGGITLPDFKL YYKATVTKTAWYWYQNRDID QWNRTEPSEITPHIYNYLIFDKP EKNKQWGKDSLFNKWCWENW LAICRKLKLDPFLTPYTKINSRW IKDLNVRPKTIKTLEENLGITIQ DIGMSKDFMSKTPKAMATKDK IDKWDLIKLKSFCTAKETTIRV\ NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSLSLAIREMQIKTTNQNH\M RYHLTPGHG
5447	35815	A	5492	1	1872	

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5448	35816	A	5493	195	1494	PPGQHLQRRCLLRVSGFSENAK KGMLEVLARAI\RQEKKIKGIQS GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKALGYKISV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYGF NAIPIKLPMTFFTELEKTTLKFI WNQKRARIAKSILSQKDKAGGI TLPDFKLYYKATVTKTACNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTDTSLSTPAAPMVD SLIARVGVMARGNAITLPVCGR DVKFTLEVLRGDSVEKTSRVW SGNERDQELLTEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLGGEL DDEQMAALSRLGNDY
5449	35817	A	5494	1	1845	
5450	35818	A	5495	1	2109	

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5451	35819	A	5496	1	2535	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAYLGV LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAEKAFDKIQQHF MLKTLSKLGIDGTYLKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSDQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNYLFFDNPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NIRPKTIKTLEENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLKSFCTGKETTIRVNRQPT
5452	35820	A	5497	3	2284	
5453	35821	A	5498	1	1245	
5454	35822	A	5499	1	1140	
5455	35823	A	5500	383	1185	
5456	35824	A	5501	1	3159	MLEVLAWAVRQEKEIKGIQLG KEEVKLSLFADNMTVYLENPIV SAQNLLKLISNFSKVSGYKVSG QKSQALLYTNNRQTESQIMSEL PFTIASKRIKYLGIHLTRDVKDL FKENYKPLLKEIKKDTNKWKNI PCSWVGRINIVKMAILPKDIIQE NFPNLARQANIQIQEIRKTPQRY SSRRATPRHIIVRFTKVEMKEK MLRAAREKASHHTYSKIDPILG SKPLLSKCKRTEIITNYLSDHSAI KLEFRIKNL

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5457	35825	A	5502	583	2515	MQKKPLTKFNNPSC*KLSIN*LI SNFSEVSGYKISVQKSQAFLYT NNR/QESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWVGRINI VKMAILPKAIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVGPNTIKTLEENLGITIQDI GTGKDFMSKTPKAMATKAKID KRDLIKLNSFCTAKETTIRVNR QPTKWEKIFTTYSSDKGLISRIY NELKQIYKKKTNNPIKKWAKD MNRHFSKEHIYAAKKHMKKCS PSLAIREMQIKTTMRYHLTPVR MAIIKKSENNSLLAAGGGNRRT ANVVAHGFANLLTLDKKTLQEI LVHYPDSERILMKKARVLLKQ KAKTAEATPPRKDLALLFPPKE ETPKLFKTLLGGTGKASLARLL KLKREQAAQKKENSEGGEEEG KENEDKQKENEDKQKENEDKG KENEDKDKGREPEEKPLDRPEC TASPIAVEEEPHSVRRTVLPRGT SRQSLIISMAPSAEGGEEVLTIE
5458	35826	A	5503	1	2463	
5459	35827	B	5504	1	1221	
5460	35828	A	5505	1	4494	
5461	35829	A	5506	1	2825	MARTSYGQHFFPTLISMNIDSG RQNNGIPKLSTSYSLKPMNTLC YLVKRDLEGVLKLRILTWESSL DYPGGPSVITKVLIRQKEGQSQ RTRYDNGSRGWSDAIAVKRPQ AKECGWPLEAGKGKEWILRKE CIPANTLMLAQCPPTLRVGGSV CSAWRMIQNSDGERRKRNRIQL QAVRLSKVIHDTFRNFPRFVHS RELSKGAEKSSSLKKGLEQVII WTKCRQCGESRCTKKVEERKV LHNTFISTSTTITTLG

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5462	35830	A	5508	1184	4791	TSMQKSSIKYWQTESSSTSKSLS TMIKWASSLGCKAGSVYANQ* M*SSI*TEPKTKTI*LSQ*MQKK PL/YKIQQPFMLKTLNKLAQNL LKLISNFSKVSGYKINVQKSQA FLYTNNRQTESQIMSELPFTIAS KRIKYLGIQLTRDVKDLFKENY KPLLKEIKEDTNKWKNIPCSWV GRINIVKMAILPQVIYRFNAIPIK LPMTFFTELEKTTFKFIWNQKR ARIAKSILSQKNKAGGITLPDFK LYYKATVT
5463	35831	A	5509	516	2233	
5464	35832	B	5510	286	4131	
5465	35833	B	5511	1	4911	
5466	35834	A	5512	1080	3119	SSGLHPWDARLVQYTQINKCN PAYKQSQRQKPHDYLNRCRKK AFDKIQQPFMLQTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSLLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIISAQNL LKLISNFSKVSGYKINVQKSQTF LYNNNRQTESQIMSELPFTIALK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL YYKATVTKTAWYWYQNRDID QWNRTEPSEIMPHIYNYLIFDKP EKNKQWGKDSLFNKWCWENW LAICRKLKLDPFLTRYTKINSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMAAKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELQQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKK\ CSSSLAIR\EMQIKTTMRYHLTP VRMAIIKKSGNNRIRRHFQPRS AMFFCCCPGGEGSGLQWELLL AAWTVLPYPCPAATVGRFLKQ AQTADHSFLGHVWRVPSSRSW TDKEILSLVVNRQNQEVVQLIG GLCGTHTISPTQHPATG

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5467	35835	A	5513	2494	4549	LQTILQGYSNSKQHGTGTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPDKNKKWGKDS LFNKWCWENWLVICIKLKLDP FLTPYTKINSRWIKDLNVRPKTI KTIEENLGNTIQDIGMGKDFMS ETLKARATKAKIDKWDLIKLKS FCTAKETTIRVNRQPTKWEKIF AIYSSDKGLIPRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQI KTAMRYHLTPVRMAI
5468	35836	A	5514	1	5582	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYQTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTQIITNYLSDHS AIKLELRIKNLTQNHSTTWKLN NLLLNDYWVYNEMKAEIKMFF ETNENEDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
5469	35837	A	5515	3371	5375	TDTSQKKTFMQPKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRSWYFEKINKIDRL LARLIKKKREKNQIDAIKNDKG DITTDPTEIQTTTREYYKHLYA NKLENLEEMDKFLDTYNLPRL KQEEVESLNRPIRGSEIVAIINSL PTKKSPGPDGFTAEFYHRYKEE LVPLLLKLFQSIEKEVILPNSFYE ASIILIPKPDRDTAKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVG

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5470	35838	A	5516	314	2695	GSACRDPDPDPLRLVGGGAAA PPCSSVSPSAWRQSRPREYYEG GRGLHAPDRETALGLGIATSER MLGICRGRRKFLAASLSLLCIPA ITWIYLFSGSFEDGKPVSLSPLE SQAHSPRYTASSQRERESLEVR MREVEEENRALRRQLSLAQGR APSHRRGNHSKTYSMEEGTGD SENLRAGIVAGNSSECGQQPVV EKC\RRNPLHFHLIADSIAEQILA TLFQTWMVPAVRVDFYNADEL KSEVSWIPNKHYSGIYGLMKLV LTKTLPANLERVIVLDTDITFAT DIAELWAVFHKFKGQQVLGLV ENQSDWYLGNLWKNHRPWPA LGRGYNTGVILLLLDKLRKMK WEQMWRLTAERELMGMLSTS LADQDIFNAVIKQNPFLVYQLP CFWNVQLSDHTRSEQCYRDVS DLKVIHWNSPKKLRVKNKHVE FFRNLYLTFLEYDGNLLRRELF GCPSEADVNSENLQKQLSELDE DDLCYEFRRERFTVHRTHLYFL HYEYEPAADSTDVTLVAQLSM DRLQMLEAICKHWEGPISLALY LSDAEAQQFLRYAQGSEVLMS RHNVGYHIVYKEGQFYPVNLL RNVAMKHISTPYMFLSDIDFLP MYGLYEYLRKSVIQLDLANTK KAMIVPAFETLRYRLSFPKSKA ELLSMLDMGTLFTFRYHVWTK GHAPTNFAKWRTATTPYRVEW

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5471	35839	A	5517	3	2079	GKPVSLSPLESQAHSPRYTASS QRERESLEVRMREVEEENRALR RQLSLAQGRAPSHRRGNHSKT YSMEEGTGDSENLRAGIVAGNS SECGQQPVVEKC\RRNPLHFHLI ADSIAEQILATLFQTWMVPAVR VDFYNADELKSEVSWIPNKHYS GIYGLMKLVLTKTLPANLERVI VLDTDITFATDIAELWAVFHKF KGQQVLGLVENQSDWYLGNL WKNHRPWPALGRGYNTGVILL LLDKLRKMKWEQMWRLTAER ELMGMLSTSLADQDIFNAVIKQ NPFLVYQLPCFWNVQLSDHTRS EQCYRDVSDLKVIHWNSPKKL RVKNKHVEFFRNLYLTFLEYD GNLLRRELFGCPSEADVNSENL QKQLSELDEDDLCYEFRRERFT VHRTHLYFLHYEYEPAADSTD VTLVAQLSMDRLQMLEAICKH WEGPISLALYLSDAEAQQFLRY AQGSEVLMSRHNVGYHIVYKE GQFYPVNLLRNVAMKHISTPY MFLSDIDFLPMYGLYEYLRKSV IQLDLANTKKAMIVPAFETLRY RLSFPKSKAELLSMLDMGTLFT FRYHVWTKGHAPTNFAKWRT ATTPYRVEWEADFEPYVVVRR DCPEYDRRFVGFGWNKVAHIM ELDVQEYEFIVLPNAYMIHMPH APSFDITKFRSNKQYRICLKTLK EEFQQDMSRRYGFAALKYLTA
5472	35840	A	5518	403	2757	
5473	35841	B	5519	128	353	
5474	35842	A	5520	2	333	
5475	35843	B	5521	25	1359	
5476	35844	B	5522	1	1113	
5477	35845	A	5523	1	2526	
5478	35846	A	5524	3	555	

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5479	35847	A	5525	1	1710	MSQGTTPWGPTPAGTTPESEVH RPFPFPVPVPVPETSERSFPVRG VCGQAKSGLRRGAARLAPAAY LFTRQQTRELIHSACVSISVNTM HGLSVAINSRRCTYYRKYVIDF SKSEIIGIPISKNIDLTVGTTVTQ LQNLNTVGIIGSRGGRGQVAAL NCDRQGHLWLFTRVTVHWRM GNDRTFWGLLDTVSELMFIPGN PKHHCGPPVKVGAYGVTFLGV HWCGACQDTPCKMKDKLLHL APPTTKKKAQYVVGLLGFWRPI YRVTQKAASFEWGPEQDKALP QVQAAVQPALLFGPYDSADPM VLEASVADRDAVWSLWQAP/IS HKMGHAQQHSIIKWK*YICDW ARAGPKGTT\APMASWGVLYD QLTEEEKTRAWFTDGSARYAG TTQKWTAAALQPLSRTSLKGS GEGKSSQWAELQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
5480	35848	A	5526	1	438	
5481	35849	A	5527	1	612	
5482	35850	A	5528	2	736	EKCAMTALSSKLISQQKAFFAK MVVDAVMMLDDLLQLKMIGI KKVQGGALEDSQLVAGVAFKK TFSYAGFEMQPKKYHNPKIALL NVELELKAEKDNAEIRVHTVED YQAIVDAEWNILYD\KLEKIHH SGAKVVLSKLPIGDVATQYF\A DRDMFCAGRVPEEDLKRTMM ACGGSIQTSVNALSADVLGRCQ VFEETQIGGERYNFFTGCPKAK TCTFILRGGAEQFMEETERSLH DAIMIVRRA
5483	35851	A	5529	3	474	
5484	35852	A	5530	374	968	
5485	35853	A	5531	1	568	
5486	35854	A	5532	1	2136	
5487	35855	A	5533	1	240	
5488	35856	A	5534	248	1034	
5489	35857	A	5535	1	1602	
5490	35858	A	5536	120	340	

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5491	35859	A	5537	2	408	DEDDDDDDEEDDDEDDDDDDF DDEEAEEKAPVKKSIRDTPA\K NAQKSNQNGRDSKP\SSTPRSK GQESFKKQEKTPKTPK\GPSSVE DIKAKMQASIEKGGSLPKVEAK FINYVKDCF\RMTDQEAI\QDLW QWRKSL
5492	35860	A	5538	194	1027	WSFISIHLLSYLSACHHLMEDS/ MDMGMRPLRPQNYLFSCELKA NKDYHFKVDNNENEHQLPLTTI NLGAGAMDELDIVEAEAMNYE GSPIKVILATLKMSVQPTVSLG G\FEITPPVV\LRLKCGSGPVHIS GQHLVAVEEDAESEDEEEEDV KLLSISGKRSAPGGGSKVPQKK VKLAADEDDDDDDEEDDDED DDDDDFDDEEAEEKAPVKKSIR DTPAKNAQKSNQNGKDSKPSS TPRSKGQESFKKQQKTPKTPKG PSSVEDIKAKMQASIEKAH
5493	35861	C	5539	212	367	
5494	35862	A	5540	14	1515	
5495	35863	A	5541	1	540	
5496	35864	A	5542	1	1881	MDAALDDLIDTLGGPEETEEEN TTYTGPEVSDPMSSTYIEELGK REVTIPPKYRELLAKPIGPDDAI DALSSDFTCGSP*LYPSQVFHLL DLLPFSPGYQPRLLQHHLA/AVP FKVAGSGGADCILHMEVRDTA SDTGAGAAALDSSVFSVGLDGF SLHSDRSKSSESSSMSSDSLRGL GFSSGSGNSGFPSLSVAGFNLYS DGIVSSSSPHFSSFSSLAFASSTS LIERRSSSGSACRVPSEADRASS
5497	35865	A	5543	1	930	
5498	35866	A	5544	1	183	
5499	35867	A	5545	1	555	
5500	35868	A	5546	162	499	FPGSGNMAKDAGLIEANGELK VFIDQNLSPGKGVVSLVAVHPS TVNPLGKQLLPKTFGQSNVNIA QQVVIGTPQRPAASNTL/VWVG SPHTPSTHFASQ\NQPSDSSPW\S AGKR
5501	35869	A	5547	2	451	LVAEFSAADNHILPNESAYDQK NIRRRVYDALNVLMAMNIISKE KKEIKWIGLPTNSAQECQNLEV ERQRRLERIKQKQSQLQELILQ QIAFKNLVQRNR\HAEQQASRP PPPNSVIHLPFIIVNTSKKTVIDC SISNDKFEYLFNFDNT
5502	35870	A	5548	37	162	

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5503	35871	A	5549	205	616	RKLHGSQSSITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADAQVRRAVNNYDIIVMSNSF NGQSEHQVWIGGQFTFIKF\PIN SVSIRCRARQEGIMSSPGQQVG
5504	35872	B	5550	1	1407	
5505	35873	A	5551	3	416	MLPARMCCGIVSG*QFHTGNSY DHDYEFELGTRS*A*LKLLFS*T LPD*QLPAGSGEGPYHLEGQLS YCHRGGEKALAALLSSPTSKTR SPSEPDPEQDEQKLRFCKRHLY GQQPRSPVEIRLQHVAIAYQTH HAYD
5506	35874	A	5552	1988	2137	LVITTLLPLACGTAK*E*VNVTS FGSRPICSTSPVLFSGL*GPVKEF DT
5507	35875	B	5553	1	561	
5508	35876	A	5554	1	492	
5509	35877	A	5555	3	1055	
5510	35878	A	5556	1	634	
5511	35879	A	5557	1	723	
5512	35880	A	5558	1	384	
5513	35881	A	5559	1	792	
5514	35882	A	5560	3	1607	HCTRMSVKWTSVILLIQLSFCFS SGNCGKVLVWAAEYSHWMNI KTILDELIQRGHEVTVLASSASI LFDPNNSSALKIEIYPTSLTKTEL ENFIMQQIKRWSDLPKDTFWLY FSQVQEIMSIFGDITRKFCKDVV SNKKFMKKVQESRFDVIFADAI FPCSELLAELFNIPFVYSLSFSPG YTFEKHSGGFIFPPSYVPVVMSE LTDQMTFMERVKNMIYVLYFD FWFEIFDMKKWDQFYSEVLGR PTTLSETMGKADVWLIRNSWN FQFPHPLLPNVDFVGGLHCKPA KPLPKEMEDFVQSSGENGVVV FSLGSMVSNMTEERANVIASAL AQIPQKVLW\RFDGD\KPDTLGL NTRLYKW\IPQN\DLLGHPKTRA FITHGGANGIYEAIYHGIPMVGI PLFADQPDNIAHMKARGAAVR VDFNTMSSTDLLNALKRVINDP SYKENVMKLSRIQHDQPVKPL DRAVFWIEFVMRHKGAKHLRV AAHDLTWFQYHSLDVIGFLLV CVATVIFIVTKCCLFCFWKFAR KAKKGKND
5515	35883	A	5561	2	1600	

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5516	35884	A	5562	2	1624	AATGKQALHCIRMSMKWTSAL LLIQLSCYFSSGSCGKVLVWPT EFSHWMNIKTILDELVQRGHEV TVLASSASISFDPNSPSTLKFEV YPVSLTKTEFEDIIKQLVKRWA ELPKDTFWSYFSQVQEIMWTFN DILRKFCKDIVSNKKLMKKLQE SRFDVVLADAVFPFGELLAELL KIPFVYRPRFSPGYAIEKHSGGL LFPPSYVPVVMSELSDQMTFIE RVKNMIYVLYFEFWFQIFDMK KWDQFYSEVLGRPTTLSETMA KADIWLIRNYWDFQFPHPLLPN VEFVGGLHCKPAKPLPKEME\E FVQSSGENGVVVFSLGSMVSNT SEERANVIASALAKIPQKVLWR FDGNKPDTLGLNTRLYKWIPQ NDLLGHPKTRAFITHGGANGIY EAIYHGIPMVGVPLLADQPDNI AHMKAKGAAVSLDFHTMSSTD LLNALKTVINDPLYKENAMKLS RIHHDQPVKPLDRAVFWIEFVM RHKGAKHLRVAAHDLTWFQY HSLDVTGFLLACVATVIFIITKC LFCVWKFVRTGKKGKRD
5517	35885	A	5563	1	225	
5518	35886	A	5564	1	3210	
5519	35887	A	5565	1	835	
5520	35888	A	5566	222	477	HPRCLSPKGILKYLTKKYLKKN NLRDWLRVVANSKESYELRYF QINQDEEEEEDED*ISFIWKILYE FLNKTWDPKKKKTKKKKK
5521	35889	A	5567	1	778	MAAAAAAAGDSDSWDADAFS VEDPVRKVGGGGTAGGDRWG GEDEDEDVKDNWDDDDDEKK EEAEVKPEVKISEKKKIAEKIKE KERQQKKRQEEIKKRLEEPEEP KVLTPEEQLADKLRLKKLQEES DLELAKETFGVNNAVYGIDAM NPSSRDDFTEFGKLLKDNTQYE ESLYYARFLEVLVRDVCISLEID DLKKITNSLTVLCSEKQKQEKQ SKAKKKKKGVVPGGGLKATM KDDLADYGGYDGGYVQDYED
5522	35890	A	5568	1	897	
5523	35891	A	5569	1	2658	
5524	35892	A	5570	1	441	
5525	35893	A	5571	3	427	

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5526	35894	A	5572	1	952	PRLVLLKMAPLDLDKYVEIARL CKYLPENDLKRLCDYVCDLLL EESNVQPVSTPVTVCGDIHGQF YDLCELFRTGGQVPDTNYIFMG DFVDRGYYSLETFTYLLALKAK WPDRITLLRGNHESRQITQVYG F\YDDCLTKYG\NANAWRYCTK VFDMLTVAALIDEQILCVHGGL SPDIKTL\D\QIRTIERNQEIPHKG AF\CDL\VWS\DPEDVDT\WAI\S PRGAGWLFGAK\VTN\EFGS*ST NLKLICRAHQLVHEGYKFMFD EKLVTVWSAPNYCYRCGNIASI MVFKDVNTREPKLFRAVPDSE RVIPPRTTTPYFL
5527	35895	A	5573	54	588	
5528	35896	A	5574	1	4287	
5529	35897	A	5575	1	507	
5530	35898	A	5576	1	1416	
5531	35899	A	5577	1	841	ILLWDVDGGLTQIDKYLYSSED YIKSGALLACGIVNSGVRNECD PALALLSDYVLHNSNTMRLGSI FGLGLAYAGSNREDVLTLLLPV MGDSKSSMEVAGVTALACGMI AVGSCNGDVTSTILQTIMEKSE TELKDTYARWLPLGLGLNHLG KGEAIEAILAALEVVSEPFRSFA NTLVDVCAYAGSGNVLKVQQL LHICSEHFD\SKEKEEDKDKKEK KDKDKKEAPADMGAHQGVAV LGIALIAMGEEIGAEMALRTFG HLLRYGEPTLRRAVPLALAL
5532	35900	A	5578	2	391	AFGVTEPGCYGVIDVDTGKSTL FVPRLPASHATWMGKL/HSVLT SQKPSVLLTLRGVNTDSGSVCR EASFDGISKFEVNNTILHPEIVE CRVFKTDMELEVLRYTNKISSE AHREVMKAVKVGMKEYELER

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5533	35901	A	5579	18	1541	RRCRANMAAATGPSFWLGNET LKVPLALFALNRQRLCERLRKN PAVQAGSIVVLQGGEETQRYCT DTGVLFRQESFFHWAFGVTEPG CYGVIDVDTGKSTLFVPRLPAS HATWMGKIHSKEHFKEKYAVD DVQYVDEIASVLTSQKPSVLLT LRGVNTDSGSVCREASFDGISK FEVNNTILHPEIVECRVFKT\DM EL\EVLRYTNKISS\EAHREV\MK AVKSGEWKEYGVGKASFEHY\ CYSRG\GMRH\TSYT\CILRAVG *GTSAVLTFTGH\AGAPNDRTIQ NGDMCLFDMGGEYYSVASDIT CSFPRNGKFTADQ\KAVYEAVL LSSRAVMGAMKPGDWWPDM\ HRLAYRIHLEELAHMGILSGSV DAMVQAHLGAVFMPHGLGHF LGIDVHDVGGYPEGVERIDEPG LRSLRTARHLQPGMVLTVEPGI YFIDHLLDEALADPARASFLNR EVLQRFRGFGGVRIEEDVVVID SGIELLTCVPRTVEEIEACMAGC DKAFTPFSGPK
5534	35902	A	5580	1	98	
5535	35903	A	5581	1	810	

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5536	35904	A	5582	1	861	MLKEIIDDTNKWKHIPCSWMG RISIVKMTILPKAIYKFNAVLIKI PPSFFTELEKTILKFLCNEKRAS RAKARLNKKNKSGGITLLDFKR YYSAIVTKTVWYWYKNRHIHQ RNRIENPEINPNTYSQLIFNKAN KNIKWGNDTLFSKWCWDNWL ATCRRMKLDPHLSPHTKINSRW IKDLILRPETTKILEDNIGKTLLD VGLGKDFMTKNPKANARKAKI NIWDLIKLKSFFTAKGTVSRVN RQPTEWEKIFIIHTSDEGLLISRI YNELKQISKKK\TNNPIKKWAK DMNRQFSKEDVQMANKYMKK CSTSLIANLICREMQIKTTMQY HLTPARMAIIKKSKISRCWHGC GDQGTLLHCWWECKLVQPLW KTVWRFLKELKVELPFDPAIPL LGTHPEEKKSLCKKDTCTCMLL AAQFTIAKSWNQPKCPSVNEWI KKLCPRWLLSKWASA*NKWK HIPCSWMGRISIVKMTILPKAIY KFNAVLIKIPPSFFTELEKTILKF LCNEKRASRAKARLNKKNKSG GITLLDFKRYYSAIVTKTVWY WYKNRHIHQRNRIENPEINPNT YSQLIFNKANKNIKWGNDTLFS KWCWDNWLATCRRMKLDPHL SPHTKINSRWIKDLILRPETTKIL EDNIGKTLLDVGLGKDFMTKN PKANARKAKINIWDLIKLKSFF TAKGTVSRVNRQPTEWEKIFIIH
5537	35905	B	5583	473	1694	
5538	35906	A	5584	1	429	
5539	35907	A	5585	572	1149	PPVSHSMTLGNSYLFAPNWTIT PAW/CNTLDPSEGFGWQASLSL PSHQQFEHTCPEWLPTYSWPCK VGPDYLSEICQPECKQHFQESL TESSKQNIYETCAIYVSSPGERIL NQRFGPHGAFILVREYDDIRFS HSGPPSTCPNFPGPSYYTARESA YALKLRALEIIQISQSTKMQRNL GNPILPAIHQQPPQ
5540	35908	A	5586	1	804	
5541	35909	B	5587	1	1995	

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5542	35910	A	5588	74	1128	LLLDL*VD*SPSRPLEMRFRV*P MKRCTTLKKNYLSFLVYISRNL *NRVKAIM/VGKAEWKTIELPL PRKTVNQKQYRIPGGIAEISTTI KELNNAGMVIPTTSPFNSPIWP VQKIDGSWRMTVDYCKLNQV VTPIAATVPYVVSSLEQIN/TSPG T/WNRKRFCNRSRLLHKLLCHL GHMTQQI*CFLRCQWHIGMLF GPEICGCTSLSGQKL/WKIFVSH AASFEWSPEQEKALQQVQAVV QAALPLGPYDPADPVLLEMSV ADRDAVWILWQAPISESQWRPP GFWSKALPSSADNYSPFERQLL ACYWTLVETERLTMGHQVTIPP ELPIMNWVFSDLSSPKMCHPQQ
5543	35911	A	5589	1	1337	MIISIDAEKAFDKIQQPFMLKTL SKLEETASPSPVVATYTPQPML PSAFPPLSEEINPVLPETTVMAS PEAVTRQDNVDSPQKPPPTPMF ASRPITRLKPRRAPSEEGIQRLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGKAKWKPLEQPP PRKIVIQKQYHIPGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSWRMTVNYHKLNQVET PIAAAVPDVVSLLEQINTSPGT WYAAIDLVNVFFSIPVYKAHQK QFAFSWQGQQYTFTFLPQGYIN SPDITLVHYIDDIMLIGSSEQEV ANTLDLLPARVASWGVPYDQL T/GGRED*GLLHRWSCRICRHH
5544	35912	A	5590	2	693	KIVN/QKQYHIRGGIAEISATIKD SKDTGVVIPTTSPFNSPIWPVW KTDGSWTITVDYHKLDQVVTPI AAAVPDVVSLLEQINTSPGTWY AAINLENAFFSIPVHKANQ/KQF AFSWQGQQYTIAVLPQ\VKFLG IHWFVACQDIPSKIKDKLLHLA PPTNKKEAQCLVGLFGFWRQHI PHLRVLLQPIYQVTLKAAIFEW GPEQEKALQQVQAAVQAALPL GPYDPTDPMVLE

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5545	35913	A	5591	1	1011	MVSTPATLPSLPKPALMASWG VPYDQLTKEEKTRVWFTDGSA RYAGTTQKWTAVALQPLSRTS LKDSSEGKSSQWAELQAVYLV VHFAWKEKWPDVGLYTDSWA VANGLAGWSETWEKQDWKIG DKEIWGRGMWMDLSEWSKAV KIFVSHVSAHQRVTSAEEEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYSWAQQT\GLPFTKADL AMATAECPICQQQRPTLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFVLTVIDTYSRYRFAY PAHNASAKTTIHGLIECLIHCYG IPHSIASDQSIHF/TTKEVQ*WAH AHGIHWSYHVSHHPEAAGL
5546	35914	A	5592	7	278	SASCTAAFHHQMEVVYTRSGS SRS*R\PTIPVIAQWDYDHNGHG GRDGGYPWAQQHELPLTKADL ATATAECPICQQQRPSLSPRCGT IPR
5547	35915	A	5593	1	237	
5548	35916	C	5594	63	116	
5549	35917	A	5595	2	739	HKMGHAQQHSIIKWK*YICDW ARAGPKGTT\APMASWGVLYD QLTEEEKTRAWFTDGSARYAG TTQKWTAAALQPLSRTSLKGS GEGKSSQWAELQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
5550	35918	A	5596	1	354	
5551	35919	A	5597	3	592	
5552	35920	A	5598	126	365	QLAEPPHWLPD*KGAGFEWGP EQKKALQ*VQAAVQAALPLGP YDPADPMVLVVSVADKDAVWI FHLSGSDRWRRTYRCL
5553	35921	A	5599	1	483	
5554	35922	A	5600	1	1908	
5555	35923	B	5601	141	1569	
5556	35924	B	5602	46	1533	
5557	35925	A	5603	61	448	WRFLGPWRIVSCWFCGWEERR EGSAFFVGIPARMSAARESHPH GVKRSASPDDDLGSSNWEAAY LGNEERKQKFLRLMGA/GKGEE DQKINEELESQYQHSMDSKLSG RYRRHCGLGFSEVEDHDGEGD

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5558	35926	A	5604	1	404	P.WRIVSCWFCGWEERREGSAFF VGIPARMSAARESHPHGVKRSA SPDDDLGSSNWEAADLGNEER KQKFLRLMGAGKKEHTGRLVI GDHKSTSHFRTG\EDHDGEGDV AGDDDDDDDDSPDP*SPDDSES DSESE
5559	35927	A	5605	2	434	LGPWRIVSCWFCGWEERREGS AFFVGIPARMSAARESHPHGVK RSASPDDDFFLFAIMNGK*KIV NSHRCSVKAKSRQQLGSSNWE AADLGNEERKQKFLRLMGAGK KEHTGRLVIGDHKSTSHFRTGE ED*KINEELESQYQH
5560	35928	C	5606	909	1096	
5561	35929	A	5607	1	309	PQPAAMAAYIWVLIRHGESAW NLETSFSGWYDATLSLAGHKE AKRGGQALRGLFQVPLAPEAV GTVWCSWRTPCALKQL*PRPL KRRLRILADRHATQPRPQQ
5562	35930	A	5608	93	914	SQSVPHPQPAAMAAYK\LVLG\ RHGESAWNLENRFSGWDDADL SPAGQRGGERFAAQALQDAGY EFDICFTSV\QKRAIRTLW\TVL\ DAFDQMWLASGEGLWGFNER HYWGS*PGLN*KQKLAAKIG*G PRLKI\WRRSY\D\VPPPPMEPDH PFYSNISKDRRYADLTEDQLPS C\ESLKDTIARALPFWNEEIVPQI KEGKRVLIAAHGNSLRGIVKHL EGLSEEAIMELNLPTGIPIVYEL DKNLKPIKPMQFLGDEETVRKA MEAVAAQGKAKK
5563	35931	A	5609	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLLKLHDERVLVAF GQRDGIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYP VSIRFGRPRLTSNEKLMLASMF HS\IKFVVLADP\RQAGIDSLLRK IYEIYSDFALKNPFYSLEMP
5564	35932	A	5610	1	663	
5565	35933	A	5611	1	2034	

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5566	35934	A	5612	374	1106	IPVSERQGSDWRFFSVYVVNKA GGLIYQLDSYAPTGLRLEKTF\S YPLDLAGSS*HDERVLVAFGQR GRHPEWGHAVL\AINGM\DVNG RYTADG\KEVLEYLG*PLLNYP VSIRF\GRPRL\TSNE\KLMLGLP CFHSLFAIG\SQACLPGTREASR HLKILGRQDTFK\LH\CYQTLT\G IKFVVL\ADPR\QAGI\DSLLRKI YE\IY\SDFALKNP\F\YSLEMPIR CELFDQNLKLALEVAEKAGTF
5567	35935	A	5613	1	336	
5568	35936	B	5614	60	2175	
5569	35937	A	5615	2	198	
5570	35938	A	5616	1	449	
5571	35939	A	5617	1	771	
5572	35940	A	5618	18	736	EAMSSKVSRDTLYEAVREVLH GNQRKRRKFLETVELQISLKNY DPQKDKRFSGT/VQVGTVLIPPS PQCPRACPSPAGSR*AGGGHVG TDVLG*FRPPAPGRRGWTDPHP GS*NMRGGVGRPRPSPPASLRS QAGCW*M*TLRVRLGWLLRSQ TLHRALGTPGLGVTCWCCPPK RRLKSTPRPKFSVCVLGDQQHC DEAKAVDIPHMDIEALKKLNK NKKLVKKLAKKYDAFLASESLI
5573	35941	A	5619	24	698	EAMSSKVSRDTLYDAVREVLH GNQRKRRKFLETVELQISLKNY DPQKDKRFSGTVRLKSTPRPKF SVCVLGDQQHCDEAKAVDIPH MDIEALKKLNKNKKTGSRSWP KKYDAFLA/SQSPLIQADSPKSL GP\SLNKGRKSSPSLLTH\NKNM VAKVDEVKSTIKFPNWRRCLCL AVAVGHVKMTDDELVYNIHLA VNFLVSLLKKNWQNVRALYIK SPMGKPQRLY
5574	35942	A	5620	1	843	

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5575	35943	A	5621	3	1215	LLIMADPRDKALQDYRKKLLE HKEIDGRLKELREQLKELTKQY EKSENDLKALQSV\GQI\VGEVL KQLT\EEKFIVKATNGPRYVVG C\RRQL*QKVSLKPGTR\VAL\D MTTLTI\MEDILPR\EVDPLVYN MS\HEDPG\NVSYSEIGGLSE\QI RGI*GEVIGLPLYKPQSYFQRVG IIPPK\GCLLYG\PPGTGKNT/LLA RAVASQLDCNFLKVVSSSIVDK YIGESARLIREMFNYARDHQPCI IFMDEIDAIGGRRFSEGTSADRE IQRTLMELLNQMDGFDTLHRV KMTMATNRPDTLDPALLRPGR LDRKIHIDLPNEQARLDIL\KIHA GPITKHG\EIDYEAIVKLSDG\FN GADLRNVCT\EAGMFAIRADHD FVSTGKTSLKAV\RKVADSKKL ESKLDYKPV
5576	35944	A	5622	104	173	
5577	35945	A	5623	1	1140	
5578	35946	A	5624	1	528	
5579	35947	A	5625	1	1083	
5580	35948	A	5626	1	471	
5581	35949	A	5627	1	2322	
5582	35950	A	5628	1	678	
5583	35951	B	5629	213	1477	
5584	35952	A	5630	2	339	FGLHKWGLGLEASSPCGPLTPS YLGFPRPHPGTLGLGRFWPFLA LQSLSETPSHARMPRVTVARTS PETLEISPLRAAT*NHRSSGHTC FRERMLRVSCRLSLDLSSSWVR
5585	35953	A	5631	1	783	

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5586	35954	A	5632	92	2746	ASRMTVLQEPVQAAIWQALNH YAYRDAVFLAERLYAEVHSEE ALFLLATCYYRSGKAYKAYRL LKGHSCTTPQCKYLLAKCCVD LSKLAEGEQILSGGVFNKQKSH DDIVTEFGDSACFTLSLLGHGH VQTERAAKGTAFSPKRLCLHTF P\WTPLEPLVEIGERPLPHQTFN\ FTS*RNFANCLHTSGTKQVTN\ HVFSHRQPETVLTETPQ\DTIEL NRLNLESSNSKYSLNTDSSVSYI DSAVISP\DTVPLGTG\TSILSKP VQ\NKPKTGRSLLGGPAALSPL TPKFWGFLPIRKPP\SPG\DGS\Y LQNYTNTPPVIDVPSTGAPSKK TFRVLQSVARIGQTGTKSVFSQ SGNSREVTPILAQTQSSGPQTST TPQVLSPTITSPPNALPRRSSRLF TSDSSTTKENSKKLKMKFPPKIP NRKTKSKTNKGGITQPNINDSL EITKLDSSIISEGKISTITPQIQAF NLQKAAAEGLMSLLREMGKG YLALCSYNCKEAINILSHLPSHH YNTGWVLCQIGRAYFELSEYM QAERIFSEVRRIENYRVEGMEIY STTLWHLQKDVALSVLSKDLT DMDKNSPESGTQRGRESPRMC GADSQIEKSQSSYFIQDLSRFDY VKFAVVTKIRAWCAAGNCFSL QREHDIAIKFFQRAIQVDPNYA YAYTLLGHEFVLTEELDKALAC FRNAIRVNPRHYNAWYGLGMI
5587	35955	A	5633	260	678	GEFSIFFWVWN*LLLWHQETFS I*NLFSSH*TSITYQATEEGFDFII QMKLIHFGDSIFIYLKLLILNRK P**EAAISI*V*TWRSRFSHFQLR *HQTQVTNHSWFTEAR*LTDLV KSKSPTIPCSRFKANTLF**SDP
5588	35956	A	5634	1	1452	
5589	35957	A	5635	2	1563	
5590	35958	A	5636	1	444	
5591	35959	A	5637	2	345	

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5592	35960	A	5638	2	1721	RSREAAAVAAAAATTAFGCRI WNPCAALTMKQSSNVPAFLSK LWTLVEETHTNEFITWSQNGQS FLVLDEQRFAKEILPKYFKHNN MASFVRQLNMYGFRKVVHIDS GIVKQERDGPVEFQHPYFKQGQ DDLLENIKRKVSSSKPEENKIRQ EDLTKIISSAQKVQIKQETIESRL SELKSENESLWKEVSELRAKHA QQQQVIRKIVQFIVTLVQNNQL VSLKRKRPLLLNTNGAQKKNL FQHIVKEPTDNHHHKVPHSRTE GLKPRERISDDIIIYDVTDDNAD EENIPVIPETNEDVISDPSNCSQY PDIVIVEDDNEDEYAPVIQSGEQ NEPARESLSSGSDGSSPLMSSA VQLNGSSSLTS\EDPV\TMDGFP FGMDNIQSFWGRVEL\LDY\LDS IDCSLEDFQAMLSGRQFSIDPDL LVDLFTSSVQMNPTDYINNTKS ENKGLETTK\NNVVQPVSEEGK ENLKSKP\DK\QLIQYTAFPLLAF LDG\NPASSV*TGRGTTASFRKF CPL*DKPIEVDELLDSSLDPEPT QSKLVRLEPLTEAEASEATLFY LCELAPAPLDSDMPLLDS
5593	35961	A	5639	2	251	
5594	35962	A	5640	70	297	QLRSPLKWKKAQRQPLAIAHV LLLRPRKKRQNGFFTVRYARLL STLPRSWRR\KQWY*AQNHVRS PEWKWHYQSLS
5595	35963	A	5641	3	985	
5596	35964	A	5642	1	3501	
5597	35965	A	5643	1	1752	
5598	35966	C	5644	1	879	
5599	35967	A	5645	21	519	LHIPVRTLSCRFVGVCWRSTPG PVCLGISSGGCRTVDIAALQLW LRGLALPEQLLRVDPHPQACRR LPREPP\GPGQTFGTREPPQAVS TKEASSSNLHAPERTVAGLTFT TEQVRALEGVFRHHQYLGPLE RNWLAREMQLS\RSR*KPGFKI AG*NTNGKCRTPS
5600	35968	A	5646	90	2401	
5601	35969	A	5647	776	1018	
5602	35970	B	5648	1	1296	
5603	35971	A	5649	1	1257	
5604	35972	A	5650	731	4841	
5605	35973	A	5651	325	9497	
5606	35974	A	5652	1	322	
5607	35975	A	5653	1	819	

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5608	35976	A	5654	56	251	
5609	35977	A	5655	149	701	
5610	35978	A	5656	3	415	
5611	35979	A	5657	3	467	AIASPRAAGIRHELTSTMAAGK NKRLTKGGKKGAKKKAV/DNII NIGKTLVTRTQRTKIASDGLKG RVFEESLADLQND\TDGYLLRVI *VAFTTERTNQI/REVFNKLIPDS IGKDIEKACQSIYPLHDDFARK VKMLKKPKFELRKLMELHGEG
5612	35980	A	5658	2	418	PRVRADGKNFRLTKGGELGAR NKVVDPFSKKDWYDVKAPAM FNIRNIGKTLVSRTQGTKIASDG LKGRVFEARLADLQNDEVAFIK CKLITDDVHGKNCLTIFHGMDL TRDKM\CSLGKKWQTMIEAHV DVKTTDGYLL
5613	35981	A	5659	3	121	
5614	35982	A	5660	1	237	
5615	35983	A	5661	25	967	FSPAAGIRHEGSLTSTMAVGKN KRLTKG\GKKGS\KKKVVDPFP R\KDWY*RRKHPLMFHYKN\IG KT\LVTQDPKGPKIA\SDGLQGF VCLKVSLADLQ\NDEVASRKF\ RLITEVCFRGKNLP*LTSHGAW DLYPVTKMCSHGQKNWQT\MI DSSR*MFKTNPMGYLALRLFLC /VGFT*KNRNQFRLRKAPPYAS ATQQVPPKSRKKM\ME\IMTPR GARQNDLEKKWVNKLIPRQAL GKDIRKGPAQSYFIPL\HDVLRL EKLKLLEGSPKF*IGESSLGASM GGRAVVPGKSHLGTQTGAKVG TSLMGYEPPVPRILV

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5616	35984	A	5662	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM

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5617	35985	A	5663	1391	2742	KKRESSLTHVMRPASF*YQSQA ETQQKKRILDQYP**TLMQKSSI K/YLAKRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLELEETTVKFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSLFNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKTLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLKSFCTAKET TIRVNRQPTKWEKIFTTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYAAKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRHAPFSIH THIMFGSLYLQIQKDLSILGFW YPRGILEPIY
5618	35986	A	5664	1	1910	MTIIINIIIIIITIITIIIIVHIITINIVIT TTILTTVIISSTIIIIITIFVFETGAI KLEIRIKKLTQNRSATWKLNNL LLNDYWVHNEMKAEIKMFFET NENKDTTCQNLWDTFKAINKID RPLARLIKKKREKNQIDAIKND KGDITTDTTGIQTTIREYYKHLY ANKLENREEMDKFFDTYTLPRL NQEEVESLNRPITGSKIEEIINSL SIKKSPGPDGFTAEFYQRYKEE LVPFLLKLFQSIEKEGIILNSCCE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKTLANRIQQHITK LIHHVQVGFIPGMQGWFNIRKS INNWKKTTLKLIWNQKRACITK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEASEIIPHTYNYLSFDKPDKN KKWGNNSLFNKWCWENWLAI CRKLKLDPFLTLYTKINSRWIK DLNFGTETIKTLEENLGNTIHDI GMGKDFMSKTPKAKATKAKID KWDLIKLKSFCTAKETTIRVNR QPTEWEKIFAIYPSDKGLISRIY KELKQVYKKKTNNPIKKWAKD TNRHFSNEDIYAANRHMKKCS SSLAIREMQIKTTMRYHLAPVR MTIIKKSGSNRQ/W*ASGHVRC

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5619	35987	A	5665	1	2460	MPHAGHARSPGHTLIKLAEWW MSRWMEWNPGFPLSIDAKCHK DLPRDIQFDSEKGVDFVLNYSK ALNQEEVESLNRPITGSEIEAIIN SLPTQKSSGPDGFTAEFYQRYK EELVPFLLKLFQSIEKEGILPNSF YEASIILIPKPGRYTHKKNNFRPI SLMNIDAKILNKILANRIQQHIK KLIHQDQVGIIPGMQSWFNIHK SINVIQHINRTKDKNHMIISIDAE KAFDKIQQPFMLKTLNKL\GIK YLRIQLTRDVKDLFKENYKSLL NEIKEDTNKWKNIPCSWIGRMN IIKMAI/LPKVIYRFNVIPIKLPMT FFSELEKSTLKFIWNQKRARIAK TILSQKNKAGGIMLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEMTPHIYNHLIFDKPDKN KQWGKDSLFNKWCWENWLAI GRQLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI SMGKDFMSKTPKAMATKAKM DKWDLIKLKSFCTAKETTIRVN RQPTEWEKNFAIYSSDKGLISRI YKQLKQIYKKKTNNPIKKWAK DMNRHFSKEDVYAANRHMKK CSSSLAIREMQIKTIMIYHLTPV TMAIIKKSGNNRCWRGCGEMG TLLYCWWDCKLVQPLWKTLW QFLRDLELGIPFDPAIPLLGIYPK DYKSCCYKDTCTPKLARDDQI HILKQHRRKELETRQKQYRAW
5620	35988	A	5666	689	1909	LIAYQPKKSRTRWIHNQILPERI KYLGIQLTRDVKDFLKEKYKPL LNEIKEDINKWKNIPCSWIGRIN LVKMAIL/PQAICRKLKLDPFLT TYTKINSRWIKDLHVRPKTTKT LEENLGNTIQDIGMGKDFMSKT PKAMATEAKIDKWDLIKRKSFC AAKETTTRVNRQPTDWEKMFA IYSSDKGLISRIYEELKQIYKKK TNNPINKWAKDMNRHFSKEDI YAANRHMKKCSSSLAIREMQIK TTVSPFAAQWVSQRYGKWQEA HPSNNDGKGYRGKPRFQSLSD VHGPQDQKKIIKESALPPTPTFI NILMNAKTIENGQFPYLLNALK QQQPHDAENLFTWGKENAAIV SPCIEVSAALSQWKVPAWPQRS GIPNRILRSPIPGLGSWVAFLDL VWVRGDPTALK

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5621	35989	B	5667	1	1962	
5622	35990	B	5668	1	1851	
5623	35991	A	5669	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGIDGTY FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSEITPHIYNYLIFD KPDKNKQWGKGSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGMDFMSKTPKAMAT KDKIDKWDLIKLKSFCTAKETT IRVNRQPTKWEKIFTTYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSPSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCW\WINWMKKTWH IYTMEYYASIKKNEFMSFAGA* MKLETII
5624	35992	A	5670	2	1967	

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5625	35993	A	5671	1039	2272	KKRESSLTHVMRPASF*YQSQA ETQQKKRILDQYP**TLMQKSSI K/YLAKRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLELEETTVKFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSLFNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKTLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLKSFCTAKET TIRVNRQPTKWEKIFTTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYAAKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAIIKKSGNN
5626	35994	A	5672	1	3477	
5627	35995	A	5673	1	2814	
5628	35996	A	5674	1	2093	
5629	35997	A	5675	1	2724	
5630	35998	A	5676	1	4680	MDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKKDPGPD GFTAEFYQRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARITKSILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRAEPSEIML PIYNYLIFDKPDKNKQWGKDSL FNKWCWENWLAICRKLKLDPF LTPYTKINSRWIK
5631	35999	B	5677	1	1989	
5632	36000	A	5678	1	2784	
5633	36001	B	5679	1	3573	
5634	36002	B	5680	1	2630	
5635	36003	A	5681	5339	10577	
5636	36004	A	5682	1	873	
5637	36005	A	5683	1	672	
5638	36006	A	5684	1	435	

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5639	36007	A	5685	1	1011	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGPGGLQPGQR VLYKQSIAQRARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMILATIIANC IVLALEQHLPDGDKTPMSERLD DTEPYFIGIFCFEAGIKIIALGFV FHKGSYLRNGWNVMDFVVVL TGRKAGLGCCGSGVESGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSELKE\DVRTHRK EAKNLEKRLDKM\VNRINSVEK TLNDPMELKTMARELCDACTS FSS*FNQVEEKVSVIEDQMDEM K*EEKFREKRVKRNEQSLQEIW DYVKRPNLRL
5640	36008	A	5686	1	1539	
5641	36009	A	5687	1	756	MDDPRLNVKPLTESLETYSGKS KGLEGDVITDSKLNDCRCPSGT KLPEEGLGSNICCSAIFAVLQPL LVIPRQTGSGVDHQQTPTDLRM TVRRKMNKQKGIASTSTKRTK KDIHTKTPSVCHQHQRPKDCSP SPATEQSWMENDLEELTEIGFR RSVITNFSELKEDVRIHHKKAK NLGKRLDEWLTRINSVEKTLND LMELKTMARELHDSCTSFNSRS NQAEEKVSVIEDQFNEIKREEK FREK\RVKRN
5642	36010	A	5688	1	1008	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGPGGLQPGQR VLYKQSIAQRARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMILATIIANC IVLALEQHLPDGDKTPMSERLD DTEPYFIGIFCFEAGIKIIALGFV FHKGSYLRNGWNVMDFVVVL TGRKAGLGCCGSGVESGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSELKEDVRTHRK EAKNLEKRLDEWLTRMNSVEK TLNDLMELKTMARELRDACTS FSSQFDQVQEMVSVIQDQISEM KREEKFREKRVKRNE/QSLQ*I WDYVERPNLRL
5643	36011	A	5689	1	672	
5644	36012	A	5690	1	807	
5645	36013	A	5691	1	1617	

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5646	36014	A	5692	1064	1893	LLEGSININKKDIYTKTQSVGRQ HQRPKVDKTTKMGRNQNRKA ENSKNQSASSPPKDC\SSSPAME QSWMENNFDELTEIGFRRSVIT NFSELKEDVQTHCKEAKNLKK RLDECLTRINSVEKKTLNDLME LKTMAQELHDTCTSFNTQFDQ VEERVSVIEDQINEIK*EEKFRE K\RVKINE*SCQEIWD*VKRPNI HLITVPESDGEKGTKLENTLQDI IQENFHNIARQANIQIQEIQRTA QRYSSRTATPRHIIVRFAKVEM KEKVLRAARKKG
5647	36015	A	5693	3	620	EAGWLLLSSVDEVMKENDELR DSISQLQKQILSLKSAKIALTESL ISFRERAEIVEKQTQALIM*VAD LQQGNDQTFQGLLDTGSELTLI PGDPKHHCGPPGPKVRAYGDQ VINGVLAQVQLIVGPVGPWTHP VVISPVPECVIGIAILNSWQNPHI GSLTGRVRAIMVGISWQGQQY TFTVLPQRYINFPALCHKTAKR HTARR
5648	36016	A	5694	1	1098	
5649	36017	A	5695	2	563	IIRRAVFRWFWG*RSWGLNMIR PQNTKDSNSNCLEKTDSPWCEL FKELYKINAFDTPDSLLMRGNE FSDPIHHTFDHMWRTKEHNEA GWLLLSSVDKVMKENDELGDS ISQLQKQILSLKSAKIALSESLIS CRERAEIVEK*T*ALIMLVADL Q*KVHAQPHHAQPRQVSTVKV RALIVLQEVTDP
5650	36018	A	5696	1	499	FVLVDVNNMWHRYASMLYER RLLIICSKLSTLTACIHGFAAML YPMYWQHVYI\PVLPPHLLDYC CAPMPYLIGIHLSLMEKVRNMA LDDVVILNVDTNTLETPFDDLQ SLPNDVISSLKNRLKKVSTTTG DGVARAFLKAQAAFFGSYRNA LKIEPEEPITFCEEA
5651	36019	A	5697	1	795	
5652	36020	A	5698	103	3531	
5653	36021	A	5699	1	2073	
5654	36022	A	5700	1	901	
5655	36023	A	5701	148	639	
5656	36024	A	5702	1	318	REYGTPQEQLNLALLTLNFLSL PKGQMLSAAEQHLQKPAAKTE A/GRMIWQRDPITKIWEIGKIIT WGRGYACVSPGQNHQSVWIPS RHLKSCHGPDAKEEIPGGS

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5657	36025	A	5703	1	612	PTRPIKHITDIPYNSEGQAIVER MNLSLKQQLQKHKKGGK/SKD YGTPHMQLNLALLTLNFLSLPK GQILSVAEQHLQKPAAKTEAEQ LVWWRDPITKS*EIGKIITWGK GYACVSPGLTQQPIWIPSRHLK PYHEPDAEEEIPGGSRGPPPPPV/ DSHVETDAEEEPHCHEQHLSNT ATHLGTDQEAVTAGGRKPEES KTTSHNK
5658	36026	A	5704	2	791	
5659	36027	A	5705	2301	2620	DGQQLIALHRLALRELQQAGH AGLPQQAKILFDGGSEIGKIRGL QRPRAKNRLSGRGPLREPSPK*F FGVQGRKTLNRTLKGAPH*NL AAKAGKPLSPCTSGRIRM
5660	36028	A	5706	1	1010	MDDIPQEAGRYRHNQAYAYSI QGDGAEDDDERIVRFHTRVTV DSDTLASDAARLTCRHGLGNQ GSDLVLYGTSTPKNLIWVRVH VVGHRPDRRFFAFDVWSPRSLI VDSCSKLEQHSTLSRAILLIYKG FCRFRNHHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGFPTGKRAVSATQLMD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQANVQQFIDEGNYTS GDNHTLRDPHYVEDKGHKYLV FEANTGTENGYQGEESLFNKA YYGGGTNFFRKESQKLQQSAK KRDAELANGALGIIELNNDYTL KKVMKPLITSNTVTDEIERANV FKMNGKWYLFTDSRGSKMTID GINSNDIYMLGYVSNSLTGPYK PLNKTGLVLQMGLDPNDVTFT YSHFAVPQAKGNNVVITSYMT RGSSR*RQRP*IPCIRSQHGNRK RIPR/SKNLYLTKRTTAAARTSS VKKARSFSRALKNAMLS*RTAP
5661	36029	B	5707	1	1149	
5662	36030	B	5708	55	3947	
5663	36031	B	5709	4	885	

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5664	36032	A	5710	461	1560	SLQTRDLPISEPPSNRIFACWGK PAWTACCNSLRARR*RAISCCP SH*KRIPRRRIFI*PKRTTAAART SSVKKARSFSRALKNAMLS*RT APSVS*S*IMITH*KK**SR*SLQ TRDLPISEPPSNR\FSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGIPDWKAGSERNAI NGAIALIEGFRPLTLEPSSLIVNS CSKLEQHSTLSRAILLIYKGFCR FRNHHQTGFSPAGPNQRGPLAA TLSGPGGEGQSAVARLTGEKK NHPGAQYANRLSPRVGRFINAA GTTGFPTGKRAVSATQLM
5665	36033	B	5711	1	1458	
5666	36034	B	5712	1	3573	
5667	36035	A	5713	606	1005	GGMLCGTLSGPDGEGQSAVAR LTGEKKHPRGDQ*QKAPLLAR W/RNPLMQLAQ/PDFPTGKRAI DTHRSVSHAHIIITIHSSTLSSDIS HTDAPNTSSNNYVIAITSPSDTA PTSRTPLHRIHHTTPIPIATLARP
5668	36036	B	5714	1	1566	
5669	36037	C	5715	29	2314	
5670	36038	A	5716	597	1384	ISYTVPEALSARSNPAACQHAS CRPAACPVASVGSPRQPAPGGA GGHRHWPRRRWRLRQRPRPSA PGRPRRPRPRPRRHRRRPRPHP HHAPPPRPSCAETRS\RRGGGRR PLPRPLPPGAAGAGHREVGDK AGAAGCGRRVVALAA\PVSPPS SPSSPSPSLLSAAVGVAGCFSAE LSDSRRLLAPGGEGPLARSPAR CDPAAGSACPAGWSSRQRSRC ELMCAAGISCWHTGHCTWCSL SFMPLVLMILAASFRPVAVSSH
5671	36039	B	5717	1	3873	
5672	36040	C	5718	356	784	
5673	36041	A	5719	1303	1664	KRRDEIIPCVLSKQLLVTFITCR ASCINESANARGEAVCVLGAR VV/SSFHQ*DGQQLIALHRLALR ELQQAVHAGLPQQAKILFDGGS EIGKIPYKSKE*PENRLSVVPVW EQESTLASV

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5674	36042	A	5720	453	915	TVSRWAMLEHILLFSREPSNKE PET*AHSM*ADDKRFAAYKKK TKGGTERWDKYGRRPANGIRT GENNAKTEHLRDRDQKR/PRER ERAR*TTEITEQEGSG*GEPVEQ MRKRRAQAWSRRKSTGSQTET RSVRVTRVGLKTASESRRIRTM EQN
5675	36043	B	5721	319	1469	
5676	36044	B	5722	164	3112	
5677	36045	A	5723	1	1102	MRWTPGHEITKALQTFQRYTGI QHVHRIGMAERMWCDRNRER HTVSSSGGNRLPNPEHFEAFQS VAQCTYNQTVQLDITAFLKTV KKNKHKFYPAFIHILARLMNAH PEFRMAMKDVDSCSKLEQHST LSRAILLIYKGFCRFRNHHQTGF SPAGANQRGPLAATLSGPGGEG QSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAAGTTGFPTGK RAVSATQLIYRELFPQPLVQLD PCSVPCMQPPTSPKSRAWVSDI ALLEFQKKKEMEKKKEKERKK ELQGGRGRRRGGGWGKGRER GGRGKKRRGGGEAIRDAEKAG RLPHPDMEIRGRVEQRVGYTIE QINHMRDVFGTRLRRAEDVFPP VIGVAAHKGGVYKTSVSVHLA QDLALKGLRVLLVEGNDPQGT ASMYHGWVPDLHIHAEDTLLP FYLGEKDDVTYAIKPTCWPGL DIIPSCLALHRIETELMGKFDEG KLPTDPHLMLRLAIETVAHDYD VIVIDSAPNLGIGTINVHPAWGS AISLLEYSPGHLAGFVASIPAPL QLVPRWDTKPVLEDASASSRFS IPQRNPTHLHPTTSFPSCNPDTV DAWMRFLITWCLYTSPYSTLM GELFPFYQGMLLESTKQGSQVR KVFVWTLVPNWNNTQPYSRAI LLIYKGFCRFRNHHQTGFSPAG ANQRGPLAATLSGPGGEGQSA
5678	36046	B	5724	90	6258	
5679	36047	A	5725	837	1485	
5680	36048	A	5726	1	2993	
5681	36049	A	5727	1	123	
5682	36050	A	5728	1	960	
5683	36051	A	5729	507	755	NKRGYKQMEEHSMLMGRKNQ YRKNGHTAQGNL*IQCHPHQA TNDFLHRIGKNDFQVHMEPKK SPHRQVNPKPKEQSWRHHAT

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5684	36052	A	5730	274	882	PDQVDRGGAHWQTDADDPWL ADHLQHCQRCGEILRHYSGGIR GNVSAVKCAEHHVPAFARLRN PQCGDFQRLDYRLFDSPGVKRR EL*TAYRFCHVAP*LMDLRSG WAAGAVYRYQSH*FTADRLRS\ VDMDEAGNHHSQQT\SQDQKI KQRTFSLISGS*TTRTHGHREGN ITHRGLSRPNTARILCASKAHLG LPLRSSLP
5685	36053	A	5731	114	329	
5686	36054	C	5732	1	1983	
5687	36055	C	5733	1	588	
5688	36056	A	5734	1	597	
5689	36057	A	5735	1	721	MTSYNEQNKKPVTDPNEMAIH EDSNQEFKIAVVNETQRSPRSSP TEHLMTPPPLPTREQQPPLTVIF HYLPKSYKTAPPLSPFPDSLFGL SQPAPRDMDEAGNHHSQQT\K QEQKTKHCMFSLTSGS*TMRTH GHREGTVIHRGLLGQFSQQLIN KSEFSNTVCREKSGRVLQVNM ESPL*MIQDALQDQTTPKGPITV FL*LFYLDHLLRSSHKVASYLST ESRSRGSITVLFIRCSEP
5690	36058	A	5736	417	696	DRNRKANTACFQHSQVGVEQ* EHMDTGKV*SI*YGNYEHTSTC ERMEIQKATTEHLNL*S*SGSFL RFTWKMLQFSKISRSFYQVLKH QQKIM
5691	36059	A	5737	325	1489	RSPTLLMHVHYIKVISWRELLLI WLRAANASINPGVEQSPSGDPK TVTGFPFLRLEAADWVEEASVP KGVHIALSSQEQRAGDPRDLEA PSNLVISERTHRSFRVSWTPPSD SVDRYKVEYYPVSGGKRQEVV RTPGVPDLRLPAIIPQAAWLLA HLPAPSAPPTELPTKHTEAQSQ RCWSLLLCSVTEVAAPSQVVK EAPPSFHTGTENGYQGEESLFN KAYYGGGTNFFRKESQKLQQS AKKRDAELANGALGIIELNNDY TLKKVMKPLITSNTVTDEIERA NVFKMNGKWYLFTDSRGSKM TIDENKIPRNPTYKGREGPLQGE LQTTAQGNKRGYKQMEEHSM LMDRKNQYRENGLTAQA\PQPP PSGI*GYTAPCFPWENLI
5692	36060	B	5738	1	873	

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5693	36061	A	5739	274	716	QACYIYTTEYYAAIKNDEF/TVL CRDMDEAGNHHSQQTVTRTKN QTPHVLTHRWELNNENTWTQE GEHHTPGPVMLDSAPPTLGHQT PGSSAFGLWDLHQRLRLPRPQT KGSTVGFPGSEAFKLGLGHYW LSFFPSLQTAYRGTLPFNH
5694	36062	B	5740	134	2283	
5695	36063	A	5741	3	872	
5696	36064	A	5742	1	480	SKLNSGDGCWSGARRGSAHSR SPLPSPLRPRAKMATEGLHENE TLASLKSEAESLKGKLEEERAK LHDVELHQVAERV/VGPGAVC HEDQKDPQRPREQSPVHGLVQ R*EEDRELVTGWEGDRVGFLH HKQGARGHHALHVGDGMCLC PIGMCHCLWWFG
5697	36065	A	5743	3	387	AKMATEGLHENETLASLKSEA ESLKGKLEEERAKLHDVELHQ VAERV/VGPGAVCHEDQKDPQ RPREQSPVHGLVQR*EEDRELV TGWEGDRVGFLHHKQDPDSER RWHMCPVGRGERAAAAELPRT
5698	36066	A	5744	1	1575	
5699	36067	A	5745	20	510	
5700	36068	A	5746	1	1392	
5701	36069	A	5747	1	1560	
5702	36070	A	5748	3	325	
5703	36071	C	5749	206	409	
5704	36072	A	5750	1	855	
5705	36073	C	5751	233	571	
5706	36074	A	5752	1	3600	
5707	36075	A	5753	1	4137	
5708	36076	A	5754	3	1357	
5709	36077	A	5755	3	194	
5710	36078	A	5756	3	269	
5711	36079	A	5757	1	1770	
5712	36080	A	5758	164	411	RKNRKPNTAFLTHKWELNNEN TWTQGGNITHQG\CWGVQG*R RDSIRRNT*CKCRVPGCSKPPW HVYTYVTNLHILHMYPRT

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5713	36081	A	5759	1	3095	MKMADAKQKRNEQLKRWIGS ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLKLLHR GADINYANVDGLTALHQACID DNVDMVKFLVENGANINQPDN EGWIPLHAAASCGYLDIAEFLIG QGAHVGAVNSEGDTPLDIAEEE AMEELLQNEVNRQGVDIEAAR KEEERIMLRDARQWLNSGHIN DVRHAKSGGTALHVAAAKGY TEVLKLLIQAGYDVNIKDYDG WTPLHAAAHWGKEEACRILVD
5714	36082	A	5760	1	591	FTVTRCYAVAQEGTYFDGSGY AALVKEGYKVQSDVNITLEVS N\PRRNGVFLGISTAIVHAIGLEL VDGKVLFHVNNGAGRITAAYE PKTATVLCDGKWHTLQANKSK HRITLIVDGNAVGAESPHTQSTS VDTNNPIYVGGYPAGVKQKCL RSQTSFRGCLRKLALIKSPQVQS FDFSRAFELHGVFLHSCPGTES
5715	36083	A	5761	340	739	
5716	36084	A	5762	1234	1897	
5717	36085	A	5763	1	4070	VTPRAAWLGLGFRGSAVLGLC WQPRSPPSRAAGMMNRTTPDQ ELVPASEPVWERPWSVEEIRRS SQSWSLAADAGLLQFLQEFSQQ TISRTHEIKKQVDGLIRETKATD CRLHNVFNDFLMLSNTQFIENR VYDEEVEEPVLKAEAEKTEQE KTREQKEVDLIPKVQEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVELILEPKDLYIDRPLP YLIGSKLFMEQEDVGLGELSSE EGSVGSDRGSIVDTE
5718	36086	A	5764	1	972	

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5719	36087	A	5765	1	2193	MVPYSLLVTWLQKALGVRQY HVASVLCQRAKVAMRPFEPKY IHYDLLEKNINIVCK*LNRPLTL SEKIVYRHPDDPTSQEIERGGTY LQQWPDSVTMQD/ATAQMAM LQFISSRL/SKVTMPSTIHCDHLI EAQLGSEKDLHQAKDINHEVY NFLATGSVKYGLSFWKPGSGII HQIILENYEYPGVLLIGTDSHTP NGGSLGGICIGVGGA/DAVDVM TGIPWELKCPKVIGVKLMGSLS GWTSPKDVILKVAGILTMKGG TGAIVEYHGPVVDSISCTGMVT VCNMGLEIGTTTSVFHYNLRM KKYMSKTCQADIANLADEFKD HLVPDPGCHYDQLIEVNPSELK LHINGPFTPDLAHPVAEVGKVA EKEEWPLDI*VGLWGSCTNSSY EDMGCSAGVAKQALAHGLKC KSQFTITPCSEQIRASIEQDGYA QTLRDVGGIVLANACGPCIGQL HRKDINKQEKNIIVTSYNRNFM GHNDTNPETHAFITSPETVTAL AIVGTLKFNPETNYLTGKDGKK FKLEAPDADELPQAEFGPGQDT YQHP\PWGTTDHISAAGP*LKFR GHLDTISNNLLSGAINIENGKAN SVHDAVTHEFGPFPDTARYKK YGISWVVIGD*NYGKGSSWEH AALEPRHL\GGRAIITKSFARIHE TNLRRQGLLPLTFADPADNKIH LVDKLTIQSLKDLT/PGKPLKYI
5720	36088	B	5766	3	1205	
5721	36089	A	5767	435	1428	
5722	36090	A	5768	1	615	
5723	36091	A	5769	79	381	DKPQPHLQHTRTSKRLNRSSQA FLQNLLPQELATSAGNLAIRPR NACSLGFLVSRVPSLAATPRAP WNSGPRLSD*LLPRSSRLSS*RL TLPDRLGSPVDH
5724	36092	A	5770	38	452	
5725	36093	A	5771	435	524	
5726	36094	A	5772	284	411	
5727	36095	A	5773	1	354	
5728	36096	B	5774	1	942	
5729	36097	A	5775	1	417	
5730	36098	A	5776	88	279	EDLGRSQSESLGPEFQG*VVAIE TIWPTEPKIFTICLSGSHSQSPW NSGPRLSD*LLPRSSQLSS*RLT LPNRLRSLQDHHRCSR

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5731	36099	A	5777	206	816	FIDSMLSPSRYQ*LSSQNWKKL L*ISYGTKNEPA*PKQS*AQRTK LEASH*LTSNCTTSLH*SKQHGT GTKTEKKT*AIPFRT*AWAKTS* LKHQKQWQQKPK*TKKIKYLG IQLTTDVKDLFKENYKPLLNEI KEDTNKWKNIPCSWIGGINIMK MAILPKVIYRFNALPIKIPMTFF TELEKTTLNFIWNQKRARIAKTI LSTKNKAGGITLADFKLYYKPT LVKTAWYWYQNREENLGNTIQ DIGMGKNFMTKTPKAMATKA KIDKRDLIKPKSFCIAKETTIRM NRQPTEWEKLFAIYPSDKALIS GIYKDLKQIYKKKNNPIKKWA KEMNRHFSKEDIYAANRHVKN AHHHWSSEKCKSKPQ
5732	36100	A	5778	502	600	
5733	36101	A	5779	51	452	ADKQLQQSLRIQNQCTKITSILI HQQQTNREPNHE*TPIHNCFKE NKIPRNPTYKGCEGPLQGELQT TAQGNKKGYKQMEEHSMLMG RKNQYRENGHTAQELEKTKVH MEPKKSPHRQVNPKPKEQSWR HHTT
5734	36102	A	5780	381	528	LPPPLPAGLC**DQQQNSNAPLI H*EKERPPDDSYRIFLPRYHFHD DRI
5735	36103	A	5781	1	477	
5736	36104	A	5782	180	496	TPIHNCYKENKIPGNPTYKGCE GPLQGELQTTAQ*NKRGQKQM EEHSMLMDRKNKYHEN/EPYSP R*FIDSMPSPSNYQ*LSSQNWK KLL*GPYGTKKEPT*PRQS
5737	36105	A	5783	1	533	MGPEICTSDKLSDEADVTVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEEHSIKWKNIPSSWVG RISIMKTAILPKVYIRIKDDEWN IYRRYTEFRSLHHKLQNKYPQV RAYNFPPKKAIGNKEAVLCHG R*HDCISRKPHRLSPKSP*ADKQ LQQSLRIQNQCAKITSILIYQ*QT NREPNHE*TPIHNCFKENKIPRN PTYKGCEGPLQGELQTTAQGN KRGTFHQMEEHSILMGRKNQY HENGHTAQGLHPDKRR

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5738	36106	A	5784	599	870	TPANQQHYRRMTLQLKENQTN RKRQQKQHQQKRPHKNPIQRS ATSKIKGDGSIQP*MLPWGQSP QKALTLATAPEQRKDTPPVRGL SLQD
5739	36107	C	5785	1	1170	
5740	36108	A	5786	317	960	KWPYCPRQFIDSMPSPSSYQRL SSQNWKKLL*SSYGTKKEPTSP SQS*AKRTKLEASRYLTSNYTT RLQ*PKQHGTGTKTEI*INGTQQ SPQK*/QPHVYNYLIFNKPEKKK QWGKDSLFNKWDMDEVGNHH SQQTITRTGNQTPHVFTHRWEL NNEITWTQGAGHHTPGPVVGL GAGRGIALREIPNANDELMVQQ TNMAHIYLCIKPARCADVP
5741	36109	A	5787	903	1050	LPPPLPAGLC**DQQQNSNAPLI H*EKERPPDDSYRIFLPRYHFHD DRI
5742	36110	A	5788	281	491	SFGYIPSNGMAGSNGISSSRSLR NRHTDFHNG*TSLQSHQQCKSV PISPHPLQHLLFPDFLMIAILTGV R
5743	36111	A	5789	1	381	
5744	36112	A	5790	1	3231	
5745	36113	A	5791	1312	1463	KGSATCSPPQANATTTTALQML GGIPWGNACGIFTRPPPQTYLN THLSTR*RPLLLLLKCVR*KGSA TCSPPQANATTTTALQMLGGIP WGNACGIFTRPPPQTYLNTHLS TR
5746	36114	A	5792	811	1065	IS*VSFMSITH**WKKKEQQLLG CWLA*M*SMLICV*RERI*THKL E*LIILCI*RMKKILEIQKGMFKL LPY*TKRIMLK/TLNRQLNSTVS SLHSRVDSLEKSNTKLIEELAIA KNNIIKLQEENHQLRSENKLIL MKTQQHLEVTKVDVETELQTY KHSRQGLDEMYNEARRQLRDE SQLRQDVENELAVQVSMKHEI ELAMKLLEKDIHEKQDTLIGLR QQLEEVKAINIEMYQKLQGSED GLKEKKEIIVRLYWSALCG
5747	36115	A	5793	1	1353	
5748	36116	A	5794	78	503	TKELLHSKRNYHQSEQATYRM GENFCNLLI*QRANIQNLQ*TQT NLQEKNKQPHQKVGEGYQQTL LKRRHLCSQKTHEKMLIITGHQ GNTNQNHNEIPSHTS*NGDH*K VRKKQGHG*SWKPSFSANYRK DKKPNTSCSHSQ

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5749	36117	A	5795	2	200	YGLMIRTIPVDPTIRTTSVSLTV RLATMNPRSRPAPVDT\APGPP HLHKNQKSSQHSQYLDLTSYC
5750	36118	A	5796	76	195	
5751	36119	A	5797	1	2445	
5752	36120	A	5798	207	475	TNLQEKNKQPHQKVGKGYEQT LLKRKHSCSQQTYEKMLIITGH QRNANQNHNDIPSHSS*NNDH* KDRKQQMLERM*RNRNAFTLL VGV
5753	36121	B	5799	1	681	
5754	36122	A	5800	1	798	
5755	36123	C	5801	78	245	
5756	36124	A	5802	16	491	EPYPDRPREPKRDPEWSWGLW DKGGL\VLSLGRTRTEAHTALS RLRASMWIDRSTRAVSVHFTLY NPPTQLFTSVSLRVEILPTGSLV PSSLVESFSIFRSDSALQYHLML PQLVFLALSLIHLCVQLYRMMD KGVLSYWRKPRNWLEVASLVS FSFEK
5757	36125	A	5803	3	2791	
5758	36126	A	5804	219	392	
5759	36127	A	5805	1	1044	
5760	36128	A	5806	1	360	
5761	36129	A	5807	1	528	
5762	36130	A	5808	127	360	
5763	36131	A	5809	1	421	GRRSRLAMRPLSMSYSFDLSDV TTPESTKNLVESSMVNGGLTSQ TKENGLSTSQQVPAQRKKLLR APTLAELDSSESEEETLHKSTSS SSVSPSFP\EEPVL\EAVFTRKKP PKFLPISSTPQPERRQPPQRRHSI EKETP
5764	36132	A	5810	328	1086	
5765	36133	A	5811	1	2076	
5766	36134	A	5812	1	450	
5767	36135	A	5813	901	1506	
5768	36136	C	5814	17	106	
5769	36137	A	5815	24	330	ARDQPI/PKKGTVEGFEPADNK CLLRATDGKKKISTVVSSKEVN KFQMAYSNLLRANMDGLKKR DKKNKTKKTKTSSSSSSSSPA AATAATTAATTAATAAQ
5770	36138	A	5816	1	2247	
5771	36139	A	5817	1	339	
5772	36140	A	5818	3	463	
5773	36141	A	5819	3	83	
5774	36142	A	5820	1	642	
5775	36143	A	5821	2	583	
5776	36144	A	5822	193	409	

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5777	36145	A	5823	3	425	
5778	36146	A	5824	1	450	
5779	36147	B	5825	82	2096	
5780	36148	B	5826	1	1554	
5781	36149	A	5827	129	522	LCTDNIEITSKVHLHCSHHGAG LGTCSPLCLSLPPPPWAPVQPEP PR*APPPAPQRPVPSTIQGRKRL QLHS*SQ*DH/DAHAKVCSFTPE PARPRTHQKEETPNTSEHQKKQ TPDTPPLRTVTLTARLHGF
5782	36150	A	5828	1	541	
5783	36151	A	5829	1	714	
5784	36152	A	5830	188	287	KELPSGGHYNCRAPSSPHPAGS S*SGHQPNSQQ
5785	36153	A	5831	71	689	SPVLDDCPQGPLPSEESW/EQPV TRQYPLRPEVHKGLQNIVKHLK APGLVRKCSSHCNTPILGVQKP NGQWRLVQDLRLINEAVVPLY PVVPNPYTLLSQTPEEAEWFMV LDLKDAFFCIPLHSDSQFLFAFE DPTDHTSQITWMVLPQGFRDSP YLFGQALAQDLGHFSSRGTLVL QYADDLLFATSSEASCQQATLD LLNFLANQ
5786	36154	B	5832	45	1148	
5787	36155	C	5833	233	319	
5788	36156	C	5834	11	133	
5789	36157	A	5835	215	849	IKRLPLMKRMWL*LQPESLEIA GILVQ*MIE*QPKKGTNSIPVSK PSP/VVQKPNGQWRQVQDLRLI SDAVIPLYPAVSNPYTLLSQILE EAEWFTVLDLKDAFFCIPLRSD SQFLLAFEDPTDHTSQLTWTVF TQGFMDTPHLFGQSLAQDLGH FSSPGTLVLQYVDDLLLAKQQA TLDLLNFLANQGYKLSKLKAQ LCELLVFSSCARMHS
5790	36158	A	5836	1	449	MNKELGISSYKFCGMGRKTSVS AAKSVSATIPISRVQGLLQVLG QEVFLLLCQDQEEQAKREKRD QRKATALAMALRQTNLGGSER IENGAGQSPSRACYQCGLQGHF KKDYPTR/EPAAPCPLC*GNHW KMHCPRGQRSCDSHLAITHL
5791	36159	A	5837	1	723	
5792	36160	A	5838	186	602	
5793	36161	A	5839	1	843	
5794	36162	B	5840	1	1779	
5795	36163	A	5841	1	1182	

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5796	36164	A	5842	23	302	LSQWKNRWTRTFLASLSVIANI LEPLLNILHVAVWLMLPN*S*V KKQVIM\FWNWWVLGLTDFKN EATDPRVCSWPCWLRSEAADL CGECYSS
5797	36165	B	5843	1	2622	
5798	36166	A	5844	279	1024	
5799	36167	A	5845	3	3619	
5800	36168	B	5846	1	1898	
5801	36169	A	5847	1	420	
5802	36170	A	5848	1	1632	
5803	36171	A	5849	1	597	KYLTKKTQAASVEAVKMLDEI LLQLSASVPVDVMPGEFDPTNY TLPQQPLHPCMFP/LATAYSTLQ LVTNPYQATIDGVRFLGTSGQN VSDIFRYSSMEDHLEILE*LRVR HISPTAPDTLGCYPFYFCGNTPS FGSKIIRGPEDQTVLLVTVPDFS ATQTACLVNLRS/LACQPISFSG FGAEDDDLGGLGWAPDSKKW
5804	36172	A	5850	1	1490	RDAARRALNLLGLGEAVWTKQ VRSVAMFSEQAAQRAHTLLSPP SANNATFARVPVATYTNSSQPF RLGERSFSRQYAHIYATRLIQM RPFLENRAQQHWGSGVGVKKL CELQPEEKCCVVGTLFKAMPL QPSILREVSEEHNLLPQPPRSKY IHPDDELVLEDELQRIKLKGTID VSKLVTGTVLAVFGSVRDDGK FLVEDYCFADLAPQKPAPPLDT DRFVLLVSGLGLGGGGGESLLG TQLLVDVVTGQLGDEGEQCSA AHVSRVILAGNLLSHSTQSRDSI NKAKYLTKKTQAASVEAVKM LDEILLQLSASVPVDVMPGE\FD PTNYTLPQQPLHP\CMFPLATA YSTLQLVTNPYQATIDGVRFLG TSGQNVSDIFRYSSMEDHLEILE WTLRVRHISPTAPDTLGCYPFY KTDPFIFPECPHVYFCGNTPSFG SKIIRGPEDQTVLLVTVPDFSAT QTACLVNLRSLACQPISFSGFG AEDDDLGGLGLGP
5805	36173	B	5851	13	441	
5806	36174	A	5852	3	279	

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5807	36175	A	5853	23	841	EKAKEFRRAEEKKKEVPAVPET LKKK*RNFAELKIKRLRKKFA QKMLQRARRKFIHEKAKH\YH KEYRQMYRT\EILMA\RMARKA GNFYVPAEPKLAFVIRIRGINGV SPKVRK\VLQLLRLRQIFNGNLL *SSTKAS\INMLRDCRSHILAWG VPQILKSVNELIYK\RGYGKINK KRIA\LTDN\ALIARSLGK\YGIL LAWEDLIHEIYTV\GK\RFKEAN NFPVGPSNLSSPPRWK*KKKTT HFCKKVEDAGNREGRTRSNRP YLEGMDLRCLP
5808	36176	C	5854	57	287	
5809	36177	A	5855	1	450	
5810	36178	A	5856	1	549	
5811	36179	A	5857	3	581	EQRKIPLVPENLLKKRKAYQAL KATQAKQALLAKKEQKKGKG LRFKRLESFLHDSWRQKRDKV RLRRLEVKPHALELPDKHSLAF VVRIERIDGVSLLVQRTIARLRL KKIFSGVFVKVTPQNLKMLRIV EPYVTWGFPNLKSVRELILKRG QA\KVKNKTIPLTDNTVIEEHLG ECYSLGVSWGRKPGSLKL

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5812	36180	A	5858	1	2652	MFGRSRSWVGGGHGKTSRNIH SLDHLKYLYHVLTKNTTVTEQ NRNLLVETIRSITEILIWGDQND SSVFDFFLEKNMFVFFLNILRQK SGRYVCVQLLQTLNILFENISHE TSLYYLLSNNYVNSIIVHKFDFS DEEIMAYYISFLKTLSLKLNNH TVHFFYNEHTNDFALYTEAIKF FNHPESMVRIAVRTITLNVYKV DNQAMLHYIRDKTAVPYFSNL VWFIGSHVIELDDCVQTDEEHR NRGKLSDLVAEHLDHLHYLND ILIINCEFLNDVLTDHLLNRLFLP LYVYSLENQDKVFLIIHHAPLV NSLAEVILNGDLSEMYAKTEQD IQRSSVLPTLSSLWQGSHLSLNQ LQSGLHKCSSHLCGAQAAADS VTGEIPAIRSLEWLISAGSKART FFFLKMLIGFWEKVDCEYQRR QVLSTRLQEALPSNRLTDVAAV HSSCMLGFGSTAPRGSWIGDPA AVHLPLPGELAEHLGSKGTTTV TKHQPQAKPSIRCFIKPTETLER SLEMNKHKGKRRVQKRPNYK NVGEEEDEEKGPTEDAQEDAE KAKGTEGGSKGIKTSGESEEIE MVIMERSKLSELAASTSVQEQN TTDEEKSAAATCSESTQWSRPF LDMVYHALDSPDDDYHALFVL CLLYAMSHNKENLLKKRKAYQ ALKATQAKQELLAKKEQKKGK GLRFKLLESFLHDYWQQKPDK
5813	36181	A	5859	1	405	LEISIMAASISGYTFSAVCFHSA NSNADHEGFLLGEVRQEETFSIS DSQISNTEFLQVIKVIGWYRFR RNTQQQMSYREQVLHKQLTRI LGVPDLVFLLFSFISTANNSTHA LEYVLFRPNRRYNQRISLAIPN
5814	36182	B	5860	1	843	

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5815	36183	A	5861	3	1260	EISIMAASISGYTFSAVCFHSAN SNADHEGFLLGEVRQEETFSISD SQISNTEFLQVIQIYNHQPCSKL FSFYDYASKVNEESLDRILKDR RKKVIGWYRFRRNTQQQMSYR EQVLHKQLT\RILGVPDLVFLLF SFISTANNSTHALEYVLFRPNRR YNQRISLAIPNLGNTSQQEYKV SSVPNTSQSYAKVIKEHGTDFF DKDGVMKDIRAIYQVYNALQE KVQAVCADVEKSERVVESCQA EVNKLRRQITQRKNEKEQERRL QQAVLSRQMPSESLDPAFSPRM PSSGFAAEGRSTLGDAEASDPP PPYSDFHPNNQESTLSHSRMER SVFMPRPQAVGSSNYASTSAGL KYPGSGADLPPPQRAAGDSGE DSDDSDYENLIDPTEPSNSEYSH SKDSRPMAHPDEDPRNTQTSQI
5816	36184	A	5862	1	742	
5817	36185	A	5863	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFPVQNCLS LARSDSREQGLVLVMESRNRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSTFSQFSPISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSSKT GLSPSGNMEKNKVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
5818	36186	A	5864	2	626	LCQHNRIKHKGIRKVYACSHCP DSRRTFTKRLMLEKHVQLMHS LKDPDLKE/TDRCHQ*GGNRNK RRH/LSSPVPSGSWKNQFSR/CA MCGFTTENLLQFHEHIPQHKSD SSSYQCQECGLWYTSHVSLSRH LFIVHKLKEPQPVSKQNGAGED NQQENKPSHEDESPNGTVSDRK CKVCVKTFETEAALNTHMRIH GMAFIKSKRMSSAKK

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5819	36187	A	5865	1	765	MQRDVYISHVRKEHGKQMKK QPCCQRDKPFSSSHSLCWHNRI KHKVIRKVYTCSHCSDSRGTFT KQLMLEKHVQLTHGIKDPDLK E/TDRRHQ*GGNRNKRRPQGPQ SQVEVERTGSGVQASQ\GAITQ PLKKLKINVFKVHKCARA\GFT TENLLQFHEHIPQHKSDGSSYQ CREHLFVVHKLKEPQPVSKQN GAGEDNQQENKPSHEDESPNG AMSDRKCKVCAKTFETEAALN THMQTHGMAFIKSKRMSSDEK
5820	36188	A	5866	878	1095	AFFLDTLYTQFSRC*SRAFVPFA HPTAMACSSRR/LIRVQEQDAA QVTHQSFKDDLCVVLGDTLHH RFFLIFRH
5821	36189	A	5867	1	1137	
5822	36190	A	5868	1	1380	
5823	36191	A	5869	55	558	
5824	36192	A	5870	1	897	
5825	36193	A	5871	1	565	
5826	36194	B	5872	22	1696	
5827	36195	A	5873	295	522	
5828	36196	A	5874	3	3678	IPAPVSGRPPPGLLAEGKLSGPR PMCRTRLGSHTAASAPARMWL FHTLLCIASLALLAAFNVDVAR PWLTPKGGAPFVLSSLLHQDPS TNQTWLLVTSPRTKRTPGPLHR CSLVQDEILCHPVEHVPIPKGRH RGVTVVRSHHGVLICIQVLVRR PHSLSSELTGTCSLLGPDLRPQA QANFFDLENLLDPDARVDTGD CYSNKEGGGEDDVNTARQRRA LEKEEEEDKEEEEDEEEEEAGT EIAIILDGSGSID
5829	36197	A	5875	1	3189	

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5830	36198	A	5876	1119	2463	LRAGGPGQGGKGPAHPGRRVD ELLLGHPTAVGCAKGTDCPTPT PGGLWV*GVQEESSDLPTAVDS SRPDIRDQAWASVHWELYVHG SSFINT*GERGAGY/AVITW/STV VEARSMPQGTSAQKAELIAFIR ALELSEALAKTVRQRCVSCRQ HHARQGPAVPPGIQAYGAAPFE DLQVDFTEMPKCGDIRKIVTGD VNTPAILGVVSSSPPSHIGNNITE DPELQPILAGLSLSMYLVTVLR NLLIILAVSSDPHLHTPMCFFLS NLCWADIGFTLATVPKMIVDM QSHTRVISYEGCLTRISFLVLFA CIEDMLLTVMAYDCFVAICRPL HYPVIVNPHLCVFFLLVYFFLSL LDSQLHSWIVLQFTIIKNVEISN FVCDPSQLLKLACSDSVINSIFM YFHSTMFGFLPISGILLSYYKIVP SILRISSSDGKYKAFSTCGSHLA
5831	36199	B	5877	1	1830	
5832	36200	C	5878	109	245	
5833	36201	B	5879	1	801	
5834	36202	B	5880	171	288	
5835	36203	B	5881	49	502	
5836	36204	B	5882	1	639	
5837	36205	A	5883	1	821	MSGQFDFLLWTPEEDNSDESD AEGEHGDGAEEEAPPPVPRPGP KPAGLGRRPCPYEQAQGGDGP EEQWMSFCWDIPRKSGAPRERI TLRRHLEDCGCKVSKKKAQICR QQKDPQEESPAQFYERLCEAYG MYTPFDPDSPENQRMIHMALV RQSAEDMRRKLQKQAGLAGM NPSQLLERASQVFVNRDAV/TP* GKQQREWRERG*YDSQYRRGG TQPCDIVPNIRRERR*YHSQYRR RARPPGPH*SERGALRPGSLPRQ AA*RVPSGPADGQ
5838	36206	A	5884	1	1860	

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5839	36207	A	5885	2745	3732	IRIGKNYFKVHMEPKKSPHRQV NPKPKEQSWRHHTT*LQTILQG YSNQNSMPGPTPQ\PSTPAPGG NLRNPQSSDLLQVTKQQGQAL AIQREAPLHRIPAPEAIPWYFQP QPATQLGSPPVDPPSSAMM/SR RAHRSRGPDRQGYPLQGD*PGE PRPQEH*RGHSQERLPSSEKQTP ICPPAQATQHPEEPDAHQPYKH LFQVCAHQGHPVAQRRN*PGY WERYHSAEDPELQPILAGLSLS MYLVTVLRNLLIS
5840	36208	B	5886	1	2379	
5841	36209	B	5887	1	6741	
5842	36210	B	5888	165	928	
5843	36211	A	5889	56	2028	
5844	36212	B	5890	1335	3804	
5845	36213	A	5891	365	1573	
5846	36214	A	5892	1	1491	
5847	36215	A	5893	25	458	
5848	36216	A	5894	1	1194	MGGNAADKFRAGVELALQSG NKVCVCSPRTTISGDAVAPRSV LPGCRHIPGEISQHSHCWAGRS LSSRKRGSLFRRMGFIKVVKNK AYFKRYQVKFRRR\RKGKT\DY YARKR\LVIQDKNKYNTPKY\R MIV\RVTNRDI\ICQMLYA/RRIE GDMIVCAAYCTPNLPKIWV*RV GLTNYAAAY\CTGLLL\ARRLL NRFGMDKIYEGQV\ELTGDEYN VESIDGQPGAFTCYLDAGLAR\ TTTGNKVFGAPEGKLWMGGLS IPHSTK\RFPG\YDSE\SKEFNA\E VTSGKHIMGPKCLQNYM\RYL ME\ED\EDAYKK\QFS\QYIK\NS VT\PDMM\EEMYK\KAHAAIRE ESSSMEKKAQGKKFKKKRWNR P\KMSLAQKKDRVAQKKASFL QSSRSGLLESLTPAIFP
5849	36217	A	5895	1	1191	
5850	36218	A	5896	21	159	PRSSVRPAGGFSSTCPPSWAAS RSCTTSHGCGHQ*CAGTGTQTR L
5851	36219	A	5897	1	1062	
5852	36220	A	5898	1	246	
5853	36221	A	5899	1	642	
5854	36222	A	5900	2	648	
5855	36223	A	5901	1	555	
5856	36224	B	5902	151	513	

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5857	36225	A	5903	1	2915	VSLAFCQPLSLSLSPLLPLASSL APERTHLPGPGSLLLSPPSFPAR PREPRGCVTAAPPDKMDTAEE DICRVCRSEGTPEKPLYHPCVC TGSIKFIHQECLVQWLKHSRKE YCELCKHRFAFTPIYSPDMPSRL PIQDIFAGLVTSIGTAIRYWFHY TLVAFARWEVVLLPACRIYKCL FLGSVSSLLTLPLDMLSRKNLL ADCLQGCF\VVTCTLCAFISLV WLREQIVHGGAPIWLEHAAPPF NAAGHHQNEA
5858	36226	A	5904	3	907	
5859	36227	B	5905	102	406	
5860	36228	B	5906	1	5241	
5861	36229	A	5907	1	519	
5862	36230	A	5908	1	3067	TRDAAMAEAALEAVRSELREF PAAARELCVPLAVPYLDKPPTP LHFYRDWVCPNRPCIIRNALQH WPALQKWSLPYFRATVGSTEV SVAVTPDGYADAVRGDRFMM PAERRLPLSFVLDVLEGRAQHP GVLYVQKQCSNLPSELPQLLPD LESHVPWASEALGKMPDAVNF WLGEAAAVTSLHKDHYENLYC VVSGEKHFLFHPPSDRPFIPYEL YTPATYQLTEEGTFKVVDEEA MEKAEVSRTCLLTVRVLQA
5863	36231	A	5909	1	429	
5864	36232	A	5910	1	690	
5865	36233	A	5911	1	376	
5866	36234	A	5912	1	471	
5867	36235	A	5913	1	606	
5868	36236	A	5914	3	2756	SPGGRTPAARDSIVREVIQNSKE VLSLLQEKNPAFKPVLAIIQAG DDNLMQEINQNLAEEAGLNITH ICLPPDSSEAEIIDEILKINEDTRV HGLALQISENLFSNKVLNALKP EKDVDGVTDINLGKLVRGDAH ECFVSPVAKAVIELLEKSGVNL DGKKILVVGAHGSLEAALQCLF QRKGSMTMSIQWKTRQLQSKL HEADIVVLGSPKPEEIPLTWIQP GTTVLNCSHDFLSGKVGCGSPR IHFGGLIEED
5869	36237	A	5915	3	404	RLKEKKLVKEVIAVSCGPAQCQ ETIRTALAMGADRGIHVEVPPA EAERLGPLQVARV/AVVTADLR LNEPCYATLPNIMKAKKKKIEV IKPGDLGVDLTSKLSVISVEDPP QRTAGVKVETTEDLVAKLKEIG

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5870	36238	A	5916	1	334	
5871	36239	A	5917	88	870	MADVRVLVAVKRVIDYAVKIR VKPDRTGVVTDGVKHSMNPFC EIAVEEAVRLKEKKLVKEVIAV\ SCGPAQCQETI\RTALA\MGA\D RGIHVE\VPPAEAERF/GVPLQV ARVLGQAWQRRRRLDLVLLGK QA\IACTDCNQ\TGQMTAGFLD WPQGTF\ASQVTLEGDKLKVER EIDGGLETLRLKLPAVVTADLR LNEPRYA\TLP\NIMKAKKKKIE VIKPGDLGVDLTSKLSVISVEDP PQRTAGVKVETTEDLVAKLKEI
5872	36240	A	5918	1	774	
5873	36241	A	5919	1	1557	
5874	36242	A	5920	1	759	
5875	36243	A	5921	305	638	
5876	36244	A	5922	364	540	
5877	36245	A	5923	9	111	
5878	36246	A	5924	1	594	
5879	36247	A	5925	169	594	
5880	36248	A	5926	37	936	
5881	36249	B	5927	91	2043	

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5882	36250	A	5928	1	2298	MSRKGPRAEVCADCSAPDPGW ASISRGVLVCDECCSVHRSLGR HISIVKHLRHSAWPPTLLQMVH TLASNGANSIWEHSLLDPAQVQ SGRRKANPQDKVHPIKSEFIRA KYQMLAFVHKLSCRD\DDGVT AKDL\SKAN*HSSVR\TGKPWK TCLRLLS\LGA\QANFFHPEKGT TPLHVAAKAGQTLQAEL\LVVY GADPGSPDVNGRTPIDYA\RQA GHHELAERLVEC\QYE\LTERLA FYLCGRKPDHKNGHYIIPQMAD SLDLSELAKAAKKKLQALSNRL FEELAMDVYDEVDRRENDAV WLATQNHSTLVTERSAVPFLPV NPEYSATRNQGRQKLARFNAR EFATLIIDILSEAKRRQQGKSLSS PTDNLELSLRSQSDLDDQHDYD SVASDEDTDQEPLRSTGATRSN RARSMDSSDLSDGAVTLQEYL ELKKALATSEAKVQQLMKVNS SLSDELRRLQREIHKLQAENLQ LRQPPGPVPTPPLPSERAEHTPM APGGSTHRRDRQAFSMYEPGS ALKPFGGPPGDELTTRLQPFHS TELEDDAIYSVHVPAGLYRIRK GVSASAVPFTPSSPLLSCSQEGS RHTSKLSRHGSGADSDYENTQS GDPLLGLEGKRFLELGKEEDFH PELESLDGDLDPGLPSTEDVILK TEQVTKNIQELLRAAQEFKHDS FVPCSEKIHLAVTEMASLFPKRP
5883	36251	A	5929	1	924	
5884	36252	A	5930	214	387	RRAFHPTPVTSARSTLHSFGQL RLPHSM*SGGTLLISMMQANQS LSLEFSKWTSFPLD
5885	36253	A	5931	1	1639	
5886	36254	A	5932	1	1098	
5887	36255	A	5933	1	546	NSSQVLQF*YLWVNEAPFRLLT MPQPYPQINITADQLWGSVAVL V*MH\NGLPGLCI*AWEKTTSG GEQYPSSSAIKQGPKEPYADFIA RLQESLKKVIADLAAQDIVLWL LAFDNANPECQAALRPIRGKAH LVDYTKVCDGIRDKLHKATLL AQAMAGLRMGKGNTPFPGACF NCGKHGH

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5888	36256	A	5934	1	648	MGQVWGLVHFTLEVFHTGDEE EQEYSEVTEDVTEHVYLPAKA KVAKEEEAGIQQARQEGDLEA WQFPVRIHPPDQQENITATFEPF PFKLLKELKQAINQYGPGSPFV MGLLKNVTVSSQMIPTDGDPLT RACLTPAQFLQFKTWWADEAS IQAARNAWAQPQINITADQLLG VGGWAGLDAQFVMQDDAIEQ LRGVCIRAREK\IT*CGEQYPSF
5889	36257	A	5935	120	254	
5890	36258	C	5936	366	479	
5891	36259	A	5937	1	933	
5892	36260	A	5938	1	840	MGKVWGLVHSTLELFHTDVEE EGEYNEVTEEVTKHVYLPAKA KAAKEGEVHPYHSAPPHYYFE ENDPPDLSFLEDTGTPRLAAAA TTKANA\KQPLLLSPSMHR/PLP TRPLLAG\QATALPQGV*PLIAP PTRPHLEHCSTQ*RPQPAPTLGE ITPVTVPQAPLHPRAVQPW/HST PTRSWLQAVMPGIAPPSRSPPW AVQLRILTYLGCLSTTPAAVQS LSQPPASVRQARVPQAPASSLC QEKPPSPPPVAPHGAAAAARPP SYHSSCASVAVVAANVLIG
5893	36261	A	5939	1	134	MGQVW*KSQSPKA*EPGVSCP RAGRREASVPRWYSS
5894	36262	A	5940	1	1158	
5895	36263	A	5941	1	673	MGIALGSPTTGPKAMKQNLSIG PAGILLPQPVMTPGCPAAAPPV APRCGYVLSEDAWGNLQGLCT GLSCGQPVAPWATDSGGAQDP VALLPPFPSRGLLGPSCMQRSQ VVKGGRQSEISSQNKKVIADLA AQDIVLQLLAFDNANPDCQAA LRPIRGKAHLVDFIKACDVIGGI PNLLLHPRGLRAITIAVFGKQ\IR TSGSNPLRSTFLSRSRSISKNCSA EV
5896	36264	A	5942	1	1182	

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5897	36265	A	5943	1056	2128	TQPPTWGQIKKLSQMVEENLR KAGQLVTMNNLMVAMIVVITT TEEQEYSEVTEEVTEQVYLPAK AKVAKEGEVHPYPSAPPHYYFE EKEWPDPPDLSFLEDTRQKVVA PVTVRAAPRATVLSSIQAGIQQ AR*EGDLEAWQFPVRIHPPDQQ GNIIVTFEPFPFKLFKEFKQAVN QYGPGSPFVMGLLKNVAVSSW MIPTDWDALTRACLTPAQFLQF KTCAMKQGPREPYVDFIARLQE SLKKMIADSAAQEIVLQLLAFD NAHPDCQAALRPIRGKAHLVD YVKACDGIGEYTPSTYEKKVN CKTASCRSFRRYPEEGIVITGDD SSMRVVVPEDLPVGQDVEVED RDIDDPDPV
5898	36266	A	5944	1	300	
5899	36267	A	5945	1	373	
5900	36268	A	5946	1	2976	
5901	36269	A	5947	287	544	
5902	36270	A	5948	831	4555	
5903	36271	C	5949	108	434	
5904	36272	C	5950	145	402	
5905	36273	A	5951	3	1104	GSRPGGHTLQSHRGRHAQGLR SPLLAPVCLGCGTWGQRRLFW SLKI*RLLCWF/CRRLQINCKNK PAIPRGPT/GPSEKSGLLLQDQG DTTNTEEENSKSLENIFGRVIKE NFQSLVRDLDI\QYKKHKEHPG NSSQKDHHLGTLSSGYPKLRQR KES*ELSDRSTRKISQS/YNLYTP NTGAPRFIKQLLTDLRNEIDSNT IIVGYFSTPLTALDRSSRQKVND ETVDLNYTLEQMDLTEIYRTFH PTTTEYTFYSTVHGTFSKIDHMI CHKMSLNEFKKTEIISSTLSDHS GIKLEINSKMNLQNHANTWKL NNLLLNEHWVKNEIKMEIEKFF KLNDSNDTTYQNLWDMAKAV LRGKFIALNTYIKKMM
5906	36274	B	5952	1	2367	
5907	36275	A	5953	21	132	WREGARQCQEDPAEFLSD*DW ADPGPPHNAPGQNWH
5908	36276	A	5954	1	1461	

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5909	36277	A	5955	31	802	SAWWNSRELLDPQSRSRSGFCF *EYPPTSGTEQESVSGNRALCSS LRMNGDQNSDVYAQEKQDFV QHFSQIVRVLTEDEMGHPEIGD AIARLKEVLEYNAIGGKYNRGL TVVVAFRELVEPRKQDADSLQ RAWTVGWCVELLQAFFLVAD DIMDSSLTRRGQICWYQKPGV GLDAINDANLLEACIYRLLKLY CREQPYYLNLIELFLQSSYQIEI GADPGPPHSPPRAMWILSDSLK RGTNLLSSTRQLSTPSTFL
5910	36278	A	5956	1	532	RLNEAEQKYKDIQDKLQIISEET NARAPECMALKADVVAKKRA YNEAEVLYNRSLNEYKALKKD DEQLCKRIEELKK/RVLTN/RLE PERLERQKKISWLKERVKAFQN QENSVNQEIEQFQQALEKDKEE HGKIKREKLDVKHALSYNQRL LKELKDSKTDRLKRFGPNVPAL LEAIDD
5911	36279	A	5957	121	475	
5912	36280	A	5958	131	2891	
5913	36281	A	5959	131	3101	
5914	36282	A	5960	44	292	CQDYRWLLASSVLCWLY*KTQ QSDTEDLLCSAPTGPPNPEEDD GKS*PEKCRQMT*KKWSINCKC FFASSHNTTLSIGLFLR
5915	36283	B	5961	26	239	
5916	36284	A	5962	131	3121	LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDPIVASEE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTTSTIIT TTVITTEQAP
5917	36285	A	5963	1	1185	
5918	36286	A	5964	495	636	PSVVLDINVSFNHWSAIFLTME\ PFCHRVRSHAMESR*GSVLP*N KPQ
5919	36287	A	5965	2	376	

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5920	36288	A	5966	3	688	GTSAGDGCPHPHTVLWPPDIMP PKKDVPVKKPAGPSISKPAAKP AAAGAPPAKTKAEPAVPQAPQ KTQEPPVDLSKVVIEFNKDQLE EFKEAFELFDRVGDGKILYSQC GDVMRALGQNPTNAEVLKVLG NPKSDEMNVKVLDFEHFLPML QTVAKNKDQGTYEDYVEGLRV FDKEGNGTVMGAEIRHVLVTL GEKMTEEEVEMLVAGHEDSNG CINY\EELVRMVLNG
5921	36289	A	5967	54	540	AVYMCDLTENQTADLIPST\EF KEA\FQLFDRTGDGKILYSQCG DVMRALGQNPTNAEVLKVLGN PKSDEMNVKVLDFEHFLP\MLQ TVAKNKDQGTYEDYVEGLRVF DKEGNGTVMGAEIRHVLVTLG\ EKMTE\EDVHMLVAGHEDSNG CINYEAFVRHILSG
5922	36290	A	5968	1	405	
5923	36291	A	5969	93	506	
5924	36292	B	5970	43	615	
5925	36293	A	5971	2	598	TRTSLHAALFSWDPVGTSLETFI SHLEVKKGMLVGIVGKVGCGK SSLLAAIAGELHRWEQVQCGG HTLH*APEQMLRGHVAVRGLS KGFGLATQEPWIQFATIRDNILF GKTFDAQLYKEVLEACALNDD LSILPAGDQTEVGEKGVTLSGG QRARIALARAVYQEKELYLLD DPLAAVDADVANPPACTGCNP
5926	36294	B	5972	137	371	
5927	36295	A	5973	1	1398	
5928	36296	A	5974	1	915	
5929	36297	A	5975	40	564	
5930	36298	A	5976	62	280	
5931	36299	A	5977	17	744	
5932	36300	A	5978	1	537	
5933	36301	A	5979	242	576	AANSLYKGSNSAALIILVGP*IS CLTHPVYMK*APS*TICLLYSM VILKALFFPQNINFIFLPVKSRHS
5934	36302	A	5980	924	3473	
5935	36303	A	5981	1	604	
5936	36304	A	5982	288	732	RNCIANYDFLILPTSF*WCSFFV LLFLFLSLSLSSLKLHSDLDKGE GTAKYTLSGDGAGP\VFTIDETT GD\IHAIRSL\DREEKPFYTLR\A Q\AVDIETRKPLEPESEF\IIKVQ DI\NDNEPKFWGWDLMVATGP QKWSPVG*VGQIKIL
5937	36305	A	5983	1	1510	

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5938	36306	A	5984	1	603	
5939	36307	A	5985	250	505	GFSPTWQ*MNTHPSLMCFSPSR TTGSAAAN*RGQQKSGVPFWS* SHVKGKDQIPVPICPCTTAPVT MESTCIC*PTHVSCKTLMV
5940	36308	A	5986	3	131	RVLVPDIRGAI*AVPKSPSIKSYP ALPRALFLLPPYPDDLGI
5941	36309	A	5987	1	913	
5942	36310	A	5988	5	177	
5943	36311	A	5989	3	383	
5944	36312	A	5990	1	1323	
5945	36313	A	5991	342	594	
5946	36314	A	5992	1	321	
5947	36315	A	5993	3	601	
5948	36316	A	5994	1	1023	
5949	36317	A	5995	1	606	
5950	36318	A	5996	1	1536	
5951	36319	A	5997	2	1394	
5952	36320	A	5998	371	1045	
5953	36321	A	5999	3	360	
5954	36322	A	6000	1	636	
5955	36323	C	6001	1	861	
5956	36324	A	6002	1	711	

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5957	36325	A	6003	18	2446	AGSPPRADAAAGLWERGHLLS AAVAAMGKRDRADRDKKKSR KRHYEDEEDDEEDAPGNDPQE AVPSAAGKQVDESGTKVDEYG AKDYRLQMPLKDDHTSRPLWV APDGHIFLEAFSPVYKYAQDFL VAIAEPVCRPTHVHEYKLTAYS LYAAVSVGLQTSDITEYLRKLS KTGVPDGIMQFIKLCTVSYGKV KLVLKHNRYFVESCHPDVIQHL LQDPVIRECRLRNSEGEATELIT ETFTSKSAISKTAESSGGPSTSR VTDPQGKSDIPMDLFDFYEQM DKDEEEEEETQTVSFEVKQEMI EELQKRCIHLEYPLLAEYDFRN DSVNP\DINIDLKPTAV\LRPYQE KSLR\KMFGNGRARSGVIVLPC GAGKSLVGVTAACTVRKRCLV LGNSAVSVEQWKAQFKMWSTI DDSQICRFTSDAKDKPIGCSVAI STYSMLGHTTKRSWEAERVME WLKTQEWGLMILDEVHTIPAK MFRRVLTIVQAHCKLGLTATLV REDDKIVDLNFLIGPKLYEANW MELQNNGYIAKVQCAEVWCP MSPEFYREYVAIKTKKRILLYT MNPNKFRACQFLIKFHERRNDK IIVFADNVFALKEYAIRLNKPYI YGPTSQGERMQILQNFKHNPKI NTIFISKVGDTSFDLPEANVLIQI SSHGGSRRQEAQRLGRVLRAK KGMVAEEYNAFFYSLVSQDTQ
5958	36326	A	6004	1	933	
5959	36327	A	6005	1	879	
5960	36328	A	6006	1	727	
5961	36329	A	6007	1	1509	
5962	36330	A	6008	1	1698	

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5963	36331	A	6009	2465	2751	VPTSSAPMPWPSRQWERSSRT MTVISSSQLMALGP*RTAQVLA AAPA*LGASSAARGIDPQAGKT QK\ETDIATMQLCANKLDKKDF FGKSDPFLVFYRSNEDGTFTICH KTEVVKNTLNPVWQPFSIPVRA LCNGDYDRTVKIDVYDWDRD GSHDFIGEFTTSYRELSKAQNQ FTVYEVLNPRKKCKKKKYVNS GTVTLLSFSVDSEFTFVDYIKGG TQLNFTVAIDFTASNGETRMSE KVGGNPLQPTSLHYMSPYQLS AYAMALKAVGEIIQDYDSDKL FPAYGFGAKLPPEGRISHQFPLN NNDEDPNCAGIEGVLESYFQSL RTVQLYGPTYFAPVINQVASLP
5964	36332	A	6010	1	1059	
5965	36333	A	6011	255	405	
5966	36334	A	6012	251	1199	
5967	36335	A	6013	1	1791	
5968	36336	A	6014	335	984	
5969	36337	A	6015	1	127	LPLRLSYEIYLYFTF*KPEHNKS HFLESHLIRNTRSALNTRK
5970	36338	A	6016	1	774	

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5971	36339	A	6017	186	2699	PRGAKPAVPAGPERPGPGPGPC SPRPMVLPTCPMAEFALPRHSA VMERLRRRIELCRRHHSTCEAR YEAVSPERLELERQHTFALHQR CIQAKAKRAGKHRQPPAATAP APAAPAPRLDAADGPEHGRPA THLHDTVKRNLDSATSPQNGD QQNGYGDLFPGHKKTRREAPL GVAISSNGLPPASPLGQSDKPSG ADALQSSGKHSLGLDSLNKKR LADSSLHLNGGSNPSESFPLSLN KELKQEPVEDLPCMITGTVGSIS QSNLMPDLNLNEQEWKELIEEL NRSVPDEDMKDLFNEDFEEKK DPESSGSATQTPLAQDINIKTEF SPAAFEQEQLGSPQVRAGSAGQ TFLGPSSAPVSTDSPSLGGSQTL FHTSGQPRADNPSPNLMPASAQ AQNAQRALAGVVLPSQGPGGA SELSSAHQLQQIAAKQKREQML QNPQQATPAPAPGQMSTWQQT GPSHSSLDVPYPMEKPASPSSY KQDFTNSKL/PHDA*CE*EFPSA RRPLPPAQPCEPAESPATE*LES ELRE/YTRGLCW\IRQYKTPFSL QSGLWARQPGVWPEQASPDGL SSPAAVPYKSRAELPVSDEAKA RKYAFPITGSTWPGAEPFQCPC ASPGYQCWDPAACRVRGQLPQ QLPLSQQPATGRCNEAASVAFG PTETKGAAAKAFTATAVPSEAT APSRGTGEATVSAPSDPPTTPVP
5972	36340	A	6018	1	1062	
5973	36341	A	6019	3	566	ASRPPVTLRLVVPASQCGSLIG KGGCKIKEIRESTGAQVQVAGD MLPNSTERAITIAGIPQSIIECVK QICVVMLESPPKGVTIPYRPKPS SSPVIFAGGQAYTIQGQYAIPQP DLTKLHQL\AMQQC\HFPMTHG \NTGFQWALES\SFPEV\KGYW\ AGLDASAQTTSHELTIPNDLIGC IIGRQGAKIN
5974	36342	A	6020	2	531	TLRSSWQVVRTGTAQAATVRG FPPHPPRP\SASTLTLEGPPLEAY TIQGQYAIPQPDLTKLHQL\AM QQSHFPMH/GDGIHSDYSAG\LD ASA\QTTSH\ELTISKRILIGLA*S GRSRAPKINGGSRQMSGAQI\KI ANPV\EGSTD*GRFTITGSAASIS LAQYLINVRLSSETGGMGSS

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5975	36343	A	6021	181	1369	PLKVQLPRTLLDMDTGVIEGGL NVTLTIRLLMHGKEVGSII\GKK GESVKKMREESGARI\NISEGNC PERII\TLAGTH*LPSFKAFAMI\I DKLGRRDISSSM\TNSTAAQLGP PVTLKLG\APAS\QCGSLIGKGG CKIKEIRESTGAQVQVAGDMLP N\STEAGHHYLLGIPQSII\ECV\K QILRGSCWETLFPSSPPKGVTIP\ YRPK\PSSSPV\IF\AGGPGQVPA QAATVRAFPTPPRPCGSTLTWE GPPLEAYTIQGQYAIPQPD\LTK L\HQL\AMQQSHFPMTHGNTGF SG\IESSF\PEVKGYW\AGL\DAS AQTTSHELTI\PNGFDWAGIIGA FKGAKIN\EIRQMSGAQIKIANP VE\GSTDRQVTITGSAASISLAQ YLINVRLSSETG\GMGNN
5976	36344	A	6022	1	690	
5977	36345	A	6023	1	399	
5978	36346	A	6024	3	397	
5979	36347	A	6025	3	249	
5980	36348	A	6026	177	477	
5981	36349	A	6027	49	451	
5982	36350	A	6028	1	1305	
5983	36351	A	6029	1	568	
5984	36352	A	6030	207	1053	PLTFGPARWRETPPSLYKEFSG LFGSFFLSSAWGAHNLRALFLL LPSSRIQPTPWVFGDLKSPAGL QVLNDYLADKSYIEGYVPSQA\ DVAVFEAVSSPPPADLCHALR WYNHIKSYEK\EKASLPGVKKA LGKYGPADVEDTTGSGATDSK DDDDIDLFGSDDEE\ESEKPKRL \REERLAQYESKKAKKPG\LVA KSSILLLVKP\WD\DETDMAKLE ECVRSIQADGLVWGSSKL\VPV GYGIKKLQIQCVVEDDKVGTD MLEEQITAFEDYVQSMDVAAF
5985	36353	A	6031	1	211	
5986	36354	A	6032	27	241	EVFGSWWQVPHEWLGSVLVV MSEFLFH*LM*ELVLKRV*CLS HLSLAPFLAM*YACSSSSPSTMI VSFFFF
5987	36355	A	6033	1	588	

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5988	36356	A	6034	279	1333	LIFCGCWLFASLTVMEAAHFFE GTEKLLEVWFSRQQPDANQGS GDLRTIPRSEWDILLKDVQCSII SVTKTDKQEAYVLSESSMFVSK RRFILKTCGTTLLLKALVPLLKL ARDYSGFDSIQSFFYSRKNFMK PSHQGYPHRNFQEEIEFLNAIFP NGAGYCMGRMNSDCWYLYTL DFPEER\VISQPDQTLEILMSELD PAVMDQF*HEDG\VTAKDVTRE SGIRDLIPGSVIDATMF\NPCGYS \MNGMKS\DGTYWT\IHITPEPEF SYVSFETNLSQTSYDDLIRKVV EVFKPGKFVTTLFVNQSSKCRT RLGLPQK\IEGFKR\LDCQEGWF KDSNFFF\TSFAKKQQQQQS
5989	36357	A	6035	1	687	
5990	36358	A	6036	1	894	
5991	36359	B	6037	1	1458	
5992	36360	A	6038	1	1062	
5993	36361	A	6039	1	1218	
5994	36362	A	6040	277	3508	RSGRIAWAQEMDAAGRGCHLL PLPAARGPARAPAAAAAAAAS PPGPCSGAACAPSAAAGAGAM NPSSSAGEEKGATGGSSSSGSG AGSCCLGAEGGADPRGAGSAA AAGAAALDEPAAAGQKEKDEA LEEKLRNLTFRKQVSYRKAISR AGLQHLAPAHPLSLPVANGPA KEPRATLDWSENAVNGEHLWL ETNVSG\DLCYLGEENCQVRFA KSALRRKCAVCKIVV/HTTACIE ELEKINFRCKPTFREG\GS
5995	36363	A	6041	45	155	
5996	36364	A	6042	1	979	
5997	36365	A	6043	3	1042	
5998	36366	A	6044	2	401	
5999	36367	A	6045	1	5772	
6000	36368	A	6046	16	5678	VTSGRLLFYFRSMGPGCDLLLR TAATITAAAIMSDTDSDEDSAG GGPFSLAGFLFGNINGAGQLEG ESVLDDECKKHLAGLGALGLG SLITELTANEELTGTDGALVND EGWVRSTEDAVDYSDINEVAE DESRRYQQTMGSLQPLCHSDY DEDDYDADCEDIDCKLMPPPPP PPGPMKKDKDQDSITGEKVDFS SSSDSESEMGPQEATQAESEDG KLTLPLAGIMQHDATKLLPSVT ELFPEFRPGKVLRFLR
6001	36369	A	6047	1	354	

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6002	36370	A	6048	1	666	
6003	36371	A	6049	129	456	TYPAVGESSRRPERSRGVPGPD AAAESHFRPGRISNPLHRAGEQ GHARAEGSGVFRPHRGRGLRL LFVQAPDQVDAPVHG*VAPPAP GARDAQTCRSHECPRTRPLDEV
6004	36372	A	6050	1	1095	
6005	36373	A	6051	171	619	
6006	36374	A	6052	1	621	
6007	36375	B	6053	1	181	
6008	36376	A	6054	1	905	
6009	36377	A	6055	1	855	
6010	36378	A	6056	2	244	
6011	36379	A	6057	3	829	LTDCLKDVDLIPPFNRMLLEVT FGKLYAWTVQNILNVLMDASA KFKELGIQPVPLQTITSENPLGP SLGSIPQARFLLMMLSMLTLQH SANNLDLLLNSGTLALTQTALR LIVLPDVELLI*DHLL*MQTSIV* LPVLALLLAQHRSFGPSCDNVE EDMNASAQGASATVLEATRKE TAPVHLPVSGPELAATMKIGTR VMRGVDWKWGD/QEAEQTER NIHPTTMMFTSTINLLQTLCLPA RVHAEIMQSEATKTLCGLLQIL VESGTTDKTRME
6012	36380	A	6058	133	5421	IFVFGCPGSPRLQMVENRYTES FFTGQNCRNNEKVTLVRIADLE NHNNDGGFWTVIDGKVYDIKD FQTQSLTENSILAQFAGEDPVV ALEAALQFEDTRESMHAFCVG QYLEPDQEGVTIPDLGSLSSPLI DTERNLGLLLGLHASYLAMSTP LSPVEIECAKWVQSSIFSGGLQT SQIHYRYNEEKDEDHCSSPGGT PASKSRLCSHRRALGDHSQAFL QAIADNNIQDHNVKDFLCQIER YCRQCHLTTPIMF

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6013	36381	A	6059	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAKSQGCSRN ARHQKARSMPLQDQHLALAIL LELAVQRGTLSQMLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLLQTFQSIICSKDTPPSEGN MHLLSGPLSPSESFLRESFFTVQ NCRNNEEVTLICKADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFCVGQYLEVR LYALSDAEDGRG\TL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTPASKSR\CSHRWALG DHSQAFLQAIADNNIQDHNVKT HQEQGRSYKEVCTPVIERLRFL SNELRPAVGNDLSIISEFKLLSSL PRWRRIAQKIIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIAIKSPKTITSENP LGPSLGSIPQARFLLMMLSMLT LQHSANNLDLLLNSGTLALTQT ALRLIGPSCDNVEEDMNASAQ GVSATVLEATRKETAPVHLPVS GPELAATMKIGTRVMRGVDW KWGDQDGPPPGLGRVIGELGE DGWIRVQWGTGSTNSYRMGK EGKYDLKLAELPAAAQPSAEDS DTEDDSASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFPAASL QRQRWVAVSLPHALVKSGTVP
6014	36382	A	6060	1	7297	
6015	36383	A	6061	32	259	SLRVTPGGRNVSEKKDRKKTG R/PPELERKSHTERLYLEEGSAE PA*VGRRAPESVNDRGGAIQRA QRGQPAPPLPR
6016	36384	A	6062	3	437	
6017	36385	A	6063	1	425	MTELPTLWKPLKNSPMFRVIAR AFCVTFILVSTHQEMLTITSENP LGPSLGSIPQARFLLMMLSMLT LQHSANNLDLLLNSGTLALTQT ALRLIGGTPVELPAELAAPAFR AAAA/VDKNPRRRGQKVAVAK SGGDRGKKSR

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6018	36386	A	6064	2	14566	RRGGRALRVRPETWEEAGEKM PSESFCLAAQARLDSKWLKTDI QLAFTRDGLCGLWNEMVKDG EIVYTGTESTQNGELPPRKDDS VEPSGTKKEDLNDKEKKDEEET PAPIYRAKSILDSWVWGKQPDV NELKECLSVLVKEQQALAVQS ATTTLSALRLKQRLVILERYFIA LNRTVFQENVKVKWKSSGISLP PVDKKSSRPAGKGVEGLARVG SRAALSFAFAFLRRAWRSGEDA DLCSELLQESLDALRAL
6019	36387	B	6065	75	581	
6020	36388	A	6066	517	5495	ESFFTGQNCRNNEKVTFVRIAD LENHNNDGGFWTVIDGKVYDI KDFQTQSLTENSILAQFAGEDP VVALEAALQFEDTRESMHAFC VGQYLEPDQEGVTIPDLGSLSSP LIDTERNLGLLLGLHASYLAMS TPLSPVEIECAKWLQSSIFSGGL QTSQIHYSYYEEKDEDHCSSPG GTPASKSRLCSHRRALGDHSQA FLQAIADNNIQDHNVKDFLCQI ERYCRQCHLTTPIMFPPEHPVEE VGRLLLCCLLKH
6021	36389	A	6067	1	1851	
6022	36390	A	6068	53	423	YHLTLLIHGTKVSATRPGHCSP GKLPSWVPISLQCTPSSPECRSV *RQL*HGHMHELLYIITKADSVI TASCLISRSEW\WGDGGTVSLV QRFVDYGSSQCQRPHRTGCASS SAPQRASSVAPG
6023	36391	A	6069	1	49	EWSGTRTWWRPWSCRT*CRT
6024	36392	A	6070	1	726	
6025	36393	A	6071	368	485	
6026	36394	A	6073	1	414	
6027	36395	A	6074	3	535	RRREFPAKERESASMSSPEE*P/ DMAKGAPPSQPPPNSVPAD/CS RSVRLSSSNFEESLRPTEDDEGQ EGQDSMSRAKANWLRAFNKV RMQLQEARGEGEMSKSLWFKG GPGGGLIIIDSMPDIRKRKPIPLV SDLAMSLVQSRKAAITSALASS TLNNEELKNHVYKKTLQALIYP ISC
6028	36396	A	6075	1	222	
6029	36397	A	6076	2	284	NGIPDFSNTTLLRGLQMPGARG PCCGSQRHINLLMGTGVFLVK MKA/NEFFFLDSETRLCKIAPEG WREQPQKTSMNTFTLFLRIKFF VSHYGLL

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6030	36398	A	6077	91	749	
6031	36399	C	6078	1	380	
6032	36400	A	6079	1	877	MPRPDLAPALLVAVLVLLYLL VSAAAPAPSSDSTPENVCPVET TTNFIWELSSPHNTSAVLLVVF HKGPSPKFEVKLKKNANGLGFS FVQMEKESCSHLKSDLVRIKRL FPGHPAEENGAIAAGDIILAVN GSPRKASSSRCRGSWAMQLSV QAGPSFASYYPAAVEVLHLLRG APQEVTLLLCRPPPGALPELEQE WQGQKYKCAWAIVNEAEVEE VVEVAGTVEFFGDQ\GA*CHHP ACSGKPLGWHGGLSRKCPRLFF RGATRVTGAQGLKEVKQQSFR SNMMWLGLRL
6033	36401	A	6080	1	1683	
6034	36402	B	6081	66	1214	
6035	36403	A	6082	1	5694	
6036	36404	A	6083	3	483	SSLTSSMEDPAAPGTGGPPANG NGN\GGGKGKQAAPKGREAFR SQRRESEGSVDCPTLEFEYGDA DGHAAELSELYSYTENLEFTNN RRCFEEDFKTQVQGKEWLELE EDAQKAYIMGLLDRLEVVSRE RRLKAARAVLYLAQGTFGECD SEVDVLHWSRY
6037	36405	A	6084	1	2646	
6038	36406	A	6085	115	1289	FSPLEPRLCSLGGWGALQAGEP CQPSRAGCGREGATMGCTLSA EERAALERSKAIEKNLKEDGIS AAKDVKLLLLGAGESGKSTIVK QMKIIH\EDGFSGEDVKQYKPV V\YSNTIQSL\AAIVRAMDTLGIE YGDKERKADAKMVCDVVSRM EDTEPFSAELLSAMMRLWGDS GIQECFNRSREYQLNDSAKYYL DSLDRIGAADYQPTEQDILRTR VKTTGIVETHFTFKNLHFRLFD VGGQRSERKKWIHCFEDVTAII FCVALSGYDQVLHEDETTNRM HESLMLFDSICNNKFFIDTSIILF LNKKDLFGEKIKKSPLTICFPEY TGPNTYEDAAAYIQAQFESKNR SPNKEIYCHMTCATDTNNIQVV FDAVTDIIIANNLRGCGLY
6039	36407	A	6086	1	1053	

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6040	36408	A	6087	2	377	IYDGFDGFAKGQIKEIGWTDVG GWTGQGGSILGTKRVLPGK/Y MEEIATQMRTHSINALLIIGGFE AYLGLLELSVFVTLKLFYQHFM HVLLTLIPNRRVPICPTSPSACC LWSVSHAFRCAYEQN
6041	36409	A	6088	1	591	
6042	36410	A	6089	1	2391	PGRAAPLGLLAMDADDSRAPK GSLRKFLEHLSGAGKAIGVLTS GGDAQGMNAAVRAVVRMGIY VGAKVYFIYEGYQGMVDGGSN IAEADWESVSSILQVGGTIIGSA RCQAFRTREGRLKAACNLLQR GITNLCVIGGDGSLTGANLFRK EWSGLLEELARNGQIDKEAVQ KYAYLNVVGMVGSIDNDFCGT DMTIGTDSALHRIIEVVDAIMTT AQSHQRTFVLEVMGRHCGYLA LVSALACGADWVFLPESPPEEG WEEQMCVKLSENRARKKRLNII IVAEGAIDTQNKPITSEKIKELV VTQLGYDTRVTILGHVQRGGTP SAFDRILASRMGVEAVIALLEA TPDTPACVVSLNGNHAVRLPL MECVQMTQDVQKAMDERRFQ DAVRLRGRSFAGNLNTYKRLAI KLPDDQIPKTNCNVAVINVGAP AAGMNAAVRSAVRVGIADGH RMLAIYDGFDGFAKGQIKEIGW TDVGGWTGQGGSILGTKRVLP GKYLEEIATQMRTHSI\NALLIIG GF\EAYLGLLELSAAREKHEEFC VPMVMVPATVSNNVPGSDFSIG ADTALNTITDTCDRIKQSASGT KRRVFIIETMGGYCGYLANMG GLAAGADAAYIFEEPFDIRDLQ SNVEHLTEKMKTTIQRGLVLRN ESCSENYTTDFIYQLYSEEGKG VFDCRKNVLGHMQQGGAPSPF
6043	36411	A	6090	1	459	

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6044	36412	A	6091	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
6045	36413	A	6092	1	3654	
6046	36414	A	6093	1	5127	
6047	36415	A	6094	1	3663	
6048	36416	A	6095	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
6049	36417	A	6096	1	5073	
6050	36418	A	6097	1	3489	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNPTQSRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIPLNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKTDRPLARLIKKKR EKNQIDTIKNDK
6051	36419	A	6098	1	3235	

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6052	36420	A	6099	1	3070	MATLIPLLFHKHPHLTQRYQFN VRGGCPTSTSAIATLDPRTAVFP LMSVFQTSAPWPFWGFTHQTP VPQPLKVKIHSSADTAADIQAN RVWSGPPANSKRPAAEEGKLT NRKDIHTKNPSVRHHHQRPKV DKTTKTGKKQRRKTGNSKKQS ACPPPKERSSSTATEQSWTEND FDKLREGFRRSNYSKLQDEIQT KGKEVENLEKSLDECITRITNTE KGLKKLENYVKNEETSGANAI NWKKGINKIDRPLARL
6053	36421	A	6100	1	3297	
6054	36422	A	6101	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
6055	36423	A	6102	1	3417	

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6056	36424	A	6103	1	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSASEPPSAPIPKAQV SSTEKLRNCIDDLKPFPALASEL SRRAKALQIAGFPPMKVPRDTI SKVCLDKTVGKLCHSGEESRK CTLICNNKHYPIQDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAKYSSLEAKLCQIESKYL ILLQEMKTPVCSEDQGPTREVI AQLLEDALQVESQEQPEQAFV KPHLVSEYDIYGFRTVPEDDEE EKLVAKVRALDLK
6057	36425	A	6104	1	4371	
6058	36426	A	6105	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKL\GIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGQ
6059	36427	A	6106	1	4449	

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6060	36428	A	6107	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
6061	36429	A	6108	1	3297	
6062	36430	B	6109	112	3300	
6063	36431	A	6110	3	3316	
6064	36432	A	6111	1	3457	
6065	36433	A	6112	1	3170	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLKELEKQEQRHSKPSRRQE ITKMRAELKEIETQ
6066	36434	B	6113	1	4753	
6067	36435	B	6114	1	3384	
6068	36436	A	6115	1	3345	
6069	36437	A	6116	1	3780	
6070	36438	A	6117	1	3720	
6071	36439	A	6118	1	3894	
6072	36440	A	6119	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
6073	36441	A	6120	1	3780	
6074	36442	A	6121	1	3852	
6075	36443	A	6122	1	3345	
6076	36444	B	6123	1	6136	
6077	36445	B	6124	1	3924	

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6078	36446	B	6125	295	4185	
6079	36447	A	6126	1	405	
6080	36448	A.	6127	1	1059	
6081	36449	A	6128	2	518	EKATCDENDSVSNIATEIKEGQ QSV\HVSPQKQSAWKVIFKKKV SLLNIATRITGGGKSGTVSSQKQ PPSKATSDKTDSALNIATEIKDG LQCGTVSSQKQPALKATTDEED SVSNIATEIKDGEKSGTVSSQKQ PALKATTDEKDSVSNIATEIKD GEKSVTVSSQKQPASK
6082	36450	A	6129	1	843	
6083	36451	A	6130	1	432	
6084	36452	A	6131	2	835	CGSAQAAAAAAAEEATEKIPAL RP/ASAVGAAGALAVLRDPRA WREAGSKS/PETPFS*CQGA/HG GGQFCPSGTAFPGKMKVMMR KRKKKGQCLPGICRSLKRRKSP RSPGM/IGYSTLSIPPEMLASYQ SYSSTFHSLEEQQVCMA/G*HR QMPGADKPVRACQRVLAGVW AGFTMRHQSRLY*ECSICGVIFR HRCVAHLLGRAIGAGLFVITPA GERGMCCKAIKLGNARVFPVT TL*NDGQCQACMHAG/TTLEDP GKNYISSSPSSSSSSSPSSPRVPS
6085	36453	C	6133	278	446	
6086	36454	A	6134	1	1152	
6087	36455	A	6135	1	639	
6088	36456	A	6136	12	1436	
6089	36457	A	6137	367	1056	
6090	36458	A	6139	1	4263	
6091	36459	A	6140	1	1311	
6092	36460	A	6141	1093	1358	MQKKPLTKFNNPSC*KLSIN*V LMGRISK*VTTTATTTTITTTTT TTTTTTTTTTATTTTTTTTTTT TTTTTTMGPTLPLIPIGLGS
6093	36461	A	6142	1	699	
6094	36462	A	6143	1	489	

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6095	36463	A	6144	5	916	ALGGTPMLGKLAMLLWVQQA LLALLLPTLLAQGEARRSRNTT RPALLRLSDYLLTNYRKGVRPV RDWRKPTTVSIDVIVYAILNVD EKNQVLTTYIWYRQYWTDEFL QWNPEDFDNITKLSIPTDSIWVP DILINEFVDVGKSPNIPYVYIRH QGEVQNYKPLQVVTACSLDIY NFPFDVQNCSLTFTSWLHT/SPG HQHLFVALARKGEIRQECLHEP GRVGVAGGAALLSGVQHGKQ* LLCRNEVLCGHPPAAPLLCGQP ATAQHLPHGHGHRGLLPAPQQ WREGLFQNYTPPGLLGLPDHRF
6096	36464	A	6145	5	756	
6097	36465	A	6146	1	471	
6098	36466	A	6147	184	1097	ALGGTPMLGKLAMLLWVQQA LLALLLPTLLAQGEARRSRNTT RPALLRLSDYLLTNYRKGVRPV RDWRKPTTVSIDVIVYAILNVD EKNQVLTTYIWYRQYWTDEFL QWNPEDFDNITKLSIPTDSIWVP DILINEFVDVGKSPNIPYVYIRH QGEVQNYKPLQVVTACSLDIY NFPFDVQNCSLTFTSWLHT/SPG HQHLFVALARKGEIRQECLHEP GRVGVAGGAALLSGVQHGKQ* LLCRNEVLCGHPPAAPLLCGQP ATAQHLPHGHGHRGLLPAPQQ WREGLFQDYTPPGLLGLPDHRF
6099	36467	A	6148	3	672	
6100	36468	A	6149	3	398	LRKIKIDLGKFSDNPDGYIDVLQ GLRQSFDLTWRDIMLLLDQSLT PNEKSAAKTAAREFGDLWFV/S FQN*SCKTTNRSSNGAPDAVHD *D/PTADPWTGPLAHALMLMTL KAPLTRKSQLHDPYYAPIQQEA V
6101	36469	A	6150	1	420	

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6102	36470	A	6151	1	878	TLLPPRPGVGSDYPNIPGCPMW GNKDPGEGTLERGKVEDASQR TSRTLKETSGKAEHRKKQDGK CSPQGKNALKMYSGEFDPVRV CVPFSLSDLKQLKIDLGRFSDNP DGYIDVLQGLGQSFDLTWRDI MLLLDQTLTPNERNATITAARE FGDLWCLSQVNDRMTTEERER FPTGQQAVPSADPH*DTESEHG DWCCRHLLTCVLEGLRKTRKK AVNFSVMSTVTQGKEENPTAFL ERLREALRKHTSLSPDSIEGQLI LKIKFITRSAADIRKQTSKVHLR PGAKLKTPY
6103	36471	A	6152	1	417	
6104	36472	A	6153	1	415	
6105	36473	A	6154	1	234	
6106	36474	A	6155	1	335	TCPIVPG/QEMIIEISKGRSGLGL SIV*GKDTPLNAIVIHEVYEEGA AAVDGRLWAGDQILEVNGVDL RNSSHEEAITALMQTPQKVRLV VYRDEAHYRDEENLEIFPVDLQ
6107	36475	A	6156	109	4687	
6108	36476	A	6157	109	4991	
6109	36477	A	6158	3	862	
6110	36478	A	6159	1	1857	
6111	36479	A	6160	3	100	
6112	36480	A	6161	1	537	
6113	36481	A	6162	125	1184	
6114	36482	A	6163	875	1506	LSIYLVTQKAA/SSEWGPEQEK ALQEVQAAVQAALILEPYDPA GPVVLEVSLADRDAVWSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQQHSIIKWKWYIHD RARAGPEGTNSSARYAATM*K W\TASALQPLSRKSLKDSSEGK SSQWAELRAVHLAVHVAWKE KWPDVRLDTDSWAV/ANGLAR WSGTWKEHDRKIGDKEVWGR GTRI
6115	36483	A	6164	1	1566	
6116	36484	A	6165	1	1098	
6117	36485	A	6166	1	538	
6118	36486	A	6167	410	625	LTLVPFSFSVVLTPLPKGNTIRY *TGIL*GWNLSWKGTLGFSVTA QPSSGTPRTALGSRTTKPLLVSL LQV

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6119	36487	A	6168	821	1428	QVTDVQDFPLKCKIQWRRTVR GDLQ/PFTRVTVHWGKGNDQT FQGLLDTGSELTLIPGDPKRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQ/NSHIGSLTGRVRA TMVGKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT G\VIPTSPFNSPI*PMQKTDGSW RMTVDYL
6120	36488	A	6169	203	850	DVEHVGKMRRRWRRRVVVAD GNVVKPMSCAGDLQ/PFTRVTV HWGKGNDQTFQDLLDTGSELT LIPGDPKRHCGPPVKIGAYGGQI INGVLAQVQLTVDAVGPWTHP VV/I/SPVPECIIGIDILSSWQ/NSH IGSLTVHLSSDPKGCHSEWGPE QEKALQEVQAAVQAALILEPY DPAGPVVLEVSLADRDAVWSL WQAPIGESQQRPLGFWSKALPS
6121	36489	A	6170	1	864	
6122	36490	A	6171	1	205	VPDFPAKPIQGPHFNSRYL/REA VHGEAVHAPFIAGQPLT**ELM SIFPQFQFFLYRRLDSHSGQSWQ I
6123	36491	A	6172	1	3039	
6124	36492	A	6173	1	1364	MIISIDAEKAFDKIQQPFMLKTL SKLEETASPSPVVATYTPQPML PSAFPPLSEEINPVLPETTVMAS PEAVTRQDNVDSPQKPPPTPMF ASRPITRLKPRRAPSEEGIQRLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPELIIGIDILSSWQNPHIGSL NGRGYINSLALCHNLIRRDLDR FLLPQDITLVHYIDHIMRLDSVK DKWLHLAPPTTKKEAQCLVGL/ FGFWRQHIS\LWRQPLACYWAL VETEHLTMGHQVTMQPELPIM NWLLSDPSSYKPAPMASWGVP YGQLTEEEKTRAWFTDGSARY TETTRKWTAVAIQPLSRTSLKD SNEGKSSHQQAKNGITVLAGVI DPDYQDEISL/LTPQWRCHPGSS VWRASSLGISHPP
6125	36493	A	6174	114	1996	

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6126	36494	A	6175	1	475	MGRNQNRKAENSKNWNASSPP KEHNSSPAREQNWREDEFNELT EVGFRRSVITNFSDLKEHVLTH CKEAKILEKRLDKWLTKITSVE KS/CK*PDG/D*KPQYENFMKHT QASIADLIKRKKRYQ*LKIKLM K*SKKTR*EKKKYKLPSENTTN TSMQIY
6127	36495	A	6176	179	393	NKRGYKQMEEHSMLMDKKNQ YYENGHTAQGN*AGEGNKGYS IRKTGSQIVPLCR*HDCISRKPD CLSPKSP
6128	36496	A	6177	1	710	MARELRDECTSFSSQFHQLEER VSVIEDQMNEMKQEEKFREKGI KRSEQSLQEIWDYMERPNLCLI GVPESDGENGIKLEDTLQDIIQK DFPNLGRQANIQIQEIQRMPQR YSSRRATPRHIIVRFTKEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITGS EIEAIINSLPTKKSPRPDGFTAEF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKLGRDTTK KENFRPISLMNIDAKILNKILAN QMQQNIKNLIRHDQAGFIPGMQ CWFNIRKSINVIQHINRTKDKN HMIISIDAEKAFYKIQQPFILKTL NKLENKIPRNPTYKGCEGPLFK ENYKLMLKEIKEDTSKWKNIP WSWIGRINIVKMAILPKVIYRLS AIPIKLPMIFFTELEKTTLKFIWN QKRACIAKSILSQKNKAGGIML PDFKLYYKATVTKAAWYWYQ NRDIDQWNRTEPSETIPHIYSHL IFDKPDKNKKWGKDFLFNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKTLEENL GNTIQDIGMGKDFMCKTPKAM VTKAKIDKWDLIKLKSFCTAKE TTVRVNRQPTEWEKIFAIYSSD KRLISRIYKELKL*PCSIV*SQVA *CLQLCSFGLGLTWQCRLFFGSI
6129	36497	A	6178	464	724	IGEVLLDNILQRVFQLGSILPITF RYTNQT*IWSWTLFWLVSY
6130	36498	A	6179	1	2022	
6131	36499	A	6180	1	882	
6132	36500	C	6181	1	1935	
6133	36501	A	6182	1	672	
6134	36502	B	6183	140	2195	
6135	36503	A	6184	26	354	

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6136	36504	A	6185	86	747	SLEDAMSLKDDDSGDHDQNEE NSTQKDGEKEKTERDKNQSSS KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA NKNG\GKWIIRL\RKGFGSRC\W ENLILAMLGEQF\MVGEEICGG CGVCPAFQEDIIS\IWNKTASDQ ATTARIRDTL\RRVL\NLPANTI MEYKN
6137	36505	A	6186	23	127	
6138	36506	A	6187	2	419	
6139	36507	A	6188	1	714	
6140	36508	A	6189	19	373	AVFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFF\SSSSSSFFFFSFFL FFFFKLKELRLVI*PLNPEN*ESC PLFSPVNLDMP*TFKDKRWKV NWARSTSRQQLLESARTKSWA EREGGTRWRAW
6141	36509	A	6190	227	420	KNFLPNCSAKELFFFFFFFFFFL LLLLLLLYFKF/MI*WFYKHLAF PLLAFILSPTAL*RGVFHH
6142	36510	A	6191	400	582	
6143	36511	A	6192	1202	1678	
6144	36512	A	6193	2	109	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL
6145	36513	A	6194	110	377	QWISRQKPYKPEKRGDQYSTFL *EC*ILVPPLFWLVGFLPRDPLL V*WAYGCP*HFFLHFNLGESNN YVSWGCSS
6146	36514	A	6195	1	381	
6147	36515	A	6196	1	759	
6148	36516	A	6197	1	609	
6149	36517	A	6198	2	1178	
6150	36518	B	6199	159	290	
6151	36519	A	6200	716	1001	SMPASTHLILVGSCSWKMVIVL PLVTHFLFTALTVPWNLPWVEL YWNM*TM*LRSMKESLMATIF TLPELKA\VLHEKLQ*LQSTEDL *HGLLGG
6152	36520	A	6201	5772	5971	TANIIMTGSNSHITILTLNVNRL NARIKRHRLENCIKSQDPSVCCI *ETHLMCRDTYRLKIKGWSN
6153	36521	A	6202	1	974	
6154	36522	A	6203	1	600	

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6155	36523	A	6204	51	424	MAPKQDPKPKFQEGERVLCFH GPLLYEAKRVKVAIKD/ITREI/H SYITVVGIKIGMNGFRRAKYSN TWTPICRNSENFKKPISKFVL*T EY*GEMPVD*FWTWNEQWRSC WLPCLYNDTSDLSAGV
6156	36524	A	6205	1	3827	MQKAIRLNDGHVAPLGLLARK DGTRKGYLSKRSSDNTKWQTK WFALLQNLLFYFESDSSSRPSG LYLLEGCVCDRAPSPKPALSAK EPLEKQHYFTVNFSHENQKALE LRTEDAKDCDEWVAAIAHASY RTLATEHEALMQKYLHLLQIVE TEKTVAKQLRQQIEDGEIEIERL KAEITSLLKDNERIQSTQTVAPN DEDSDIKKIKKVQSFLRGWLCR RKWKTIIQDYIRSPHADSMRKR NQVVFSMLEAEAEY
6157	36525	A	6206	1	900	
6158	36526	C	6207	172	501	
6159	36527	A	6208	499	848	KIRVPAAVAGLSPPLGPWSLRS PSQPERCCPWRNSSWWTAPRTS IITAAKGVSPARLSSISCTTRGS WVKTPTPTRARMVIASSNLERP SALSRM*PTSQSMTRKRWWRL WPSTTL
6160	36528	A	6209	3	495	SCAQTFPKLDTFLEHIKSHQEEL SYRCHLCGKDFPSLYDLGVHQ YSHSLLPQHSPKKDNA/CLQVF PCERYLRRHLPTHGSGGRFKCQ VCKKFFRREHYLKLHAHIHSGE KPYKCSVCESAFNRKDKLKRH MLIQYDEVRQGLGMVPGTQKV LNKCFCHNVKKKK
6161	36529	A	6210	667	2142	
6162	36530	A	6211	1	396	
6163	36531	A	6212	213	446	
6164	36532	A	6213	101	580	VAGVGSLPRSMEDDAPVIYGLE FQARA\LTPQT\AETDAIRFLVG TQSLKYDNQIHIIDFDDENNIIN KNVLLHQS/AGEIWHISASPADR GVLTTCYNRTSDSKVLTCAAV WRMPKELESGSHESPDDSSSTA QTL\ELLCHLDNTAHGNMACV VWEPMGDG
6165	36533	A	6214	1	933	

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6166	36534	A	6215	3	404	RLKEKKLVKEVIAVSCGPAQCQ ETIRTALAMGADRGIHVEVPPA EAERLGPLQVARV/AVVTADLR LNEPCYATLPNIMKAKKKKIEV IKPGDLGVDLTSKLSVISVEDPP QRTAGVKVETTEDLVAKLKEIG
6167	36535	A	6216	1	408	
6168	36536	A	6217	88	871	MADVRVLVAVKRVIDYAVKIR VKPDRTGVVTDGVKHSMNPFC EIAVEEAVRLKEKKLVKEVIAV\ SCGPAQCQETI\RTALA\MGA\D RGIHVE\VPPAEAERF/GVPLQV ARVLGQLAKK\EKVDLVLLGK QA\IACTDCNQ\TGQMTAGFLD WPQGTF\ASQVTLEGDKLKVER EIDGGLETLRLKLPAVVTADLR LNEPRYA\TLP\NIMKAKKKKIE VIKPGDLGVDLTSKLSVISVEDP PQRTAGVKVETTEDLVAKLKEI
6169	36537	A	6218	1	1023	
6170	36538	A	6219	110	842	
6171	36539	A	6220	1	122	
6172	36540	A	6222	1	1257	MNDATAVQEGSQMYSWQKLT PTGPFIMQPEGMGRLFAINKMA EGPFPEHYEPIETPLGTNPLHPN VVSNPVVRLYEQDALRMGKKE QFPYVGTTYRLTEHFHTWTKH ALLNAIAQPEQFVEISETLAAAK GINNGDRVTVSSKRGFIRAVAV VTRRLKPLNVNGQQVETVGIPI HWGFEGVARKGYIANTLTPNV GDANSQTPEYKAFL/GQHREGV RN*LHHAAFSGA*LQCFQYAH NSRKNN
6173	36541	A	6223	737	941	WLRMMEHRILFPLWKRESKKA HYVQSSVLLCLGMLR*KYKGK KGKKERKKKDEKRKGNGKKRI KIHSI
6174	36542	A	6224	1	1072	
6175	36543	A	6225	1	585	
6176	36544	A	6226	1	930	
6177	36545	A	6227	28	392	AGEVPLQLPPAAVCSACLQRPA LWWNSSFFL*SCLHALFH*VDL QSLIAFLLLD*SSY*YLCMLHEV LVLCFSAPSGHLCSSLS*LF*LAI HLTFFQGS*LPCIGLEHASLAQR SLLLPTF
6178	36546	A	6228	1	271	SAIVTFVCFMKFSCCVFQLHQV FHVL\FKLVILVSSSCNLFSRFLA SLHWVTTCSFSSEEFVITHLLKP APVNSSNSFSVQFCSLAGKEL

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6179	36547	A	6229	1	1089	MGWRPRWLPYLYWGFQSDLC PHCKRKAQEEDSLAAQAASHP RLSANSKNNSWGKQYSYALFK AMRHMLCIGYGRQAPAAVSDV WLTMLSM\IVGATCYAMFIGH/ ATALIQVLDCSRRQYQEKVVLP REHPNIGSSQEGGTWHQTVGL QQTSDKFDANDPILKDQTQEW SGSATFTSDGKIRLFYTDYSGK HYGKQSLTTSAANTGTENGYQ GEESLFNKAYYGGGTNFFRKES QKLQQSATTRDAELANGALGII ELDNDSPLKKRGATQRSSEENI TLKAYKRDVRSLLMLTRNEDV ADSLNSSKKRQNYQLPSIRSVT RCKKIGVCAKGIGCGQGTHYLS VSILNTADRDRRKLGFTRTSMY
6180	36548	B	6230	1	1140	
6181	36549	A	6231	3	204	GSDYELGLW*PWLTSEATDLH GECYSS*SGASGVVRSSLWARG LAGFRSEAADLRGRESVAVTN
6182	36550	A	6232	1	1296	
6183	36551	B	6233	1	1686	
6184	36552	A	6234	1	627	
6185	36553	A	6235	570	736	SATFGRSSRSGCSG\FPAASRRG RLPLSPPPWPAV\RVYPCGMLD NKASAAHPPKKK
6186	36554	A	6236	1	103	
6187	36555	A	6237	699	887	GLQPPAPRETRPLY*TLAWNLH FLFVSPLDSCDLVRSVLTCLSPP GNSPSFDMHRYQLPCVH
6188	36556	A	6238	2	803	
6189	36557	A	6239	2	1277	YKETYLIHLFHTFTGLSIAYFNF GNQLYHSLLCIVLQFLILRLMG RTITAVLTTFCFQMAYLLAGYY YTATGNYDIKWTMPHCVLTLK LIGLAVDYFDGGKDQNSLSSEQ QKYAIRGVPSLLEVAGFSYFYG AFLVGPQFSMNHYMKLVQGEL IDIPGKIPNSIIPALKRLSLGLFYL VGYTLLSPHITEDYLLTEDYDN HPFWFRCMYMLIWGKFVLYKY VTCWLVTEGVCILTGLGFNGFE EKGKAKWDACANMKVWLFET NPRFTGTIASFNINTNAWVARYI FKRLKFLGNKELSQGLS\MLFLF LWHGLHSGYLVCFQMEFLIVIV ERQAARLIQESPTLSKLAAITVL QPFYYLVQQTIHWLFMGYSMT AFCLFTW\DKWLKVYKSIYFLG HIFFLSLLFILPYIHK\AMVPRKE

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6190	36558	A	6240	56	324	
6191	36559	A	6241	68	487	
6192	36560	A	6242	52	457	
6193	36561	A	6243	263	787	SLEV*KWPGVACRLQL*P/MVP APKS*ESKSAGSLNTPSAICRDA SGRGLARPWLRKSKCLACHLV DTRSKTAGGLAPVPSAHLISVR EREPGLCAVLVSQLEFRVGVGL VGPTLGARREPCWPQAMGDLA PEPVAALRLISRRALPAFPWGR ARDLQPAMPEPPTHSMGSCAPE PPR
6194	36562	A	6244	3	236	
6195	36563	C	6245	1	1608	
6196	36564	B	6246	1	1083	
6197	36565	A	6247	823	1055	KQKDGTGAPWSRGRRSSGRLG THRSPRRGWEAQAWRAAGPET CPAGRQLRPGEKSSAAPG*RSR RKDAYEMDTAKKK
6198	36566	B	6248	1	390	
6199	36567	A	6249	27	363	
6200	36568	B	6250	1132	1268	
6201	36569	A	6251	11	489	
6202	36570	A	6252	356	638	
6203	36571	A	6253	1	507	
6204	36572	A	6254	80	336	
6205	36573	B	6255	100	912	
6206	36574	B	6256	821	2992	
6207	36575	A	6257	2	602	
6208	36576	A	6258	1	519	
6209	36577	A	6259	3	228	STGVPVSQ\RTCLLEKASVLFNT GALYTQIGTRCDRQTQAGLESA IDAFQRAADMSPPGLTRRSLGP TRWHQGTPH
6210	36578	A	6260	1	963	
6211	36579	A	6261	1	925	
6212	36580	A	6262	1	397	
6213	36581	A	6263	1	2625	
6214	36582	A	6264	11	241	SLQHLNPATFLPVSKSPVKHNC VEVLDSVYSSGPNHRDHP*TSV DWELYMDGSSFTNPCKVTLKK TTSPAPVTPGS
6215	36583	A	6265	1	1662	
6216	36584	B	6266	1	897	
6217	36585	A	6267	3	258	
6218	36586	A	6268	1	279	
6219	36587	A	6269	1	258	
6220	36588	A	6270	1	639	
6221	36589	B	6271	1	1935	
6222	36590	A	6272	698	1643	

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6223	36591	A	6273	91	386	IFDFLFLLYVSGCNSIAEPQHFT TTVTRCSPTVAFVEFPSSPQLKN DVSEEKDQK\KP\ENEMSGKGG SWVLFTKGEVQEWRESGLNPT KFNMGPLIYS
6224	36592	A	6274	1	2538	
6225	36593	A	6275	1	471	
6226	36594	A	6276	152	520	CPLTLLLPSRGAGLGTCSPPCLS LPPTPWAPVRPEPPRRAPPPAPR RPVPSTGKEQTTQGLRNASARR GTGRQLHL\SPGVGSTG*SQGL
6227	36595	A	6277	831	1449	HPGQWLRRVCWVSSGAGPLAL CSISCPALAAFPRVGLGTCSPPC LSLPPTPWAPVRPEPPRRAPPPA PR/PPSPIDHPRAEEYE/PHGAGL AGSSTCSPSAESTG*SQLGS*VV RVRGFILEVSETKNPPIPDTFGL PPGSSSAASTLVQVTRL*ISAISL PHLLSRPCSNTARGPVPAPVPG AAVRAPAAGGRWCGGARGRG RRGGGH
6228	36596	C	6278	1	426	
6229	36597	A	6279	1	535	MKHSGAQLASPSGS\PLGPQVE LPASPVPCACTSQPLGGRWDW APWSRGWCSSGRLGPHRSPWS GWE\LRHGGLQVPSPAPREGS* GPARNP/GTAPGRPAAPS\GGPP SPRPPRTPAGPQALRAAPVP\LA PLPPHLPAS*GSGLQPWPA*KE APTVQCQAEGLLKCRQSGSPGR GGAESE
6230	36598	B	6280	1	1743	
6231	36599	A	6281	1	428	GTREEHLKRSGREIALPIEACV MLLLETGMKEEGLFRIGAGASK LKKLKAALDCS\ILTWDEFYSD PHAVAG\ALKSYLRELPEPLMT FNLYEEW\AQVASVQDQGQKT FKDLWRTCQKLPPQNFVNFRY LIKFLAKLAQTSDV
6232	36600	A	6282	135	512	LPFRGAGLETCSPPCLSLPPPPW APVRPKPPR*APPPAPRRPVPST TQGSLGPHCFYEL*HSP*RSAAS LLKPARP*AHREERTTP/GRSAL/ TSCNTHREGLQ/PSLRKKETPNT SEHQKEQTPDAPP

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6233	36601	A	6283	698	2233	IQAAMQAAPQFGPSTED*CCPIT SEAPWAIMDAKLR\LKPPSHPPL VSPHLNPQVWDTSSPSLATEHA SLTISLKPNHPYPAQSQYSIPQH ALKGSKPVITRLLEHGLLKPINS PYNSPILPVQKLDKSYRLVQHL CLIYQIVLPIHPMVPNPYTLLSSI PFTTHYSVLDLKHAFFTIPLYPS SQPLFAFTWTDPDTHQAQQITL AVLPQCFIDSPHYFSQAQISSSS VTYLGIILMKTHIGLGAVEQGV VLVGEARAAQEPMEWVGGSG MVGCRSRALPRGKAAKARREI ERSAVTIVPVLDFNPAFHIIPDTT PDHHDCISLIHLTFTPFPHISFFP VPHLEHTWFIDGSSTRPNCHSP AKAGYAIVSSTSIIEATALPRST TSQQAKLIAYTDSKCAFHILHH HAVIWEERNFLTMQGASIINAF LIKTLLKDILLPKEAGVIHCKGH QKASDPITQDNAYADKVAKKQ LAFQLLSLTAVFLLLIRPLSPTSP LKLPLINLFPHKANDS
6234	36602	A	6284	1	1239	
6235	36603	A	6285	1	477	QRPPHGVFVLGVAGRVHGPEL ASHKAGPQLGDVGVCAGQGG QVGPLVLQPVVEHIQQLPG/AG HCAHQ*QGSPS*SSLPRPERSLQ CRRPQGATATIRSTWWGPRGP VCTAALVPLCWPGWPVQKDEL QAVRSHSALASAMQTCSLAGP GLGSSHARLTA
6236	36604	A	6286	1	1134	
6237	36605	A	6287	673	836	
6238	36606	A	6288	1	225	
6239	36607	A	6289	1	468	
6240	36608	A	6290	495	1637	ESQVLSNVSPHVKV*NMASWE GKDLTVPQPDTRKGSVLRRISK RGRNASCS*DKRKASVSCLSLG NGMSRYKTRLYAPSTEIGKNRL RAGGGTCGQQYCFVKH
6241	36609	A	6291	1	507	
6242	36610	A	6292	215	389	
6243	36611	A	6293	1	255	
6244	36612	B	6294	69	1055	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6245	36613	A	6295	23	1596	IKPQRWGETRAEMLKILKTREP FLLQRIASPRQQWNKAGQRRS WFFERL/NKIDRLLARLIKKKRE KNQIDAIKNDKGDITTDPTEIQT TIREYYKHLYANKLENLEEMD KFLDTYTLPRLNQEELESLNRPI TGSEIEAIISSLRTKKSPGPDGFT AEFYQRYKEELVLFLLKLFQSIE KEGILPNSFYEASIILIPKPGRDT TKKENFRLISLMNIDVKILNKIL ANRIQQHIKKLVHHDQVGFIPG MPDWFNICKSINIIHHINRTNGK NHMIISIDAEKAFEKIQQCFMLK TLNKLGIDGMYLKIIRAIFDKPT ANVILNGQKLEAFPLKTGTTQG CPLSPLLFKIVLEVLARAIRQEK EIKRIQLGKEEAKLSLFADDMIV YLENPIVSAQNLLQLRSNFSKV LGYKINMQKSQAFLYTKNKQT ESQIMSELPFTIATKRIKYLGIQL TRDVKSLFKENYKPLLSKIKED TNKWKNIPSSWIGRISIAKMAIL PKVIYTFNAIPIKLPMTFFTELEK
6246	36614	A	6296	1	1488	
6247	36615	A	6297	1	1401	
6248	36616	A	6298	2	1256	
6249	36617	B	6299	84	955	

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6250	36618	A	6300	735	2718	RSFPRSRPSPFLLLSRYLRIHMV FSVLPFGLQNPKYLLSGSLQEK FRTPGINSHKTLDPNRVIIKVRR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITTDATEIQTTIREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPITGSEIEAIINSL PTKRSPGPDGFTAEFYQTYKEE LVPFPLKLFQSTEKEGILPNSFY EASIILIPKPGRDTTKKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHYDQVGFIPGMQGWFNKRK SINVIQHINRTNDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCPLSPLLFNI VLEVLARAVRQEKEIEGIQLGK EEVKLSLFADDMIVYLENPIVS AQNLLKLISNFSKVSGYKINIQK SQAFLYTNNRQTESQIMSELPFT TASKKIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPC SWVGRINIMKMAILPKVICRFN AIPIKLPMPFFTELETTTLKFIWN QKRARKSILSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEIMPHIYNYLIF DKPEKNKQWGKDSLFNK*CWE NWLAIWRKLK
6251	36619	B	6301	1	2907	
6252	36620	A	6302	1	2358	
6253	36621	A	6303	1	1866	
6254	36622	A	6304	1	885	
6255	36623	A	6305	1	1059	MKNNSESFEPLLLIPRQRGSGV DLQQTPTDLQLRVLTVRRKTN KQDIHTKTPTVRHHHQRPKNP WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKEVEKQEQT QSKASRRQEITKIRGELKEIETQ KTLQKINESRSWFFEKINKIDRL LARLIKKKREKNQIDTIKNDKE DITTDSTEIQTTIREYYKHLYAN KLENLEEMDKFLNIYTLPRLNQ EEVESLNRPITGSEIEAIINSLPT KKSPGPDGFTAEFYQSYQEELV PFLLKLFQSIEKEGILSNSFYKA NIILIPKPGRDTTKKENFRPISLM NIDAKILNKIL/ANRIQQHIKKLI HHDQVGFIPGMQGWFNI
6256	36624	A	6306	1	1692	

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6257	36625	B	6307	1	2871	
6258	36626	A	6308	2	2315	
6259	36627	A	6309	1	1210	MMSFHELSVHTAIDGHSHSSCS AWCSPIDRDYFEQENNSSSSCC CCCYHCHRKHCGGKGLSFPGE MPLSPGHFNKMMYSVSELMQG SGSGTFIPLPAELSLWLLVTNTK GQRMIKNDAEIQTTIREYYKHL YANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITSSEIVAIIN SLPTKKSPGPHGFTAEFYQRYK EELVPFLLKLFQSIEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLMNSDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIISIDAE KAFDKIQQPFMLKTLNKL\GIK YLGIQLTWDVKDLFKENYKPL LKEIKEDTNKWKNIPCSWVGKI NIMKMAIPPKATSPLESYKREK
6260	36628	A	6310	1	2745	MEGEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDTF

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6261	36629	A	6311	1	2052	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDKTYQNLWDAFNAV CRGKFVALNAHKRKQEGSKID TLTSQLKELEKQEQTHSKASRR QEITKVRAELKEIETQKTLQKIN ESRS\ARLIKKKREKNQI/DAIKN DKRDITIDPTEIQTTIREYYKHL YANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITGSEIVAIIN SLPTKKSPGPEGFTAEFYQRYK EELVPFLLKLFQSTEKEGILPNS FYEASIILIPKPGRDTTKKENFRP ISLMNIDAKILNKILAKRIQQHI QKLIHHDQVGFIPGMQGWFNIC KSINVIQHINRTKDKNHMIISID AEKVFDKIQQRFMLKTLNKLV LEVLARAVRQEKKIKGIQLGKE ELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSEYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDVNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTSFTELEKTTFKFIWNH KGARIAKSILSQKNKAGGITLPD FKLYYKATVTKTAWY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6262	36630	A	6312	2	2143	SSDGSWWTGFQWREWRQAGR SVNSWDNPKQEVRASSKDKSR GSIQEAMRMQSSAKLLCSAWT LAYSIAVRTLSSDSEGQPPLVIH RQTGSGEDLQQTPTDLQLRVLT IRRKTNKQKGHPHQNPISSRRQ EITKIRAELKKIETQKPFKKINES RSWFFEKINKIDRLLARLIKKKI EKNQIDAIKNDKGNITTNPTEIQ TTIREYYKHLYANKLEHLEEM DKFLDIYTLPRLNQEEVESVNR PITGSEIEAIINSLPTKKSPGPDRF TAELYQRYKEELVPFLLKLFQSI EKEGILPNSFYEASIILISKPGRD TTKKENFRPISLMNIDAKILNKI LANQIQQHIKKLIHHHQVGFIPG MQGWFNILKSINVIHHINRTKD KNHMIISIEAEKAFDKIQQPFML KTLNKLGIDGTYLTYLKIIRAIY DKPTANIILNGQKLEAFPFKTGT RQGCPLSPLLFNIVLEALARAIR QEKEIKGIQLGKEDVKLSLFAD DMIVYLENPIVSAQNLLKLISNF SEVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVKM AILPKTLNQKFSYWFRVNKHYI HQRTFPLKETEFNTIATLYNGA SP/CTAPKSTGTNGHQASGLPRF *RIAFCSALVKSKRKLYQGYLP GQTDRREEGVSWCPGGP
6263	36631	A	6313	1	3018	
6264	36632	A	6314	1	2016	
6265	36633	B	6315	1	1215	

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6266	36634	A	6316	1	2268	MAGYPSETKPPEERSDSNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDLQLRVLTVKRKTNKQKG HPHQNPIRTSPSSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFIKEVLRDLQ RDLDSHTIIMGEFNTRLSTLDRS MRQKVNKDIQELNSALHQADL IDISRNLHPKSTEYTFFSAPHRT YSKIDHIVGSKALLSKCKRTEII TKCLSDHSAIKLELRIKNLTQNC STTWKLNNLLLNDYWVHNEM KAEIKMFFETSENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKTDTLTSQLKELEKQEQT HSKASRRQEITKIRAELQEIETQ RTLQKISESRSWFFEKINKIDRS LARLIKKKREKNQIEAIKNDKG DITTNPTETQTTIKEYYKHLYK NKLENLEEMDKFLNTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRCKEEL VTFLLKLFQSIEKEGILPNSFYE ASINLIPKPGRDTTKKENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSQIVPVCR*H DCVSRKPHHLSPQSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE*TPIHNCFKENKIPRNPT YKGCEGPLQGELQTTAQ*NKR GHKQMEEHSMLMDRKNQHRE NRHTAQGNL*IQCHSHQATNDF
6267	36635	A	6317	1	1797	
6268	36636	A	6318	2	2063	
6269	36637	A	6319	1	1212	

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6270	36638	A	6320	1	2718	MALFRVGMTTRRLGHANKFTR DLLVKRLLLYEFVVEIIPGLRTK TTLVGPLETGYTSSDSVNSPHF MLDIALSHNVKSTQLLLRPWR NIDCSRNHKNAKKEEQMGDDE INRQQECSSSPAMEQSWTENDF DELREEVFRRSNYSELQEEIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQEITKIRAELKEIE TQKTLQKINESRSWFFEKINKID RPLARLIKKKREKNQTDTIKND KGDIITDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPITGSEIEAIINSL PTKKSPGPDGFTAEFYQRYKEE LVPFLLKLSQSIEKERILPNSSYE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KLISKFSKVSGHKINVQKSQAF LYTDNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIPCSWVG RINIVKMALLP\RFSAIPIKLPMT FFTELEKTTLKFIWNQKEP/CIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNYLIFDKPDK KKEWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKMNSRWI
6271	36639	A	6321	1	2307	
6272	36640	A	6322	1	1989	
6273	36641	A	6323	1	3285	
6274	36642	A	6324	3	4732	
6275	36643	B	6325	1	2693	

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6276	36644	A	6326	603	2976	DNTARGTIRQQHLLFTNIRCSA ASAADTQANRVWSGPPANSNR PAA\RVLTVRRKTNKQKGHPH QNPICTSPSSKTKETQTTIREYY KHLYANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRITESDIE AIINSLPTKKSPGPDGFTAEFYQ RYKEELVPFLLKLFQSIEKEGIL PNSFYEASIILIPKLGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSINVIHHMKRTKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GFQLGKEEVKLSLFVDEMILSL ENPMVSAKNLLKLISNFSKVSG YKINVQKSQAFLYTSNRQTESQ IMSELPFTIASKRIKYLGIQLTGD VKDFFKENYKPLLNEIKEDTDK WKNIPCSRVGRINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAC HRVGRAQQHSISKWKWYIHDW SQVGPEGTNDSARYPDTTQKW TAAALQPLSRTSLKDSHEGKSS QWAELRAVHLVLRFAWKEKW PDVQLYTDSWAVASGLAGWS GTWKKHDWKIGDKEIWGRATP VIAQWAHEQRGHGGRDGDYA
6277	36645	A	6327	3193	6107	SMKTGLEKKMKRNEQSLQEIW DYVKRPNLPLIGVPESDGDNAT KLENTLQDIIQENCPNLARQANI QIQEIQRTPQRYSSRRATPRHIIV RFTKVEMKEKMLRAAREKGRV THKGKPIRLTAALSAETLQARR DRRPIFNILKEKNFQPRISYPAK LSFVSEGEIEYFTDKQMLRDFL MTRPALKELLKEALNMETTGA PRFIKQVLRELQRDLDTHTIITG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADL
6278	36646	A	6328	1	1808	
6279	36647	A	6329	1	4695	

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6280	36648	A	6330	1	2915	MIMGDFNTPLSTLDRSTRQKVN KDTWELNSALHQADLIDIYRTP HPKSTEYTFFLAPHHTYSKIDHI AGNKALLSKCERTEIITNCLSDH SAIKLQLRIKKLTQNHSTTWKL NNLLLNDYWVHNEMKAEIKIF FETNKNKDTTYQNLWDTFKAV CRGKFIALNAHKRKQERSKTDT RTSQLKHLENQEQTHSKASRRS WFFEKINKIHRPLARLIKKKREK NQIDAIKNDKGDITTNPTEIQTTI REYYKHLYTN
6281	36649	B	6331	1	6730	
6282	36650	A	6332	1	378	
6283	36651	A	6333	3	1700	
6284	36652	A	6334	1	1759	
6285	36653	A	6335	2	409	
6286	36654	A	6336	1	2051	MFGRSRSWVGGGHGKTSRNIH SLDHLKYLYHVLTKNTTVTEQ NRNLLVETIRSITEILIWGDQND SSVFDFFLEKNMFVFFLNILRQK SGRYVCVQLLQTLNILFENISHE TSLYYLLSNNYVNSIIVHKFDFS DEEIMAYYISFLKTLSLKLNNH TVHFFYNEHTNDFALYTEAIKF FNHPESMVRIAVRTITLNVYKV DNQAMLHYIRDKTAVPYFSNL VWFIGSHVIELDDCVQTDEEHR NRGKLSDLVAEHLDHLHYLND ILIINCEFLNDVLTDHLLNRLFLP LYVYSLENQDKVFLIIHHAPLV NSLAEVILNGDLSEMYAKTEQD IQRSSVLPTLSSLWQGSHLSLNQ LQSGLHKCSSHLCGAQAAADS VTGEIPAIRSLEWLISAGSKART FFFLKMLIGFWEKVDCEYQRR QVLSTRLQEALPSNRLTDVAAV HSSCMLGFGSTAPRGSWIGDPA AVHLPLPGELAEHLGSKGTTTV TKHQPQAKPSIRCFIKPTETLER SLEMNKHKGKRRVQKRPNYK NVGEEEDEEKGPTEDAQEDAE KAKGTEGGSKGIKTSGESEEIE MVIMERSKLSELAASTSVQEQN TTDEEKSAAATCSESTQWSRPF LDMVYHALDSPDDDYHALFVL CLLYAMSHNK/GKSPEKEEGLS GTQSHPGKAGTFGKEGAEERK
6287	36655	A	6337	2	2753	
6288	36656	A	6338	1	577	
6289	36657	A	6339	1	849	

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6290	36658	A	6340	1	1293	
6291	36659	A	6341	1	861	
6292	36660	A	6342	154	6208	RRAPGKIPGQASAFLGRTWSRP CLRTQLCVIVSCLAKAGVQGYL VGSPGGAKRFLFSERTGSFSKL AAMSSWLGGLGSGLGQSLGQV GGSLASLTGQISNFTKDMLMEG TEEVEAELPDSRTKEIEAIHAIL RSENERLKKLCTDLEEKHEASE IQIKQQSTSYRNQLQQKEVEISH LKARQIALQDQFLKLQSAAQSV PSGAGVPATTASSSFAYGISHHP SAFHDDDMDFGDIISSQQEINRL SNEVSRLESE
6293	36661	A	6343	3810	5310	SQGTCVPDRPCNVSG*RI\SIEEI EAGRIPNPHLGPVEERLALHVL QQQGLVPEHVESRPLYSPLQPD IEQAFPSFGRKSRWIRVIPFPRFF LRCIIWNTRDVILDDLSLTGEK MSDIYVKGWMIGFEEHKQKTD VHYRSLGGEGNFNWRFIFPFDY LPAEQVCTIAKKDAFWRLDKT ESKIPARVVFQIWDNDKFSFDD FLDPYAIVSFLHQSQKTVVVKN TLNPTWDQTLIFYEIEIFGEPAT VAEQPPSIVVELYDHDTYGADE FMGRCICQPSLERMPRLAWFPL TRGSQPSGELLASFELIQREKPA IHHIPGFESEDTDLPYPPPQREA NIYMVPQNIKPALQRTAIEILA WGLRNMKSYQLANISSPSLVVE CGGQTVQSCVIRNLRKNPNFDI CTLFMEVMLPREELYCPPITVK VIDNRQFGRRPVVGQCTIRSLES FLCDPYSAESPSPQGGPDDVSL LSPGEDVLIDIDDKEPLIPIQNYA
6294	36662	A	6344	1	527	
6295	36663	A	6345	5251	5711	PPQRGPPSSSCYSRSQRSVSRCP SRHRPSAASPRPGRPSGRSGLLA GLRLWAGAGCFQCPPCLQRGL FSPEALRPQAPAHKGLFSGSLW PQQRSHQGLRAAATS*DRRAG ALCKWCPRPSGTPRGEHLS*EN ESLPP**RWAHQTAPQESQTS
6296	36664	A	6346	1	924	
6297	36665	A	6347	1	894	
6298	36666	A	6348	1	525	
6299	36667	A	6349	6	343	
6300	36668	A	6350	1	2693	
6301	36669	A	6351	26	353	
6302	36670	A	6352	1	9182	

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6303	36671	A	6353	1	8655	EAAKDLADIAAFFRSGFRKNDE MKAMDVLPILKEKVAYLSGGR DKRGGPILTFPARSNHDRIRQE DLRRLISYLACIPSEEVCKRGFT VIVDMRGSKWDSIKPLLKILQE SFPCCIHVALIIKPDNFWQKQRT NFGSSKFEFETNMVSLEGLTKV VDPSQLTPEFDGCLEYNHEEWI EIRVAFEDYISNATHMLSRLEEL QDILAKKELPQDLEGARNMIEE HSQLKKKVIKAPIEDLDLEGQK LLQRIQSSESF
6304	36672	A	6354	1	1338	
6305	36673	C	6355	152	404	
6306	36674	A	6356	137	1278	MDSQPNSTRGQSGRR/MEIKGI QLGKEEVKLSLFADDMIVYLEN A\TSQPKISLS**ATSAKSQDTKS MCKNHKHSYTPITDKQRAKS* VNSHSQLLQRE*NT*ESNL*GT* RTSSRKTTNHCSMK*KRIQTNG RTFHAHG*EESIS*KWPYCPR*F IDSMPSPSSYQ*LSSQNWKKRL SSSYGTKKEPASPSQS*AKRTKL EAS/LLPDFKLYYKATVTKTAW DMDEAGNHHSQQTITRTKNQT PHVLTHRWELNNENTWTQEGE HHTPGLVVRRSPDPEQNFKAVR CLDLPD/PSSSFLAVLTFHFKPA FLQSLR*DKPRS/SPALGTWHKP *KITPKKQ/HQAITKPNTEYRTA VKPSVVGALPDINSFLKLGGLH RITNGCLLD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6307	36675	A	6357	1	2569	MRTKTQHTRISWDAFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKREK NQIDTIKNDKGDITTDPTEIQTTI REYYKHLYANKLKNLEEMDKF LDTYTLPRLNQEEVESLNRPITG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIHHDQVGFIPGMQ GWFNIRKSINVIQHVNRAKDKN HMIISIDAEKDFDKIQQPFMLKT LNKLGIDGTYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVVEVLASAIRQEKEI KAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFIIASKRIKYLGIQLTRDVKDLF KENYKPLIKEIKEDTNKRKNIPC SRVGRINIVKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKRAHIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYSYQNR DIDQWNRTEPSEITPHIYNYLIF DKPEKNKQWGKDSLFNKWGW ENWLAIWRKLKLDPFLTPYTKI NSRWIKDLNVRPKTIKTLEENL GITIQDIGMGKDFMSKTP/TSNG NKRQN*QMGSNETKELLHSKR
6308	36676	A	6358	1702	2252	FLSLFFFISLASSLSILLIHIMNSW IPHSPIFTDLNVESSRLCPLGDIM M*IPLTWYLIVTCTHLSREITTV PRGLARLWSFTRICPRTHCKPIP A\VLLRAGCPPSCWWDQDTHS QLPSKRSSYTLFFCTVTEYPFLD *WP*NHGTPC*TAPLWSMF/PCS CWYPVTGPGVSCSPSCVQVFSL FISHL*VRTCGVWFFVLAIVC*E *WFPASSMSQAVLVTVAL*YSL KSGSVMPPA\FSFGLGLTWRCR LFFGSIRTLK*IFPIL*RKSLVA* WGWH*IYKLRWAVWPFSRY*F FLPMSM/VMFFHLFVSSFISLSS GL*FSLKRSFMSLVSWIPKYFIL FEAIVNGSSLMIWLSVCLLLLH KNACDFCTLILYPETFLKLLISL RRFWAETMGFSRYTIMSSANR DNLTSSFPN

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6309	36677	A	6359	207	1209	IPRHIHPPKTKPGRS*/TP*IDQ*Q ALKLRQ/CINSLPTKKSPGPDGF TAKFYQSPSLTGKNDKEPEILPY FHADFLVVPGTHQASPVLMVL GHKSFPHRNSPPSVCMANFFTQ KPPSQSIHNAVNTHTDPPLFLVL LKDRGLLVIWCHESQGDELWH LVLLDSKCCFGSMTHRMEWSG PSAAGLLEFAGGPLQTLFAWVS AVEAAEQRILLNSKCCCLIIPLE ALSQRGIWPWQGSPVPRPWTTT TLWPVRNQATQQETSLMPCQL EGKEPLALPTKEAEIEGRRTGEI KKVERDSNTNKEELLLDLAFK VSSLFDKLEEVVELLVIGELQL YPSK
6310	36678	A	6360	544	678	AFFHVSFGCINVFF*EVSVHML CPLFDGVVFFLVNLFEFFVDSG
6311	36679	A	6361	7	94	VRTSGVWFFVLAIVC*E*WFPA SSMSLIY
6312	36680	A	6362	381	431	ATKQDSVSKKKEEEEEEEEEEE EEEEEEEEEEEEEEEEKEK/GNK ERKK/DKGKARQVQARQIYLLS LHLGRIRKVPNNNKA*SSCP
6313	36681	B	6363	1	603	
6314	36682	A	6364	1	987	
6315	36683	B	6365	1	444	
6316	36684	A	6366	977	1177	RTSISSPVSSTCSPLVMPTLLPQP TVPWRMWRPCTQ*RNAGTFSP AVAMGLPVEAVICLSV*DSPA
6317	36685	A	6367	1148	1395	
6318	36686	A	6368	33	663	VHVLCGDTDETGNHHSQQTIA RTKNQTPHVLTHRERLSLRRGL HSCAYSLHRWLGARHAQKGSR NTKGCGGQGPRTSERGPASGEF SENCTSLLGQRGVFSPGRRALL HSPSDG\SVPLGAVDSSP\PASTR RDWSHWAVGKPSPEREPAGKV T*TTRQLQPASP*REHPLLNSQH GHCLKISLPLLPTVLSPSPPLSLC SNVTFSTRPLT
6319	36687	A	6369	1	1314	
6320	36688	A	6370	120	410	
6321	36689	A	6371	1	492	

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6322	36690	A	6372	3	945	EEVPRSMSKKKKRKRRKSRKR EEEEEEEEEEEEEEEEEEEEE EERR\EGEGEEEEEEEEGKEKID PSHLELKMVRNKNTMYEVCLM PIGIKPQVNVGAMQCILVAPYIS PIVGVINFNDQVNSQGGGSKME DGIHFRGKVMLHVGKRKQRVK KGLGYAFISSMKTNEYTKLVPV EWGLAEKIPKNVEATLELGNRR SKKTGGILPLLLWNFELERDEL GYLVEEISKQPSIQQMTWVLLK AFRFIQEAEPKSSENLNPDNVIE KKNPFSEGKFMLAAEICISNEE WNGNVNPQDYGGKWLQGMA EVFTATPSITGLEA
6323	36691	B	6373	1	792	
6324	36692	C	6374	348	884	
6325	36693	A	6375	1	588	
6326	36694	B	6376	1	5339	
6327	36695	B	6377	520	3146	
6328	36696	A	6378	1	2044	
6329	36697	A	6379	1	585	
6330	36698	A	6380	1	2433	
6331	36699	B	6381	53	441	
6332	36700	A	6382	2	425	
6333	36701	A	6383	1386	2569	FLRKHRESGKDEEMTALCSFPG VAGEDELQVIQPEKSVSVAAGE SATLRCAMTSLIPVGPIMWFRG AGAGRELIYNQKEGHFPRVTTV SELTKRNNLDFSISISNITPADAG TYYCVKFRKGSPDDVEFKSGA GTELSVRAKPSAPVVSGPAVRA TPEHTVSFTCESHGFSPRDITLK WFKNGNELSDFQTNVDPAGDS VSYSIHSTARVVLTRGDVHSQV ICEIAHITLQGDPLRGTANLSEAI RVPPTLEVTSQPI\RAENQANVT WQVSNFYPRGLQLTWLENGNV SRTETASTLIENKDGTYNWMS WLLVNTCAHRDDVVLTCQVEH DGQQAVSKSYALEISAHQKEH GSDITHEPALAPTAPLLVALLLG PKLLLVVGVSAIYICWKQKA

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6334	36702	A	6384	1	2453	MEPAGPAPGRLGPVLCLLLAAS CAWSASRQLPAVQVLRGDVTC GSDHVFLLAYIKHLAVAGRRA LKATVHVHQRTLLRPGGCGSV PGKRAVTLISKCSDGQPAFPGA PAGNTNTFLVCSCGFPDLQSSR GPERALCAFIQCLMVRPEEQRE KNWPGPRGRSMARPGWNAKPP VVQAKAFKNWAVLELSTVSAR NLTGSRIPRENTKVILIGTIWVL CFLGSALGVCDPGGTHSHLAM HVVIFGPVGSNNPSIVIIIIIIRPIL QIKSQRSRVGETFPGVSWVAEL ESKSKHTFSQCQALLQPWGRK LSSCSQRTYNLLLVCIQSMNVI DKHLRKHRGSRVAGEEELQVI QPDKSVLVAAGETATLRCTATS LIPVGPIQWFRGAGPGRELIYNQ KEGHFPRVTTVSDLTKRNNMD FSIRIGNITPADAGTYYCVKFRK GSPDDVEFKSGAGTELSVRAKP SAPVVSGPAARATPQHTVSFTC ESHGFSPRDITLKWFKNGNELS DFQTNVDPVG\ESVSYSIH\STA KVVL\TREDVNSQSFW*GPTVT LQGDPLRGTANLSETIRVPPTLE VIQQPVRAENQVNVTCQVRKF YPQRLQLTWLENGNVSRTETA STVTENKDGTYNWMSWLLVN VSAHRDDVKLTCQVEHDGQPA VSKSHDLKVSAHPKEQGSNTA AENTGSNERNIYIVVGVVCTLL
6335	36703	A	6385	1	405	
6336	36704	A	6386	91	2926	PACPSPRLPFTNTDTHIDTSSPA SRSTRCLCISTHGVLAQSGGSSG GPAVPTVQRGIIKMVLSGCAIIV RGQPRGGPPPERQINLSNIRAGN LARRAAATQPDAKDTPDEPWA FPAREFLRKKLIGKEVCFTIENK TPQGREYGMIYLGKDTNGENIA ESLVAEGLATRREGMRANNPE QNRLSECEEQAKAAKKGMWSE GNGSHTIRDLKYTIENPRHFVD SHHQKPVNAIIEHVRDGSVVRA LLLPDYYLVTV
6337	36705	A	6387	2	448	
6338	36706	A	6388	1	645	
6339	36707	A	6389	1	294	

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6340	36708	A	6390	23	321	RGREHTQGIPGAGKRWH*FKV LLTQ/CW*SEFSVIRQFKAGPGG LDQFRDRSK/RWLRDLRGRLLG SLNASLVLRALFSGNWGLTAN QL*LAVGAKGDPEA
6341	36709	A	6391	1	1599	
6342	36710	A	6392	1	561	
6343	36711	A	6393	1	1833	STLASSEGQGGFWRGPRALILL LLFLGPCHARSHDGKYSREKN QPKPSPKRESGEEFRMEKLNQL WEKAQRQERYPCRRRRRVKQV AAGTPRVFLKTPEMGVFELCRP SGPHYLISNAGVRLDLLNSPVL SIPESLRGKVNDLQNKKELLER KGRGETGLARPMHDLTAAQGG YGCALVHGAQVEGAGAQGWA GTVHATCRGETGTACQEALVT ATACSSCQRGQTRAPQGQHTL ESMGLNCLPQGAASGSDHHCG PRISDLPGSAARTSRWPASSELH LPPVRLAELHADLKIQERDELA WKKLKLDGLDEDGEKEARLIR NLNGHWRAEDAHQDGGVNK WDIPTVVGVGVAAIALVAVKL FFLPINIRCVLSESPATLHSLQV ASVLWSLEFLPYGSRSPVVIQET VILAKYGLDGKKDARQVTSNS LSGTQEDGLDDPRLEKLWHKA KTSGKFSGEELDKLWREFLHH KEKVHEYNVLLETLSRTEVHPG PQDGVASTGREHSPMETLFQEE LKHFEAKIEKHNHYQK\QLEIA HEKLRHAESVGDRRSV*SASPR ESTPCLEGRTKGAGLPR*KKHL QD\LSGRI\SRARHKRTLKALGS
6344	36712	A	6394	1	185	DFFDNSAQVTIAGIPCDIRHVSP RKIECTTRAPGK\V*GSPPLSQAI EGFFLKLEMLLRDWN
6345	36713	A	6395	1	1512	
6346	36714	A	6396	117	268	QSLLLEYLHLYLHLCYLHLANK QELTLTWYKE*CTFFLPSV*NPF HQNLA
6347	36715	A	6397	1	500	

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6348	36716	A	6398	1301	2565	TLLTILPFYLFKNRTSLTGYLRI WILSTKLFCLSTLWLAPTLFLIP/ LPDPHDCISLIHLAFTPFPHTSFF PIPHPDHTWFIDGSSTWPNRHSP AKVGYAIVVSSTSILEATALPPS TTSQQAELIALTRALALAKGLH VNIYTDSKYAFHILHHNAVIWA ERGFLSTQRSSIIIASLIKTLLKA ALLPKEAGVIHCKGHQKASDPI AQGNAYADKTKFLDLAFPPLR LSFTCQITQAVSQALGIQWNLH TPYRPQSSGKDWTVFLPLALHR IRARPREATGYSPFELLYGRTFL LSPNLVPDTSPLGDYLPVLWQA RQEIHQAANLLLSTPDSQLYED TLAGRSVLIKNLTPQTLQPRWT GPYLVIYSTPTAVRLQDPPHWV HRSRIKLCPSDNQPNLSSSSWKS QVLPTTSLKVTLISEEQ
6349	36717	A	6399	581	2517	LFLGYSHTSLLPFPPVQSLLHLL PLYLHTLTHKYGIPLLPPWRPIM HPLPSH*NLITLTLLNANIPSCST L*KD*SLLSLTCYSMAF*/QPINS PYNSPILSVQKPDKPYSSFRYVY SLFVESPTITIVPGPDFNLASHIIP DTTPDPYDCISLIHLTFTPFPHVS FFPVPHPFHTWFIDGSSTRPNCH TPAKAGYAIVSSTSIIEVTTLPHS TTSQQAELIALTRTLTLAKGLC VNIYTDPISCTTMLFYGLKCFLT MQGSSIINASLIKTLLKAALLPK EAGVIHCKGPQKASDPIAQDNT YADKVAKKAASVPTSIPHSSFS PSHLVTPTYSPTETSTYQSLPTQ GKWFLDQGKYLLPASQAHSILS SFCNLFHVGYKPLARLSELLISF PSWKSILKEITSQCSICYSATPQ GLFRPPPFPKHQAWGFVPTQD WQIDFTHMPQVGKLKYLLVW VDTFTGWVEAFPTGSEKATVVI SSLLSDVIPRFCLPTSIQSNNGLA MISQITQAVSQALGIQWKLCTP YHPQSSGKVKWANGLLKTHLT KLSLQLKKDWTVLLPLALLRIR ACLRNATGYSPFELLYRCSFLL GPSLIPDTRPTWTAPPKTWHPY YLLSSHTPIHRSQLLIHALLLFTL PVYTVSPSHHS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6350	36718	A	6400	281	1095	DCSKRNRHSQVIAEGNICKIQE VRRKEDTQGGEKDPESLLLPPL LAPGPTE/YSTYYNISVAKAELL NKLKDQPEMAEIGLGEEEVDH ELAQKKIQLIESISRKLSVLREA QRGLLEDINANSALGEEVEANL KAVCKSNEFEKYHLFVGDLDK VVNLLLSLSGRLARVENALNSI DSEANQEKLVLIEKKQQLTGQL ADAKELKEHVDRREKLVFGMV SRYLPQDQLQDYQHFVKMKSA LIIEQRELEEKIKLGEEQLKCLR ESLLLGPSNF
6351	36719	A	6401	1	972	
6352	36720	A	6402	514	736	
6353	36721	B	6403	446	991	
6354	36722	A	6404	521	903	NIKPASQISPG*I*VHSSPTQRLS APPSAA/GRLLSLSLPAGLVGGD TARCIPAGRLRPLCSWLDPGKL LHLSLKSKGSGGRSGAGTLQEG NQSVCIQAEKPPLKPAIQTQSG MNVLRCRAYSWVIDWD
6355	36723	A	6405	11	545	
6356	36724	A	6406	3	2920	
6357	36725	A	6407	1	2388	
6358	36726	A	6408	275	479	
6359	36727	A	6409	1	3810	
6360	36728	A	6410	7	1047	
6361	36729	A	6411	1	705	
6362	36730	C	6412	304	638	
6363	36731	A	6413	99	759	WAYLDFWM*HIPHLGVLL/SAH LLSDLNSCQF*MGSRTEGSATG PGSCSAALPLGPYDPADPMVLE VSMADRDASPHDPLAKFLFPVP MTLHSALLEVLVPEGGTLPPGD TTTIPLNW/IVKIAT*TLWVPPTF KFTGCRLNTMWKLPRLGASTL *SNSLRCTLTSFSHDWSGWDAG HQVIRPHGFAGYNTCGCFHRL MLSACGFSRQMVQAVNGSTTL GSGG
6364	36732	A	6414	1	685	
6365	36733	A	6415	1	1359	
6366	36734	A	6416	3	7714	
6367	36735	A	6417	1	723	
6368	36736	A	6418	1	528	

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6369	36737	A	6419	38	530	HSPRRSAASLLSQRDHEPHQKE ETPNTSEHQKEKTPDTPPLRTV TLTVRVHGFILEVSETKNPPIPD TKLRG/ERLQGFGLAGFRSE/GC RPSP*VLQLIKAVWTQRPLGGR WDWAPWSRRWCSSGRLRPHR NQWSGWEAQAWGLQVPEPCP AGRQLRPGEKSSTAP
6370	36738	A	6420	1	649	
6371	36739	A	6421	1	987	
6372	36740	A	6422	1	924	
6373	36741	A	6423	1	435	
6374	36742	A	6424	1	147	
6375	36743	A	6425	1	1107	
6376	36744	A	6426	3	913	
6377	36745	A	6427	1	159	
6378	36746	A	6428	313	1083	
6379	36747	A	6429	1	1245	MAQELRDTCTSFSSRFDQVEER VMVIEDQINEMKQEEKFREKR VKRNKQSLQEIWDYVKRPNLR LIGVPEKNLEETDKFLDTYTLPR LNQEEVESLNRPITDSEIEAIINS LPTKKSSGPDGFTAEFYQRYKE ELP/RQRHNKKREF*TNIPDEHR CKSPQ*NTGKPNPAAHQKAYPP *SSGLHPWDARLVQHTQINKRN PAYKQNQGQKPHDYLSRCRKG L*QNSAALHAKNSQ*IRY*WDI SQNNKSYL*QTHSQYHTEWAK AGSIFFENWHKRGMPSLTTPIQ HSVGSSGQGNQAGERNKGYSI RKRGSQIVPVYR*HNCISRKPH HLSPKSP*AGKQ/SSAKSQD/DKI NVQKSQAFLHTNNRQTESQIMS E/APIHNCYKENKISRNPTYKGC EGPLQGELQTTAQRSKKGHKQI
6380	36748	A	6430	39	314	KSECLIYTKGSQRLASNGTKLD GE*L**VDRIRLQKIGNDKLLPA KGGCSNPSQRS*KPRKKIRQMA N*NKQHRGDLK*PDGAENHGT RTT
6381	36749	A	6431	213	843	VDRSRLQKVSNNKLL*AKGECS NPLQGS*KP*KKIRRMAN*NKH CREDLK*PDGVENNGTRTS*FM HKLQ*PI*SSGRKGISD*R*N**N KIHQG*NEGKSVKGSQRERSSY PQRKAHQTNSGSLSRNPTSQKK VGANIQHS*RKEFSTQNFISSQT KLHK*RRNKIFYRQADAERFCH HQACVTRAPEGSTKHGKKQPV PAPAKTGQIV

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6382	36750	A	6432	1	2112	MRAFVVLMDVSKLPSERGGPG LRSNQQHMRMFLTSVDRGSVS LLADAVAAATPQGTKSQPRGPS NLAADLRVAEESSGMENLFLK MSFDSIRPAQDGQCTPEISMVTP SPGWSVHTGDLDGHPLPRMVS AHRRSRWSPPPQDGQCTPEISM VIPSPGCSVHTGDLDGHPLPRM LSAHRRSRWSPPPQDAQCTPEIS MVTPSPGWSVHTGDLDGHPLP RMVSAHRRSRWSPPPQDAQCT PEISMVTPSPGCSVHTG
6383	36751	A	6433	1	648	
6384	36752	A	6434	1	1539	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE/ SAN*NQQCREDLK*PEAEIHGT RTS*HMHKLQ*PI*SSGRKGVSD *GSNQ*NK*WGEWNQVGKHSA GYYPGELPQPSKAGQHSNSGNT ENTTKILLEKSNPKTHNCQIHQ G*NEGKSVKGSQRERTREARA NKFKS*QKARYN*DQCRTERD RNTENPSKN**IQEPVF*KDQQN **NASKTNKEEKREESNRRNKK **KNRTVKPHVSFTLLPALSHVS EKNEAESMNSLIPPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKSMA RELHDTCTSFNSRFDQVEERVS AIEDQTNEINNGENGTKLENTL QDIIQENFPNLARQANIQIQEIRR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKGLERQEQTN SKASRRQDITKISAELKEIETQK TLQKINEFRSRFFKKINKIDKTL ARLIKKKREKNQTDAIKNDKR DITTDPTEIQTTIREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEAESLNRTITGSEIEAIINSLPT
6385	36753	B	6435	137	586	
6386	36754	A	6436	129	506	
6387	36755	A	6437	1	237	
6388	36756	A	6438	182	1034	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6389	36757	A	6439	203	650	SAIVCGSPLRLRMQAVSSRINSA HSRGAIYSQASSSAACPSVSIAF LRR*IEANVS/WIRTLLSTLCTPK CGPGFKHRIVLCKSSDLSKTFPA AQCPEESKPPVRIRCSLGRCPPP RWVTGDWGQ/CDSRDPRPGRR RRDFCRNGRAGAGH
6390	36758	A	6440	207	426	AECTRCAIPK/HSCYPVLLIVVS P*KKQ\NCSLGELSCWRRESCRS SWSNKALPSLTRCLRGFVCGLS CYKGSS
6391	36759	A	6441	524	783	TAVLAARISNQWILSCWS/AVG CTPKCGPGFKHRIVLCKSSDLS KTFPAAQCPEESKPPVRIRCSLG RCPPPRWVTGDWGQLSPTREK
6392	36760	A	6442	1	1524	
6393	36761	A	6443	1	8738	
6394	36762	A	6444	1	642	
6395	36763	A	6445	1	549	
6396	36764	A	6446	8	434	
6397	36765	A	6447	1	2922	
6398	36766	A	6448	18	1158	FLDFDCPYGSAHITGLRFWLPW YRKRQRYWGSHGNCMPPPSLR VPERCPSHTEPRNLTGA*ELLLL GLSEDPELQPILAGLSLSMYLVT VLRNLLISLAVSSDSHLHTPMC FFLSNLCWADIGFTSAMVPKMI VDMQSHSRVISYAGCLTQMSLF AIFGGMEE\NMLLSVMAYDWF VAICHPLHYPVIMNPHLGVFLD LGAFFLSLLDSQLHSWIVLQFTF FKNVEISNFV*DPSQLLNLACSD SVINSIFIYLDSIMFGFLPISGILW SYANNVPSILRISSSDRKSKAFS TCRSHLAVVCLFYGTGIGVYLT SAVAPPLRNGVVASVTYAVVT PMLNPFIYSQRNRDIQSALRRLR SRTVESHDLLHPFSCVGKKGQA
6399	36767	A	6449	2	1535	
6400	36768	A	6450	1	635	
6401	36769	A	6451	222	1040	
6402	36770	A	6452	2	1135	
6403	36771	A	6453	1	576	

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6404	36772	A	6454	2	694	QCGGIQRSHGSWSQEASDSVW QLQSMWMLDKLTGVFAPRPST GPHKLR\ECLSRIIF\LRNRLKYA LTGDEVKKI\CMQRFIKI\DGKV RT\DITYPVG\FMDVI\SIDKTGR EFPVLIYDTKG/RAFAVHRITP\E EAQVPSCAKVRRDLCGAQKGIP HLVTH\DARTIPLPRSPSSKVND\ TIQI\DLEDWARFT*FSSKFDNW *TCCMGDWEGA*P*GRNWVLI HQQRRRAPWDLF
6405	36773	A	6455	1	243	
6406	36774	A	6456	3	766	
6407	36775	A	6457	1	741	
6408	36776	B	6458	500	8643	
6409	36777	A	6459	1	7863	MKPRTLTVRVTALKVARLESV PSDVQMCSEFLPSDSAAQLASP SGSRTGAAGGAAYQSCAVLPH SSALWVVDGTRCRGAGGSAHQ GGSATQEPTERVEGSGMAGCR SRVLPHWKAANVLGMSVESAP AVEEEKGEELEQKEKEKEEDTS GNTTHSLGAEDTASSQLGFGVL ELSQSQDVEENTVPYEVDKEQL QSVTTNSGYTRLSDVDANTAIK HEEQSNEDIPIAEQSSKDIPVTA QPSKDVHVVKEQNPPPA
6410	36778	A	6460	2	669	ERRRRKLTIPCPPPHPAPPTGGQ ACRENAEGIL*AANTSEPGKDA EK*KIKV*LAP/CSHSGSSLQSDP HFGCSLGPS/DPALGLSGCILPPC SGSYLAPAPNSRIPKPGLKPW/H /ESYLPSAVRPHGTQAPGLWPE RGL*PAGFLLRPEPVRAASER/Q EAVSPER*VPRPPKAQQLHGQS PDPSSLCTALRQDHTHWLDARS VYPDWRGQPWPPLHQDCGHG GWR
6411	36779	B	6461	241	369	
6412	36780	A	6462	1	510	
6413	36781	B	6463	1	630	
6414	36782	A	6464	229	561	SCRGYSRILLLFHKSSWCSQVIS IFRYNIICSRLPRSWKWRLPVY MNWL*YHWFKQYHSSINFISFR SMWFIIIINFKRSPAFILSGSWSIS IARWQIFVFFTTFGSRTKV

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6415	36783	A	6465	1271	1710	TEGLGHRSSETPGGAALDALTG ERPRVACFPAARGRGLRPRPRL MIGPFETGGGQRLLTLRPRRRR QRRRP/WQGLERPHVRNWGIEL ETLRDAFRPQPSVWRTARGEA GKRKGRLVECLGSQRKVLEGV LLYAVTRGSFPNLFTPRD
6416	36784	B	6466	1	772	
6417	36785	A	6467	1	1272	
6418	36786	A	6468	3	236	
6419	36787	C	6469	1	457	
6420	36788	B	6470	148	324	
6421	36789	A	6471	1	1407	
6422	36790	A	6472	1	651	
6423	36791	A	6473	619	835	
6424	36792	A	6474	52	535	
6425	36793	A	6475	319	647	LCRRIYMYFCVMKNWMQSLW KLCTNKR*RIDKPTLHQVVVRK *LTPLGMKNQVDSLELLETRSL KKDPVELGSKSLRRCCCQTEPV NLLPHVSIGTLKI*SRILRLQRP
6426	36794	A	6476	39	515	
6427	36795	B	6477	1	807	
6428	36796	A	6478	3	247	GANICCW*GLQE/VFHSW*KTQ EPSWLHLVDPTTGLQVELPASP APFARIPQPLGGRWDWAPWSR GWCSSGRLGQHRSPWSG
6429	36797	A	6479	27	363	
6430	36798	B	6480	1132	1268	
6431	36799	A	6481	1628	2008	
6432	36800	A	6482	953	1087	
6433	36801	A	6483	2	443	QLAGRCGGRGMSGNRGC\WGA CGPAGVPGG/CWAWCALHSEE PASPALRSISRRALAAFPRGRAR DLQPAMPEPPTPSVGSCAAQAS PTSAAPCSMAPSPIDHPRAEECV ARRGTGRHDELIVALPFMMIPW HSSIQPFTIHPFNWNFG
6434	36802	C	6484	175	423	
6435	36803	B	6485	122	608	
6436	36804	A	6486	644	1149	KTMHWKAPLMSWHMHRASSQ KQTRTGTQT/MEAQLQQLQRY QEALLQVLRKGEKKAFNMGNI SEVLQRADESCSQFYERLYEAF QLCSPFDPEATENQCMVNAVF VGQTQGDIRRKLQKLECFTGM NVTQVLEVATKVYTNCEEETQ GKGQFAGGSTYGKGGECPKTK
6437	36805	A	6487	1	2847	
6438	36806	B	6488	329	742	
6439	36807	A	6489	1	1035	

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6440	36808	A	6490	13	630	INPPPPPFRPEPPSSSNSPKMTDH KGERGEATRYMFSRPF\RK\HG VVPLGPHICRI\YRKGDIVD\IKG MGYCSKKGIAPTKCY\HGQNLE GVLPMLPQHACWPFVVNQPVL GQSFFPRELMCRIEHI*ALLRAR DKLPETVLKENDSEKERSPNEK GTWGSNLKRHPGSTPEEAHFV RTQWGRSLELAGTLFPMNFMG IIGVKEIK
6441	36809	A	6491	1	1020	
6442	36810	A	6492	1	330	
6443	36811	C	6493	250	372	
6444	36812	A	6494	1	345	
6445	36813	A	6495	2	335	TVRAYNVPQHAVGIVVNRQVK GKIPAKRINVGIKHFKHSTS*EN FLKRMKENDQKKKEAKEKVT WIQLKHQSAPPRE/AQCERTNG KEPELLEPLPYEFMHNTYIHIYV CVH
6446	36814	A	6496	2	490	
6447	36815	A	6497	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQ/RKAPGKNLVYISLVLRA L*G*DLTHHIIILFPFFFL**PAPP REAHFVRTNGKEPELL
6448	36816	A	6498	54	553	
6449	36817	A	6499	131	803	TMFCQTGSSVRRVGPGPWAEN RTAMLRPCGGTFARKTRLSRLG NSPKMNEQQRGKRRGTPIIMFS KGLLRKHG\VVPLAHIFMR\IYK \KGDIVRHPRGMGYLVPKRELP PQSCYPWPKPGRSLTNVTPAML VGHLL*NKQV*GQRFLPKRNL MWRI*APFRHFLRSPRLASLKT CGRENGSRKKERKPKGGKVTW GFQLKRRHLGFPPQEEATFLLK EPIGGREP
6450	36818	A	6500	1	489	

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6451	36819	A	6501	29	2028	ENEEEGEKMASTDYSTYSQAA AQQGYSA\YTAQPTQGYAQTT QQAYGQQSYGTYGQPTDVSYT QAQTTATYGQTAYATSYGQPP TGYTTPTAPQAY\SQPVQG\YGT GAYDTTTATVT\TTQASYAAQS AYGTQPAYPAYGQQPAATCPT RTED*\NKPTETSQPQSSTGGYN QPSLGYGQSNYSYPQVPGSYP MQPVTAPPSYPPTSYSSTQPTSY DQSSYSQQNTYGQPSSYGQQSS YGQQSSYGQQPPTSYPPQTGSY SQAPSQYSQQSSSYGQQSSFRQ DHPSSMGVYGQESGGFSGPGE NRSMSGPDNRGRGRGGFDRGG MSRGGRGGGRGGMGSAGERG GFNKPGGPMDEGPDLDLGPPV DPDEDSDNSAIYVQGLNDSVTL DDLADFFKQCGVVKMNKRTG QPMIHIYLDKETGKPKGDATVS YEDPPTAKAAVEWFDGKDFQG SKLKVSLARKKPPMNSMRGGL PPREGRGMPPPLRGGPGGPGGP GGPMGRMGGRGGDRGGFPPRG PRGSRGNPSGGGNVQHRAGDW QCPNPGCGNQNFAWRTECNQC KAPKPEGFLPPPFPPPGGDRGRG GPGGMRGGRGGLMDRGGPGG MFRGGRGGDRGGFRGGRGMD RGGFGGGRRGGPGGPPGPLME QMGGRRGGRGGPGKMDKGEH
6452	36820	A	6502	1	693	
6453	36821	A	6503	3	657	
6454	36822	A	6504	1	434	
6455	36823	A	6505	208	443	

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6456	36824	A	6506	3	2650	LLPAFLLLCSDSHFLQFCSQFAP RKTQGSGSVNNIQANIIAKKSN NHLMKKNDQKFKDLPQMAGH PIHHQAQGPPGAKNPQEQQRRP MGQTTLPAEQEESRVKCKNCG AFGHSARNKTCPIKRWSGALPL QVLGSHKEKENLKPAKAQLPFT TPGPFTTNDREKERSPSSTMNPS EMQRKASPRRWKHHNQTPSIH KVNKMVMSEEQMKLPSTKKA EPPTWAQLKKLTQLPKKSLEN\ TKVTQTPENTLLAALMIVST/A GAAAANYTYWAYVPFPPLIRA VTWMDNPIEVYVNNSAWVPGP TDDRCPDKPEEEGMMINISTGY RYPPICLGRAPACLMPAIQNWL VEVPTVGTTSRFTYHTGLLTFR DVAIEFSQEEWKCLDPALEDSY TRRKANSCGKPYKCNECGKAF TQNSNLTSHRRIHSGEKPYKCS ECGKTFTVRSNLTIHQVIHTGE KPYKCHECGKVFRHNSYLATH RRIHTGEKPYKCNECGKAFRGH SNLTTHQLIHTGEKPFKCNECG KLFTQNSHLISHWRIHTGEKPY KCNECGKAFSVRSSLAIHQTIHT GEKPYKCNECGKVFRVGRGVSI GTTCLLSVFQVITVSSRKSRASP ENRATQSILILAPPTSRGSGPGP ASVLRRLAQTRKRMAWTESCT AACAFPSCLVLLYRGRGVPTDL QVPAPLFSTQSKLKRPGSRTKSS
6457	36825	A	6507	54	360	CSTMNPSEMQRIAPPRRQRHRS RAPSAHKMNRMVMSEEQMKL PSTKKAEPPTWAQLKKLTQLA KKK\LENTKVTQTPENMLLAAL KTVSTVSAGVPSSSEESD
6458	36826	A	6508	525	3656	SSTMNPSEMQRKAPPRRRRHR NRAPLTHKMNKMVTSEEQMK LPSTKKAEPPTWAQLKKLTQLA TKYLEN\TKVTQTPENTLLAAL MIVSMVVSLPMPAGAAAANYT YWAYVPFPPLIRAVTWMDNPIE VYVNNSAWVPGPTDDHCP\AK PEEEGMMINISTGYRYPPICLGR APACLMPAIQNWLVEVPTVGT TSRFTYHTIDLMTEKWVVLASV EVLLRFPLKPGEDPTARYVSNK KCQPSVDWPTTISQRRGY
6459	36827	A	6509	1	246	
6460	36828	A	6510	1	246	

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6461	36829	A	6511	1	279	
6462	36830	A	6512	1	363	
6463	36831	C	6513	109	245	
6464	36832	A	6514	2	429	LMTFCWDTPRQSGVPRERMPH TGTWRTVGIRCPKKKLRSANSS MMRGKVQPFRP/DIQAYGAAPF EDLQVDFREMPKCGGNKYVLV LGRTYSGWVEAYPTRTEKTRE VTPVLLRDLIRRFRPPLWIGSDN GPAFLAALVQKTAK
6465	36833	C	6515	31	895	
6466	36834	A	6516	2	4735	
6467	36835	A	6517	263	418	
6468	36836	A	6518	120	295	YDPLPTWILGKISQRGAEEPAQ HPGCQL*LPPP/SPPRTSSSPSCA GLTSVSPRPRFPR
6469	36837	A	6519	1	1758	MKIRRRFPSSLQLSADLQVPVR KAPRQGVSQEKRTKPSLELMIS GTISQEDIRNNVTRGCTPPAIQR VISSSPLLAIRNNVTEGVYTPCD TGGRVHLPVILLLISRDGGHDIS FNIAVDVHSPCDTDPNIQGVEY DMTPNIAMNVQPPGTISQKRCT LPAILGLISYASSVNIRSNITGWL YIDRYVGSHVILYPLGIRMGVT GEMKGERRRGLHAATKWLEE HAPADYQNPQEYGRTQLPGTQ PQLDPHEREDMQRLNRDREAL LEGFKRGAQKATNVNKVSEVI QGKEESPAQFHQRLCEACAKQ VLVNGDAVSREEKRKENERQA RRNADLLVSCSNQSGPPKEARE ELWTKDYRPGQDLRLLSQATL TFHPTVPSPSTLLGLLPAEDSWF TCLDLKDAFFPIRSAPESQKLFA FQWEDPESALAKTVRQRCVSC RQHHA\GKVQPFRP/DIQAYGA AAFEDLQVDFTEMPECGGNKY LPVLGRTYSGWVETYPTRAEK AREVTRVLLRDLIPRLELPFRIG SDNGPAFVADLLQKTATVLGIT RKLHAASRPQSSGKGIQNNRTG GVYTPCDIESHVILFRSGY
6470	36838	A	6520	1111	1342	MFVPHIGFQNTAALCLLRLGVL FP*PVGFPAGSCLLI*WNRHWH VPDFSCVTTPQEWCGGVSDVC CGHPHAEPFHLQ

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6471	36839	A	6521	1	1144	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRALAATALLVQEANKLTLG QKLNIKASRAVVTLMNTKGHH WLTNATLTDYQTLLCENPRITIE VCNTLHPATLLPVSKSPVKPGC VEVLDSIDSSRPDLWDQPWASV DWELYLDGSSFFNPQGEVEG\S RGDTSELPPCWVCGIPALTQRL EKQHLPPSGHQGSLKHLIWDLL LLTKKRTFSSMI
6472	36840	A	6522	1	554	
6473	36841	B	6523	63	620	
6474	36842	A	6524	1	796	SRTKNYQPVQDLRLLHQAKLT FHPTVPNPSTLLGFPPAEDSWFT CLDLKDAFFPIRLAPERQKLFAF QWEDPESGWPPCWRALAATAL LVQEANKLTLGQKLNIKASRA VVTLMNTKGHHWLTNATLTD YQTLLCENPRITIEVCNTLHPAT LLPVSKSPVKPGCVEVLDSIDSS RPDLWDQPWASVDWELYLDG SSFFNPQGEVEG\SRGDTSELPP CWVCGIPALTQRLEKQHLPPSG HQGSLKHLIWDLLLLTKKRTFS
6475	36843	A	6525	3	2640	
6476	36844	A	6526	2745	3732	IRIGKNYFKVHMEPKKSPHRQV NPKPKEQSWRHHTT*LQTILQG YSNQNSMPGPTPQ\PSTPAPGG NLRNPQSSDLLQVTKQQGQAL AIQREAPLHRIPAPEAIPWYFQP QPATQLGSPPVDPPSSAMM/SR RAHRSRGPDRQGYPLQGD*PGE PRPQEH*RGHSQERLPSSEKQTP ICPPAQATQHPEEPDAHQPYKH LFQVCAHQGHPVAQRRN*PGY WERYHSAEDPELQPILAGLSLS MYLVTVLRNLLIS
6477	36845	A	6527	1	1860	
6478	36846	A	6528	1	1458	
6479	36847	B	6529	1	1503	

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6480	36848	A	6530	3	515	TISQKRCTLPAILGLISYASSVNI RSNITGWLYIDRYVGSHVILYP LGIRMGVTGEMKGERRRGLHA ATKWLEEHAPADYQNPQEYGR TQLPGTQPQLDPHEREDMQRL NRDREALLEGFKRGAQKATNV NKVSEVIQGKEESPAQFHQRLC EAYRMYTPLDHDSPENQRMIH MALVRQSAEDMRRKLQKQAG LAGMNPSQLLEIASQVFVNRDA VSPKENSKENGGQARRHDDLF SPVEPDCVEVLDSIHSSRPDLRD QPWPSGDW/RTICGWEQLLQPP RRERCRVCSDNPGH/WLLKPHR CPRPLQARKLNSLLSLGP*NSTR DCVRPIVCILPLITIALKISA
6481	36849	B	6531	96	2524	
6482	36850	B	6532	61	2025	
6483	36851	A	6533	674	2913	
6484	36852	B	6534	120	1849	
6485	36853	A	6535	1	426	
6486	36854	A	6536	2	475	
6487	36855	A	6537	1	501	
6488	36856	A	6538	15	593	SMWWNSAREPCPWRIVDDCGG AFTMGVIGGGVFQAIKGFRNAP VCRLLSEAPLFIYSCSRSVSPTV NVSSERAESRPTLFMAVSLHMA WCLAHIGIRHRLRGSANAVRIR APQIGGSFAVWGGLFSTIDCGL VRLRGKEDPWNSITSGA\LTGA VL\AARSAPLAM\VGSAMMGGI LL/ALIEGVSILL/TR*TATV
6489	36857	A	6539	2	557	RRFRASAMEEYAREPCPWRIVD DCGGAFTMGVIGGGVFQAIKG FRNAPVGIRHRLRGSANAVRIR APQIGGSFAVWGGLFSTIDCGL VRLR\GKEDPWNSIT\SGA\LTG AVL\AAR\SGPLAMGGLQQ*WG GILFAPHLRAFGILLTRYTAQ\Q FRNAPPFLEDP\SQ\LPPKDGTPA \TGYP\SYQQYH
6490	36858	A	6540	223	2274	

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6491	36859	A	6541	2795	3762	FLHFHLRNAVPHQQWNKAGW RMTLRS*EKKASDDQITLSYGR TFKPK/DKEVENFEQNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERISVMED EMNEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DGENGTKLENTLQHIIQENFPN LARQANVQIQEIQRTPQRYSSRI AIPRHIIVRFTKVEMKEKMLRA AREKGRVTLKGKPIRLTADLSA ETLQARREWGPIFNILKENNFQ PRISYPAKLSFISEEEIKYLTDKQ MVRDFVTTRPALKELLKEALN MERNNRYQLLQNHAKF
6492	36860	A	6542	245	1293	TGAVPIRPSWQRWGKNRTEKL ETLKRRAPLLLQRNAVPHQQQ NKAGWRMILTS*EKKASDDQIT LSYGRTFKPK/DKEVENFEKNL EECITRITNTEKCLKELMELKTK APELREECRSLRSRCDQLEERV SAMEDEMNEMKREGKFREKRI KRNEQSLQEIWDYVKRPNLHLI GVPESDVENGTKLENTLQDIIQ ENFPNLARQANVQIQEIQRTPQ RYSSRRATPRHIIVRFTKVEMK EKMLRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK YFIDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK
6493	36861	C	6543	116	283	
6494	36862	A	6544	51	281	KSQNQLLSSKGEYADGQQDQV SIPAPSPYTLSGPQTQSCPVRPE LGL*GASSAVQAPAVRYLTRFL LFVMSNLHSP
6495	36863	B	6545	1	897	
6496	36864	B	6546	91	8030	
6497	36865	A	6547	126	362	

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6498	36866	A	6548	936	2064	ERADCLFKRKTNNQKGHLHRK PICTSPSSKTKSR*NHKDGEKTE QKNWKL*NAERLSSS/IRNAVP HQQQNKAGWRMILTS*EKKAS DDQITLSYGRTFKPK/DKEVENF EKNLEECITRITNTEKCLKELME LKTKARELHEECRSLRSRCDQL EERVSAMEDEMNEMKREGKFR EKRIKRNEQSLQEIWDYVKRPN LRLIGVPESDVENGTKLENTLQ DIIQENFPNLARQANVQIQEIQR TPQRYSSRRATPRHIIVRFTKVE MKEKMLRAAREKGQVTLKGK PIRLTADLSAETLQARREWGPIF NILKEKNFQPKISYPAKLSFISEG EIKYFIDKQMLRDFVTTRPALK ELLKEELNMERNNRYQPLQNH
6499	36867	A	6549	1	767	MAGAPPPASLPPCSLILDCCASN QRDSVGVGPSEPGVGYSLVVR RFLSRSEKRNIRVGVTRFSSEM NPVPQMEMQKSPSSASLTLGA VDRSCSYSAILAPPLGFCFYPLY ENSTLQSAKKRDAELANGALGI IELNNDYTLKKVMKPLITSNTV TDEIERANVFKMNGKWYLFTD SRGSKMTIDGINSNDIYMLGY/D IKLFNRPLQAAEQNRACAANGS *SKRCDIHLLSLRSAASQRQQC GYHKLHDKQRLLRG
6500	36868	B	6550	50	327	
6501	36869	A	6551	333	1301	FLHFHLRNAVPHQQWNKAGW RMTLRS*EKKASDDQITLSYGR TFKPK/DKEVENFEQNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERISVMED EMNEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DGENGTKLENTLQHIIQENFPN LARQANVQIQEIQRTPQRYSSRI AIPRHIIVRFTKVEMKEKMLRA AREKGRVTLKGKPIRLTADLSA ETLQARREWGPIFNILKENNFQ PRISYPAKLSFISEEEIKYLTDKQ MVRDFVTTRPALKELLKEALN MERNNRYQLLQNHAKF
6502	36870	A	6552	352	2304	
6503	36871	A	6553	1	1617	

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6504	36872	A	6554	1	257	MGPIHKISHYVYANISKSEKVL KSEHFRSQAFQPGQQSETVSEK KKKTRKKRKKRKKKRKKKKK KKKKKKKKKKKKKKKKKKKK SE*DRLGKKEEDEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEI
6505	36873	A	6555	5	156	RKKGGG/EREEEGEGEEEEEEE EEEEEEEEEEEEEEEEEEEVVL LTPGTGAEDFKKH
6506	36874	A	6556	1	279	
6507	36875	A	6557	3	120	TEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEGEEEE\EEEEE
6508	36876	A	6558	3	123	
6509	36877	A	6559	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEEKIFLGHRVGI
6510	36878	A	6560	1	588	
6511	36879	A	6561	1	204	
6512	36880	A	6562	75	234	
6513	36881	B	6563	100	2510	
6514	36882	A	6564	47	4976	
6515	36883	A	6565	3	4755	SCRCRRRRRGPAPAMAQILPVR FQEHFQLQNLGINPANIGFSTLT MESDKFICIREKVGEQAQVTIID MSDPMAPIRRPISAESAIMNPAS KVIALKAGKTLQIFNIEMKSKM KAHTMAEEVIFWKWVSVNTV ALVTETAVYHWSMEGDSQPM KMFDRHTSLVGCQVIHYRTDE YQKWLLLVGISAQQNRVVGA MQLYSVDRKVSQPIEGHAAAF AEFKMEGNAKPATLFCFAVRN PTGGKLHIIEVGQPAAGNQ
6516	36884	B	6566	47	482	
6517	36885	A	6567	1	555	MNARPHKVD/GRVVEPKRAV* EDSQRP\AFVAGIKEDTEEHHLR DYFQQYGKMEVIEIMTDRGSG KKRGFAFVTFDNHDSVDKTVV QKYHTANDHNCEGRKALSKQE MASASSSQRGHSSSGNFRGGHG GGFGGNDIFGYGENFSGHGGFS GSCGGGGYGSSGGGYNEFGND GSNTGGGGSYNDFGN
6518	36886	A	6568	1	645	

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6519	36887	A	6569	2	944	GRGLRKLFIGGLSF*FIDESLKS QVGEWGTLTDCVVMRDPNTK RSRGFGFVTYAT\VEEVDAAMN ARPHKVDGRVVEPKRAVSRED SQRPGAHI/TLVKKIFVGGIKED TEEHHLRDYFEQYGKIEVIEIMT DRGSGKKRGFA\FVTFDDHDSV DKIVIQKYHTVNGHNCEVRKA LSKQEMASASSSQRGRSGSGNF GGGRGGGFGGNDNFGRGGNFS GRGGFGGSRGGGGYGGSGDGY NGFGNDGSNFGGGGSYNDFGN YNNQASNFGPMKGGNFGGRSS GPYG\GGGQYF\AKPR\NQGGY GGSSSSSSYGSGRRF
6520	36888	A	6570	1	1512	
6521	36889	A	6571	2864	3677	RCQLDHLPCHLCCCCHR/CIPSL RDPQQAPGSTRLSRAPHIESRV GRKPPEEPANPTMNSLTLRDKQ /HDASTC/DWKRAL*VPESGLPR ALLKYIRCPNMSSAQKPRELSK RRN*K*PCVKRTPFRPT*E/DLP YSGKKTGVKGLICPVPGTAVK APQRPPGPQQPHPAPQSASETA WFPVADRRVFSENPGWTAAKT LGTLSSPCQAGAGVGRQDGDP GQELTSQEKPWVGRKIPEHAV ADKGYRQQCGAGEARGGPVF WAAAPRTSWQQASYT
6522	36890	A	6572	1	666	
6523	36891	A	6573	2926	3304	EYSLGHRHYNWKC*ALGQKDQ VTFATKFAPTSHRTRKQPELWR /QDPGSYGEKQPAWCSVPPGRF SGGLVGLGFLDGGIVVQPLRRP CCQDCVCGFPTLRSSTKTSTEL GPSFLPCERQGKETISVT
6524	36892	A	6574	1	665	

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6525	36893	A	6575	3	1121	SSTFPRMPWRLVTSWTAYIPEL EGSTSDPDSPAVAQKGEKPVKL GNSLWGSHTEPVPRPGTGPRPL SFVHRLPTMDPHKVNALRAFV KMCKQDLSVLHTKEMHFLRE WVESMGGKLSPATQKVKSEEN TKEEKPDSKKVEEDLKADEPSS EESNLLIDNEDVIEPDPDAPQEM GDENAEITEEMMDQANHKKVA AIEALNDGELQKAIDLFTDAIKL NPQLAILYAKRASVFIKLQKPN AAIRDCDRAVEIY\SAQPYKWR/ GKYEQKREEREIKERIERVKKA REEQERAQREEEARGQSVAQY GSFPDGLPGGMLEMRGGMPGK PGITGLNEIFSDPEVLAAVQDPK VMV/AFFQDVAQNPANMSQYQ GNPKVM
6526	36894	A	6576	3	1351	PEAGGERERERAQREEDSTRQS RAQYGSFTGGFPGGMPGNFPG GMPGMGGPSARSRRAQRLSLE PDRSPPSYAHHLPTMDPRRVNE LRAFEKMCKQDPSVLHTEEMR FL\RECVESMCGKVPPATHKAM SEENTTEEKPDSEKAEEDLQAD\ EPSSEESDLRKLIKEGVIEPDTD APQEMGDENAEIPEE\MMDQA NDKKVAAIEALNDGELQKAIDL FTDAIKLNPRLAILYAKRASVF VKLQKPN\AAIRDCDRAIEINPD SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDYDEDASAML KEVQPRAQKIAEHRRKYERKR EEREIKERIERVKKAREEHERA QREEEARRQSGAQYGSFPGGFP GGMPGNFPGGMPGMGGGMPG MAGMPGLNEILSDPEVLAAMQ DPEVMVAFQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGQ
6527	36895	A	6577	2	433	GPPLNLSSPRGGILKTYGCELCG KRFLDSLRLRMHLLAHSAGAK AFVCDQCGAQFSKEDALETHR QTHTGTDMAVFCLLCGKRFQA QS\ALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHTGDH PYECEFCGSCFRDE
6528	36896	A	6578	1	687	
6529	36897	A	6579	2	449	

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6530	36898	A	6580	852	1084	TDAGCYYAARQCGTAVPSRDV HIRHQGTPVPQF*TAPLRARS/E VSPARRRARMLSSSASFASANIT TSSAWSDTLQP
6531	36899	A	6581	1	681	
6532	36900	A	6582	1	483	
6533	36901	A	6583	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS
6534	36902	A	6584	1	678	
6535	36903	A	6585	3	634	
6536	36904	A	6586	4	479	CSAKTAIRGVSECLIHHHGIPHS TASDQGTHFTAKEVWQWAYA HGIHWSYHVLHHPEEA/GKER WNGLLKSQLQCQLGDNTLQG* GKVLQQAVYVLN*HPIYGTVSP IARIH/GSRNQG/VETELTPLTITP SDPLAKFLLPVPPTLHSAGLEIL VPEGEIR
6537	36905	A	6587	1	1539	MVGKAKWKPLELPLPRKMVSQ KQYRILGGTAEISVTIKDLKDA RVVIPSTSPFYSPIWPVQKIDGS WRMTEDYRKLNQVVTPTAAA VPDVVSLLEQINTSPGTRYAAID LTNAFFSIPFHKAHQKLFAFSW QGQQYTFTVLPWGDINSPALCH NLIRRDPDCFSLPQDITLVHHID DIMLTGSREQEVADTRDFLVKD KLLHLAPPTTKKQAQHLVGLF GFWRQHIPLLGVLLQPIYRVTQ KVASFEWSQEQKTALQQVQAA VQAVLPLGPYNPADPMVLEVS VADRDAVCSLWQAPIGESQWR PLGFWSKALPSSADNYSPFERQ LLA/CHKVGHAQQHSISKWK*Y IHDRAQADYHPWT\QACLIHCQ GIPHSIASDKDAHFTTKEVWQW THAHEIHWCYHVLHHPEAAGL TERWNRLLKSQLQRQLGDNTL QQGSGKVLQKAMYALNQHPIYG TISPIARIHGSSNQGVEVAPLTIT PSDPLAKFLLCVPTTLRSAGLD VLVPEGGMTQQQFH

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6538	36906	A	6588	1	566	MGRNQSRKAENSKNWSASSPP KDHSSLPAMEQSWMENDFDEF TEVGFRRSVITNFSELKEHVLTY CKEAKNVEKRIYRSRNQGMEV KVAPLTITPSDPLANFFASVPAT LHSAGLEVLVPEGGTLPLGDTT MIPLNWKLRLRTGYFGLLLRLS QQAKKGAMVLA/GVVDPDYQ NEISLLLHN*GKTHDH
6539	36907	A	6589	221	357	
6540	36908	C	6590	228	342	
6541	36909	A	6591	745	849	
6542	36910	A	6592	1	240	
6543	36911	A	6593	2	495	FVRLVGRGDCDPLLSVCLTTMP LYEGLGSGG\EKTAVVIDLGEA FTKCGFAGETGPRCIIPSGIKRA GMPKPVRVVQYNINTEELYSYL KEFIHILYFRHL\LVNPRDRRV\V IIES\VLCPS\HFREDTHSCFFFKY FE\VPSVLLA\PS\HLMALLTLGI NSWHGPRL
6544	36912	A	6594	1	579	
6545	36913	A	6595	1	621	
6546	36914	A	6596	1	351	
6547	36915	A	6597	1	447	
6548	36916	A	6598	114	880	
6549	36917	A	6599	1	2625	
6550	36918	A	6600	1	1674	
6551	36919	A	6601	1035	2235	QTHSQYHTEWAKTGSIPFENW HKTGIPSLTTPIQHSVGSSGQGN QAGEGNKGYSIRKRGSQIVPVC RRHD/VYI*KTPLSQPEISLS**A TSAKS/LGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPM PFFTELEKTTLKFIWNQKRARIT KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKMNSRWI KDLNVRPKTIKTLEENLGITIQD IGMGKDFMSKTPKAMATKAKI DKWDLIKLKSFCTAKETTIRVN RQPTK

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6552	36920	A	6602	369	1917	AGEGNKGYSIRKRGSQIVPVCR RHD/VYI*KTPLSQPKISLS**AT SAKS/LGYKINVQKSQTFLYTN NRQTESQIMSELPFTIASKKIKY LGIQHTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTSKFIWNQKRARITK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYLYQNRDIDQWN RTEPSEMTPHTYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQDI GMGKDFMSKTPKAMATKDKID KWDLIKLKSFCTAKETTIRVNR QPKKWEKIFATYSSDKGLISRIY NELKQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAIIQKSGNNRCWRGCGEIGTL LHCWWDCKLVQHILTHRWEL NNEITWTQEGEYHTLGTVVGW GEGGGIALGDIPNAR
6553	36921	A	6603	1	2781	

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6554	36922	A	6604	1320	2403	LQTILQVYSNQNSMVLVPKQR YRSMEQNRALRNNATYLQLSD L*QT*EKQAMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKR*T*NSKKQSPSP PPKERSSSPATEQSWTENDFDE LREEGFRRSNYPELREDIQTKG KEEIQTTIREYYKHLYANKLEN LEEMDKFLNTYTLPRLNQEEVE SLNRPITGSEIVAVINSLPTKKSP GPDGFTAEFHQRYKVELVPFLL KLFQSIEKEGILPNSFYEASIILIP KPGRDTIKKENFRPISLTNIDAKI LNKILANRIQQHIKKLIHYDQV GFIPGMQDWFNIRKSINVIQHIN RTKVKNHMIISIDAEKAFDKIQ QRFMLKTLNKLAQNLLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRLNIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTVKFIWNQKRACITKSI LSQKNKAGGITLPDFKLYYKST VTKTAWYWYQNRDIDQWNRT EPSEIMPHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGV DKDFMTKTPKAMATKPKIDKW DLIKLKSFCTAKETTIRAFDELD DVHPHEEIEACRVWQNYGTHP
6555	36923	A	6605	2202	2515	KSLQCEHSSHIQDLPLACLGLR KHYMVAQYL*HSHS/ASGGGSR YDVLKISVSCSSTIDI*LAFVSLG *DKRTS**TNLAESSPNFFHWV WIFLASKKFCSVPAR
6556	36924	A	6606	1934	2077	AIPFRIQAWARTSCPKHKKQWQ QKPKLTNGI*FN*RASAQQKKL PSE
6557	36925	B	6607	1	2325	

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6558	36926	A	6608	1524	2877	IRKRGSQIVPVCRRHD/VFV*KT PSSQPKISLS**ATSAKS/LGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKSILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQCNRTEPSEIMPH IYNYLIFDKPERNKQWGKDSLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGITIQDIGVGKDFMSKTP KAMATKDKIDKWDLIKLKSFC TAKETTIRVNRQPTTWEKIFAT YSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSSSLAIRERQIKT TMRYHLTPVRMAIIKKSGNNR DMDEIGNHHSQ
6559	36927	A	6609	1	2226	
6560	36928	A	6610	1	674	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VQNFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQEN/CPQSSKAGQRSD SGNTENATKILLEKSNSKTHNC QIHQS
6561	36929	B	6611	1	5175	
6562	36930	A	6612	1666	2032	LQTILQGYSNQNSMVLVPKQR YRSMEQNRALRNNATYLQLSD L*QT*EKQAMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKH*T*NHKNPRRKP RHYHSGHRHGQGLHV
6563	36931	A	6613	1596	2169	AGEGNKGYSIRKRGSQIVPVCR *HD/VYI*KTPLSQPKISLS**ATS AKS/LGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIM KMAILPKVIYRFNAIPIKLPMTF FTELEKTKVHMEPKKCPHHQG NPKPKEQSWRHHTT

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6564	36932	A	6614	1667	3103	AGEGNKGYSIRKRGSQIVPVCR *HD/VYI*KTPLSQPKISLS**ATS AKS/LGYKINVQKSQAFLYTNN RQTERQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLLQE IKEDTSKWKNVPCSWVGRINIV KMAILPKVIYRFNAIPIKLPMPF FTELEKTILKFIWDQKRARIAKS ILRQKNKAGGITLPDFKLYYKA TVTKTAWYWYQNRDIDQCNR TEPSEITPHIYNYLIFDKPEKNK QWGKDSLFNKWCWENWLAIC RKLKLDPFLTPYTKINSRWIKD LNIRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATNAKIDK WDLIKLKSFRTAKETTIRVNRQ PTKWQKIFATYSSDKGLMSRIY NELKQIYKKKTNNPIKKWAED MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAIIKKSGNNRLTLLNNHNNPQ PLISIKEPREKEELNLQV
6565	36933	A	6615	3134	3288	
6566	36934	A	6616	1	2630	
6567	36935	B	6617	877	7936	
6568	36936	A	6618	2	1589	
6569	36937	A	6619	1	240	
6570	36938	A	6620	200	486	
6571	36939	A	6621	1	558	
6572	36940	A	6622	1	3885	

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6573	36941	A	6623	1	2302	KLPVTNRAAHGLCASLGPDFM TFKVPSSWRHSDSICREWFTLA GAPSRDVLLVSAIITVSLSVTVV LCGLCHWCQRKLGKRYKNSLE TVGTPDSGRGRSEKKAIKVSRP CPPPAKASATHPTCKSPRSQEK VESPGDLDRDFWNNNESTVQQ KWSSYPPKEFILNISPYAPYGDP RLSLNGTLLSGAKVAAAAGLA VEREGRLGEKPAPVPPPGEDAL RSGGAAPSEPGSGGKAGRGRW RTVQSHLAAGKLNLSNFEDSTL STATTLESIPSSTGEPKCQRPRT LMRQQSLQQPLSQHQRGRQPS QPTTSQSLGQLQAHMASAPGP NPRAYGRGQARQGTSAGSKYR AAGGRSRSNPGSWDHVVGQIR NRGLDMKSFLTTSSRAAKWNF TNSETVPALDLDSAVVLIPWISS KEDTGDSHYGRVAIYHKGLSFS SDGLVYPGAKGREGRMVVLSL VLGLSEQDDFANIPDLQNPGTQ QNQNAQGDKRLPAGGKAVNT APVPGQTPHDESDRRTEPRSSV SDLVNSLTSEMLMEDWPPAVF SSGWAIATAHPASLHSPLIGYSF LAARGGLLLFEADFCWCKRSG STFPDCDGVANLAATEMALSQ LRFSKETAMRESLVMLSPGSEE DEAHEGCSRENLGRIQFSVGYN FQESTLTLKIMKAQELPAKDFS GTSDPFVKIYLLPDKKHKLKTK
6574	36942	A	6624	1	576	
6575	36943	A	6625	1	155	
6576	36944	A	6626	4746	5258	DAGAQPSLPRYLIYHQPSRFFRI TSTVTPFSKPISSLLWLV*/GLHG DILL/RLLQS*RC*CRSHPEYHSG PPGRWQGPSPAPQKCSRTTSRS RSSR*HPPPPRPGGSAPSSPASYS WTPPRTVPGSWARRWRRHLSR PSWATQPSWTATLWSQPLWRL KWEDCLSPGRSRLQ
6577	36945	A	6627	1	588	

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6578	36946	A	6628	444	1056	GPLLREPHQLCHFPVAGFVLDA GLPEAAAAPHDRGPELAGPQA AGQHPAQVAHQPRAAAQQRQ GRRAREEAGAQAQEEPRGPQE RRRRLAEGLRRQCGHPAGRDG RGGYRRAAQGPARGGRTPEWQ QSGGARRTPSVGHPRRARAD\W CLTGANDALSCSSPTCGKFLKT VSKVPVCRRGLAVNRKEAEGR SSESPTSSATFQSPALSWMLVS QRLLLPHMIGAQSSPGPKRPGN TLRKWLTSPVRRLSSGKADGH VKKLAHKHKKSREVRKSADAG SQKDSDDSAATPQDETVEEDTV AQPRGRREGAGRQSGSRAAGP GGRRASAIRGGHARTDVGKRN GTRTRKELMPLHGKRKDAAEH DEPTSASRPAGERPELTLAAVQ TEYNCSFPS
6579	36947	A	6629	128	1103	
6580	36948	A	6630	1	602	
6581	36949	A	6631	3	1618	
6582	36950	A	6632	1	602	
6583	36951	A	6633	3	1618	
6584	36952	A	6634	1	912	
6585	36953	A	6635	195	396	VLPLHRQI**LLH*SKKHNHYK GKQQDLR/CSSTVPRRPQGILPII SFSNVPVGSRRLKAPLVFIGPG

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6586	36954	A	6636	2	1813	FNTPLSTLDRSSRQKVNKDIQD VISALHEAGLIDIYRTLHPKSTE YTFFSAPHHTYYKIDHIVGSKA LLSKCKRTEITTNCLSDDRAIKL ELRIKKLTQNYTTTWKLNNLLL SDYWVNNEMKAEIKMFFETNE NKDTMYQNLWDTFKAVCRGK FIAVNAYKRKQERSKIHTLTSQ LKEPEKQEQTHSKASRRQEITKI RAELKEIDTQKTLQKISVSRSW FSERINKIDRLIARLMKKKREK NQIDAIKNDKGDITIDPTEMQTT IREYYKNLYANKLENLEEMDK FLDTYILPRLNQEEVELPNRPIT GSENEAIINSLP/TKKSPGPDEFT AKFYQRYKG\LARAIRQEKERE DTQLGKEEVKLLLFAEDMIVYL ENPIVSAQNLLKLINNFSKVSGY KINVQKSQAFLHTNNRQTESQI MSECPLTIASKRIKYLGIQLTRD VKDLFKENYKPLLNKIKEDT\N KWKNIPRSWLGRNNIVKMTILP KVI/YKKTTLNFIWNQERARIAK TILSKKNKAGGITLPDFKLYYK ATVTKTARYWTLTIKKGSVWPI SLKSEKRGHRTRPLWKLCHND VQGELLKTIQFLFGSPLGHSSLD
6587	36955	A	6637	1	2988	MPPHSEQPHSPSTRQKRKVPLF VRQCPSFVIQAPKAKMDTFDGR KKQFTRFLFLFSMDQLGQGRFS MQTLSFALAVYRKDSPLVACQ VQALGNLEPSSVEAHVSSHGIAI DRKGWHVSLFSIQPGDCFPKAL VEDSPRDRARRQQSSKEEGWC RDRRRLKFHSKKGAAAIVVKS KKYESPSFGVCFESLLNPPRLTS RREKTISSSKRCRQCHAEETTV VFWAKESQTGEQTGRGAGQRR MGMIICKACSMLPAE
6588	36956	B	6638	362	1463	
6589	36957	A	6639	1	1061	
6590	36958	A	6640	1	1581	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6591	36959	A	6641	46	862	AAFPAPRTLFFLSRPLRPTACAA FRPEFWRLNMKLPARVFFTLGS RLPCGLAPRRFFSYGTKILYQN TEALQSKFFSPLQKAMLPPNSF QGKVAFITGGGTGLGKGMTTL LSSLGAQCVIASRKMDVLKAT AEQISSQTGNKVHAIQCNVKYP DMVQNTVSELIKVQGHPSTVIT N*STERSSISFLLPTIYA*DWFRF CSTQVLLPKQVWKPMSKSLAA EWGKIWNAIQC
6592	36960	A	6642	1	2902	MVKGSLQQEELTILNIYAPNTE APRFIKQVLRDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKINKD TQELNSALYQADLIDIYGTLHP KST\EYTFF\SAPHHTYSQNWTT IVGSKALLSEHKRTEIIT\NYLSD \HSA\IKLELRIKKLTQN\RSATW KLNNLLLNDYWVHNDMKAEI KMFFETK\ENK\DTTYQNLW\DT FKAVCRGKFIAK\NAHNRKQE\ RSKIDTLTSQLKELEKKEQTYL KASRRQEIT
6593	36961	A	6643	1	5127	
6594	36962	B	6644	1	3570	
6595	36963	A	6645	1	3663	
6596	36964	B	6646	143	3122	
6597	36965	A	6647	1	3235	
6598	36966	A	6648	1	3249	
6599	36967	A	6649	1	3297	

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6600	36968	A	6650	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
6601	36969	A	6651	1	3402	
6602	36970	A	6652	1	3288	
6603	36971	A	6653	1	3168	
6604	36972	A	6654	1	3516	
6605	36973	A	6655	1	3693	

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6606	36974	A	6656	1577	3354	TEPKTKTT*LSQ*MQKRPLTKF NNLSC*KLSIN/IVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELGKTALKFIWNQKRARITKSI LSQKNKAGGITLPDFQLYCKAT VTKTAWFPSGDVGLEADFSPSH TLKTQFFSCLAEFAAASCFFQR MNGFGMAMTTTYSTGAAESPL PSCSIDQGDDTKLHRARSPGRT FPAAAGIPAAAAPDGPPLSLLH KLWFPVELGGRALPRAEESHGE VAALGVMVVAQGGKNQGEEA RSTPWLRPTSHLPPCSSSSAWW TEQTDAHPLLFLLCLGIYLLNA LSNLSMVALVRSDGALRSPMY YFLGHLSLVDVCFTTVTVPRLL AGLLHPGQAISFQACFAEMYFF VALGITESYLPAAMSYDRATAA CRPLRYGALVTPWALRLAARY DRLASVVYAVITPTLNPFINSLR NKEVKGALKRGLRWRAAPQE
6607	36975	A	6657	1	3514	MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFFSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRIKNLTKSRSTTW KLNNLLLNDYW
6608	36976	A	6658	3	3316	
6609	36977	A	6659	1	4794	
6610	36978	A	6660	1	3570	
6611	36979	B	6661	1	3384	
6612	36980	A	6662	1	3429	
6613	36981	A	6663	1	3780	
6614	36982	A	6664	1	3894	

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6615	36983	A	6665	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
6616	36984	B	6666	1	3145	
6617	36985	A	6667	1	4398	
6618	36986	A	6668	523	3852	
6619	36987	A	6669	1	3934	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
6620	36988	B	6670	1	5215	
6621	36989	A	6671	1	7171	
6622	36990	A	6672	3	493	
6623	36991	A	6673	1	729	
6624	36992	A	6674	3	800	
6625	36993	A	6675	1	327	
6626	36994	A	6676	2	462	KSSWLEEDDDPVVARVNRRMQ HITGLTVKTAELLQVANYGVG GQYEPHFDFSRRPFDSGLKTEG NRLATFLNYMSDVEAGGATVF PDLGAAIWPKKGTAVFWYNLL RTGEGDYR\TRHAACPVLVGCK WVSNKW\FHES\GQEFLRPCGST EVD

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6627	36995	A	6677	3	717	RHRLRNRLKDVGGEAFYPLLE DDQSNLPHSNSNNELSAAATLP LIIREKDTEYQLNRIILFDRLLKA YPYKKNQIWREARVDIPPLIRG LTWAALLGVEGAIHAKYDAID KDTPIPTDRT/QLKWDIPRCHSV R*TVIHAPEGHAKFRRVLK\AW VVSHPDLVYWQGLDSLCAPFL YLNFNNEALVYACMSAFIPKYL YNFFLKDNSHVIQEYLTVFSQM IAFHDPELSNHLNEIGFIPD
6628	36996	A	6678	1	508	
6629	36997	A	6679	1	888	
6630	36998	A	6680	2	584	
6631	36999	A	6681	2	152	QVAKGMDALLQHLEDCGYR/S SKKKAQICRQQVTKWGDGSAL MGTSTTASL
6632	37000	A	6682	733	894	
6633	37001	B	6683	1	1626	
6634	37002	A	6684	1	1971	MAQVWANDNPPGLAVNQAPV LIDVKPGAQPIRQKQYPVPREA LKGIQPGTKDYQPVQDLRLVN QATVTLHPTVPNPYTLLGLLLA EDSWFTCLDLKDAFFSIRLAPES QKLFAFQWEDPQSDLGCILLLY VDDLLLGHSTAVECAKGMDVL LQHLEDCRYKMSKKKAHICRQ QVRYLGFTIRKGERS\WEREKM AVGVLTQTVGPWPRPVAYLSK QLD/EVSKGWPLCLRTLAATAL LAQEADKLTLGQNLNIKAPHA VVTLMTTEGHHWLTNARLTKY QSLPCENPHITIEVCNTLNPTTL LPVSESPGEHNCVEVLDSVYSS RPDLRDQPWASSVDWELYMD GSSFINSQGERCAGYAVVTLDA VIKAKLWLQGTSAQKAELIALT RAVELSEGQESLEELLGRYFYV SHLPAFAKAVAQLCITCRQHNA RQSPTVSPHIQAYGAAPFEDLQ VDFTEMPKCGGNKYLLVLTCT YSGWVEAYPTRTEKPYKKGKN DPSCTKGQCNPLELVITNPLNP HWKKGERVTLGIDRARLDPRV NILVRGGEVYERSPEPVFQTFY DELNVPVPEIPGKTRNLFLQLA ECVAQPLNVTSCYVCGGTVTG YQWPWKARELVPVDPVPDEFL AQKNYPDNFWVLKPSITGQYCI
6635	37003	A	6685	1	1461	
6636	37004	A	6686	1	1005	

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6637	37005	A	6687	1	174	
6638	37006	A	6688	519	588	
6639	37007	A	6689	2	4527	GRAGLGWSSGGRGSRACSEGP AEARGREGDKGSAALSPPLPLT LGEEMAAERGARRLLSTPSFWL YCLLLLGRRAPGAAAARSGSAP QSPGASIRTFTPFYFLVEPVDTL SVRGSSVILNCSAYSEPSPKIEW KKDGTFLNLVSDDRRQLLPDGS LFISNVVHSKHNKPDEGYYQCV ATVESLGTIISRTAKLIVAGLPR FTSQPEPSSVYAGNNAILNCEV NADLVPFVRWEQNRQPLLLDD RVIKLPSGMLVI
6640	37008	A	6690	1	879	
6641	37009	A	6691	407	594	
6642	37010	A	6692	1	3621	
6643	37011	B	6693	1	609	
6644	37012	B	6694	1335	1599	
6645	37013	A	6695	1	354	
6646	37014	A	6696	181	683	SRYFILLRKPTFPAMALLPVLFL VTVLLPSLPAEGKDPAFTALLT TQLQVQREIVNKHNELRKAVSP PASNMLKMEWSREVTTNAQR WANK/CTLQHSDPEDRKTSTRC GENLYMSSDPTSWSSAIQSWY DEILDFVYGVGPKS/PQYCPAG NNMNRKNTPYQQGTPCPG
6647	37015	A	6697	199	969	
6648	37016	A	6698	1	564	
6649	37017	A	6699	153	427	
6650	37018	A	6700	1	978	
6651	37019	A	6701	3	419	
6652	37020	A	6702	9	255	VRAPAQGPDLAGGRRRCGSGA SCTPSPRGPASWSRSAAQVPRS SRWRAGSASS*N/GRQPAPPTSQ PPRAQPFAQPPGPWPLS
6653	37021	B	6703	96	283	
6654	37022	A	6704	172	365	PTYHLYPCHFWYQHRTRRIPRK SERLFPTPPPQLSWKGTWDY*I CLLCCNDSEGRDFLVLRVLK
6655	37023	A	6705	3	1171	
6656	37024	A	6706	2	740	
6657	37025	A	6707	256	461	
6658	37026	A	6708	1	414	
6659	37027	A	6709	1330	1386	YIDSILPK*NHDTLQSYCRYM\H SRQRAAS*PLSTGKLQQCLGLD LVLC

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6660	37028	A	6710	207	1173	GGDRDRMTANHESYLLMASTQ NDMEDWVKSIRRVI\GDLSGGG IFGQKLEDTVRYEKRYGNRLAP MLVEQCVDFIRQRGLKEEGLFR LPGQANLVK\ELQDAFDCGEKP SFDSNTDVHTVASLLKLYLREL PEPVIPYAKYEDFLSCAKLLSKE EEAGVKELAKQVKSLPVVNYN LLKYICRFLDEVQSYSGVNKMS VQNLATVFGPNILRPKVEDPLTI MEGTVVVQQLMSVMISKHDCL FPKDAELQSKPQDGVSNNNEIQ KKATMGQLQNKENNNTKDSPS RQCSWDKSESP/TEKQHEQWIP HSSIRQQNQQPKEQWSQAI
6661	37029	A	6711	173	881	
6662	37030	A	6712	1605	1844	
6663	37031	B	6713	123	699	
6664	37032	A	6714	1	462	
6665	37033	A	6715	1	2607	
6666	37034	A	6716	1	918	
6667	37035	A	6717	1	549	
6668	37036	A	6718	1	687	
6669	37037	A	6719	1	258	
6670	37038	A	6720	90	1621	HGLDLRTMNRSRQVTCVAWV RCGVAKETPDKVELSKGGVKR LIAEAEEKLQEEGGGSDEEKTG SPLEEG\MQSARTQARP\REPLE\ DGDPED\DRTLDDDELAEYDLD KYDEEGDPDAETLG\ESLLGLT VYGSNDQDPYVTLKDTEQYER EDFLIKPSDNLIVCGRAEQDQC NLEVHVYNQEEDSFYVHHDILL SAYPLSVEWLNFDPSPDDSTGN YIAVGNMTPVIEVWDLDIVDSL EPVFTLGSKLSKKKKKKGKKSS SAEGHTDAVLDLSWNKLIRNV LASASADNTVILWDMSLGKPA ASLAVHTDKVQTLQFHPFEAQT LISGSYDKSVALYDCRSPDESH RMWRFSGQIERVTWNHFSPCH FLASTDDGFVYNLDARSDKPIF TLNAHNDEISGLDLSSQIKGCL VTASADKYVKIWDILGDRPSLV HSRDMKMGVLFCSSCCPDLPFI YAFGGQKEGLRVWDISTVSSV NEAFGRRERLVLGSARNSSISGP FGSRSSDTPMES
6671	37039	A	6721	1	549	

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6672	37040	A	6722	1	1318	AKQQLNLRTHMADENKNEYA AQLQNFNGEQHKHFYVVIPQIY KQLQEMDERRTIKLSECYRGFA DSERKVIPIISKCLEGMILAAKS VDERRDSQMVVDSFKSGFEPPG DFPFEDYSQHIYRTISDGTISAS KQESGKMDAKTTVGKAKGKL WLFGKKPKPQSPPLTPTSLFTSS TPNGSQFLTFSIEPVHYCMNEIK TGKPRIPSFRSLKRGWSVKMG/ AALEDFSHLPPEQRRKKLQQRI DELNRELQKESDQKDALNKMK DVYEKNPQMGDPGSLQPKLAE TMNNIDRLRMEIHKNEAWLSE VEGKTGGRGDRRHSSDINHLVT QGRESPEGSYTDDANQEVRGPP QQHGHHNEFDDEFEDDDPLPAI GHCKAIYPFDGHNEGTLAMKE GEVLYIIEEDKGDGWTRARRQ NGEEGYVPTSYIDVTLEKNSKG
6673	37041	A	6723	1	741	
6674	37042	A	6724	1	1063	MPFYISDLSICGDRILRALCPQD LPTYSLHSRGKMRASCSRKFLD NNSSRLVSCNMGALISIWGTTT PPLHATILDSQPTVHPPLAKDCL PCGLQASASDLRARALQRLCQ QLPWVGSQPHTRSPSPQRGGKT GLFAGLASSVSMRPASPPSPAA DSCSACRFFARRPPLRVTWVKP SSALALCVSISDSIPGNLKALPA ETRAQLHHAEASLSQPPLQLRP FPKTSQAGDLQDLGPYVCVRK AVGKGDKQIRAVVKEHSVRSQ ERIWHYPGITTANMPGHLGQNT ESGRDKLPMFGVWFPGCRFWG LWVWRLP*LKLAAPCRPSRSLR SSPISRRASTTRCLTVSGCPAAP
6675	37043	A	6725	25	573	
6676	37044	A	6726	1	483	

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6677	37045	A	6727	1	996	MVGKAKWKPIELPLLRKIVNQ KQYHIPGGVAKISATIKDLKDV GVVIPTTSPFNSPIWPVQKTDGS WRKW\LS*QGQQFT/FTVLPHG YINSLALCHNLIRRDLDHFSLPQ DITLVHYIDDIVLTGSSEQEVAN TLDLLTSLDWALVETECLTMG HQVTMQPELTIMNWALSDPSN YKVGCAQQHSIIKWKWYIRDQ ARAGTTCKWTAAALQPLSRTS LKDSGERKSSQWAELRAVHLI MHFAWKEKWPDVQLYTDSWA VANGSAGWSGTWKNHDWKIA TTVIAQWAHEQSSHGSRNGGY TWAQQHGLPLTKADVATATDE CPICQQQRPTLSP
6678	37046	A	6728	2	1380	CLAGLFGFWSPCIPHLGVLLQSI YLVTQKAA/SSEWGPEQEKALQ EVQAAVQAALILEPYDPAGPVV LEVSLADRDAVWSLWQAPIGE SQQRPLGFWSKALPSSA/DHKA CHAQQHSIIKWKWYIHDRARA GPEGTNSSARYAATM*KW\TAS ALQPLSRKSLKDSSEGKSSQWA ELRAVHLAVHVAWKEKWPDV RLDTDSWAVANGLARWSGTW KEHDRKIGDKEVWGRGTRIELS EWSKTVTIFVSH/VLLPRLPSIRG LTECLIHQHGIPHSIASDQGTHF TAKELQQWAHAHGIHWSYHVP HHPG\WGKVLQKAVYALNQRP IYEWKEESCLHTGVADALRGN WAEGHREHKALWLGLWSTWS QHPLRSLKTTRHHPGLGVLSED ICEAGGATEELSRASGFATGYG KRKEDTKKHKQHSVSDIIEQQH SLGLTEKTVKGTPTQGISMRPG LYHKATEFQE
6679	37047	A	6729	1	2229	
6680	37048	A	6730	1	789	RDLQPFTSVTVHCRKGNDQTF GGPLDAGSELTLIPGDPKHHCG PPVKVGAYGGQVINGVLA\HPL IWLVQKTDGS/WRMTVDYCKL NQVVIPIAAAVSDVVSLLEQINT SPGTWYAAIDLANAFFSIPVHK AQQKQFAFSWQGQQYTFTVLP QWYINSPALCHNLIRRDLDCFS LPLDITLVHYIDDIMLIGSSEQE VANTLDLFVRHLRARGWEINPT KIQGPSTSVKFLGFQWCGACQA IPSKMRDKLLHLVPPTTKKEAQ

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6681	37049	A	6731	1	553	MTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIG\PRQLLACY/WALVETEHL TISHQVTMRPELPIMNWVLFDP SSHKVGCAQQHSIIKWKWYVH DWARAGPEGT
6682	37050	A	6732	3	266	
6683	37051	A	6733	3	582	
6684	37052	A	6734	3	403	
6685	37053	A	6735	1	2712	
6686	37054	A	6736	875	1506	LSIYLVTQKAA/SSEWGPEQEK ALQEVQAAVQAALILEPYDPA GPVVLEVSLADRDAVWSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQQHSIIKWKWYIHD RARAGPEGTNSSARYAATM*K W\TASALQPLSRKSLKDSSEGK SSQWAELRAVHLAVHVAWKE KWPDVRLDTDSWAV/ANGLAR WSGTWKEHDRKIGDKEVWGR GTRI
6687	37055	A	6737	1	633	MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAFLPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPSS GDIKEYFPNAFVLLTTASLQGQ DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
6688	37056	A	6738	2	1103	DLWPFTRVTLHRGKRNDQTFQ GLLDTGSELMLIPEDTKHHCGP PVKVEAYGGQVINGVLAQIQLT VGPVGSGTHPVVIYPVPECIIGI GILSSWQNPHIGSLTSRKTDGS WRMTVHYHKLNQMVTPIAAAI PDVVSLLEQVNTSPGSWYAAID LANAFFFIPVHKAHQKQFAFSW QGQQYTFTVLPQWYINSPALCH NLIRRDLDCFSLPLDITLVHYID DIMLIGSSEQEVANTLDLFVRH LRARGWEINPTKIQGPSTSVKFL GFQWCGACQAIPSKMRDKLLH LVPPTTKKEAQCL\QLLACY/W ALVETEHLTISHQVTMRPELPI MNWVLFDPSSHKVGCAQQHSII KWKWYVHDWARAGPEGT

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6689	37057	A	6739	1	2058	
6690	37058	A	6740	2	1173	WEVRQYTFTVVPQGHINSLVLC HDVVRRDLGHFFLPQDITLVHY IDDIMLIGSTPPITKKKAQHLVG LFGFWRQLVPHLGVLLWPIYQ VTQQAASFEWGPEKEKALQQV QAAVQAALPLGPYDPADPMVL EVSVADRDAVWSLWQDPIGES QWRSLGFWSKALPSSADNYSPF ERQLLACYWVLVETERL\QWV TPAEEDFNNQVDRMTHSVDTT QPLSPATHVITQWAHEQSGHG GRDGGYTRVQQHGLPLTKADL ATAGKVFQKAV*ALN*HSIYGT LSLIARIHRSRNQGVEVEVAPLT ISPSDPPAKFLLPVPPTLRSAGLE FLVPEEGMLPSGDTTVPLNWKL RLPPGHFGLLFPLHQQANKGVT VLVGVTDLDYQDEISLLPHNG
6691	37059	A	6741	823	2487	KELKLWKNRHKLLSYPTVGAA VTQLQNLTAMGVIGSHGARGQ VVALNRQRQGDLQPFTRVTVH WGKG/NMQIFGGLLDTGSELTL IPGDPKHHCGPPVKVGAFGG\Q VINGALARVQLIVGPVGPWAHP VVISPVPECIIDIDILSSWQNPHIS SLTGRVRAIMVGKAKWKSLEL PLPRKIVNQKQYHIPGGIVEISA TIKDLKDAGEVIPIPTTFPLNSPI WPVRKTDGCWRMTVDYCELN QVVTPTAATVPDVVSLLEQINT SPGTWYADIDLANAVFSIPVHK AHQKQFAFSWQGQQYTFTVLP QEYINSLGLCHNLIQRDLDHFSL LQDITLVHYIEDIMLIGSTEQEIA NTLDLLFMAKEVWQWAHAHG IHWSYHVSHHPEAAGLIEWWK GLLKLQLQCQLGDNTLEGWGK VLQKTVYALNQHPIYGTVSPIA RIHRSRNKGVEVAPFTITPSDPL PQFLLPVPATLCSAGLEVLAPE GGTLPPGDRTTIPLNWKLRLPP EDFGLLPSLSQQAKKGVTVLAG VIHPDYQDEISLLLHNGCKEDL
6692	37060	A	6742	3	350	
6693	37061	A	6743	1	3339	
6694	37062	A	6744	1	2271	

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6695	37063	A	6745	3	1377	AHLAADDFCTK*GWVSG\LPQG LDKLTLPGANLEMQPENLKED LVYLKKNHEELSMAIKRNESM AKGLQRALLQQQPEDDSKCFP RPQDLIRLYDIILQLTLEDREGK GLSFSFACVDKDVSVKMDTVP GVNLSCILNEMRDQDKKLVEK SCKDAQGWFFSLKALLEGSLVE TEVCYRTQLAQLQGLIRSMEQQ LCELCCDAEHQDHEHQVLLDV KTQLEQEIATYSRLLEVEDAQL ATQYSLSLASQPTREDLEKAIL KFIWNQNRAQIAKTILSKKSKA RGIMLPSFKIYYKTTVTKTAWC WYKNRHIDQWNRIENPEIRPHT YNHVIFDKPDKRKQWGKDSLF NKWCWENWLAICSKLTLDPFL NPYTKVNSRWIKDLNLQPKTIK ILKENLGNAIQDTGKGKDFMTK MPKAIATKAKIDKWDLIKLKSF CTALRNYQQSKPTTYRMGENF
6696	37064	A	6746	1	882	
6697	37065	A	6747	13	1402	STGSTHACDLLFSPSPVCLPPAA ATMTTSIR\QFTSSS\SIKGSSGL GGG\SSRTSCRLSGGLG\AGSCR LGSAGGLGSTLGG\SSYSSCYSF GSGGGYGSSFGGVDGLLA\GGE KA\TMQNL\ND\RLGSYLDKVPC PWKEANTELEVKI\RDLVTRGR APGPARDYSQYYRTIEELQNKI LTATVDNANILLQIDNARLAAD DFRTKFETEQALRLSVEADING LRRVLDELTLARADLEMQIENL KEELAYLKKNHEEEMNALRGQ VGGEINVEMDAAPGVDLSRILN EMRDQYEKMAEKNRKDAEDW FFSKTEELNREVATNSELVQSG KSEISELRRTMQALEIELQSQLS MKASLEGNLAETENRYCVQLS QIQGLIGSVEEQLAQLRCEMEQ QNQEYKILLDVKTRLEQEIATY RRLLEGEDAHLTQYKKEPVTTR QVRTIVEEVQDGKVISSREQVH
6698	37066	A	6748	2	452	FLLPSSFSCTHSLLSPTITIVPGP DFNLASHIIPDTTPDPHDCISMIH LTFTPFPHISFFPVPHPDHA*FID GSSTRPNRHTPAKAGYAIAQAT IPPLRTSHFLSIVEIYPQGNNFSV FHVLFYYSSGIIQAPSLPYTLRR DRRPGTSRA
6699	37067	A	6749	1	1791	

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6700	37068	A	6750	1	219	
6701	37069	A	6751	2	528	TLTVESKSIKAYKLSLQFPHFTC PKTGHALQVSSGFVESPTVTIVP GLDINLASHTIPDNTPEPHDCIS LIHLTFTPFPHVSFFPVPHPDHT WFIDGSSTRPNCHSPAKTGYAI VSSTLIIDATALPPSTTSQQAELI ALTRALTLAKGLPINIHTDSKY AFHILHHHAVI*AER
6702	37070	B	6752	1	1744	
6703	37071	A	6753	1	1376	MCKRMPGLQASQTVCPFYDKN YLDLKRKGTEIKRRERLKCGTK IERRKRLRDSERLEKRIKRGCLP DLKLSTEIQINRLRGLYTLLRKE RRFGLQETINYAEVTGIYVKELI EDREHLNSGKYIFNIFDIKVPRV VFGIIDPYMLWEKKEGTKEGIK EGMKRESQKRIKWERSFITFIAL NTADRTLMSSAGCYRKQVKIHI DALPPPNSQTLKKRGGASLIISF RRQSGPSAAGLWEFARGPFQTL FAWLSPAEAAEQQRLLPASSAE SFIAEGDPPDAGQSSPPSSLHAA AATALMLLEALKITNYAQLTLY SSPNFQNLFSSSHLTHILSADWL LQLYSLFVESPTITIVPGPDFNPA FHFIPDTTPDPHDCISLIHLTFTP FPHISFFPVPHPDHTWFIDGSST RPNRHTPAKAGYA/DGRNTSYC VLSPVGNSPLVPNPGSARCTEG GLLYARA
6704	37072	B	6754	400	820	
6705	37073	B	6755	1	1190	
6706	37074	A	6756	1	1002	
6707	37075	B	6757	1	3216	
6708	37076	A	6758	1	4020	
6709	37077	A	6759	1	1155	
6710	37078	A	6760	2	346	SSYLMHILSAPNLLQLYSLFVES PTITIVPGPDFNLASHIILDTTPD PHDYLSDPPDIHS/TFP/DISFFPV PHPGHTWFNDGSSTRPNRHSPA KAGHAIVFSTSIIEATALPPSTT
6711	37079	A	6761	189	1201	
6712	37080	A	6762	1	231	
6713	37081	A	6763	1	834	
6714	37082	A	6764	470	479	PRNPSSFLQVQVQHRFLQLFVP FHFVFFLASLYVMVTLTTWFR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT
6715	37083	A	6765	21	706	
6716	37084	A	6766	1	158	

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6717	37085	C	6767	78	401	
6718	37086	A	6768	536	694	
6719	37087	C	6769	1	1410	
6720	37088	B	6770	1	1836	
6721	37089	A	6771	306	487	VGFLGILF/CFEAIVNVSSLMIW LSVCLLSVYKNACDFCTLILYP ETLLKLLISSSSLYLW
6722	37090	A	6772	714	1096	FFLPMSMECSSICLYPL/CISLRS GL*FSLKRSFTSLVSWIPRYFILC KSQGMRWLGLGSEA*YSCLLIL IRKITQNSVEVLGRRKFLGGGM EREWVMFLRAASSGIRGSVGT NFKSESRHQISCASV
6723	37091	C	6773	1	2796	
6724	37092	A	6774	126	490	FFLPMSMECSSICLYPLLFPGAV VCSSP*RGPSHPL*VGFLGILF/C FEAIGNGSSLMIWLSVCLLLVY KNACDFCTLILYPETLLKLLISL RRFWAETMGFSRYIIMSSANRD NLTSSFPN
6725	37093	A	6775	1	550	
6726	37094	A	6776	578	865	MCPRDYGMLCLCSH\CFKEHLY FCLHFVMYPVVIQEQVVQFPCS *AVLSEFLNPEF*FDCTVV*ETV CYNF*SFTFAEKSFTSNSVVNFG IGVVWC
6727	37095	A	6777	1	2091	
6728	37096	C	6778	1	1458	
6729	37097	B	6779	1	504	
6730	37098	A	6780	70	511	NHASPGIRNLFLHPRGLRAITIA VFCKQNTYIRLEPFKINVLEQIT KHIEKLQCGGVVKQLSRRGNN QHISSTYDINRADTQVRRAVNN YDII\A*ATVSMASRSIRCGSVGS LPSSNLPINSVSIRCRARQEGIM SSPGQQVGFIA
6731	37099	A	6781	3	306	
6732	37100	A	6782	1	3567	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRSLRSRCDQLEERVSV MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLKNTLQDIIQENF PNLARQAKVQIQEIQRMPQRYS LTRATPRHIIVRFTKVE
6733	37101	A	6783	386	550	
6734	37102	A	6784	1	594	

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6735	37103	A	6785	1	1324	MGKKQSRKTGNSKRQSASPPP KERSSSPAMEQSWMENDFDEL REEGFRRTNYSELQEGIQTKGK EVKNFEKNLDECITRITNTEKCL KELMELKAKARELREECRSLRS RCDQLEERHHTTPIPKLTTYLE VKLSPANVKEQVITNCLSDHSA IKLELRIKKPTQNPSTTWKLNN LLLNDYWVNKEMKSEIKMFFE TNENKNTTYQNLWDAFKAVCR GKFIALNAHKGKQERSKIDTLT SQLRELEKQEQTHSKVSRRQEI TKIRAEPKEIETQKTLQKINESR SWFFERINKIDRRLARLIKKKRE KNQRDAIKNDEGDITTDPTEIQT TIREYYKHLYANKLENLKEMD KFLNTYTLPRLNQEEAESLNRPI AGSEIVAIINSLPTKKSPGPDGFT AEFYQRYKEKLVFGAGYFGM WALAALPSNLLKLSQLCQEAA EVNVLVQFVCIC*SCLNSVRRQ
6736	37104	C	6786	1	1719	
6737	37105	B	6787	1	1098	
6738	37106	C	6788	1	1782	
6739	37107	A	6789	3095	3217	CRCLQMAM*WS*AIALSMKIS MSPRKPEV*IKVLAGLCCL
6740	37108	A	6790	1	5364	
6741	37109	C	6791	1	2505	
6742	37110	A	6792	37	1214	KLLQDLPFSINSSAVEKISMSTT GQVIRCKAAILWKPGAPFSIEEV EVAPPKAKEVRIKVVATGLCGT EMKVLGSKHLDLLYPTILGHEG AGIVESIGEGVSTVKPGDKVITL FLPQCGECTSCLNSEGNFCIQFK QSKTQLMSDGTSRFTCKGKSIY HFGNTSTFCEYTVIKEISVAKID AVAPLEKVCLISCGFSTGFGAAI NTAKVTPGSTCAVFGLG\GVGL SVVMGCKAAGAARD/IIGVDVQ QGRKF*GRAQELGATEC\LNP\Q ALKKPHFKEVLFDMTDAGIDFC FEAIGNLDVLAAALASCNESYG VCVVVGVLPASVQLKISGQLFF SGRSLKGSVFGGWKSRQHIPKL VADYMAEKLNLDPLITHTLNL DKINEAVELMKTGKW
6743	37111	B	6793	1	2280	
6744	37112	A	6794	1498	1764	LVYLKVMGRMEPSWKTLCRIL SRRTSANLSKAGQCSDSGNTEN TTKILLKKSNSKTHNCQIHQS*N EGKNVKGSQRERSGYPQRGRPS

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6745	37113	A	6795	3	640	
6746	37114	A	6796	1	996	
6747	37115	A	6797	1	933	
6748	37116	A	6798	74	1128	LLLDL*VD*SPSRPLEMRFRV*P MKRCTTLKKNYLSFLVYISRNL *NRVKAIM/VGKAEWKTIELPL PRKTVNQKQYRIPGGIAEISTTI KELNNAGMVIPTTSPFNSPIWP VQKIDGSWRMTVDYCKLNQV VTPIAATVPYVVSSLEQIN/TSPG T/WNRKRFCNRSRLLHKLLCHL GHMTQQI*CFLRCQWHIGMLF GPEICGCTSLSGQKL/WKIFVSH AASFEWSPEQEKALQQVQAVV QAALPLGPYDPADPVLLEMSV ADRDAVWILWQAPISESQWRPP GFWSKALPSSADNYSPFERQLL ACYWTLVETERLTMGHQVTIPP ELPIMNWVFSDLSSPKMCHPQQ
6749	37117	A	6799	1	229	
6750	37118	A	6800	1	1011	MVSTPATLPSLPKPALMASWG VPYDQLTKEEKTRVWFTDGSA RYAGTTQKWTAVALQPLSRTS LKDSSEGKSSQWAELQAVYLV VHFAWKEKWPDVGLYTDSWA VANGLAGWSETWEKQDWKIG DKEIWGRGMWMDLSEWSKAV KIFVSHVSAHQRVTSAEEEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYSWAQQT\GLPFTKADL AMATAECPICQQQRPTLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFVLTVIDTYSRYRFAY PAHNASAKTTIHGLIECLIHCYG IPHSIASDQSIHF/TTKEVQ*WAH AHGIHWSYHVSHHPEAAGL
6751	37119	A	6801	2	739	HKMGHAQQHSIIKWK*YICDW ARAGPKGTT\APMASWGVLYD QLTEEEKTRAWFTDGSARYAG TTQKWTAAALQPLSRTSLKGS GEGKSSQWAELQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
6752	37120	A	6802	1	354	
6753	37121	A	6803	3	592	

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6754	37122	A	6804	126	365	QLAEPPHWLPD*KGAGFEWGP EQKKALQ*VQAAVQAALPLGP YDPADPMVLVVSVADKDAVWI FHLSGSDRWRRTYRCL
6755	37123	A	6805	1	636	MEFNDSMHNTFDHIWRTKEYD EAGWLLLSSLDKAMKENDELR DSNSQIQKQILSLQSSKIILNLTE GTVVTQLQNLNSVGIIGSQGGR GQVAALSLQRQGASFEWSPEQ EKALQQVQTAVQAALPLGPYD PSDPMVFEVSVADGNAVWSLW QAPIGELQWRTLEFWSKALPSS ADNYSPFGRQLLACYWALVET EHLTVDHQVT/M*PELPIM
6756	37124	A	6806	1	672	
6757	37125	A	6807	308	470	
6758	37126	A	6808	1	1908	
6759	37127	A	6809	1	1218	MGIIGSRGGRGQVAALKRQRQ VTKKAASFEWGPEEEKALQQV QAAVQAALPLGPYDPADPIVLE VSVADRGAVWSLWQVPIGESQ QRPLGFWSKALPSSADNDSPFE RQLLACYCALVETERLDMGHQ VTMRPEVLIINCVLSDPSSH/Q\G WRLCMDSATWTSTYQ/A*PGY GHC*VPNLPAAETNTDPSIWHH S/YG*LASYLVIG*LHWTSSIME GAEVCPHWNRHLLRI*VCLSCT QCFCED/SHPWIHE/ASYLPSWH ST*HCL*SRHSPYS*RSVAVGSC SWNSLVLPCSPSS*SSWINRMV EWPFEVTITMPTR*QYSAGLGK SSSEGCVCSESASNIWYCFSRSQ DSWVQESRGGSGSGTIHHHF** PTSKIFASCFLDIMFCWT*GCS/S *WRNAATRRHNNNFI
6760	37128	A	6810	901	1142	GPEDLQGLFILSFQDPLL/SHPV CLEALAPFPSPPVVPISSFPPHVA GEFWLYPSGAA/RASSDAQSWT VIAVSPLRGLNSWG
6761	37129	B	6811	1	1452	
6762	37130	A	6812	122	1838	
6763	37131	A	6813	101	249	MTHVTALRTSSNLMRN*RKVG EAKSQQEH*S*QACHLKSRMSS SRLWIN
6764	37132	A	6814	1	1074	
6765	37133	A	6815	310	397	LTIWQDSNPGSCL*GCSVCAHA /CVGGQHMVCF*PSYSLYLKSE PKEGTGRNKDPDLNSQNRKGF LEQIHFQ
6766	37134	A	6816	1	583	

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6767	37135	A	6817	1	486	
6768	37136	A	6818	2	1001	
6769	37137	A	6819	1	2307	
6770	37138	A	6820	3	393	
6771	37139	A	6821	1	1776	
6772	37140	A	6822	1	1140	
6773	37141	A	6823	1	558	
6774	37142	A	6824	2	798	PRVRIFFSITWYSLRVLTEISLW GGLILVVIITIQYDMTRTRNKYL HTNSLVALANMSAQFR\SLHQY AA\QRIIRLFSLLSKKHNKVLEQ ATQSLRGSLSSNDVPLPDYAQD LNVIEEVIRMML\EIINSCL\TNS LHHNPNLGITPWLLQ\RRSLWN NFR\THPSFQGINGKILIWVIF/LS /SRLQGLAGKLGAELSVERVLEI IKQGVR\SLPKDRLKKFPELKFK YVEEEQPEEFFIPYVWSLVYNF SSRPVLGIPQDIPAVSPWVSD
6775	37143	A	6825	3	206	PSASRPAWHAPALHPSPVPARG WQPPTGLHPLREQRGLGQHM* QSSGQQPQGGVGPGSHFPGAL WAQL
6776	37144	A	6826	200	601	EMGSCDQWQRPCVPWEAVVM PRDP/LKMALAVVWPKMKAPR VTKRTP*LTSTHQLAGLTSSISE SLA*MRHSPGKTKMKQAARPP MTEITLPMSGMKS/VQQQGEQE PDQRLQHSPPPLPPHVLLHWHP LVAQPQA
6777	37145	B	6827	25	1407	
6778	37146	A	6828	1786	1795	HC*LNALPSGETWGQKRGLPG TQLPLPL/VPLRAPKGRSPKGSK GPTHHTWALSSFSLTPSQVTVG TEDQATSASGRPWLRIGTGPGG GRVWAGRDS\RGVPALTVLHV LSSLGRETP*RPCLRGPTAPAGP KRAPGKWLPWSQAPPCGCCPR *LSHVL*DRNRCAW*KGGGRG L/LRAPTPVPELAPHPCGPAPTL SKPLSSPNMPAQGLTQE*PGSV ANLPPYGPALLCLGRREWDER GQVG*VPTESEME*RRTEPLKT PGDCSAAASKIPSFFSNRTPFPPL CPHKNKLKGT
6779	37147	A	6829	1	311	
6780	37148	A	6830	1	402	
6781	37149	A	6831	1	750	
6782	37150	C	6832	130	450	

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6783	37151	A	6833	1	875	MRLLRLKLKVEQHVELYQKYS NNSWRYLSNRLLAPSDSPEWLS FDVTGVVRQW/VWSRGGEIEGF RLSA\HCSCDSRDNTLQVDINGF TTGRRGDLATIHGMNRPFLLFM ATPLERAQHLQSSRHRRALDTK YCFS\STEKNCCVRQLYIDFRKD LGWK\WIHE\PKGYHANFCLGP CPYIWSLDTQYSKVLALYNQH NPGASAAPCCVPQALEPLPIVY YVGRKPKVEQLSNMIVRSCKC NLGPAPPRPAPAGPAPPRPAPV ALPMGAVFKDTRAPSPPGAPLK MERGKKKKKK
6784	37152	B	6834	162	635	
6785	37153	A	6835	2	1846	
6786	37154	A	6836	322	2104	
6787	37155	A	6837	1	352	
6788	37156	B	6838	92	1774	
6789	37157	A	6839	260	1016	
6790	37158	A	6840	479	1937	DVEHVGKMRRRWRRRVVVAD GNVVKPMSCAGDLQ/PFTRVTV HWGKGNDQTFQDLLDTGSELT LIPGDPKRHCGPPVKIGAYGGQI INGVLAQVQLTVDAVGPWTHP VVIFPVPECIIGIDMLSSRQNPHT GSLTGRVWTIMVRKAKWKPLE LPLPRKIVNQKQYHIPEGIVEIS ATIKDLKDAGVVIPTTSPFNSPI WPVQKTDGSWRMTVGYCKLN QVVTPIAAAVPDVVSLLEQINT PPGTWYAAIDLANDF
6791	37159	B	6841	20	26	
6792	37160	B	6842	2	207	
6793	37161	B	6843	187	405	
6794	37162	A	6844	451	770	LFLFLLSSHPRRSSASWYRHRH PHHPSAARLPVADSASSSSSPSS SSPSPSSSSSSSSPPSSSSFVYPHC QPPAPHFPH*HSR*QGRLFHFLP LPQLPSSPLSPWW
6795	37163	A	6845	1	417	
6796	37164	A	6846	191	314	
6797	37165	A	6847	129	212	

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6798	37166	A	6848	1	192	CALNAGL/IGENEAKKRRSKVT QEADFPGSMDGASNFVRGDAI AGILIMVINIVGGLLVGVLQHG MSMGHAAESYALLTIGDGLVA QIPALVISTAAGVIVTRVSTDQD VGEQMVNQLFSNPSVMLLSAA VLGLLGLVPGMPSLVFLLFTAG LLGLAWWIRGREQKAPAEPKP VKMAENNTVVEATWNDVQLE DSLGMATGLLT*PIFRAQWTGQ VTLFAAMPSPGSSSWSLTLSAG CWSACCNMA
6799	37167	B	6849	65	1129	
6800	37168	B	6850	46	1038	
6801	37169	A	6851	2	413	PSFQGPVSLPSITVVSIDSQASKP LKTPQLWCQLRQYSFKHSFLV VPTCPVPLLG*DTLTKLSASLTI PGLQPHLIATHLNPQVEDTSIPS LATYHAPLTISLKPNHPYPSQC QYPIPQHALKGLKPVITHLLQH
6802	37170	C	6852	35	346	
6803	37171	C	6853	239	484	
6804	37172	A	6854	1	1020	
6805	37173	A	6855	3	131	
6806	37174	A	6856	1	956	MAGALPPASLPPCSLISDCCASN ERSSMGIGPSEPCAGYNLLVCR LTKKKRIRSTNKVWDYVKRPN LRIIGVPEEEENSKSCENILGEIIE ENFPSLATDLDIQIQEAQRTPQK FITERSLPRYIVIRLSKVKTKERI LRAVRQKHQIFLTQRLKTNTAQ SPQKLPGPSQTLLVTLTREITIVP GLDFNPASHIIADTTPDPHDCIS LIHLTFIQFPHISFFPVPHPDHTW FINGSSTRPNRHSPAKAGYAIVS STSIIEATTLPSSTTSQQAEFIAL TQALILAKGLCINIYADSKY/AF HILHHHAVIWAERDTFTG
6807	37175	A	6857	1	1269	
6808	37176	A	6858	1	741	
6809	37177	B	6859	411	1257	

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6810	37178	A	6860	438	3997	SPLPHSTPISHPAACFKKIKACY HLPATAWPFKAYKLSLQFPHFT CPKTRQGLQHNSHKNTRALPD YRLRLISQTPIPSTKQQLLSFLG MVSKVRILTQELGPRPIAFLSKQ LDLTVLTQPSCLHAAAAAALIL LKALKITKYAQLTLYSSHNFQN LFSSSYLMHILSAPWLLQLYSLF VESPTITIVPGTDFNPASHIILDT TPDPHDCISLIHLTFTPFPRISFFP VPHPNHIWFIDGSSTRPKCHSPA KAGY
6811	37179	A	6861	245	505	
6812	37180	A	6862	346	522	PAPEFWVHG*NVSPLSL*SKEQ EDRGFISQGRSPDLSHGTKFHV RPCEETTKQALCEQH
6813	37181	A	6863	3	879	SGDLPWEINPPSSYTLLCEKDPP TTSGPQTNQPKKH\LTNFKSETK ETRFIRGPTTPAPVTDWEGSLPL VFNHSRDTSLIIHPGFRGVRPRR DACLGPSPLAASPTFLGKGPAA PRQTELGPNSSSASAPPPYNPFI ASPPHTWSGLQFPSMTSPPPPA QQFTLKKVAGAKGIVKDLINLT FKVYNNRKKLQFLASTVRQTP ATSPAHKNFQTPELQQPGVPPE PPPRGACYKFQKSGHRAKECLQ PRIPPKPHPICVGPHWKSDCPTH LAATPRAPGTLAQGSLTPSQIFL
6814	37182	A	6864	143	331	DTSTPSLVTDHASLTISLKPNHF YPD*CQYPIPQHALKGLKPVITC LLQHGLLKPINSPYPRA
6815	37183	A	6865	1	783	
6816	37184	A	6866	32	415	WRHALKGLKPVITRLLQHGLL RPINSPYNSPFLLVLEPDKPYRK RK*ISPPNRHILASVEVLKNQVN SHEFERSALIHTLTSGLAPCSLH KMCSKLPRSFLSVGSGTGKEAR SKILTFRTASRHLVL

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6817	37185	A	6867	1	1374	MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKPTETKTAW YWYLNRDIDQWNRTEPSEITPH TYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPF FTPYTKINSRWIKDLNVRPETIK TLEENLGITIQDIGVGKDFMSKT PKAMATKDKTGKWDLIKLKSF CTAKETTIRVNRQRVAALLNSA VFQNAVEVVVWPSSEVHVKFL FCKIISCAGQKQPIKFDGSSSLS GVATAMMSATIAHLKRIKACY RSPVTAWTFKAYKLSLQFPHFT CPKTGQALQ*HT*KGLKPVIAH LLQHGLLKPINSPYNSLILPVQK PDKPYRKLESFTSKAIKWHQIPS \PGKHLC**GS*RSPVTAWTFKA YKLSLQFPHFTCPKTGQALQEA GVIHFKGHQMASDPITQGNTYA NKVAKEAASVLTSVPHGQFFSF SSVTPTYFPTEIDFTYMPQVRKL KHLMV
6818	37186	A	6868	122	281	
6819	37187	A	6869	2	2144	
6820	37188	A	6870	224	418	LSQWRHALKGLKSVITRLL*HG LLKPINSPYNSPIVPVLKPDKTY RKVESFTAKTIKRCQIPLL
6821	37189	A	6871	5	289	
6822	37190	A	6872	1	2205	
6823	37191	C	6873	1	2082	
6824	37192	B	6874	1	1614	
6825	37193	A	6875	1	2067	
6826	37194	A	6876	1	1152	
6827	37195	A	6877	1	798	
6828	37196	C	6878	488	788	
6829	37197	A	6879	90	765	NTVFGLVVLPLELKLRIFRLLD VRSVLSLSAVCRDLFTASNDPL LWRFLYLRDFRGDFRNDIYSWT TKDFEYYINLVDKTEARFEKVD SDFESFTVGKMPSNSIACTEKSF MKGRVSQCDKKPVITRLLQHG LLKPINSPYNSPILPVLKPDKPY KLVQDLHRINQIVLPIHPCGAQP HTLFCPQYLPPQLTIPVPDLKDA FFTIPLQPSSQ\PLFAFT*TDPDT

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6830	37198	A	6880	1824	2286	PRVLRPNSPRNISPISNRIFSD*R CPIASEASWTITDALG/RLLQWR HGLLNPINSPYNSPILPVQKPDK PYRLVQALLSLPQLPLFLAWTSI WPPTLFRITLLNPMTVSL*ST*H SLHFPMFPSFLFLTLITLGLLMA VPLGLIATHQQRRAML
6831	37199	A	6881	930	1289	LSQWTDGLLKPMNSPYNSPILP VLKPDKPYK*VQDLRLINQIVL PIHPVV\PNPYTLLSSIPPSTTHY SVLDLKLAFFTIPLHPSSQPFFAF TWTDPDTHQAQQIT*AVLPQSF SDSPHE
6832	37200	A	6882	2	196	IHGCKFIQCKRILSNFTEVADHV HDQIRL*TGIRLLTQPQPRLSCR HQVAQHSVCRYLCQLPLL
6833	37201	A	6883	2	1441	LNQEEGESLNRPITGSEIEAIINS LPTKKSPGPDGITAEFYQRYKE ELVPFLVKLFQSTEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLMNIDAKILNKILANRIQQHIK KLIHNGQHINRTNDKSHIIISIDA EKTFGKIQQPFMLKTLNKLGID GTYLKIIRAIYDKPTANIILTGQ KLEAFPMKTGTREGCPLSPLLF NIVLEVLARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLRLISTFSKVSGYKINVQ KSQAFLYTNNRQTESQILSELPF TIASKRIKYLGIQLTRDVKDLFK ENYKALLNEIKEDINKWKNIPC SWVGRINIVKMAILPKVIYRFN AIPIKLPMTFFTELEKTTLKFIW NQKSARIAKSILSQKNKAGGIM LPDFKLYYKATVTKTAWYWY QNRDIDQWNTTEPSEIMLHIYN Y/LIFNKPEKNKKWGKDSLFNK WCWENWL

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6834	37202	A	6884	69	2415	DKTSRGTIRQQRLRFTNIRCSAA TAADIQANRVWRGPPANSNRP AA\RVLTVRRKTNKQKGHPHQ KPICTSPSSNTKEIQTTIREYYKH LYANKLENAEERDKFLNIYTLP RLNQKEVESLNRPITGSEIEAIIK SLPTKKSPGPDGFTAKFYQRYK EELVPFLLKLFQSIEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLMNIDARILNKILANLIQQHIK KLIHHDQVGFIPGMQGWFNICK SINIIQHMNRTKDKNHMIISIDA EKPFDKIQQPFMLKTLNKLDID GTYLKIVRAKYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLAREIRQEKEIKGIQL GKEEVKLSLFVDDMIIYLENPIV SAQNLLKLISNFSKVSGYKISVQ KSQAFLYTNNRQTESQTMSELP FTIASKRIKYLGIQLTRDVKDRF KENYKSLLSEIKEDTNKWKNIP CSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFIR NQKRARIAKSILSQKNKAGGIT LLDFKLYYKATVTKTAWYWY QNRHVDQWNRTEPSEIMLHIY NYLIFEKPDINKQWGKDSLFNK WCWENWLAICRKLKLDPFLTS YTKINSRWIKDLNVRPKTIKTLE ENLGNTIQDIGMGKDFMSKTPK AMATKAKLDKWDLIKLKSFCT AKETTIRVNRQPTGWEKIFATY
6835	37203	A	6885	1	2358	
6836	37204	B	6886	1	1443	

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6837	37205	A	6887	452	2913	KMGLAREWILRFLVLILQEIRS MRQKENKDIQDLNSALHQADL IDIYRTLHPKSTEYTFFSAPHCI/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKLTQ\NRS ATWKLN/MLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLW DTFKAVCRGKFIALNAHKRKQ ERSKIDTLMSQLKELEKQEQTH SKVSRRPIPSSEIEAIINSLPTKKS PGPDGFTAEFYQRYKEELVPFL LKLFQSIEKEGILPNSFYEASIILI PKPGRDTTEKENFRPISLMNIDA KILNKILANRIQQHIKKLLHHDQ VGFIPGMQGWFNICKSINVIQHI NRTSDKNHTIISIDAEKAFNKIQ QLFMLKTLNKLGTNGMYLKIV RAIYDKPTANIILNGQKLEAFPL KTGTRQGCPLSPLLFNIVLEVLA RAIRQEKEIQGIQLGKEEVKLSL FADDMIVYLENPIVSAQNLLKLI SNFSKVSGYKINLQKSQAFLYT NNRQTESQIMSELPFTTASKRIK YLGIQLTRDVKDLFKENYKPLL NEIKEDTNKWRNIPCSWVGRIN IVKMAILPKVTYRFNAIPIKLPM TFFTELEKTILKFRWNQKRAHI AKTILSQKNKAGGIRLPDFKLF YKATVTKTARYWYENRDIDQ WNRTEPLEIMPHIYNHLIFDKPD KNKQWGKDSLFNKWCWENWL AICRKLKLDPFLTSYTKINSRWI
6838	37206	A	6888	1	1677	

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6839	37207	A	6889	2	2400	SMRQKENKDIQDLNSALHQAD LIDIYRTLHPKSTEYTFFSAPHCI /RTYSKIDHTLGSKALLSKCKIT EIITDSQTTVLSELRIKKLTQ\NR SATWKLN/MLLNDYWVHNEM KAEIKMFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLMSQLKELEKQEQT HSKVSRRPIPSSEIEAIINSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEASII LIPKPGRDTTEKENFRPISLMNI DAKILNKILANRIQQHIKKLLHH DQVGFIPGMQGWFNICKSINVI QHINRTSDKNHTIISIDAEKAFN KIQQLFMLKTLNKLGTNGMYL KIVRAIYDKPTANIILNGQKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIRQEKEIQGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINLQKSQA FLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWRNIPCSWV GRINIVKMAILPKVTYRFNAIPI KLPMTFFTELEKTILKFRWNQK RAHIAKTILSQKNKAGGIRLPDF KLFYKATVTKTARYWYENRDI DQWNRTEPLEIMPHIYNHLIFD KPDKNKQWGKDSLFNKWCWE NWLAICRKLKLDPFLTSYTKIN SRWIEDLNVRPKTIETLEENLG
6840	37208	A	6890	1	1515	
6841	37209	A	6891	1	1428	

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6842	37210	A	6892	150	1920	NYQCREVLKGPDGAENHGTRT T*RMHK\LSSQFSQLEERVSGM EDQTNETKDTHRLKIKGWRKIY QANGKQKKAEAAILVLDKTDF KPTKIKGDKQGHYIMVKGSIQQ GQLTILNIYAPNTGASRLIKQVL RDLQRDLDSHTIIMGDFNTRLS TLDRSTRQRLNKDIQELNSALH QVDLIDIYRILHTKSTEYTFFSA PHHTYSKIDHTVGSKALLSKGK RTEIITNRLSDHSAIKLELRIKEL TQNRSTTWKLNNLLLNDYWNL WDTFKAVCRGKFIALNIQKRK QERSKIDTLTSQFKELEKQEQT HSKASRRQEITKIRAELKERETQ KSLQKISESRSWFFEKINNIDTP LARLIKKKREKNQIDTIKNDKG DITTDPTEIQTTIRQYYKHLYAN KQENLEEMNKFLDTYTLPRLN WEEAESLNRPITGSEFEAIINSLP IKKSPGPDGFTAKFYQSYKEEL VPFLLKLFQSIEKEGILPNSFYE ASIILIPKPGRDTTKKDNFRPISL MNIDAKILNKILANKIQQHSKK LIHHNQVGFIPGMQGWFNTCKS INIIQHINRTKDKNHMIISIDAEK AFDKIQQPSC
6843	37211	A	6893	1	1797	

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6844	37212	A	6894	2	1880	APNTGAPRFIKQVLSDLQRDLD SHTIIMGDFNTPLSTLDRSMRQ KVNKDIQELNSALHQADLIDIY RTLHPKSTEYTFFSATHHTYSKI DHIVGSKALLSKCKRTEIITNCL SDHSAIKLELRIKKLTENRSTTW KLNNLLLNDYWVHNEMKAEIK MVFETNDTLPRLNQEEVESLNR PKTGSEIEAIINSLPTKKSPGPDG FTAEFYQRYKEELVPFLLKLFQ SIEKERILPNSFYEASIILIPKPGR DTTKK/EENFRPISLMNIDAKIL NKILANRIQQHIKKLIHHDQLGF IPGMQGWFNICKSMNVIQHINS PKDKNHMIISVDAEKAFDKIQQ PFMLKTLNKLGIDGTYLKIIRAI YDKPTASIILNGQKLEAFTLKTG TRQGCPLSPLLFNIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIISAQNLLKLIGN FSKVSGYTINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDFFKENYKPLLNE IKEDKNKWKNIPCSWVGRINIV KMAIPPKVIYRFNAIPIKLPMTF FGMIFLSQKYGHVTLLFRLLQW LLNVARNNNKVFYKIYKVGHK LSSAYVLCLTCSHFSVSFL
6845	37213	B	6895	13	1506	
6846	37214	A	6896	1	6635	MTPESRDTTDLSPGGTQEMEGI VIVKVEEEDEEDHFQKERNKVE SSPQVLSRSTTMNERALLSSYL VAYRVAKEKMAHTAAEKIILP ACMDMVRTIFDDKSADKLRTIP LSDNTISRRICTIAKHLEAMLIT RLQSGIDFAIQLDESTDIASCPTL LVYVRYIPLKLRLGGLLQPEKPI VLKVESRDGTIQYNSQQHINLS AAWLKTAVQGREAPGKQPSKQ QHSAKRKTHRTQLKKESGDGP HPKFGGGNLASP
6847	37215	B	6897	1	3045	

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6848	37216	A	6898	1	2764	MARELHDKCTSFSSRFDQLEES LSAMEDQMNEMMREEKFREK RRKRNEQSLQEIWDYVKRPNL HLIGVPESDRENGPKLENTLQDI IQENFPNLARQGNIQIQEIQRMP QRYSSRRATPRHIIVRFTKVEM KEKMLRAAREKEIQTTIREYYK HFYANELENLEEMDKFFETYTL PRLNQEEVESLNRPITGSAIEAII NSLPTKKSPGPDGFTAEFYQRY KEELVPFLLKLFQSIEKEGILPNS FHEASIILIP
6849	37217	B	6899	1	3549	
6850	37218	A	6900	387	541	
6851	37219	A	6901	1	545	
6852	37220	A	6902	71	370	RRCKVRPSARGVLRYAVCVCV CVCVYPCVHVCTCVRMCLCVC VCVCE/CSVEIHCGGQGCARCIC LQPQEGGCTEQAVALHCAAQL WRNRLKLMKQPVARV
6853	37221	A	6904	1	738	
6854	37222	A	6905	1	567	
6855	37223	A	6906	1	1416	
6856	37224	A	6907	3	1267	
6857	37225	A	6908	1	552	NALPGRKSRVFSGCVSADTWK PPSSAKVTETKGASPAFLRAGQ PRLVPGETLEKSLGPGKDPQVE PQHPVHLPGISSEGFPWDGFNE QTPKD\LPNRDGGAWVLGYRA GPACPFLLHEEREKSNRSELYL DLHPDHSLTEQDDRTPGRLQA VWPPPKTKDTEEKVGLKYTEA EYQAAILHLKRE
6858	37226	A	6909	1	561	
6859	37227	A	6910	219	1343	RRLCHTQPTLGMRERSELVNV CVHSVFSLPSVQAMQEKDEAK AETIQALYHQTLEALQTLLKAL FIEDPTPAGLKSILEALGPWMNS GKAHERARAVNTNVSVLNHM LLTLPFFMPLGFPALGLLLGRLI LHIGDPDEEIGCEALDGIIILYTI LELQKRARDKEETNKKELYES NKHFLGPYNPVSPCQNILRVIEE FGDFLGPQQIKDLLLAALEGLK GSSEAPGKDSREMMQLASEVM LSSVLEWYRHRALEVIPEIMQGI YMQLSHIQEPRARQVALLPVSL LASSFMTEVVVALLMCPLPLNR QPAACASSCPSTAAWAV*GAST LSCSWPCSFRSITTSASTCLAAW LLPRTPRRVHSPLPSYLCAGW

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6860	37228	A	6911	3	730	
6861	37229	A	6912	2	1218	ERKCMQGKYAGAMESEPCVCT EADFDCDYGYERHSNGQCLPA FWFNPSSLSKDCSLGQSYLNST GYRKVVSNNCTDGVREQYTAK PQKCPGKAPRGLR\VVTADGKL TA\EQGHNVTLMVQLEEGDVQ RTLIQVDFGDGIAVSYVNLSSM EDGIKHVYQNVGIFRVTVQALV RLPPHISQCDEVFRFFEARPEDV NPPKDQALLLGELGPAVELCLK EERFADAIILAQAGGTDLLKQT QERYLAKKKTKISSLLACVVQK NWKDVVCTCSLKNWREALAL LLTYSGTEKFPELCDMLGTRME QEGSRALTSEARLCYVCSGSVE RLVECWAKCHQALSPMALQD MHVISTDENQVFAAVQEWNQN DTYNLYISDTRGVYFTLALENV QSSRGPEGNIMIDLYEVTI
6862	37230	A	6913	1	1659	
6863	37231	A	6914	540	824	KPRLENYVKNAEASGADAINW KKGY/LVMEDEMNEMKREGKF REKRIKRNEQSLQEIWDYVKDQ IYVRLVYLKVTGRMEPSWKTL CRILSRRTSPI
6864	37232	A	6915	1	939	
6865	37233	A	6916	285	458	QVFSQLEGRIALGKFQRPSSLPT GKWTQRCWWGAQWE*D*LFG LHGWWVRPVIAGFP
6866	37234	A	6917	32	171	
6867	37235	A	6918	294	461	
6868	37236	A	6919	2	255	LIPCPATVNNVSDIMGMYMKE CSASLITREMQIRTTIMRHHLTS IGTEMIRK/SKNNECWSGRECQ TVGAGQCVRAPCASRSRARH
6869	37237	A	6920	2	393	
6870	37238	B	6921	87	633	
6871	37239	A	6922	78	260	TQYLRWKCRNHRLLRRSCWEL *TRAVPIRPSWLQNRYQGTSRF CVCFEESSGTPSTQLEI
6872	37240	A	6923	1	369	FVLHEKCLGPFIWTGNTNVEM VKKICAPT*TKHVVW*LES*M WEEPRWPN\GKAPVYSSQREQR RRRVISAFPSEGVLPSTFKNKKF TVKQPQVGRSVGIPEEGIVIIGD GQLQGCLLPLKTF
6873	37241	A	6924	3	201	LKEMQINTTMRYHS\TPSRTS*\I KKTDNNKFWMRMTEKLETSY CWWECETMQPRWKVSLQYLL PLI

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6874	37242	A	6925	1	2064	
6875	37243	A	6926	95	752	
6876	37244	A	6927	2237	5072	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
6877	37245	A	6928	3	331	
6878	37246	A	6929	364	853	
6879	37247	A	6930	2	531	RPRVRELVGGSAIQALKEWNTT GKLRINH*KRCGSTQHHGSKYA TDKEERPD\ACPLQPQPPQIQNG PMNGCEKDSSSTDSANEKPALI PREKKISILEEPSKALRGVTGPNI EKSAKDLQRCTVSLTRYRVMIK EEVDSSVKKITAAFAELHNCIID KEASLMAEMGTVNEQAMRC
6880	37248	A	6931	1	456	ISILEEPSKALRG\VTEGNRLLQ QKLSLDGNPKPIHGTTERSDGL QWSAEQPCNPSKPKAKTSPVKS NTPAAHLEIKPDELAKKRGPNI EKSVKDLQRCTVSLTRYRVMIK GEVDSSVKNIKAACAEFPICIID KEVSLMAEM\DKVKGRKPW
6881	37249	A	6932	333	964	
6882	37250	A	6933	240	691	
6883	37251	A	6934	1	2076	
6884	37252	A	6935	14	485	RRSLESVLSRKLNPF*KATGTSR SESAVWAIIDAVSSPQKRLLDSE FIDPLMNKKARISHLTNRVPPTL NGHLNPTSEKSAAGLPLPPAAA AIPTPPPLPSTYLPISHPPQIADS HSPAAPVQGIQPFLTADQYWLE NRYPSQHLSRVTASRARHQT
6885	37253	A	6936	1	643	
6886	37254	B	6937	1	408	
6887	37255	A	6938	2	197	
6888	37256	A	6939	103	298	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEKI FLGHRVGI
6889	37257	A	6940	117	257	

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6890	37258	A	6941	46	219	LKECNCIVCNSKNKCLKG*KKK EEEEEEEEEEEEEEEE\EEEEEEE EEEEEEEEEEEGRRGRGRGRRR RRRRRRKKK
6891	37259	A	6942	1	1314	MVSRIWSWISEAQCPLCRPSGT YGPGEAALLLWLCIEAAAAAA AARSTTTPIITNHQSNTIAEQNP PRHENGDPKTYIIHVLAEQVLE RLPHGVALRHDPLAPVVSRAG GVGHQRCAADDALQPLLQGRP EPGLAERHGVQDNLILKVSHTH TQKSAEKRAVSDPSSTVHRPQP LPPSTVHQSTIPSNPDSSSAYCL PSTRHGFSSYTDSFVPPSGPSNP MNPTIGNGLSPQRVHYQHLPTH AGGKRNAALEYGVPRKYYHM LKITASDYEKTKPFQVGDKVM GSGWRKVGMQT*FL*LKKEEE EEREEEE\EEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEENSLSLTE
6892	37260	A	6943	1	160	
6893	37261	A	6944	1	306	
6894	37262	A	6945	1	933	MWLARELEESLAVSLQGEPGL LAGAGRLQGSPFSHPMEPGRQS ETLSQKKKKKEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEGEEEEGEEEE DQLDTM\FGTHQQTSPTQRSAR RRPCSVQGPRS*SPFSHPMEPGR QSETLSQKKKKKEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEGEEEEGEE EEDQLDTMLWDSSTNLTNTAL SKEKTMFSSRAKIVKPNGEKPD EFESGISQALLELEMNLDLKAQ LWELNITAAKEIEVGGGRKAIII FVPVPQLKSFQKTQVQLRRILP KPTQKSCTNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVK LDGSHLIKIHLDEAQQNNVEHK VEPFSGVYKKLMGKDVNFEFP
6895	37263	A	6946	1	1365	
6896	37264	A	6947	416	610	EFKKPVLEGGA*RGEGGSPCV WSFFDPVHFNYQAGLFRVALP GEQCRTGRLVARVYTGISGASF
6897	37265	A	6948	1	846	

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6898	37266	A	6949	3	620	HVTLLIVVTQSHLVIHNLFEGMI WFIVPISCVICNDIMAYMFGFFF GRTPLIKLSPKKTWEGFIGGFFA TVGFGLLLSYVMSGYRCFVCP VEYNNDTNSFTVDCEPSDLFRL QEYNIPGVIQSA\IGW\KTVRMY P\FQIHSIA\LSTFASLIGPFGGFF ASGFKRAFKIKDFANTIPGHGGI MDRFDCQYLMATFVNVYIACV LRPL
6899	37267	A	6950	50	554	
6900	37268	B	6951	446	625	
6901	37269	A	6952	1	2149	
6902	37270	A	6953	1	1704	
6903	37271	A	6954	1	1853	
6904	37272	A	6955	1	1305	MVKGSIPQEELTILNIYALNTGA PRFIKQVLRDLQRDLDSHTIIMG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADIIDIYRTLHPKST EYTFFSAPHHTYSKIDHIVGSKA LLSKCQRIEIITNCLSDYSAIKLE LRIQKLTQNCSTIWKLNNLLLN DYWVHKEMKAEIKMFFETNEN KDTTYHHLWDTFKAVCRGKFI ALNAHKRKQERFEMDTLTSQL KELKKQEQTHSKASRRQEITKI RAERKEIETQKTLQKINESGSW FVEKINKIDRPLARLIKKKREKN QIDAIKNDKGVITTDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DTYNLRRLNQGEVESLNRPITG SEIEAIINSLP/TKKSPGPNGFTA KF*QEELTILNIYALNTGAPRFI KQVLRDLQRDLDSHTIIMGDFN TPLSTSDRSTRQKVNKDIQELN SALHQADIIDIYRTLHPKSTEYT FFSAPHHTYSKIDHIVGSKALLS KCQRIEIITNCLSDYSAIKLELRI QKLTQNCSTIWKLNNLLLNDY WVHKEMKAEIKMFFETNENKD TTYHHLWDTFKAVCRGKFIAL NAHKRKQERFEMDTLTSQLKE LKKQEQTHSKASRRQEITKIRA ERKEIETQKTLQKINESGSWFV EKINKIDRPLARLIKKKREKNQI DAIKNDKGVITTDPTEIQTTIRE YYKHLYANKLENLEEMDKFLD
6905	37273	A	6956	1	1926	

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6906	37274	A	6957	2	1025	WRRIYQANGK*KNK/QKKAGV VILVSDKTDFKPTKIKRDKEGH YIMVKGSIQQEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRIKKLTQNSSTTWK LNNLLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCKA VCREKFIALNAHKRKQERSKID TLTSQLKE/LEKQEQTHSKASRR \NLEEMDKYLDTYTLPRLNQEE FESLNRPITGSEIEAIINSLPTKKS SGPDGFTAKFYQ
6907	37275	A	6958	1	1661	
6908	37276	A	6959	2	1632	WRKIYQANGK/HKKAGVAIRV SDKTDFKPTKIKRDKEGHYLM VKGSIQQEELTILNIYATNTGAP GFIKQVLSDLQRDLDSHTIIMED FNTPLSTLDISMRQKVNKDTQE LNSALHQEDLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQSRSTTWKLNNLLLN DYWVHKEMKADIKMFFETNES KDTTYQNLWDAFKAEELESLN RPITASEIVAIINSLPSKKSPGPD GFTAKFYQRYKEELVPFLLKLF QSIEKEGILPNSFDEASIILIPKLG RDTTKKENFRPISLMNIDAKILN KILANQIQQHIKKLIHHDQVGFI PGMQGWFNIHKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQSF MLKTRNKLGIDGTYLKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGIQLGKEDVKLSLFADD MIVYLENPIVSAPNPLKLISNFS KVSGYKINVQKSQAFLYTNNR
6909	37277	A	6960	1	2169	

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6910	37278	A	6961	2	1255	EGKFRENRIKRNEQSLQEIWDY VKRTNLRLIGVPESDWENGTKL ENTLQDIIQENFPNLAR*AKIQRI RSQDPSTHLTSRDTHRLKIKGW RKIYQANGKQKKAAVTILVSD KTNFKPTKIKRDNEGHYIMVKG SNQQEELTILNIYAPNTGAPRFI KQVLRDLQRDLDSHTIITGDINI PLSTLDRSTKQKVNKDTQELNS ALHQVDLIDIYRTLHPKSIEYTF FSAPHHTYSKVDHILGSKALLS KCERIEIITNCLSDHSAIKLELRI KNLTQNHSITWKLNNLFLNDY WVHNEMKAEIKMFFETSENKD TTYQNLWDAFKAVCRGKFIAL NAHKRKQERSKIYTLTSQLKEL EKQEQTHSKASRRQEIIKIRAEL KEIETQKTLQKLNESISHQLEW QSLKSQKTTGAGEDVEK
6911	37279	A	6962	1	1122	
6912	37280	A	6963	551	1536	EILSPPGLPYKSS*KKH*TWKGT TGTSCC/INHAKIVTHRLKIKGW RKIYQANGKQKKAGVANLVSD KTDFKPTKIKRDKEGHYIMVKG SIQQEELTTLNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLLTLDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHIYSKTDHILGSKALLS KCKRTEIITNYLSDHSAIKLELRI KNLTKNRSTTWKLNNLLLNDY WVHNEMKAEMKMFFETNENK DTTYQNLWDTFKAMCRGKFIA VNAHKRKQERSKIDTLTSQLKE LEKQEQTHSKASRRQEITKI
6913	37281	B	6964	28	1209	
6914	37282	A	6965	1	1284	
6915	37283	B	6966	1	1056	
6916	37284	B	6967	124	963	
6917	37285	A	6968	3	1162	
6918	37286	A	6969	1	1364	
6919	37287	A	6970	1	1003	
6920	37288	B	6971	1	1129	

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6921	37289	A	6972	1	1917	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKL\GIKYLGIHLTRDVKDLF KENYKPLLKEIKEDTNKWKNIP CSWVGRINIVKMAILPKMCL*R RWTPLCLLTAAASLNRE*ERLV QPLLWRQMYCGPRHCRQVPQH RRLNWSPSLRLS
6922	37290	A	6973	1	2673	

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6923	37291	A	6974	261	2667	TWCSGRYMVGCR/DWHLLLV/ KGLRKLTIVAEGEGGAGMSLG ESGNKIKRDKEGHYIMVNGSIQ QEELTILNIYAPNTGAPRFIKQV LRDLQRDLDSHTIIMRDFNTPLS ALERSTREKVNKDIQELNSALH QADLVDIYRTLHPKSTEYTFFS APHRTYSNIDHIVGSKALLSNC KRTEIITKCLSDHSTIKLELRIKK LTQNRSTTWKLNNLLLNDYWV HNEMKAEIKMFFETIENKDTTY QNLWDTFKAECRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKASRRQEITKIRAELKET ETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNLIDAIKN DKGDITTDPTEIQTTIREYYKHL YANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITGSEIVAIIN SLPTKKSPGPDGFTAEFYQRHT VSILISYCQGGSLMSQVYWNQQ EKPPSSSNAPPGLSVNKAQHRH VCCRGEMLKRVQVHYVRAGES DSASFHCVAQGPRAFGKPLILS KENHLLTVTAIAKLNHKLCEIK SMGVFINTEPLYDSCLEQKHAL FASPPATTHSTTMISKAKVIPML SLTPGSFQTVESSLAPSAGKFQG TETSSLKTLINLCCPKLPSPSPA HLGGLPGGSQERPSRQYLYESA RTTVLLGLGCPLKQIQLRSQHS SPLEYLESLPKKDRKKREKIQIN

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6924	37292	A	6975	1	1687	MLKGSIQQEELTVLNIYAPNTG APRCIKQVLSDVQRDLDSNTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNSLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKEIQTTIR EYYKHLYTNKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITGS EIVAIINSLPTKKSPGPDGFTAEF YQRYKEEMHINRAKDKNHMIIS IDAEKAFDKIQQPFMLKTLNKL GIDGTYFKIIRAIYDKPTVNIILN GQKLEAFPLKTGTRQGCPLSPL LFNIVLEVLARAIRQEKEIKGIQ LGKEEVKLS\LFADDMIVYVEN PLPSQPQNLL*GWLSNFSK/MSS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQFTR DVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVK\MAILP
6925	37293	B	6976	1	2431	

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6926	37294	A	6977	1	1921	MGESVQSLLTLAQKRSMMIQV AVAPRTPTLLLKLYKEKASKTQ LKKVNLVVQDGQSLESIEVHD HEPADTYKLLSLVKEPAEEIPR VIQNVFGHRSKKENLKDSYGLR QSSTMVATTWNNVSLMQHHSL RRPNRHLTASYPHFHFQEIPVNF FHSGRDSESFGWNQHIKKDKE GHHIMVKGSIQQEELTMLNIYA PNTGAPRFINQVLSDIERDLDSH KIIMGDFNTPLSTLDRSTRQKV NKDTQELNSALHQADLTDIYRT LHPKSTEYTLFSAPHHTYSKIDH IVGSKALLSKWKRTEIITNCLSD PRAIKLELRIKKLTQNRSSIWKL NNVLLNDYWVHNEMKAEIKIF FETNENKDTSCQNLWDTFKAV CRGKFIALNAHRRKQERSKIDT LTSQLKELEKQERTHSKASRRQ EITKIRAEMKEIETQK\TLQKINE SRSWFFEKINKIDRPLARLIKKK REKNQIDAIKNNKGDITTDPTEI ETTIREYYKHLYTNKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEVVAIINSLPTKKSPGPDG FTAEFHQRYKEKLISELLPMPN HTALKKQTQDLSDCKAMFLYY QSVSVQTAIINYHRLRGLNNRN LFLTVLEYSSLRSGCEHSRVL

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6927	37295	A	6978	1	1848	MSLTKMLICAALLGLFCMLLGL RWQVAELIGMTLALSSTAIAM QAMNERNLMVTQMGRSAFAV LLFQDIAAIPLVAMIPLLATSSA STTMGAFALSALKVAGALVLV VLLGRYVTRPALRFVARSGLRE VFSAVALFLVFGFGLLLEEVGL SMAMGAFLAGVLLASSEYRHA LESDIEPFKGLLLGAVFTPRVVV NIYSSELRTAKNYQANGKQKK PGVAILVSDKTAF/KPTEIKRDK EGHY\IMVKGSIQQEELTILNIY APNTGAPRFIKQVLSDLQRDLD SHTLMMGDFNTPLSTLD\RSTR QKVNKDTQELNSALHQADLIDI YRILHPKSTEYTFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLTQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDMTYQNLWDT FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKAIQ KINESRSWGPPGNCQQNYRNSE SGEKSAPEGQAQHAGPTEGKV PTFLYVGKEKFPPSYLLTRKSSH LPTCGDPICGEKCWRVPTTSGQ GNKADQWGGVGIGDTDHDSA
6928	37296	A	6979	1	2235	
6929	37297	A	6980	1	2955	

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6930	37298	A	6981	3	2156	KSLKDLMELKIMAQELCDEWT SLSSRCNQLEERVSVMEDEMN EMKDKHRPKIKEWRKIYQANG QQKKTRVANLVSDKTEFKPTKI KRDKEGHYIMVKGSIQQEELTI VNIYAPNTGAPRFIKKVLSDLQ RALDSHTIIMGDFNTPLSTLDRS TRQKVNKDIQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHYTY PKIDHIVGSKALLSKCKRTEIIT NCLS\DHSAIKLELKIKKLTQNL STTWKLNNLLLKDYWVHKEM KAEIKMFFETNKNKDTTYQNF WDTFKAVCRGKFIALNAHKRK QEGFKIDTLTLQLKELEKQEQT HSKASRRINKIDRPLARLIKKKR EKNQIDTIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGAEIVAIINSLPTKKSPGPDG FTAKFYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASIILIPKPGR DITKKENFRPISLMNIDAEILNKI LASQMQQHIKKLIYHNQVGFIH GMQGWFNIHKS\INVIQHINRTK DKNHTIISLDAEKAFDKIQQPF MLKLKTLNKLGIDGMYLKIIRA IYDKPTANIILHWQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AVRKEKEIKRTQIGREEIKLSLF ADDMIVYLENPIVSAQNLLKLIS NFTKVSGYKINVKKSQAFLYN
6931	37299	A	6982	3721	8717	MLPIKRHRLANWIK\SQDP\SVC CIEET\HLTCRDAHRHKIKGWR KIYQANGKQNKTKQQKKQGLQ ILVSDKRDFKPTKIKRDKEGHYI MVKGPIQQ\EELTILNIYAP\NTG APRFIKQVLSDLQRDLDSHTLI\ MGD\FNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAP\HHTYSKIDHIL GSKALLSKCKRTEIIT\NYLSD\H SA\IKLKLRIKNLTQNHSTT\WK LNNL

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6932	37300	A	6983	599	1074	NPRAWEKQQPPTSPQEFCLVCF VVHLQKSTREALNNKNIKPLLS TFSQVPG/SINHSSCENVLAIISL AIGGVTEGICTASTPFVLLGDVL DCLPLDQCDTIFTFVEKNVATW KSGTASLPAAFMAGVEHLWLF QVNGANCQWIYPSGVWRTVAL FSQLH
6933	37301	A	6984	1	312	
6934	37302	A	6985	2	484	QSRALLWPMLVDVIQPKPWKA PGSLGLPSCISAITVQSSPGLRLC SCGQGPRVNTPGTKLPQPNRPV SLSFSQMKLLTSSHWKSFHCPA *INPAQSSPGPWP*PQLSGCPAF QFLSFG*KSLLSSGNTASSSPLW FLCWCFLNLVLQAKLPDGFRPA HRV
6935	37303	A	6986	234	405	ELKICSCDPITVRYNADDSTVSL SFSQMKLLTSSHWKSFHCPA*I NPAQSSPGPWP
6936	37304	A	6987	1	2021	PTRPAAAQWRARAAEKMSPTP PLFSLPEARTRFTKSTREALNNK NIKPLLSTFSQVPGSENEKKCTL DQAFRGILEEEIINHSSCENVLAI \ISLAMGEVTEGICTASTHFVLL GDVLDCLPLDQCDTIFTFVEKN VATWKSNTFYSAGKNYLLRMC NDLLRRLSKSQNTVFCGRIQLF LARLFPLSEKSGLNLQSQFNLE NVTVFNTNEQESTLGQKHTED REEGMDVEEGEMGDEEAPTTC SIPIDYNLYRKFWSLQDYFRNP VQCYEKISWKTFLKYSEEVLAV FKSYKLDDTQASRKKMEELKT GGEHVYFAKFLTSEKLMDLQL SDSNFRRHILLQYLILFQYLKGQ VKFKSSNYVLTDEQSLWIEDTT KSVYQLLSENPPDGERFSKMVE HILNTEENWNSWKNEGCPSFV KERTSDTKPTRIIRKRTAPEDFL GKGPTKKILTGNEELTRLWNLC PDNMEACKSETREHMPTLEEFF EEAIEQADPENMAENEYKAMN NSNYGWRALKLLARRSPHFFQP TNQQFKSLQEYLENMVIKLAKE LPPPSEEIKTGEDEDEEDNDALL KENESPDVRRDKPVTGEQIEVF ANKLGEQWKILAPYLEMKDSEI RQIECDSEDMKMRAKQLLVAW QDQEGVHATPENLINALNKSGL SDLAESLTNDNETNS

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6937	37305	A	6988	155	811	EFYRTGKVHRAPGVQEVTEDP RDPLAQLATRDRKERRGSLDH LALRVREAQLDQLVPPESVAA KDLKAPRAPKAPVVPLGSPALR APVGTQAPRAHQAKRDSPALR ALLASRDFRAPLGSLGCLDLGD CQACLGYQACQAPRAPPALLA HQERWCPWPCRMSQPQHRRT MAARLTGRTSQTNATIFQLRKK FLRMQSFSVKTSLHILFS*TLER NSNG
6938	37306	A	6989	91	918	
6939	37307	A	6990	199	380	CSTSSRTY*IPSRCFSKG*HWRH TVNSNFGPMGNPSHPTTSSAHH TVPLIESQPSSTSKK
6940	37308	A	6991	1	483	
6941	37309	A	6992	178	298	
6942	37310	A	6993	864	1298	RLQNRTILASDLSGSDRWRRTY RCL*RHGPRFSSCRLSCRRPFDK TCRLMCHQRLSGFPQEQTQRDS RCIQLLFRQRFAAASCPTHQVH VHRWRKPMVFLILESDLKYTV LSLPEECHTGAHEQSSHCLLLSL ASVDVHCSQRP
6943	37311	A	6995	2	348	KKKRKKKIEEEEEEEEEEEEEE\ REEEGDEEQEEEEE\EEEEEEEE EEEEEEEEEEDDDDDNGLLQTL PGLHEMRVNLTRSDGIISVWHF PFWHFSFLMPYEEGALLRLHLP
6944	37312	A	6996	1	192	
6945	37313	A	6997	1	507	MEKNEKEQEEEEKKEKNSKKK EEEEEEEGGGEEEEEEGEGGEE EEEEEEEEEEEEEEEEEEEEEE EEE/DKEEEEEEEEEEEEEEEE EEEEEEEEEEEEEE\EEEEKVVE EEDEFIWFLGNSLYFPSFSHFA WSQIPSREDEGERRLRVNSMIM DFTSNTNHVQLIVAR
6946	37314	A	6998	1	257	MGPIHKISHYVYANISKSEKVL KSEHFRSQAFQPGQQSETVSEK/ EEEDEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEI
6947	37315	A	6999	1	156	
6948	37316	B	7000	1	757	
6949	37317	A	7001	1	279	

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6950	37318	A	7002	1	1226	MPSSKGVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGIDSNFEPELVFLEFFEALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYTILNQDAQNKSP SAVMSHESDAAHSDSARSSSSK LELSPDVNKIRKSEAMVKEKKK ADKKGEKSARSPSSLSDNLDFS KQDGNTTRQEMSPAGVPLLGM QLNEVKPKKDRQNVQQNE/GC HPIRRVHSDQTHSGKL*RGKGS W/DCMREKASQPFKAVVPIV*V /VPFENLQEGEEGRLCEECPDEP RRVHVAGRSMYEGEVVNGMR NGFGMFKCSTQPVSYIGHWCN GKRHGKVGEVATWRAEKKKK EEEEEEEEEEEEE\EEEEEEEEEE EEEEEEEEEEEEE\EEEEEEEEEE EEEEEEEEEEEEEEEKIRP
6951	37319	A	7003	3	123	
6952	37320	A	7004	2	458	
6953	37321	A	7005	239	432	CLWLFQEEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEEKIFLGHRVGI
6954	37322	C	7006	7	162	
6955	37323	A	7007	39	2154	
6956	37324	A	7008	1	639	
6957	37325	A	7009	1	651	
6958	37326	B	7010	1	684	
6959	37327	A	7011	3	428	TRFQGVYLPLLWEQSF/CWKSPI ALGYTRGHFSALVAMENDGYG NRGAGANLNTDDDVTITFLPLV DSERKLLHVHFLSAQELGNEEQ QEKLLREWLDCCVTEGGVLVA MQKSSRRRNHPLVTQMVEKW LDRYRQIRPCTSLF
6960	37328	A	7012	2	800	

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6961	37329	A	7013	1	930	DHNSSPAMEQNWMENAFDELT EVGFRRWVITNFSKLKEHVLTQ CKEAKKLEKRLEELLTRITSLEK NINDLMELKNTSQELREAYTTE ERISEIEDQLNEIKHEDRIREK/R/ VKRNEQSLQEIWDYVKRPNLH LT/GVPESDGENGTKLENTLQDI IQENFPNLARQANIQIQEIQRTP QRYSSRRATPRHIIIRFTKVEMK EKMLRAAREKGQVTHKGKPIR LTADPLAETLQARREWGPIFNIL KEKNFQHRMSYPAKLSFISVGE IKYFTDKQMLRDFVTTRPALQE LLKDALNMERNNQNQSLQKHA KL
6962	37330	A	7014	1	870	
6963	37331	A	7015	1	585	
6964	37332	A	7016	1	1032	
6965	37333	A	7017	2	770	
6966	37334	A	7018	1	2910	
6967	37335	B	7019	239	462	
6968	37336	A	7020	3	694	
6969	37337	A	7021	1	1212	
6970	37338	A	7022	1	1140	
6971	37339	A	7023	1	570	
6972	37340	A	7024	1	486	
6973	37341	A	7025	1	1476	MEVNREKQLNELEVIGSEEQNL EEEGLMIGGVAVRLVPDDIVIP GGVNATNGTEARDALRVKVA MSVTLLSGIIQYLLSALGWSYY TVDGVSQKNPRALGVTADQLH AIFTTMSDEQASFRFGFVAIYLT EPLVRGFTTAAAVHVFTSMLK YLFGVKTKRYSGIFSVVYSTVA VLQNVKNLNVCSLGVGLMVFG LLLGGKEFNERFKEKLPAPIPLE FFADHNSSPAREQKWMENEFD EWTEVSFRRWVITNSSELKEHI LTQCKEAKNLEKRLEELLTRITS LEKNINDLMELKNTAQEFHEA YTSINS/RNQTEERVSEIEDQLN EI*CKDKIR\EKKRMKRNEQSLQ EIWDCVKRPNLRLTGVPESDGE NGTKLENTLQDIIQENFHNLAR QANSQIQEIQRTPQRYSSRRATP RHIIIRFTKVEMKEKMLRAARE KGRVTHKGNPIRLIADLSADTL QARRQWEPIFNILKENFQTRISH
6974	37342	A	7026	1	1080	

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6975	37343	A	7027	1	3501	MIVYLENPIVSAQNLLKLISNFS KVSGYKIYKIDVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY PGIQLTRNVKDLFKENYKPLLN EIKEDTNKWKNIPCSWIGRINIV KMAILPKVIYRFNAIPIKLPMTS FTELEKTTLKFIWNQKGARIAK TILSKKNKVGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEASEITPPIYNHLIFDKPDKN KKWGKDSLFNKWCWENWLAI CRKLKLDPFLTS
6976	37344	A	7028	164	714	IGVNRHLIQESPSWNLAGAPLE QIFQRKEQAAIFAILQPLLVISRQ TGSGVDPQQTPADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTIINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
6977	37345	B	7029	1	579	
6978	37346	A	7030	1	927	
6979	37347	A	7031	1	1362	MAAGRHLPVGADRHLIQESTG WHLAGAPLGWSFQRKEQTAIF AVLQPLLVIPRQTGYGVDLQQ MPADLQQRFLTVRRKTNKQKG IVSTSTKRTSSEGHQHQRRKVD KFTEMGRNQHKKAENSKNQN ASSP\PKDHNSLPAREQNWTEN EFDELTEIDFRRWVITNSSQTKG SMF*P*CKEAKNLEKRLDELLT RITSLEKNINDPMELKNTAREL REANKSINS*IDQGRKERV\SEIE DQLNEIKREDKIREKRMQRNK QTLQEIWDYVKRPNLHLIGVPE SDRENGTKLENTLQDII\QENFP NLARQANIQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AARKKGQVTHKGKSIRLSADFS AETLQARREWGPIFNILKEKNF QPKISYPAKLSFISEEEITSFTDK QTLRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKM
6980	37348	A	7032	1	598	
6981	37349	A	7033	3	787	
6982	37350	A	7034	61	284	RLLEPQGPLRAGSSPAGK/IGGT LERRGMPWPGP/HSEGGLSPLL LGASLAAAPHGEMPSVRVHPV RPSSRDCSSRV
6983	37351	B	7035	743	1683	

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6984	37352	A	7036	1	1137	
6985	37353	A	7037	1	663	
6986	37354	A	7038	1	197	
6987	37355	A	7039	1	291	
6988	37356	A	7040	3	342	
6989	37357	A	7041	1	439	
6990	37358	A	7042	3	253	
6991	37359	C	7043	1	210	
6992	37360	A	7044	1	165	
6993	37361	A	7045	1	346	
6994	37362	A	7046	1	389	
6995	37363	C	7047	1	464	
6996	37364	A	7048	1	1806	
6997	37365	A	7049	491	1640	
6998	37366	A	7051	188	383	
6999	37367	A	7052	1	759	
7000	37368	A	7053	1	1683	
7001	37369	A	7054	1	972	
7002	37370	A	7055	1	429	
7003	37371	A	7056	3	753	DQTFWGLLETG/S/ELMLIPGDP KCHCGPPVKVGAYGGQEIKGV LAQVQITVGPVGTRTHPVVISP VPECIIGIDILSSWQNPHTGSLTG RVRVIMVEKAKWKPLELPLPR KIVNQKQYCIPGGIAEISATIKD LKDTGVMIPTTSPFNSPIWPVQ KTDGSWRITVDYQVVTPIAAA VPDVVSLLEQINTSPGTWQHIT HLDVLLWRIYQVTQKAASFEW GPEQEKALQQVQAAVQA\LCH LGHMTQQIQWCL
7004	37372	A	7057	2	430	
7005	37373	A	7058	1	1515	

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7006	37374	A	7059	1	1523	MGEERRWRPSSNGKHGAFAEL DKGWLVWLEGKGVIGARRSW RAHSALIKICVQQIKDSLPGKM SKGLLQQQQKPKHLLHDLYKA MSTRWGVQKARLNCTALPPTG CVTLDPSFLTEPQFPRQLSEDLL LTREALEKEVQLRRQLQQEKEE LLYRVLGANASPAFPLAPVTPT EVEKERELELRDRLDEQQRVLE GKNEEALQDPRLVDPLTSCTVH FEKPQMLNARLWKHAGREAV ACKVRGSELPKTMGTYPLHQH DLDVRHGVKGDHFGALRFDCP AGFWTCMGPLAPSFWPISPIWN GPPLDISGYPATSTQKSTMCLRI IDTRLHPESRLKQQSNFALNAR EKALQQVQAAVQAALPLGPYD PADPMVLEVSLADRDAVWSL WQAPIGESQQRPLGFWGKALPS SADNNSPLERQLLARYWALVE TEYLTMGHQVTM*P/ELPIMNW VLSDPSSHKVVYAWQHSIIKW K\DRA*AGLAGTSKLHEEVAQ MPIVSTPATLPSCRIL
7007	37375	A	7060	1	2190	
7008	37376	A	7061	286	430	
7009	37377	A	7062	205	514	LWSLCAPVLQVPCLRAAFPVFT RRHAPSAGRGFTRSYVSAGSW TETQQGLWGSLTKLGADGLLL GISKHLVEFLQIFQISGCWGHYC YLQILFFALNSISPSYHVLLFNV QFGFIFNFMVLCVP*AGTHIAPC KSSSRTRGMSSCENWKGCSKA RHLQYWSTKTPQSLSFFCCGIH FVTAVCQP
7010	37378	A	7063	1	487	
7011	37379	A	7064	1	1212	
7012	37380	A	7066	140	453	
7013	37381	A	7067	1	3341	MGKKQNRKTGNSKNQSASPPP KERSSSPATEQSWMENDFDELR EEGFRLSNYSELPEDIQTKGKE VENFEKNLEECITRITNKRNFKP TKIKRDKEGHYIMVKGSIQQEE LTILNIYAPTGAPRFIKQVLSDR QRDLDFHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHSKSTEYRFFSAPH HTYSKIDHLLGSKAFLSKCKRT EIITNYLSDHSAIKLELRIKNLTQ NRSTTWKLNN
7014	37382	B	7068	1	1785	

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7015	37383	A	7069	1	1141	MVTWNFIQERNGSGMDQCDD GGGKILDPVYILTVELTGFAKG WKMFSVKDQSVNVLGFAGYPL ITQTARKGAGKIPTWASLRQYQ KGLGSKYQLRRALRPDCALGN GQGVRYCNSLDEEEKRELKLFS SQRKRENLGRGNVRPFPVTMT GAICEQCGGQINGGDIAVFASR AGHGVCWHPPCFVCTVCNELL VDLIYFYQDGKIYCGRHHAECL KPRCAACDEIIFADECTEAEGR HWHMKHFCCFECETVLGGQRY IMKEGRPYCCHCFESLYAEYCD TCAQHIGHAGSFIKEC/SRRLLP GEAEI/SRRATVICLVRVSVRPE AASKSPNMRRKRKRKGACPLS SVGPVIPSVP*NTQRT*RPQSRP LGAPWNPWPCLMQ
7016	37384	A	7070	1	2388	VHQYYSCLPEEKVPYVNSPGEK LRIKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSSQRKRENLG RGNVRPFPVTMTGAICEQCGG QINGGDIAVFASRAGHGVCWH PPCFVCTVCNELLVDLIYFYQD GKIYCGRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECETVLGGQRYIMKEGRPYC CHCFESLYAEYCDTCAQHIGID QGQMTYDGQHWHATETCFCC AHCKKSLLGRPFLPKQGQIFCS RACSAGEDPNGSDSSDSAFQNA \GPRSPGAVPKLARTRARR\GAH AEPAQPAASEF*PAVSRRRPPVT ADGHAQPVQPDTQPQPGPHLE EPGRALPLWEQDGAEPDPEPSA AP\RQCNIRTSYSPGGQGAGAQ PEMWGKHFSNPKRSSSLAMTG HAGSFIKECREDYYPGRLRSQE SYSDMSSQSFSETRGSIQVPKYE EEEEEEGGLSTQQCRTRHPISSL KYTEDMTPTEQTPRGSMESLAL SNATGLSADGGAKRQEHLSRFS MPDLSKDSGMNVSEKLSNMGT LNSSMQFRSAESVRSLLSAQQY QEMEGNLHQLSNPIGYRDLQSH GRMHQSFDFDGGMAGSKLPGQ EGVRIQPMSERTRRRATSRDDN RRFRPHRSRRSRRSRSDNALHL ASEREAISRLKDRPPLRAREDY DQFMRQRSFQESMGHGSRRDL
7017	37385	A	7071	1	807	

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7018	37386	A	7072	500	2666	YCLRLAQVGIFPAPSRAWPVDL DPESRLCCFPSLGSLANPTAVG LEEDREQDVGTSSRGGAWDTRI KRELEKMSEKCGGQINGGDIAV FASRAGHGVCWHPPCFVCTVC NELLVDLIYFYQDGKIYCGRHH AECLKPRCAACDEIIFADECTEA EGRHWHMKHFCCFECETVLGG QRYIMKEGRPYCCHCFESLYAE YCDTCAQHIGEAIFGSQLGPSV MRSPLFWGVGIAAAALDAVLIR AHQRTQGCHHELSALLAFEKG SEKKEEEEGGQVSRSSSLKVQA QELSATEDKGHISPFFWEAVYH YASGECRGPGPPYSHSLRLYSQ QALPTGRGPSSSQFPFCQFYCC YKKSLLCDCLSKSPALEKAMR GIDQGQMTYDGQHWHATETCF CCAHCKKSLLGRPFLPKQGQIF CSRACSAGEDPNGSDSSDSAFQ NA\GPRSPGAVPKLARTRARR\G AHAEPAQPAASEF*PAVSRRRP PVTADGHAQPVQPDTQPQPGP HLEEPGRALPLWEQDGAEPDPE PSAAP\RQCNIRTSYSPGGQGAG AQPEMWGKHFSNPKRSSSLAM TGHAGSFIKECREDYYPGRLRS QESYSDMSSQSFSETRGSIQVPK YEEEEEEEGGLSTQQCRTRHPIS SLKYTEDMTPTEQTPRGSMESL ALSNATGTKTCSVTFQAKETCR YQDAQFGKVKARVKERQSLWS
7019	37387	A	7073	1	2239	
7020	37388	A	7074	1	282	
7021	37389	A	7075	2	430	GFGAQDPKSLALRTHCQTSGW/ SLTEQDPYNNVIRTTIEALAATL GGTQSLHTNVFDEALGLPTDFS ARIARNTQIIIQEESELCRTVDPL AGSYGGAIIQQIDVAGGLAKRI EAGLSKRMIEEASAREQALIDQ GKRVIVGVT

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7022	37390	A	7076	1	1561	MVTLILYFRFYRLNGDTLRRIQI HLLDKYRKVPPEPVHADIPVGA RRFSRPCSWFLRITKRGYRRTV HAMAGQKEKLLGAGMSDYLA KPIEEERLHNLLLRYKPGSGISS RVVTPEVNEIVVNPNATLDWQ LALRQAAGKTDLARDMLQML LDFLPEVRNKVEEQLVGENPEG LVDLIHKLHGSCGYSGVPRMK NLCQLIEQQLRSGTKEEDLEPEL LELLDEMDNVAREASKILGPDK THLRRIRRDVLATDPRPARDRR KACLHACVLRTPPLGAARAIIQ QIDEAGGMAKAIEAGLPKRMIE EASAREQSLIDQGKRVIVGVNK YKLDHEDETDVLEIDNVMVRN EQIASLERIRATRDDAAVTAAL NALTHAAQHNENLLAAAVNA ARVRATLGEISDALEVAFDRYL VPSQCVTGVIAQSYHQSEKSAS EFDAIVAQTEQFLADNGRRPRI LIAKMGQDGHDRGAKVIASAY SDLGFDVDLSPMFSTPEEIARLA VENDVHVVGA\SSLAAGRSR
7023	37391	A	7077	1	354	
7024	37392	A	7078	1	1116	
7025	37393	A	7079	1	450	
7026	37394	A	7080	1	252	
7027	37395	A	7081	1	242	
7028	37396	A	7082	1	242	
7029	37397	A	7083	1	9228	
7030	37398	A	7084	3	664	
7031	37399	A	7085	3	718	
7032	37400	A	7086	380	1038	WTRWRASAADNLAHGRWGEQ KLVVTTGASGAPDRQAARCAA SAKISWYRSKGSKHPLTPKEVE KTGWGLKIPG/MGQQQLPERV KEAARILELDGLLKRRPRELSG GQRQRVAMARAIVRDPAVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVEVDGDDTLEIL GADNLAHDAGRAEAGGDWRI RSARRSSTCAH

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7033	37401	A	7087	380	920	WTRWRASAADNLAHGRWGEQ KLVVTTGASGAPDRQAARCGC IWRKISWYRSKGSKHPLTPKEV EKTGWGLKIPG/MGQQQLPERV KEAARILELDGLLKRRPRELSG GQRQRVAMARAIVRDPAVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVE
7034	37402	A	7088	1	258	
7035	37403	A	7089	3	208	
7036	37404	A	7090	34	125	
7037	37405	A	7091	1	393	
7038	37406	A	7092	1	690	MVAPVYIRDQYSALITNIGKGD HTTFVKPNIPATGEFKGVGFLE APRGMLSHWMVIKDGIISNYQ AVVPSTWNSGPRNFNDDVGPY EQSLVGTPVADPNKPLEVVRTI HSFDPCMAWVGNILLTDEAIGV RIVEALEQRYILPDYVEILDGGT AGMELLGDMANRDHLIIADAIV SKKNAPGTMMILRDEEVPALFT NKISPHQLGLADVLSDLRFT\GE FPKKLPWVQA
7039	37407	A	7093	82	224	
7040	37408	A	7094	1	239	
7041	37409	A	7095	1	1062	
7042	37410	A	7096	1	221	
7043	37411	A	7097	1	1067	
7044	37412	A	7098	1	1545	
7045	37413	A	7099	1	2820	
7046	37414	A	7100	1	1223	
7047	37415	A	7101	1	3087	
7048	37416	A	7102	1	1182	MDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKKSPGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTKKENFRPISLMNIDAKILY KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLAQNLLKLISNFNKV SGYKINVQKSQAFLYTSNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRAHIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYCYQNRHIDQWNR\PSEI TPHIYNYLIF

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7049	37417	B	7103	1	1722	
7050	37418	A	7104	1	3513	
7051	37419	A	7105	1	2546	MSELPFTIATKRIKYLGIQLKSD VKDLFKENYKPLLNEIREDTYK WKNTPCSWIGRINIMNMAILPK VIYGFNAILIKLPLTFFTELEKTT LKFTQSLKRAHIAKTILSKKNK AGGIMLPDFKLYYKATVTKTA CTIHNSKDLEPTEMPSNDTLDK ENVAYIHHGILCSHSKGRVHIL CRDMDEAGNHHSRQTNTGTEN QTLHVLTHKWELNDENTWTQ GGEHHISGPVRTNNKNHMIISIG AEKAFDKIQQPFMLKTLNQLGI DGTYLKIIRDIFDRPIANILLNGQ KREASPLKTGTRQGCPLPPLLF NIVLEILARAIRQEKEIKGIQLG KEEVKLSLFADDMIIYLENPIVS AQNLLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQILSELPF TIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPC LSIGKINIMKMAILPKVIYRFNAI PIKLPMTFFTELEKTTLKFIWNQ KRARIAKTILSQKNKDGGITLPD FKLYYKATVTKTAWYQYQNR DIDQWNRTEPSEIIPHVYNHLIF DKPDKNKKWGKDSLFNKWCW ENWLAICGKLKLDPFLTPYTKI NSRWIKDLNVRPKTIKTLEENL GNTIQDIGMGKDFMSKIPKAM ATKAKIDKWNLIELKSFCTAKE TTISVNRQPTEWEKIFAICLSDK GLISRIYKELKQRHKKKTNNPIK
7052	37420	A	7106	1	2575	
7053	37421	A	7107	1	875	
7054	37422	B	7108	1	3421	
7055	37423	A	7109	1	3790	MELKTKARELREECRSLRSRRN QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSSRRATPRHIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE
7056	37424	A	7110	134	307	

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7057	37425	A	7111	2	173	RPPRSEVPGPLSPGRPPAAGLRG R*PAGVRGLREPRAFSGVRVER RSLFIGKDMFDS
7058	37426	A	7112	888	1016	VPGEIHALHSADRQHENA*NAR TRWQHAQSGRSPLFLALSRE
7059	37427	A	7113	573	872	SPSLLPDPDAHVGC*SRSRKRPD RIRRFDSR*NGLFYCRKTS*PFH *G*MCQ*YQTDPRSNAQCHPVL LRLWWPGDEYDFLCRSGSVGS VRQSGRASGL
7060	37428	A	7114	1	654	
7061	37429	A	7115	71	2776	
7062	37430	A	7116	31	1016	TVLPERPYNRKSSRRNRCGNGP PARSFCPSSGRSRRRSSSPATGP/ HTAIASALPRIAFGKISDSSTQH TGPQDMAKAAT*NSLRGSMRY SFKPMVGRWIKSCLRPVWC
7063	37431	A	7117	279	1243	SVLLMCAADYLPRPPDVQTCN AVRVWLRYHRSNHGTPPDFSP GPVSAWYYAH/QPKIPIWSQ/QR GFTD/R*TRHKCPQRFAVPDK*I SSPD*AMNYYRKIHRPAPRHTA PTQKARLMADKSSLRHRHNSA NKRRSASPLSSAGYP/GKRIRAQ NLIPASTTNGQLRIRQRRISQAR **TKRMARKGSISPISAVSNSLN SS*ASIIVSSCIRCSALSPLSNIHK S*TAGPWGASSRKTNIGLSRQRI FPAWQSPCSRRTVKSSRQCAVT AAISSSVAFRNAAFNPEGISVAS SNSLRGSMRYSFKPMVGRWIKS CLRPVWCIRPK
7064	37432	B	7118	1	726	
7065	37433	A	7119	1	138	
7066	37434	A	7120	56	133	
7067	37435	B	7121	1	1524	
7068	37436	B	7122	1	1521	
7069	37437	A	7123	1	1494	
7070	37438	B	7124	4	1698	

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7071	37439	A	7125	1	1725	MELKTKARELREECRSLRSRCD QLEERPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLAKQVN VQIQEIQRTPQRYSLRRATPRHII VRFTKVEMKEKMLRAAREKGR VTLKGKPIRLTADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNRS WFFEKINKIDRPLARVIKKKRE KNQIDAIKNDKEDITTNPTEIQTI IREYYKHLYPNKLENLEEMDTF LDTYTFPRLNQEEVESLNTSITG SEIVAIISIAYQPKKVQDQMDPQ PNSTRVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKCLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTDLEKTTL NFIWNQKRARITKSILSQKNKA GGITLPDFKLYYTATVTKTAW YWYQN\RWYWYQNRDIDQWN RTEPSEITPHVYNYLIF
7072	37440	A	7126	1	2478	

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7073	37441	A	7127	1	1746	METQKTLQKINESRSWFFEKIN KIDRPLARLIKKKREKNQIDTIK NDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEAESLNKPITGPEIEAII NSLPTKKIPGPDGFTAEFYQRY KEELQHIKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMIISIDAEKASDKIQQPFMLK TLNKLGIDGTYLKIIRAIYDKPT ANIILNGQKLEAFPLKTGTRQG CLLSPLLFNIVLEVLARAIRQEK EKKCIRLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQIE SQIMSELPFTIASKRIQYLGIQLT RDVKDLFKENYKPLLNEIKEDT NKWKNIPCSWIGRINIMKMAM LPKVIYRFDAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPDKNKQWG KDSLFNKWCWEIWLAIGRKRK LDPFLTPYTKINSRWIKDFNIRP KTIKTLEESLG\IQDISMGKKFTS
7074	37442	A	7128	1	1908	
7075	37443	A	7129	1	1494	
7076	37444	A	7130	2	1562	
7077	37445	B	7131	1	1569	
7078	37446	A	7132	1	1593	
7079	37447	A	7133	1	1520	
7080	37448	B	7134	1	2796	

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7081	37449	A	7135	101	1686	SIAYQPKRVQDQMDSQPNSTR ANIILNGQKLEAFPLK\TGTRQF SKENFE\PLSPLLFNIVLEVLARA IRQEKEIKGIQLGKEEIKLSLFA DDMIVYLENPIVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKQNYKPRLKE IKEDTNKWKNIPCSWVERIYIV KMAILPKVIYRFSAIPIKLPMTFF TELEKTTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKDT VTKTAWYWYQNRDIDQWNRT EPSEIMPHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLALCR KLKLNPFLTPYTKINSRWIKDL NVRPQTIKTLEENLGITIQDIGM GKDFRSKTPKAMATKAKSDK WDLIKLKSFCTAKETTIRMNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDIN RHFSKEDIYAAKRHMKKCSSSL AIRQMQIKTTMRYHLTPVRMAI IKKSGNNRDMDEIGNHPSQ
7082	37450	A	7136	1364	3024	TEPKTKTT*LSQ*MQKRPLTKF NNASC*KLSIN/IVLEVLARAIRQ EKEIKGVQLGKEEVKLSLFADD MIVYLENPIVSAQNLLNLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNER KEDTNKWKNIPCSWVERINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYSYQNRDIDQWNRTE PSEILPRIYNYLIFDKPEKNKQW GKDSLFNKWCWENWLAICRKL KLDPFLKPYTKIKSGWIKDLNV RPKTIKTLEENLGITIQDIGMGK DFMSKTPKAMATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTER EKIFATYSSDKGLISRIYKELKQI YKKRTNNLIKKWVKDMNRHFS KEDVYAAKKHMKKCSSSLAIR EMQIKTTMRYHLTPVRMAIIKK SGNNRITIVLLPGSLIVRSFHVTL NAILLHPGLTLFSPSAGRRDIPR VAFSYLAFSAQPSHNTPVN
7083	37451	A	7137	1	2274	
7084	37452	A	7138	2	2348	

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7085	37453	A	7139	1	2202	
7086	37454	A	7140	1	2823	
7087	37455	A	7141	1052	3831	RHKKPFKKSMNPGAGFFERINK IDRPLARLTKRKREKNQIHAIK NDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEIESLNRPITGAEIVAII NSLPTKKSPGPDGFTAEFYQRY KEELVPFLLKLFQSIEKEGILPNS FYEASINLIPKPGRDTTKKENFR PISLMNIDAKILSKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIC KSINVIQHINRTKDKNHMIISID
7088	37456	A	7142	1	327	
7089	37457	A	7143	1	446	
7090	37458	A	7144	382	1485	
7091	37459	A	7145	1	378	
7092	37460	A	7146	2	217	
7093	37461	A	7147	1	483	
7094	37462	A	7148	1	1260	
7095	37463	A	7149	1	891	
7096	37464	A	7150	5	182	RQGLLVSPRLVQKGEIRTPGLK RSSRLDLQKC*DYRHEPSSLAS EAPSVWVLLPPWRQS
7097	37465	A	7151	1	1914	

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7098	37466	A	7152	1	2200	MKLTTHRENMALTNGFCHHIA AQQNLYTNTLLAARIKQRLTEQ FELMLRQAQIDFAGKAHSLTEA QANTTQVSAERDRLFKNYQRY LKGSQAAVNPFSERDIDDARQN FLAQDALAQIQSQLDSLVNGEQ SQIVSLKAQLAEAKYNLEQTIV RAPSNGYVTQVLIRPGTYAASL PLRPVMVFIPDQKRQIVAQFRQ NSLLRLAPGDDAEVVFNALPG KVFSGKLAAISPAVPGGAYQST GTLQTLNTAPGSDGVIATIELDE HTDLSALPDGIYAQNPKNLKIV ELKAPQLPRSLDDAQIALAVIN TTYASQIGLTPAKDGIFVEDKES PYVNLIVTREDNKDAENVKKF VQAYQSDEIPCRTRSKHCTPAE SGACKTESAARHAGPNLYQCR RIRSANRSAISVKGWRTPCIPDS LPAVEWLTYGSGYLAGMKLGD TPLVEYTRDRLHRETLRSFGRY ELTTAYTPAGQLQSQHLNSLLS DRDYTWNDNGELIRISSPRQTR SYSYSTTGRLTGVHTTAANLDI RIPYATDPAGNRLPDPELHPDST LSMWPDNRIARDDNYLYRYDR HGRLTEKTDLIPEGVIRTDDERT HRYHYDSQHRLVHYTRTQYEE PLVESRYLYDPLG\RRVAKRVW RRERDLTGWMSLSRKPQVTWY GWDGDRLTTIQNDRTRIQTIYQ PGSFTPLIRVETATGELAKTQRR
7099	37467	A	7153	719	1575	
7100	37468	A	7154	1	239	
7101	37469	A	7155	1	735	FNDDSPEARKITRRWRIGEAAD LVGVSSQAIRDAEKAGR\LP\HP D\MEIRGRVEQRVGYTIEQINH MRDVFGTRLRRAEDVFPPVIGV AAHKELNNDYTSKKVMKPLIT SNTVTDEIERANVLKMNGKWY LFTDSRGSKMTIDGINSNDIYM LGYVSNSLTGPYKPLNKTGLVL QMALDPNDVTFTYSHFAVPQT KGNNVVITSYMTNRGFFEDKK ATFAPSFLMNIKGNKTSVVKNS ILEQGQLT
7102	37470	A	7156	1	4368	
7103	37471	A	7157	1	1452	
7104	37472	A	7158	1	516	
7105	37473	A	7159	1	743	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7106	37474	A	7160	3	1743	DSPE\ARKITRRWRIGEAADLV GVSSQAIRDAEKAGRLPHPDME IRGRVEQRVGYTIEQINHMRDV FGTRLRRAEDVFPPVIGVAAHK GNDPQGTASMYHGWVPDLHIH AEDTLLPFYLGEKDDVTYAIKP TCWPGLDIIPSCLALHRIETELM GKFDEAQPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEPDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTDTSLSTP AAPMVDSLIARVGVMARGNAI TLPVCGRDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTPAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG KYFLRWLMRKIFHIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQQASNLHE QKKAGVIFEAEEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMVLNLDRSRVPTECIEKI EAILKELEKPAP
7107	37475	A	7161	1	438	
7108	37476	A	7162	1	3216	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPG FGDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRL/VKRAPTC WPGLDIIPSC\LALPRIETELMGK FDEGKLPTDPHLMLRLAIETVA HDYDVIVIDSAPNLG
7109	37477	A	7163	1	513	

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7110	37478	A	7164	1	2027	MRGHREKAAACKPRTRASEGT TPASTFILDFQPPNCNYTSGDNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWYLFTDSRGSKMTIDGINSN DIYMLGYVSNSLTGPYKPLNKT GLVLQMGLDPNDVTFTYSHFA VPQAKGILCEEDNYTAGDNHM MRAPHCEEDRAHKFVVFDANA GTESGHQGESSLFNRACGGGGT FFFSKESQKLQQSAKKRDCINA GHEMTKAIAIAQFNDDSPEARK ITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMRDVFGTRLKR AEDVFPPVIGVAAHKGGVYKT SVSVHLAQDLALKGSLLLPKND FLFKLGLEGHLPLGKIHSPPTGA DVARGSSGLPKSELFLPERNTQ ELQQDSEEGPLALQVLQSNLM DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQNNDGIC EIHVAKYVEIFGLTSAEASKDIR QALKSFAGKLVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQRAL QCTYQPISHSLLYRVTEPVYAV
7111	37479	A	7165	1	750	
7112	37480	A	7166	1	723	
7113	37481	B	7167	1	1156	
7114	37482	A	7168	1	999	
7115	37483	A	7169	1	529	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFVAGDEKGYESFPWF IKTCA\HPSRGLYSVHINPYLIPS LSGYRTGLRSFGLVKQKKSPIR MPCVYTNPCVSIVSRMAQASSL
7116	37484	A	7170	1	1038	
7117	37485	A	7171	1	1098	

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7118	37486	A	7172	1	838	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTE TMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGSL PTDPHLMYYYQAPCMKSNNAL IVILGTVTLDAVGIGLVMPV\CR ASCGISSIPTASPVTMACC
7119	37487	B	7173	1	1212	
7120	37488	A	7174	1	738	
7121	37489	A	7175	1	654	
7122	37490	A	7176	1	448	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHK\AGNLSCQLH**IGQR AGRGGLRIGRQGGFSFHQ
7123	37491	B	7177	1	753	
7124	37492	A	7178	1	345	
7125	37493	A	7179	1	516	
7126	37494	A	7180	1	1989	
7127	37495	B	7181	1	1191	
7128	37496	A	7182	1	669	
7129	37497	A	7183	1	574	
7130	37498	A	7184	1	934	
7131	37499	A	7185	1	1281	
7132	37500	A	7186	1	324	
7133	37501	A	7187	3	817	
7134	37502	A	7188	1	587	
7135	37503	B	7189	1	610	
7136	37504	A	7190	1	882	
7137	37505	A	7191	1	1077	
7138	37506	A	7192	1	418	
7139	37507	A	7193	1	840	
7140	37508	A	7194	1	337	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRN\VFGSGLRRPTAELKCA SQT
7141	37509	A	7195	1	1142	
7142	37510	A	7196	1	1080	
7143	37511	A	7197	1	1170	
7144	37512	B	7198	1	1296	
7145	37513	A	7199	1	1179	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7146	37514	A	7200	1	507	
7147	37515	A	7201	1	411	
7148	37516	A	7202	1	793	
7149	37517	B	7203	366	1502	
7150	37518	A	7204	1	1107	
7151	37519	A	7205	1	2388	
7152	37520	B	7206	1	2260	
7153	37521	A	7207	1	1067	
7154	37522	B	7208	563	1467	
7155	37523	B	7209	1	1272	
7156	37524	A	7210	1	1722	
7157	37525	B	7211	1	1917	
7158	37526	A	7212	1	2679	
7159	37527	A	7213	1	1207	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPG FGDFA\HFGNHHQNRIFALLGQ TSVDRLLQLSQGGQAVKGNQLL PVSLVKRKTTLAPNTQTASPRA LADSLMQLARQVSRLESGQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMRDVFGTRLRR AEDVFPPVIGVAAHKGGVYKT SVSVHLAQDLALKGLRVLLVE AARGLKKRGLAGTAQGPGEPG EAPKGKKGKTEPGHERKGNWT GKGPQIREGTSPNPPREHGGEC APPPPSAKRKQPKAQKRKANSN AHPRQPKPKKKRPKRQTNSRTN TRSGKRQNKQPEEPK
7160	37528	A	7214	1	2757	
7161	37529	A	7215	1	2984	

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7162	37530	A	7216	1	2387	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKAKGLTALSPQTDWNR KRNSSKPLAQVQEEDSAWHPE CLQKTRQAWCDNLKTCHTSHG SVMAETAVINHKKRKNSPRIVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNPLTQFRLSE TKEITNPYAMRLYESLCQYRKP DGSGIVSLKIDWIIERYQLPQSY QRMPDFRRRFLQCINAGHEMT KAIAIAQFNDDSPEARKITRRW RIGEAADLVGVSSQAIRDAEKA GRLPHPDMEIRGRVEQRVGYTI EQINHMRDVFGTRLRRAEDVFP PVIGVAAHKGGVYK\TLISVHL AQDLALKGLPGLLR\EGNDPQG \TTSMYHGWVPDLHIHAEDTLL PFYLGEKDDVP\YAIKPTCWAG AWHFFLPCRALHRIETELMGKF DEGKLPTDPHLMLRLAIETVAH DYDVIVIDSAPNLGIGTINVVCA ADVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEPDVFIRD KLMERRNRRTGRTEKARIWEV
7163	37531	A	7217	1	917	

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7164	37532	A	7218	1	1862	MKLMETLNHCINAGHEMTKAV AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAY DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELWGK/FDEGR SFMPGPP/HHHPLGRSSQ*QVSN SLDRAAKGN*KPLCHCPCSGTT HATLRLIKEQRPYVPYAHLQQA VVDPRRGGHMVLI/NVVRVTG DVGKGQIRMRTVVEQAIDQRSS TGAWRNALSIWEPVCNEIFYRL IKPRWEIRWGKRAPVIPKHTLN TQPVEDTSLSTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGEAICPVRMFRMKLMETLN QCINAGHEMTKAIAIAQFNDDS PGSEENNPALENR
7165	37533	A	7219	1	2724	
7166	37534	A	7220	1	3252	FNDDSPEARKITRRWRIGEAAD LVGVSSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVFGTRLRRAEDVFPPFNDDSP EARKITRRWRIGEAADLVGVSS QAIRDAEKAGRSTATRILEIRGR VEQRVGYTIEQINHMRDVFGTR LRRAEDVFPPVIGVAAHKGGV YKTSVSVHLAQDLALKGLRVL LVEGRSFPQTEACLLQYSSWDV SSEKPAALNKNKSEMRGDFAD FGTTIKQDFRLLGQT
7167	37535	A	7221	1	465	
7168	37536	A	7222	1	291	

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7169	37537	A	7223	1	1710	MLCTKWDKLGLEKNAGKNKN AYKWYGWPANAPDEPHIEQLV GECRVMRQLKRLISRIAPSPSSV MVVGESGTAIPVVSHAEFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDFGYLEFEGGANFSWGEM YGFFDWENFYNGRHNKPGSEQ RYTFKNTNRIYLGDTGFNLYLH AYGTYGSANRVNFHDDM\FLA GFGFQF*PAGGW/WGSNPFFAK\ RYTRSKPYYT\GDNGYV\AGWV AGYNFMLGSEKFTLTNWNEYE FDRDATYAADFLPLYDVDCQD NGNLEYDTYSQPEWKHNLFDH YLAVLYRFKDESGKEQFSGAV VKTREATPGKEIEAITRRMLDFS PRLKKLADCPSPRPVFEALCICS MLDALLLLCPLDYHASCDNYS YALLDPQGFPLPHRRLWGPYID VDVPMLHLIQHAWAQDALLSC LYSDLLYMSSFPYPAGTLTRLM GVTSYNHKNTLLTYCITLMSTI RFAYDGDEEIAMKYTDFLKGE LSMNIRPLHDRVIVKRKEVETK SAGGIVLTGSASAKSTRGEVLA VGNGRILENGEVKPLDVKIGDI VFFNDGYRGEI
7170	37538	A	7224	678	1588	RTQHKASLHGRASAFCPPRLFA PQAPRLFDHRGFLTFASANFAA VAFCPPRLFPPTGAAAVCPLPLF APRRFLPPPPPRLFRCHGFFPPC LGFLTSAAFFLPPPRLFALRRRG FLPFAAAAAFFPTRLFAPPPTQL FAPSPPWLFAAAAFCPPWLSAP TPPRLFVPAAAAFCCRDFLPPSP PLFRHRDFLPPPPRIFVPAAAAL RAGAADSAAGSTGVLGQDLWS RCVVGTGMEAPGSRGGGGGLR EDIPLPPEFPSGPALSSCR*GNRR PEGEMTCQEPLLS/CSWIP*VKE FETNPDNIVRPH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7171	37539	A	7225	1	1627	MTKQLELPQSPGEVPGSDYPLL IACAYIGFLTWGGGFSGSMPLL AATPGNPVEHIAGLIPVGDTLFS GFNIFITVALIVVMPFITRMMMP KPSDVVSIDPKLLMEEADFQKQ LPKDAPPSERLEESRILTLIIGAL GIAYLAMYFSEHGFNITINTVNL MFMIAGLLLHKTPMAYMRAIS AAARSTAGILVQFPFYAGIQLM MEHSVTGIEAAMLDLLGQHLG VNVASLLGDGQQRSEVEMLGY LFFVGNRKATPLPYQSQPDDSC DWYRLRHEEAMTPDAVVRLAE AAYEKYGFNDFKLKGGVLAGE EEAESIVALAQRFPQARITLDPN GA\WSLNEAIKIGKYLKGSLAY AEDPCGAEQGFSGREVMAEFR RATGLPTATNMIATNWREMGH AVIAQ\SVDIPLADPHFWTMQG SVRVAQMCHEFGLTWGSHSNN HFDISLAMFTHVGAAAPGNPTA IDTHWIWQEGDCRLTQNPLEIK KGKIAVPDAPGLGVELDWEQV QKAHEAYKRLPGGARNDAGP MQYLIPGWTFDRKRPVFGRH
7172	37540	A	7226	3	655	
7173	37541	A	7227	1	633	
7174	37542	A	7228	1	630	
7175	37543	A	7229	362	1491	PTLSVIHESMRFFIRHQPENLTL VVLSRNLPQLALPICVFVINCW KLAVSNWHLPISTGCAVTKDG RWSPEFTITGQA/WDLPVVGYR NGVAQPLRLWQATHAHPFDLT KFNDGDFLRAEQQGINAEKLTK VLYPNDNHTAGKKLRLMQQYF QCACSVADILRRHHLAGRKLH ELADYEVIQLNDTHPTIAIPELL RVLIDEHQMSWDDAWAITSKT FAYTNHTLMPEALERWDVKLV KGPLPRHMQIINEINTRFKTLDL QDAEHRPLKMRGCLLCQCHTL FQGKHRFFTGAGGNRQNNVIE HLVAASRYRFTTASRRPLFTAG FTLLTAFLFHSNFAEGVNSLMF MKNLTISGGFLLLAITGPGAYSI DRLLNKKW
7176	37544	A	7230	1	660	

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7177	37545	A	7231	545	1322	KHAEHLGQATHAHPFILTKFNP GYFL\RRQTTRGINAEK\LAKIFF \PKANHFAGKKLRLMQQYFQC ACSVADILR\RHHLAGRKLHEL ADYEVIQLNDTHPTIAIPELLRV LIDEHQMSWDDAWAITSKTFA YTNHTLMPEALERWDVKLVKG LLPRHMQIINEINTRFKTLVEKT WPGDEKVWAKLAVVHDKQVH MANLCVVGGFAVNGVAALHS DLVVKDLFPEYHQLWPNKFHN VTNGITPRRW\IKQCNPALAALL
7178	37546	A	7232	641	874	KYPTPGRDLRMFITGLSERL*EI TSLLKRSITGDKYSLRPLTANSV TSVTHFSFGRVALKSLSSVRAV SLDLNRCFK
7179	37547	A	7233	1	693	
7180	37548	A	7234	980	1305	TWLRICSIRHSKSLILTSI/HVLH SDQGWQYRMRRYQNILKEHGI KQSMSRKGNCLDNAVVECFFG TLKSECFYLDEFSNISELKDAVT EYIEYYNSRRISLKLKGSDSN
7181	37549	A	7235	1	3219	
7182	37550	C	7236	1	7521	
7183	37551	A	7237	1351	2117	CDRILCSACCAEPQPVSHLHRL RRSFSERQPDGNGSQNPASRDR/ DVVDVTVIAWIEHRGGHEAPS GPGEDGMDAPAIAAGTFSPREA STLPVQVS*VCRLNCCSRDVPK ATRVPL/EKLAGPLRHPLFMLF QTCLHLSLFTHHFADDSRRLQIF SVGFVAGLKQQYRRDLLQGDV NPRMATAVGNDQVWFQSGNG FQARLRARSDGLPRFQVRTHFG QDAFCIVIVGNTDRDDVHGGQ RIGEREFQHHNPLWRFFEC
7184	37552	A	7238	690	868	

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7185	37553	A	7239	2607	3692	TWLRICSIRHSKSLILTSI/HVLH SDQGWQYRMRRYQNILKEHGI KQSMSRKGNCLDNAVVECFFG TLKSECFYLDEFSNISELKDAVT EYIEYYNSRRISLKLKGLTPIEY RNQTYMPRVNCPLFDTLRIPDI GGVVRARAIAKLLNDTDMAIID KRRPRANVSQVMHIIGDVAGR DCVLVDDMIDTGGTLCKAAEA LKERGAKRVFAYATHPIFSGNA ANNLRNSVIDEVVVCDTIPLSD EIKSLPNVRTLTLSEKYTAARFT RDLIAGITVGIIAIPLAMALAIGS GVAPQYGLYTAAVAGIVIALTG GSRFSVSGPTAAFVVILYPVSQ QFGLAGLLVATLLLGDLFDSDG
7186	37554	A	7240	1326	3930	NVLRGISAAFFVG*AKAPRNGT Q
7187	37555	A	7241	3	195	RVDDFVGGAGAPASPGL*QCG QLQKLIGISIGSLRGLGTKCAVS NDLTEQEIRTLEHCPNSFF
7188	37556	B	7242	75	402	
7189	37557	A	7243	1	309	
7190	37558	A	7244	3	187	
7191	37559	A	7245	383	1778	
7192	37560	A	7246	2	447	IREKLIRLQHENKMLKLNQEGS DNEKIALLQSLLDDANLRKNEL ETE/Q*VLVPINFPLTTAFAVSH RFRLVNQRLLEVQSQVEELQKS LQDQGSKAEDSVLLKKKLEEH LEKLHEANNELQKKRAIIEDLE PRFNNSSLKIEELQEALR
7193	37561	B	7247	80	1042	
7194	37562	A	7248	1	192	
7195	37563	A	7249	3	62	
7196	37564	B	7250	219	230	
7197	37565	A	7251	246	594	
7198	37566	A	7252	1	316	
7199	37567	A	7253	1	1059	
7200	37568	A	7254	1	516	EDALEQEKKELQIQVEHYEFQT RQLELKAKNYADQISRLEERES EMKKEYNALHQRHTEMIQTYV EHIERSKMQQVGGNSQTESSLP GRSRKERPTSLNVFPLADGT/CT CTDRGQARACGGPLAPE*PRPA AVQLQLPGFVAVPWSERLLPV AGVPRSLGREPRLQAALHGS
7201	37569	A	7255	1	1176	
7202	37570	A	7256	1	749	
7203	37571	A	7257	1	691	

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7204	37572	A	7258	2	810	VMMTGYNNGRCPRNSLYSDCII EEKTVVLQKKDNEGFGFVLRG AKADTPIEEFTPTPAFPALQYL\ ESVDEGGVAWQAGLRTGDFLI EVNNENVVKVGHRQVVNMIR QGGNH\LFLKVVTVTRNLDPDD TARKKAPPPPKRAPTTALTLRS KSMTSELEELVDKASVRKKKD KPEEIVPASKPSRAAENMAVEP RVATIKQRPSSRCFPAGSDMNS VYERQGIAVMTPTVPGSPKAPF LGIPRGTMRRQKSIGKKCGTPP QKLPLGFQTQP
7205	37573	A	7259	1	1416	
7206	37574	A	7260	2	1142	
7207	37575	A	7261	1	576	
7208	37576	A	7262	21	289	
7209	37577	A	7263	2	372	
7210	37578	A	7264	170	655	VRRRILGALFTWICSVTRESTSK PLSSALLSAKLLHRARSRTGLS GRNPKTISQDLQFAAIGSPLTES LNLHSRQALRDCCWTHTIPPNP *ICTHARR/WRDCCWTHTIPPNP DTVWRFPLSSPVSAAPKQERAS SEPCSWSHWCRCSLSWLSSIPTE GCTPVCSSICLLMATFPMFSLIK IVR
7211	37579	A	7265	1	1725	
7212	37580	A	7266	307	686	PRRTPMKSCKIKEVPIFVFPLRT TRENCLRPIKGYAIYEKAPRSIL KDVHLTRNQCVPIPDRYKWWS WQVCRRPKQWGWTQGPVAPK RSAEFFAAHA*KRRRVMLNLR GLDVDSLVIEHIQVNKAP
7213	37581	A	7267	1	276	
7214	37582	A	7268	1	726	
7215	37583	A	7269	3	231	
7216	37584	A	7270	1	217	
7217	37585	A	7271	3	283	KRKTEGDAKGDKAKVKDESQR RSARLSAKPAPPKPEPKPKKAP AKKGEKVPKGKKRKADAGKE REGYWRSQVKCIHFL*LYFW*L YSLKYYFI
7218	37586	A	7272	1	1188	
7219	37587	A	7273	5	365	
7220	37588	A	7274	1	453	

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7221	37589	A	7275	1	441	RQPAHPGTSSAAAAPRKRSAAA HAGVAVAASARLPPCAGCGLR AAPPLLASSARLRALRRP\GGL WAAGCAPAAGQLCTAAGSAAP GALQRCGGRHGITRPWCAEIAS AG*GSGGSRWGCWPCPCLLRT CTSHPLSSPLPFTHGSLQASFSL TRDCVSSTKTLWVWLEVQR
7222	37590	A	7276	2	1957	
7223	37591	A	7277	1	678	
7224	37592	A	7278	1	720	
7225	37593	A	7279	190	2947	QALQRGLLSR/DRAPCSSKLSW RS/SPRRRAGTGPVQEEVALKP VLLRHPVQPVIRVKLPRICLLEE AGQLRGVHRLESVEEYYEADG AEWGPPDTAMLESLPEMAGKH SLPQLLDSSSASQPGAIQIIYS\IL YQIHYLKHLLSSYWGASQWKH TRHTHYFESLW*EHLPS*KYQK REKWADLTRSLENP\GQQPRDS WEPSGFWALPQAGDSCQTSQSP RKPTGPPKPSPPPEEGRLLR/CPT MPVMRKSLTE
7226	37594	A	7280	3	439	
7227	37595	A	7281	1	273	
7228	37596	A	7282	2	1664	
7229	37597	A	7283	1	7511	
7230	37598	A	7284	1	5046	
7231	37599	A	7285	42	8716	
7232	37600	A	7286	2	201	
7233	37601	A	7287	2	797	CS/GSPPTCRQAQTSLEVALYM FLQNPDTEAVLVAMSCFCHLCE EADTQCGVDEVSVHNLLPNSN TFMEFACQQCDVNSPPVGPVSE HKGSMISVMSSEGNADTPVSK YMDQLLSLMVCNLEKVGLQIP TNDKDLVLLTDTNTQFVEQTL DIMKNLLDNHTEGSPEHLEQAS IETMMLNLVRNKMVEYLTDW VMGTSNQAADDDVKCLTSRI/D HPGGTLL*GQPRPELPAGLPRQ PASPGPRHPGASCGWPRAPPDS APGGPGRER
7234	37602	A	7288	56	8669	
7235	37603	B	7289	278	2333	
7236	37604	A	7290	1	423	

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7237	37605	A	7291	2	1688	PLYFHSPPAWLCSPSPPSARLYL ELRKLPATLPWSSVTDTGSYSA GRRERGGEGEGRGRRVRVADH RSALPRTGPQGSEEELANMQGL \VERLERAVSRLESL\SAESHRPP GN\CGEVNGVIA\GVAPSRGKPL HKLMDSMVAEF\LKNSRILSGD VETLAEIVHSAFQAQRAFLLMA SQYQQPHENDVAALLKPISEKI\ KEIQTFQRE/RTRGSNMFNHLSA VSESIPALGW\IAVSPKPGPYVK EMNDAATFYTNRVLKDYKHSD LRHVDWVKSYLNIWSELQAYI KEHHTTGLTWSKTGPVASTVS AFSVLSSGPGLPPPPPPLPPPGPP PLFENEGKKEESSPSRSALFAQL NQGEAITKGLRHVTDDQKTYK NPSLRAQGGQTQSPTKSHTPSP TSPKSYPSQKHAPVLELEGKKW RVEYQEDRNDLVISETELKQVA YIFKCEKSTIQIKGKVNSIIIDNC KKLGLVFDNVVGIVEVINSQDI QIQVMGRVPTISINKTEGCHIYL SEDALDCEIVSAKSSEMNILIPQ DGDYREFPIPEQFKTAWDGSKL
7238	37606	B	7292	44	355	
7239	37607	A	7293	1	3623	SEKEKEELERLQKEEEERKKRL QLYVFVMRCIAYPFNAKQPTD MARRQQKISKQQLQTVKDRFQ AFLNGETQIMADEAFMNAVQS YYEVFLKSDRVARMVQSGGCS ANDSREVFKKHIEKRVRSLPEID GLSKETVLSSWMAKFDAIYRG EEDPRKQQARMTASAASELILS KEQLYEMFQNILGIKKFEHQLL YNACQLDNPDEQAAQIRRELD GRLQMADQIARERKFPKFVSKE MENMYIEELKSSVNLLMA
7240	37608	B	7294	1	1555	
7241	37609	A	7295	1	1056	
7242	37610	B	7296	54	2173	
7243	37611	A	7297	1	984	
7244	37612	B	7298	95	1350	

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7245	37613	A	7299	1	2569	MDGAKAFFSAVAAGFVIILTCQ LQWQWQHGGVHAHQLWQLA SGYRDACFCVSTYSSGPSEFPGP TLGTLNELAIDLEERKHRRKAK VWKGEGGGLRSPRQSLLAFRA VLASRGTRSCHVSPYLGVSGAL SSPNPHPSTTGAGPIPPVQRWGL PQINQKNREIAIPLTLGMSTHLR RGCKNMSRFSPSLHCCTTPISTN FTDPGSHCKGAHGDICLLIQNL KGALPMSINRSYFNAHPLLQISE AVTFKDVAVVFTEEELGLLDPA QRKLYRDVMLENFRNLLSVGN QPFHQDTFHFLGKEKFWKMKT TSQREGNSGGKIQIEMETVPEA GPHEEWSCQQIWEQIASDLTRS QNSIRNSSQFFKEGDVPCQIEAR LSISHVQQKPYRCNECKQSFSD VSVFDLHQQSHSGEKSHTCGEC GKSFCYSPALHIHQRVHMGEK CYKCDVCGKEFNQSSHLQTHQ RVHTGEKPFKCGQCGKGFHSRS ALNVHCKLHTGEKPYNCEECG KAFIHDSQLQEHQRIHTGEKPF KCDICGKSFRVRSRLNRHSMVH TGEKAFRCDTCGKNFRQRSAL NSHSMVHIEEKPYKCEQCGKGF ICRRDFCKHQMVHTGEKPYNC KECGKTFRWSSCLLNHQQVHS GQKSFKCEECGKGFYTNSRRSS HQRSHNGEKPYNCEECGKDYK RRLDLEFHQRVHTGERPYNCK
7246	37614	A	7300	2	326	
7247	37615	A	7301	166	443	

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7248	37616	A	7302	1	2692	MDPGTLQSASQGPTAINPCDYV LKRRNIQTSWQRLTPIIKWHVYI LMIGPGEKEAGRNLGIFGKWTP FPKIPAKRLRESNCPVDAQEIW LPQAFREYLGRRGNFGPGRRTC EFWEVESICSVESWELWLRQA DSGDSGKCSPDACGIIDTSGLR AGHCYLTRLWHVSGRIPPSFKL HHPGVCKFPKVGGKMTTFKEA VTFKDVAVVFTEEELGLLDPAQ RKLYRDVMLENFRNLLSVGHQ PFHQDTCHFLRE\EKFWMMGT ATQREGNSGGKIQTEMET\VPE AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNPSQIKA RLSIIHVKTETSEGRTCKKSFSD VSVLDLHQQLQSREKSHTCDEC GKSFCYSSALRIHQRVHMGEKL YNCDVCGKEFNQSSHQQIHQRI HTGEKPFKCEQCGKGFSRRSGL YVHRKLHTGVKPHICEKCGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRHSMVHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKRFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVHSG ETTFKCEECGKGFYTNSQRYSH QRAHSGEKPYRCEECGKGYKR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGEK PFKCEECGKRFTQNSQLYTHRR
7249	37617	A	7303	1	585	KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAP/ASTQSVLADG TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRG/RL MKTV/TQGSQQPSLADPASHLP VGDHLTYSNETEPVRALLPDEK KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREFE EQFFKQTGRSPQKEDRIPMADE YY
7250	37618	A	7304	1	366	

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7251	37619	A	7305	1	1265	RYRPGIPGSTISSLVEEHAPPSW EPQHQNVEATVLVDSVLRPSM GNFKSRKPKSIFKAESGRSHGES QETEHVVSSQSECQVRAGTPAH ESPQNNAFKCQET\VRL\QPRID QRTATSPKDAFETR\QDLNEEE AAQVHGVKDPAPASTQSVLA\D GTDSADPSPVHKDGQNEADSA PEDLHSVGTSRLLL/YHITDGDN PLL\SPRLFPLSGQSQRFNLDPES APSPPSTQQFMMPRSSSRCSCG DGKEPQTITQLTKHIQSLKRKIR KFEEKFEQEKKYRPSHGDKTSN PEVLKWMNDLAKGRKQLKEL KLKLSEEQGSAPKGPPRNLLCE QPTVPRENGKPEAAGPEPSSSG EETPDAALTCLKERREQLPPQE DSKVTKQDKNLIKPLYDRYRII KQILSTPSLIPTIVSQDTCMLLLC
7252	37620	A	7306	797	1390	PRMGARPRAPAAQPPPAAAQR PPARPATPTACGSSAHRAPSPA RSRRSPCTPRAAPAAPGPKAAR QWAGTATRSSRPQRSARRSPRD SSRCWAISSRSKRAATACTPGA KRRVATKARGALWSKPKSKA MRLWPWCLSGRLGS*KAQEVA QDPGSDEGRGRLVESGLQDEG WVPQGGEGGVAGQDASHRGSF RGALK
7253	37621	A	7307	605	697	
7254	37622	A	7308	1	1263	
7255	37623	A	7309	257	1190	
7256	37624	A	7310	394	485	
7257	37625	A	7311	21	674	
7258	37626	A	7312	277	396	GLLPGWKI*CSRVFVTSAIHVE VAELEANLPCTCKVHFPDPNKL HCFQLTVTPDEGYYQGGKFQF ETEVPDAYNMVPPKVKCLTKI WHPNITET
7259	37627	C	7313	74	316	
7260	37628	C	7314	211	390	
7261	37629	A	7315	1	2601	
7262	37630	A	7316	1	1365	
7263	37631	A	7317	358	760	SIPLLFRKSSLSRK*CSAASIFSG SSKFKRSVNKEFNPQTTSFNVL VGAQPVPSIECSLNKLRHISPVS VIVGVPDSLVQAFHFGRHHVV RIRELQFQTEIFHPGSNPHLGLL LAENNEACLDQENALYMYKV
7264	37632	A	7318	1	1728	
7265	37633	A	7319	1	558	

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7266	37634	A	7320	2	1884	PAGAGPGQEAGAGPGPGAVAY ATGAEEGEMKPVAAGAAVPPG EGISAAPTVEPSSGEAEGGEAN LVDVSGGLETESSNG\KDTLEG AGDTSEVMDTQAGSVDEENGR QLGEVELQCGICTKWFTADTFG IDTSSCLPFMTNYSFHCNVCHH SGNTYFLRKQANLKEMCLSAL ANLTWQFRTQEEHPKTMFSKD KDIIPFIDKYWECMTTRHRPGK TTWPNNIVKTMSKERDVFLVK EHPDPGSKDPEEDYPKFGLLDQ DLSNIGPAYDNQKQSSAVSTSG NLNGGIAAGSSGKGRGAKRKQ QDGGTTGTTKKARSDPLFSAQR LPPHGYPLEHPFNKDGYRYILA EPDPQAPDPEKLEIDCWAGKPIS GDLYRACLYERVLLALHDRAP QLKISDDRLTVVGEKGYSMVR ASHGVRKGAWYFEITVDEMPP DTAARLGWSQPLGNLQAPLGY DKFSYSWRSKKGTKFHQSIGKH YSSGYGQGDVLGFYINLPEDTE TAKSLPDTYKDKALIKFKSYLY FEEKDFVDKAEKSLKQTPHSEII FYKNGVNQGVAYKDIFEGVYF PAISLYKSCTVSINFGPCFKYPP KDLTYRPMSDMGWGAVVEHT LADVLYHVETEVDGRRSPPWE
7267	37635	A	7321	1	267	
7268	37636	A	7322	60	888	RGAALARTRLSVRPVGPAGTRR SHALGPRPGARSSFRLRCELRR CMCGNNMSTPLPAIVPAARKA TAAVIFLHGLGDTGHGWAEAF AGIRSSHIKYICPHAPVRPVTLN MNVAMPSWF\DIIGLSPDSQED ESGIKQAAENIKALIDQEVKNGI PSNRIILG\GFSQGGALSLYTALT TQQKLAGVTALSCWLPLRASFP QGPIGGANRDISILQCHGDCDPL VPLMFGSLTVEKLKTLVNPAN VTFKTYEGMMHSSCQQEMMD VKQFIDKLLPPID
7269	37637	A	7323	1	1182	

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7270	37638	A	7324	1	2469	MVDRARPTVLVTEVPLKSKHT AQMGLVLTANESQPLVHETAL KNKKPQSWFPNPCVSYNRKPG LQD*GRAERPELGEQATEAALL KAPAESVRQEHRSTNT/PQTRSC CPQYFPRAGCLPSRGHDVEPQH EAGDGPCRGIRNG*KLLSSFFG QQVRT**R/CSELTPKQEFFKGS ESSNRTSGGLFGVVPGAAETGD VCVYTFKELEGQTSDEEGSRLE NDFLEITDEDKKKSTKDRYDKY KEVGEHPPLSSSPVEHEGVLKG QKSYRCDECGKAFNRSSHLIGH QRIHTGEKPYECNECGKTFRQT SQLIVHLRTHTGEKPYECSECG KAYRHSSHLIQHQRLHNGEKPY KCNECAKAFTQSSRLTDHQRT HTGEKPYECNECGEAFIRSKSL ARHQVLHTGKKPYKCNECGRA FCSNRNLIDHQRIHTGEKPYECS ECGKAFSRSSGLISHHRVHTGE KPYSCIECGKAFNQNSQLIEHQ RMHRGKKVYKCKECGKAFGLS KCLIRHQRLHTGEKPYKCNECG KSFNQNSHLIIHQRIHTGEKPYE CNECGKVFSYSSSLMVHQRTH TGEKPYKCNDCGKAFSDSSQLI VHQRVHTGEKPYECSECGKAF SQRSTFNHHQRTHTGEKSSGLA CQEGNKEISKGPQKPPGYRLCP LQAVGGGEFGPTRVHISFSLSD LKQIKVFFPGGPLMLEKQKKKS
7271	37639	A	7325	1	1596	
7272	37640	A	7326	2	3394	MAHAGGGSGGSGAGGPAGRG LSGARWGRSGSAGHEKLPVHV EDALTYLDQVKIRFGSDPATYN GFLEIMKEFKSQSIDTPGVIRRV SQLFHEHPDLIVGFNAFLPLGY RIDIPKNGKLNIQSPLTSQENSH NHGDGAEDFKQQVPYKEDKPQ VPLESDSVEFNNAISYVNKIKTR FLDHPEIYRSFLEILHTYQKEQL NTRGRPFRGMSEEEVFTEVANL FRGQEDLLSEFGQFLPEAKRSLF TGNGPCEMHSVQ
7273	37641	A	7327	1	738	
7274	37642	A	7328	1	399	
7275	37643	A	7329	3	223	
7276	37644	A	7330	1	1040	
7277	37645	A	7331	1	465	
7278	37646	A	7332	1	288	

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7279	37647	A	7333	109	4770	
7280	37648	A	7334	109	4687	
7281	37649	A	7335	109	4860	
7282	37650	A	7336	1	336	
7283	37651	A	7337	1	441	
7284	37652	A	7338	305	446	
7285	37653	A	7339	2	461	
7286	37654	A	7340	59	620	FQKIGL**/FIDLKDGLFTIPLAE QDCEWFAFTIPVVNNLQPAKRF HCFTDGSNNGKASYSGSKNKV FQMSYTSAQKAELVAVIELIEN AQLRFHTDEQLMTLFTQLQTA VRSRMHPFYITHIRAHTPLPGPL TEGNQMADRLVANAISSARHF QQHLL/THSHPPGDRSRSCHRW RKKLEESGTSSHE
7287	37655	A	7341	1	1410	
7288	37656	A	7342	1	1740	MGQVWALVHSTLETFHTDEEE GEYNEVTEQVCLPAKAGSAAV DLCCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQIVTS TSVPWKAKPGDHIAQLLIVPKK F\EGLKEPLQVERQSSCQGLGY/ PFLMAAIVKPPEPIPLKWLTDKP IWTEQWPLSKEKLEALEDLITQ QLKKGHIAPTFSPWNSPVFIIKK KSAEQDCEWFVFTILAVNNLQL KPAKRFHWKVLPQGPNQQPIWI PSRYLKPYHKPDAKEEIPEGSQ GFPVAAMSRLTLRRTPTVTSNT HRTQPPTWGQIEKLPQMAEENL RKAGQPVTISNWILPRITKFKPI EGAENVFTDGSSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIIQRCPTCQVMLSAAE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKIPGESRGPPVAAMSRLTLR RMPTVMSNTHRTQPPTWGQIK KLSQMAEENLRKAGQPVTMNN LMIAVITTAFNKG
7289	37657	A	7343	1	1239	

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7290	37658	A	7344	1	777	MPQNSLEECALELGKKSLQEN VNNFPKTKLFQFLKLTNWILPKI TKFKPIEGAENVFTDGSSNGKA SYFGLKGKVFQTPYTAAQKVE LVAVIEVLTAFDMPVSMISDST YVVHSTQLTENAQLRLHTDEQ LMTLFSQLQTAVR\CFAVMGIP ASTTT/DNAPGYTSQALATFFS MWNIKRITGIPYNSQGQAIVER MNLSLKQQLQKQTEGDREYGT PQMQLNLALLTLNFLSLPKGQ MLSAAEQHLQKPAVKTEAEQLI
7291	37659	A	7345	1	1307	
7292	37660	A	7346	1	2040	
7293	37661	A	7347	1	1898	MAGAPPPAWLPHCSSISDCCAR NERGSVGVAPSKPARSAAVDL CCTKAVSLLPGEPPQKVPARVC GPLPAGTVGLLLGRSSLSLKEV QIHTGVIDSDYKVEIQIVVSTSV PWKAEPGERIAQLLVVPYVGT GKSEIKQTEGFGSTNKQGKAAY WVNQITDKHLTCEITIQGKKFK GLVDTGADVSIISLQHWPSMWP IQSTQFNIVGVDGSSNGKASYF GSKCKVFQMPYTSAQKVELVA IIEVLTTFDMPINVISDSSYVVHS TQLIENAQLQFHTDEQLMTLFT QLQTAVRSRMHPFYITHIRAR\H TPLPGPLTEGNQMADCLVATA VSNARHFHNLTHVNASGLKCR YSNTWKAAKAIIQRRPTCQMV HSSSFTGGVNPQGLEPNSLWQ MDVTHVPSFGRLAYVHVCVDT FSHFVWATCQSGESSACVKHH LLQGFVVMGIPASIKTDNVPGY TSQALATFFSMLNIKRITDIPYN SQDVEADANADVGVDVDADA DVDAEEEVFTDADADAEVDVD EDADAERLRCNADEDSDLDLD VDAEMDADVDTNLDVDAAVD VDVDADADVDADTDVDVDTG LNLEADLDLDVDADVDTDADV DRDADVEVAVDADATVNADV DYVDVDTDSD
7294	37662	A	7348	2	565	
7295	37663	A	7349	1	996	
7296	37664	A	7350	18	260	
7297	37665	A	7351	1	594	
7298	37666	C	7352	232	603	
7299	37667	A	7353	1	1236	
7300	37668	A	7354	568	1370	

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7301	37669	A	7355	1	1800	
7302	37670	A	7356	1	498	
7303	37671	A	7357	1	3400	MDCSEKWRDPLDAVCVLPATE EPVVQGSALYLVAHHDDYCV WYSLQRTSPEKNERVRQMRPV CDCQAHLLWNRPRFGEINDQD RTDRYVQALRTEIPLTLKGAKL QREEKEGDMPCRANILVTELFD TELIGEGALPSYEHAHRHLVET SLGEQVIVPPVDVESCPGAPSV CDIQLNQVSPADFTVLSDVLPM FSIDFSKQVSSSAACHSRRFEPL TSGRAQVVLSWWDIEMDPEGK IKCTMAPFWAHSDPEEMQ
7304	37672	A	7358	1	687	
7305	37673	A	7359	1	660	
7306	37674	A	7360	112	474	
7307	37675	A	7361	352	441	
7308	37676	B	7362	1	831	
7309	37677	A	7363	460	612	
7310	37678	A	7364	251	496	LFVSI/WQVFH*GRRGFLLVRN DCVQIWCEMISHSGFDLHFSDG Q*/WMSISSC/DFLAA*MSSFEK CLFMSFAHFLMGLFVFFL
7311	37679	B	7365	1	729	
7312	37680	A	7366	1	774	
7313	37681	B	7367	1	516	
7314	37682	A	7368	10	504	
7315	37683	C	7369	520	1656	
7316	37684	B	7370	1	1206	
7317	37685	A	7371	677	1126	AVTLTTKVCSFTPEASETTNPPG GTNNSRRTALRAVALTAKVRS FTPRGSAASFLKSVRPRTHQFRT Q*HVHQIEFSPGGLWESCPRAS SSTGDPGRPPERRGAAARKTVG VQGVGYSLPRKLCPLFSRTTYP HTSLRKDCLESDTTAE
7318	37686	A	7372	2	394	HLFIYLLVVLLWCPGWPQTAG LKGSSCLSLLSNWNYRPPL*AL LLGTQKLPRVWNFIMVRRIQDG VKPSVSIAEREMKSRKSAASLL SQRDHEPTRRKKLRTHPNIRRN KLQTRHLKSCNTHCEGPWRHS
7319	37687	A	7373	1	204	
7320	37688	A	7374	1	879	
7321	37689	A	7375	139	4488	
7322	37690	A	7376	1	933	
7323	37691	A	7377	335	582	VLQLLRQHVWSCSFLLVGSWS HWLQERSCRSSQ*VLQLIKAV WTQRTQEPSWLHLVDPAPGLQ VELPASPTRYAHTPQPLGG

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7324	37692	B	7378	1	3101	
7325	37693	A	7379	365	625	VAKIFSHVVGCLFTLMVVSFAV QKLFSLIRSHLSILAFVAIAFGVL DMKSLPTPMS*MVMPRFSSRVF MVLGLKFKSLIHLELIFV
7326	37694	A	7380	994	1167	NKGGHKQMEEHSMLMDRKNQ YRENGHTAQGNL*IQCHPHQAT NDFLHRIGKNKLASNM
7327	37695	C	7381	143	3529	
7328	37696	B	7382	54	1158	
7329	37697	A	7383	1662	1919	LLNVFALAFLVLLIEMLGCQFW IFPAFSCRHLVL*ISLYTLL*MRP RDSGMWCLCSRWFQRTSLFLA SFRYVPSSHSGAGCSVSM
7330	37698	A	7384	63	1650	SPGHI*SSV*REIYSTKCPQEKA GKI*NSHPNITIKRTGEARANTF KS*QKARNN*DQSRTEGDRDT KNPSKNQ/CNPGAGFLKRSTKLI DR*QD**RRK*RRIK*T**KMIK GI/VTTDPTEIQTTIREFYKHFYA NRLKNLEEMDEFLETYTLPRLN QEEVESLNRPITGSEIEAIINSLP TKKSPGPDGFTAEIYQRTNDKN HMIISIDEEKAFDKIQQPFMLEM LNKLGIYGMYIKIIRTIYDKSTA NIILNVQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLARAIRQEKEI KGIRLRKEVFKMFLFADDMIVY LENPIISAPNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIATKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALNAKTILSQKNK AGGIMLPDFKLPYKATWYWNQ NTEIDQWNKTEASEITPHIYNHL VFDNPDKNKK
7331	37699	A	7385	392	493	
7332	37700	A	7386	1	1223	
7333	37701	A	7387	386	553	KMIKGISPLIPQRYKLPSENTINT STQIN*KI*KKWIHSSTHTPSQD* TRKKLNL
7334	37702	B	7388	285	1581	
7335	37703	A	7389	1	1473	
7336	37704	A	7390	755	1042	SSYATKKEPALPSQSEAKKTKL ETSCYLTSNYTTRLQ*PKQHGT GTKTEI*ANGTEQSPQK*YHTA TTIWSLTNLTKTRNGERIPYLIN GVGKTG
7337	37705	C	7391	1	2334	

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7338	37706	A	7392	1	1539	
7339	37707	B	7393	1	2361	
7340	37708	A	7394	5071	5535	GTAFLWRRRGALRFRVSSFSVL FFPHLCGFIYFWSLMMVMYRC VFGVDVLSVC*FSF*QTGPSAA GLLEYPAV*GVSVPLLGGASQL GCSGVRGQGPT*GGSLPVLRSP AACWENHCSLQSCQTGTFKSA EVTAVFLFVCALPPEVEPTEAG
7341	37709	A	7395	1	459	
7342	37710	A	7396	3	1063	
7343	37711	A	7397	39	895	
7344	37712	A	7398	2	277	
7345	37713	A	7399	34	845	
7346	37714	A	7400	1	3399	
7347	37715	A	7401	1	3126	
7348	37716	A	7402	1	387	
7349	37717	A	7403	1	3578	RDLVVGCGGFVKSDVEINYSLI EIKLYTKHGTLKYQTDCAPNN GYFMIPLYDKGDFILKIEPPLGW SFEPTTVELHVDGVSDICTKGG DINFVFTGFSVNGKVLSKGQPL GPAGVQVSLRNTGTEAKIQSTV TQPGGKFAFFKVLPGDYEILAT HPTWALKEASTTVSVTNSNAN AASPLIVAGYNVSGSVRSDGEP MKGVKFLLFSSLVTKEDVLGC NVSPVPGFQPQDESLVYLCYTV SREDGSFSFYSLPSG
7350	37718	A	7404	34	460	
7351	37719	A	7405	105	245	VSSEKVSLGVPCPAASAAASGD ASR*MATGRGGGGGGVAALPE SAP
7352	37720	A	7406	1	1289	
7353	37721	A	7407	462	5250	
7354	37722	A	7408	714	887	
7355	37723	A	7409	1	109	PLRQLLCVKRGFC*HH*HEGCQ SRLLLRCLLCSTAI
7356	37724	A	7410	1	1845	
7357	37725	A	7411	192	1507	
7358	37726	A	7412	2	688	
7359	37727	A	7413	1	518	
7360	37728	A	7414	1	276	

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7361	37729	A	7415	984	3112	MWQETFFRMENLQLIIILILGSP SQLHFPVIRNNQGWTLYHQWP HFLNRFSSRLSNSSLLNQLKFTC ANCKKPLQKGQTAYQRKGSAH LFCSTTCLSSFSHKPAPKKLCV MCKKDITTMKGTI/VLAQVDSS ESFQEFCS\TSCLISL/YEEQQNP TKG\ALNKSRCTICGKLTEIRHE VSFKNMTHKLCSDHCFNRYRM ANGLIMNCCEQCGEYLPSKGA GNNVLVIDGQQKRFCCQSCVSE YKQVGSHPSFLKEVRDHMQDS FLMQPEKYGKLTTCTGCRTQC RFFDMTQCIGPNGYMEPYCSTA CMNSHKTKYAKSQSLGIICHFC KRNSLPQYQATMPDGKLYNFC NSSCVAKFQALSMQSSPNGQFV APSDIQLKCNYCKNSFCSKPEIL EWENKVHQFCSKTCSDDYKKL HCIVTYCEYCQEEKTLHETVNF SGVKRPFCSEGCKLLYKQDFAR RLGLRCVTCNYCSQLCKGGAT KELDGVVRDFCSEDCCKKFQD WYYKAARCDCCKSQGTLKERV QWRGEMKHFCDQHCLLRFYCQ QNEPNMTTQKGPENLHYDQGC QTSRTKMTGSAPPPSPTPNKEM KNKAVLCKPLTMTKATYCKPH MQTKSCQTDDTWRTEYVPVPIP VPVYIPVPMHMYSQNIPVPTTV PVPVPVPVFLPAPLDSSEKIPAAI EELKSKVSSDALDTELLTMTD
7362	37730	A	7416	1	1071	
7363	37731	A	7417	88	2118	
7364	37732	A	7418	2	2930	
7365	37733	A	7419	1	1677	
7366	37734	A	7420	172	13329	
7367	37735	A	7421	2	946	
7368	37736	A	7422	255	933	WIEAAPQAQEVQGDGLWLPCG AAGAGGLQSARSYGTVGEASV AEHPW/CAPGGCMAGCGSLAA AASPGLVPGHLP/QPTAAPSHPH RASLRVALLSGQWGLTCGQLL ASAPLLQSWAWDTRLLMCRRL SCSSEEGERIAQLLLLPYLKLGS STVKRTGGFGNTNPAGKAVYW VNQVSDKRPICTVAIQGKDFEG LVDTEADVSIIAINQWPQHWPK QKASIGIVGVGAA
7369	37737	A	7423	718	2385	
7370	37738	A	7424	1	180	

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7371	37739	A	7425	1	1713	
7372	37740	A	7426	1	774	
7373	37741	A	7427	2	158	
7374	37742	A	7428	1	174	
7375	37743	A	7429	252	1245	ELGECGCRQGSVSHCGRGSRPL LPRVRGKRHLPRARLARCQEAL SPWGFCRFRNHHQTGFSLAGA NQRGPLAATLSGPGGEGQSAV ARLMGEKKNHPGAQYATRLSP RVGRFINAAGTTGFPTGKRAPT CWPGAD\IIPSCLALPRIETELM GKFDEGKLPTDPHLMLGLAIET VAHDYDVIVIDSAPNLGIGTINV VCAADVLIVPTPAELFDYTSAL QFFDMLRDLLKNVDLKGFEPD VRILLTKYSNSNGSQSPWMEEQ IRDAWGSMVLKNVVRETDEVG KGQIRMRTVFEQAIDQRSSTGA WRNALSIWEPVCNEIFDRLIKPR
7376	37744	A	7430	1	1113	
7377	37745	B	7431	56	1234	
7378	37746	A	7432	667	1048	LLLFRDLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPW\MEEQIRDAARFPV GKPVVPAALMNRPTRRGEAVC VLGARVVFLFTSETGNS
7379	37747	A	7433	1	1428	
7380	37748	A	7434	1	1125	
7381	37749	A	7435	1	756	SDRRYEWDRGPSLIIRPTIRVGP WSQTNNQTDDTSGTVV/RRPFP PVIGVVFHKGGVYKTSVSVHL AQDLALKGLRVLLVEGNDPQG TASMYHGWVPDLHIHAEDTLL PFY\DPHLMLRLAIETVAHDYD VIVIDSAPNLGIGTINVVCAADV LIVPTPAELFDYTSALQFFDMLR DLLKNVDLKGFEPDVRILLTKY SNSNGSQSPWMEEQISDALRIS QRRNISSKFILQSACITLTTFIST CWAIIVTQSG
7382	37750	A	7436	1	1329	
7383	37751	A	7437	1	1185	
7384	37752	A	7438	1	1065	
7385	37753	B	7439	67	1033	
7386	37754	A	7440	1	1192	
7387	37755	A	7441	1	1413	
7388	37756	A	7442	1	1176	
7389	37757	A	7443	1	1302	
7390	37758	B	7444	1169	3356	
7391	37759	A	7445	14	3974	

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7392	37760	A	7446	677	1033	RATASSISTTRPCESTSNAPSCN SPIRSRSPLPIIRPRASITLILVSM MRMVRATISCAILVSRCQPAISP PLCTAFFRPICAAGVPVFTLFTT TP*SLPLLLISAPSMPLKMELES T
7393	37761	A	7447	1558	1748	CSNASARFFAAVNPSGLGMILM *SRFIVFTKLSAIPLLSGLRTAVF FGSSPNIRANWRVSLAR
7394	37762	A	7448	1	595	LKNSKPQVVMAAAGIFLIMCG VWLGFGGVLDPTKSSGYLIVDI YNEIICMLSNRIAGLGLSIMAVG GYARYMEGTPASRAMVSLLSR PLKLIRSPYIILSAT*VIGQIMP\Q FITSASGLGMLLMVPLFPTLVSL GVSRLSAVAVIATTMSIEWGIL ETNSIFAAQVAGMKIATFFCHA HNPVASRVILSVAISGTRAR
7395	37763	A	7449	1	978	
7396	37764	C	7450	32	316	
7397	37765	A	7451	1	2465	
7398	37766	A	7452	1	1416	MIILIDAEKAFDKIQQPFMLKTL SKLGTDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILP\R DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFHKWC WENWLAVCRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLKSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL

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7399	37767	A	7453	3	2272	RSTRQKVNKDTQELNSALHQA DLIDIYRTLHLKSTEYTFFSAPH HTYSKIDHILGSKALLSKCKRTE IITNYLSDHSAIKLELRIKNLTQ NRSTTWKLNNLLLNDYWVHN KMKAEIKMFFETNENKDTTYQ NLWDTFKAVCRGKFIALNAHK RKQERSKIDTLTSQLKELEKQE QTHSKASRRQEITKIRAELKEIE TQKTLQKINESRSWFFERINKID RPLARLIKKKREKNLIDAIKND KGDITTDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYTLPRL NEEEVESLNRPITGAEIVAIINSL PTKKSPGPDGFTAEFYQRYKEE LVPFLLKLFQSIEKEGILPNSCY EASIILIPKPGRDTTKKENFRPIS LMNIDAKILNKILAKRIQQHIKK LIHHDQVGFIPGMQGWFNIRKS INVIQHINRAKDKNHMIISIDAE KAFDKIQQPFMLKTLNKL/DIGR NYCKVHMEPKKSPHRQVNPKP KEQSWRHHTT*LQTILQGYSNQ NSMVLVPKQRYRSMEQNRALR NNAAYLQLSDL*QT*EKQAMG NGFPI**MVLGKLASHM*KAET GSLPYTLYKNQFKMD*RLKR*T *NHKNPRRKPRHYHSGHRHGQ GLHV*NTKSNGNKSQN*QMGS N*TKELLHSKRNYHQSEQATY KMGENFHNLLI*QRANIQNLQ* TQTNLQEKNKQPHQKVGKGHE
7400	37768	A	7454	1	3020	
7401	37769	A	7455	1	3046	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
7402	37770	B	7456	197	1917	
7403	37771	B	7457	1	1954	

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7404	37772	A	7458	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGIDGTY FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSEITPHIYNYLIFD KPDKNKQWGKGSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGMDFMSKTPKAMAT KDKIDKWDLIKLKSFCTAKETT IRVNRQPTKWEKIFTTYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSPSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCW\WINWMKKTWH IYTMEYYASIKKNEFMSFAGA* MKLETII
7405	37773	A	7459	1	1713	

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7406	37774	A	7460	281	2882	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPQRYSSRRATPRHIIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASIILIPKPGRDTTKKE NFRTISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSINVIQHINRTKDKNH VIISIDAEKAFDKIQQLFLLKTL NKLGIDGTYLKIKRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLARAIRQEKEI KGIQLGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTETQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIMKMAILHK VIYRFNAIPIKLPMTFFTELEKTT LKFTWNQKRARIAKSILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFFTPYTKINSRWIKDLNVRPKT
7407	37775	B	7461	1	2633	
7408	37776	A	7462	3	1336	

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7409	37777	A	7463	2	2458	SWFFEKINKIDRPQARLIKKKRE KNQIDTIKNDKGDITTDPTEIQIT IREYYKHLYANKLENLEEMDK FLDTYTLPRLNQEEVESVNRPIT GSEIEAITNSLPTKKSPGPDGFT AEFYQRYKEELVPFLLKLFQPIE KEGILPNSFYEASIILIPKPGRDT TKKGNFRPISLMNIDAKILNKIL ANQIQQHIKKLIHHDQVGFIPG MQG\WLEVLARA/IRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PTVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCSWIGRINIVKMAILPKVI YTFNAIPIKLPMTFFTELEKTTL KFIWKQKRSHIAKSILSQKNKA GDITLPDFKLHYKATVTKTAW YWYQNRDIDQWNTTEPSEIML HIYNHLIFDKPDKNKQWGNDS LFNKWCWENWLAICRKLKLDP FLTSYTKINSRWIKDLNVRPKTI KTLEENLGNTIQDIGMGKDFMS KTPKAVATKAKIDKWDVIKLK SFCTAKETTIRVNRQPTEWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSSLAIREMQI KTTMRYHLTPIRMVIIKKSGNN RAPGGRGGCGCSFGRLKRSCVP ALKRVADLPAQRSSSAKGETAS
7410	37778	A	7464	2	2101	
7411	37779	A	7465	196	792	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTLLHCWLDCKLVQPL WKSVWRFLRDLELEIPFDPAIPL LGIYPNEYKSCCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVQ SLVG/TWVNWETTFSVTIAVQK PTRLSH
7412	37780	A	7466	3	610	
7413	37781	A	7467	1	1986	

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7414	37782	A	7468	965	4421	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFFSAPHHTYSKI DHILGSKALLSKCKRIEIITNYLS DHSAIKLELRIKNLTQSRSTTW KLNNLLLNDYWVHNEMKTEIK MFFETNENKDTTYQNLWDAFK AVCRGKFIALNAYKRKEERSKI DTLTSQLKELEKQEQRHSKPSR RQEITKMRAELKEIETQKTLQKI NESSSWFFERINKIDRPLARLIK KKREKNQIDT
7415	37783	A	7469	1	1674	MGQLQRNARDLQESVMSIRM MPMEYVFSRYPRLVRDLAGKL GKQVELTLVGSSTELDKSLIERI IDPLTHLVRNSLDHGIELPEKRL AAGKNSVGNLILSAEHQGGNIC IEVTDDGAGLNRERILAKAASQ GLTVSENMSDDEVAMLIFAPGF STAEQVTDVSGRGVGMDVVKR NIQKMGGHVEIQSKQVTGTTIRI LLPLTLAILDGMSSLLTHGIGQF ADVACAGPLLAAELDALGKAL KEPARPMVAIVGGSKVSTKLTV LDSLSKIADQLIVGGGIANTFIA AQGHDVGKSLYEADLVDEAKR LLTTCNIPVPSDVRVATEFSETA PATLKSVNDVKADEQILDIGDA SAQELAEILKNAKTILWNGPVG VFEFPNFRKGTEIVANAIADSEA FSIAGGGDTLAAIDLFRIADKNS YISTGGGAFLEFVERLTTLTQLL HDQGYVTQAIGKWHMRETTEP QPQNVGFDDFRGFNSVSDMYT AWRDVHVNPEVALSPDRPAYI NQSPLSKDDVHALRGGDQQAI AD\ITPKYMADLDQRCTEYGAQ LLDKMAKSA
7416	37784	A	7470	1	3360	
7417	37785	A	7471	2	543	
7418	37786	A	7472	1387	1805	QAIAFDVQPGRGDYAGNQRHH NQYNQHQAH*SWQRCGIGDGL ARFARHNATKPANKPGETGDR FNHQKNHGGQQDPVLHQLIEV MLVGRGGDQAVGQATLGIDTN VGLHAKV/LTDCLSWSDASPDR VAALCSWSSWVPQ
7419	37787	A	7473	4088	4228	SPPSA*VKALPGPKHHGGLKPV HPIPGASLVLARRWSMFRRWG LIT
7420	37788	A	7474	332	538	

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7421	37789	A	7475	1	1983	
7422	37790	A	7476	856	964	
7423	37791	A	7477	1	1563	
7424	37792	B	7478	1	1086	
7425	37793	A	7479	372	886	
7426	37794	A	7480	2028	2368	RPPGNSLNVSRMGTRSSYSCRR HSPAFLSWGKGRCHLCNKAHL LAGA*HYSFLSGSAPY*N*VNG QI**R*TAHRSTPDAPTGH*NCC S*L*CHSY*QRA*PGYRHD*CR MCC
7427	37795	A	7481	146	402	LGFLLRLSEMPRKQGDYRTRI/C EIRGRVEQRVGYTIEQINHMRD VFDRRYEWDHGPRLIIRPTIRVG PWSQSDYQTDDTSGTVVPD
7428	37796	A	7482	3	149	
7429	37797	A	7483	5	753	ARKVVAVAARHKCPA/CISFSA SHRLYRYWEEEMNPAPVEAMR TFQQFIDEGNYTSGDTHTLRDP HYVEDKAHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDGINSNDIYML GYVSNSLTGPYKPLNKTGLVLQ MGLDPNTNIQTDDTSGTVVQT NNQTADTSGTMVPD
7430	37798	C	7484	182	709	
7431	37799	B	7485	1	1488	
7432	37800	A	7486	2	1034	YLISQRGLIRRSKISLQTGSQIER AFLQAPVEER*SMACSK/YSSHP DLTFTNFIRFTYNIF*NHASPGIP NLLLHPRGLRAITIAVFGKQNT YIRLEPFKINVLEQITKHIEKLQC G/ECSQTTQQAWEQSAHQQHIR H*SCRYPG*ARCQ*VHQARTL* DQRS*ADHEAYRKTAVRRCSQ TTQQAWEQSAHQQHIRH*SCR YPG*ARCQ*L*HHSHEQQFQWP VG/CIRCGSVGSLPSS\ICPLTQF QYGAEPDRKE*CQAPASKWAL LHK*HRPFPQDRKAGECLLHEY EDLVPIRDTLRLFPGGRYLPRA KHVAPSEPDPTIRVGPWSQSDY QTDDTSGTVVPD
7433	37801	A	7487	2	426	
7434	37802	A	7488	138	346	RWRLQNLSFCSSC/SRIWL*RGY VFCSWKPREQSSQSPLACSAAC LTLRTQSCLGTAGQTDDTSGT MVQY

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7435	37803	C	7489	1	1290	
7436	37804	A	7490	48	439	HHHSGLDD/HRRKILNTAYRSR KLQASC*KSAERAWKTKASLT VNGWMKKIRCKTPMCRPTVR* SIRILIITTPLPRVPSRS*LKPPTS CT*CIFTQPTRC*KMTTCWRCS TSRKSSGHVCVSPGSVAVTI
7437	37805	A	7491	1126	1340	KARWMLQTRKRAVRRSNWRK RNIWCAPAAICKRSTTLITSF*K PVKMACPFICAMLRRSRLARRC AGALPN
7438	37806	A	7492	12	960	
7439	37807	A	7493	1	1806	
7440	37808	B	7494	1	1318	
7441	37809	A	7495	1	1385	MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNSIDS WKNAGRVFKDSDKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHYGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGE RKTYQNVQQFIDEGNYTSGDN HTLRDPHYQNTYIRLEPFKINVL EQITKHIEKLQCGGVVKQLSRR GNNQHISSTYDINRADTQVRRA VNNYDIIVMSNSFNGQSEHQV WIDRKAGECLLHEYEDLVPIRD TLRLFPGGRYLPRAKHVAPSEP DPEQDEQKLSCCTYRKRYRVL VGELGDEQMAALSRLGNDYRP TSAYERGQRYASLLQNEFAGNI SALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAF*SASPDRADSSPG*EKRATT D/SRQFGGVDTAGNNLT*NIFRI SQRRNISSKFILQ*ACITLTTFIST CWAIIVTQSG/LMQPSAHHPAR QPEHDIAFGKCSSSVSVHLA/LG SGSEGATCFARGR*RPPGNSLN VSRMGTRSSYSCRRHSPAF\HRS TPDAPTGH*NCCS*L*CHSY*QR A*PGYRHD*CRMCC
7442	37810	B	7496	1	3597	
7443	37811	A	7497	1	666	
7444	37812	A	7498	1	738	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7445	37813	A	7499	1	727	MKVLIVESEFLHQDTWVGNAV ERLADALSQQNVTVIKSTSFDD GFAILSSNEAIDCLMFSYQMEH PDEHQNVRQLIGKLHERQLNVP VFLLGDREKALAAMDRDLLEL VDEFAWILEDTADFYRRTAPVA RE*TRYPPGSCWPPLF/TAPLMK YS\DIHEY\SWAAPGHQGGVGF TKTPAGRFYHDYYGENLFRTD MGIERTSTAVSLLDHSGAFGQS EKYAARVFGADRSWSVVVGTS GSNRTI
7446	37814	A	7500	1	744	
7447	37815	A	7501	1	250	
7448	37816	A	7502	1	850	
7449	37817	A	7503	1	1085	GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQIKEEDVLK FLAAGTHLGGTNLDFQMEQYI YKRKSDGIYIINLKRTWEEL\LR QPRA\MVPIENPAD\VSVISSR\N TGQVCGTVRAV\LRFLAATGAT PIGG\RFTPGTF\TN\QIQASLPGS PRAFLWVT*PPGAEPPALSRSAS LC*PFLPLALVNPD/SPLRRYVII AIPCNNKGAH\SVGLMWW\ML AREV\LRMRGTISREHPW\EVM PDLYFYRDPEEIEKEEQAAAEK AVTKEEFQGEWTAPAPEF/TLA TQPEVADWSEGVQGAPLVP\IQ QFP\TEDWSAQPATE\DWS*A\P LAQATEWVGATTDWS
7450	37818	A	7504	1	1053	
7451	37819	A	7505	2	654	
7452	37820	A	7506	674	805	TLMQKSSIKYWQTESSSTSKSL STMIKWASSL*REIYSTKCPQEK AGKIQN*HPNITIKRTRKARANT FKS*QKARNN*NQSRTEGNRDT KNPSKN**/MPGAGFLKGSTKLI DR*QD**RKKERRIK*/IAIKNDK GDITTNPTEIQTTIREYYKHLYA NKLENLEEMHKFLDTYTLPRLN QEEVESLNRPITGAEIV\E*SIAY QPKKVQDQMDSQANSTRGTRR NWYHSF*TIPINRKRGNP*TLM QKSSIKYWQTESSSTSKSLSTMI KWASSLGGKAGSIYANQ

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7453	37821	A	7507	1	1577	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDIYRNLHP ESTEYTFFSAPHHTYSKIDHILG SKAPLSKYRRSEIKINCLSDHSA IKLELRIKKLTQNRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLLARLIKKKR EKNQIHAIKNDKGDMSTNHTEI QTTIREYYKHLYANKLENLKEI DKFLETYSLPRLNQEEVESLNR PITGSEIEAIINSLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNIPCSWVGRINIVKMAIL PKNWKKTTLKFIWNQKRARIA KSILSQ/IEQSWRHHAT*LQTILQ GYNNENSMVLVSKQRYRSMEQ NRALRNNATYLQPSDL
7454	37822	A	7508	58	330	FTENDDFQFHPCPYKGHELIIFY GCIVFHGVYVPHFLNPVYHCW TFGLVPSLCYCE*CRNKHTCAC VFIAA*FIVIWVYTQ*WDGWVK WYF
7455	37823	A	7509	1246	1522	DCLGNAGSFLVPYELGHYGHF HNIDSSYQ*AW\MFFHLFVSFFI SLSSGL*FSLKRSFTSLVSWIPR YFILFEAIVNGSSLMIWLSVCLL
7456	37824	A	7510	140	577	YSMVYMCHIFLIQSIIVGHLGW FQVFAIVNNVTINIRVHVSL*QH DL*SFGYIPSNWMAGSNGISSSR SLRNRHTVFHNG*TSLQSHQQC KSVPISPHPLQHLLFPDFLMIAIL TGVRWYLIVVLICISLMASDDE HFFMCFLAA
7457	37825	A	7511	399	677	NQREQRHNIPESLGRIQSSV*RE IYSTKCPQEKAGKIQN*HPNITI KRTRKARANTFKS*QKARNN* NQSRTEGNRDTKNPSKNQ*IQE LVF
7458	37826	A	7512	1446	1855	IYKLPWAVWPFS*Y*FFLPMS/G GVFFHLFVSSFMSLSSGL*FSLK RSFTSLVSCIPRYFILSEAIVNGS SLMIWLSVCLLLVYKNACDFCT LILYPETLLKLSISLRRFWAETM GFSRCTIMSSANRDNLISSFRN

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7459	37827	A	7513	1	2982	
7460	37828	A	7514	5202	5430	
7461	37829	A	7515	2	454	
7462	37830	A	7516	2	744	
7463	37831	A	7517	1	2422	MCPILREHRGSTEGKRRQKRLP LELTLKDEEVLAHRQEIEVAKA SPSKGNIIIHFGYKGVEYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKLELTKAEK HVHNFMMDTQLTKRHCPWAA TIQPKLSFLISLPGCDYRGESAR ARPLSHPPLQLGLGKDARYLRI CDRSLLCVCAAAGNAGLRPRD SPHTLLHWRSRSPYFFSPKPVPP QLLGGQPAAHSRRDDLGEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPAPGQGDVMPIVLVRPT NRTRRLDSTGAGMGPSSHQQQ ESPLPTITHCAGCTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPPP RSSHLHCQQQQQSQDKPCPPFA PLPHPHHHPHLAHQQPASGGSS PCLRCNSCASSGAPAAGAGDNL SLLLRTSSPGGAFRTRTSSPLSG SSCCCCCCSSRRGSQLNVSELTP SSHASALRQQYAQQSAQQSAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHHPHPAHHQH HQPQARRESNPFTEIAMSSCRY NGGVMRPLSNLSASRRNLHEM DSEAQPLQPPASVGGGGGASSP SAAAAAAAAVSSSAPEIVVSKP EHNNSNNLALYGTGGGGSTGG GGGGGGSGHGSSSGTKSSKKK NQNIGYKLGHRRALFEKRKRLS
7464	37832	A	7518	1	579	

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7465	37833	A	7519	1	1184	MSSANRSILEVPHLDILLQELPG VSKVVTVEVRGNWQRWLKVR DLTKGVTYFFRVQARTITYGPE LQANITAGPAEGSPGSPRDVLV TKSASELTLQWTEGHSGDTPTT GYVIEARPSVFGNGSFQVSKEE NQYFSEGLTSIEVPSQQVQQEG AVAMALMVPDEGLWDMFVKD IPRSATSYTLSLDKLRQGVTYEF RVVAVNEAGYGEPSNPSTAVS AQVEAPFYEEWWFLLVMALSS LIVILL\VVFALVLHGQNKKYK NCSTRQGISTMEESVTLDNGGF AALELSSRHLNVKSTFSKKNGT RSPPRPSPGGLHYSDEDICNKY NGAVLTESVSLKEKSADASESE VSVGAYFRAVTISPYFCKDAGF AVRTIALGLAETAGSKADARK
7466	37834	A	7520	1	1347	
7467	37835	A	7521	512	1051	MAYCKSTPAVGLRVTV*SLSRL SLICYTFCIGAPSHLSVGSLIIAT SFIVSNRPCRAPYVDTIYRLPSP LRLAGHRTLPLKPSFPRRSPPLL YYPSPRPPAHYPLSPSSEPNRRY TMALTAVPYPYTSPLQAFPFLH SRIPQLQLFLLTNSFTSRTPVEP VQVLEILSQWKATTKWHYG
7468	37836	A	7522	352	546	
7469	37837	A	7523	1	360	
7470	37838	A	7524	3	349	
7471	37839	A	7525	1077	2142	SAVRYSVAITTADRRTAAGAIS YPTK*S*SEPIQEGQPEEQ/RAN YPNGTYPTSLRHLERLWLRSAL SVKARF/YHQQYSLKKYRYKHI ADNVCQWLDEVFLRPKEMSDI HKLTFIEKRERLKNSVFKSLHD VRTVEDPSGTQLEVVSNNPWD PKRQLLKWDGTKWTGWDIPD YSAAPPEAVPSLNNPQTFSEQK LDEALYHGAVLRVRPKAMTVA VIIAGLLPILWGTGAGSEVMSRI AAPMIGGMITAPLLSLFIIPAAY KLMWLHRHRWLKCKSARRPQ YQSGYTDDRHSRSVKASPTAG LPSLTHEQQQKAVERIQELMAQ GMSSGQAIALVAEELRANHSGE RIVARFEDEDE

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7472	37840	A	7526	116	191	RLKFTETNLYTNIYVGSIHIHLN LEIIHMSLH**MDRTNINIRVQIC FCEFKSLVLLDKPGRQELIDDL NKRTDNFLTDSGISVSDWIDAA TWEVFSSLRELELLGIKNIRLAS QDLHGVILSSETVAEDIWCRILD TVTRKGEHSRRIHSADDKSYLR PDLLEWFKQRVEDDQSRSGRKI YVKRDLPHILTPFRAPMASVCA KRKGQVLHQQYSLKKYRYKHI ADNVCQWLDEVFLRPKEMSDI HKLTFIEKRERLKNSVFKSLHD VSEFLGRVLLHATDPAAPRKPA YSLHAIRGKSRGRKNS
7473	37841	A	7527	1	177	
7474	37842	A	7528	1	399	
7475	37843	A	7529	3	209	
7476	37844	A	7530	1	288	
7477	37845	A	7531	2	256	
7478	37846	A	7532	414	1188	TSFLTTGGKKGS\KKKVVDPFS KKD/WL*YVKHPAMFNIRNIGK DVGSPRTQGTKIAS\DGLKG\RV FE\VSLADLQHDEVAFRKFKLIT \EDVQGKNCLTNFHGMDLT\RD K\MCSMVKKW\QTMI\EAH\VD VKTT\DG\YLLRLFCVGF\TKKR NNQIGKPF*AQ\HHRVRQIGKK MMEIMTREVQTNDLKEVVNKL IPDSIGKDIEKACQSIYPLHDVF VRKVKMLKKPKFELGKLMELH GEGSSSGKATGDETGAKVERA
7479	37847	A	7533	1	1140	
7480	37848	A	7534	131	410	
7481	37849	A	7535	1	861	
7482	37850	A	7536	1	406	MWEILELPRDLLNGFAQNADS NMDNKVQAEVALDGNGELVG YYSKASAGDTQANRVWSGPPA NSNRPAAEGPERNTININKKDIN TKTPSVGHRHQRPKVDKTTKT R\KTRAEKLKILKTRVPLIFQRT AALRQR
7483	37851	A	7537	1366	1629	TQSPVQTKPTPITTRGGGFLPTQ PFPVILQRQFCPE*LVAFMGS*E DVP*GSFRVSAESSIL*RAP*GA QSTCKPVNRNEKISKRIVH
7484	37852	A	7538	502	648	

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7485	37853	A	7539	1	1169	PPLLIPRQTGSGVDLQQTPTDLQ LRVLTVRRKTNKQKGHPHQNSI CTSPSSKTKDFKPTKIKRDKEG HYIMVKGSIQQEELTILNIYTPN TGAPRFIKQVLRDLQRDLDSHT IIVGDFNTPLSTLDSSKRQKVDK DIQELNSALYQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCNRTEIITNCLSDHS AIRLELRIKKLTENRSTTWKLN NLLLKDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTGKAAC RGIFIAINAHKRNQKRSKMDTL TSQLKELEKQEQRHSKASRRLN QEEVESLNKPRTGSEIEAIINSLP TKKSPGADGFTAEFYQRYKEE/ PGTIPSETIPINRKRGNTP*LIL*G QHHPDTKA
7486	37854	A	7540	1	404	MDEFLNTYTLPRLNQEEVESLN RPITGSEIVAIINSLPRKKSPGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTIKENFRPISLMNIDAKILN KIILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAFDKIQQP FMLKTLKKFGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKKWKNIPCSWVGRINIM KMAILPKVIYRFNAIPIKLPMTF LTELEKTTLKFIWNQKRARIAK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYWYQKRDIHQWN TTEPSEITPHIYNHLIFDKPEKNK QWGKDSLFNKWCWENWLAIW RKLKLDPFLTPYTKINSRWIKD LNVRPKTIKTLEENLGITIQDIG MGKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRQ PTKWEKIFTTYSSDKGLISRIYN ELKQIYKKKSDNPIKKWVKDM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPPSLL IPRQTGSGVDLQQTPTDLQLKV LTVRRKTNKQKVHPHQNPICTS PSSKTKELEKQEQTHSKASRRQ EITKIRAELKEIETQKNLQKINES RSWFLEKVNKIDRLLARLIKKK REKDQIDAIKNDKGDITTDPTEI QATIREHYKHLYANKLENLEE

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7487	37855	A	7541	3	1284	SAADTQANRVWSVPPTNSNRP AAEGPDC*KEN*QKGHPHQNPI CQSPSSK\PKVDKTTKMGKKQN RKTGNSKNQSTSPPPQEHSSSPA MEQRITNAEKYLKDLMELKTT AQELHDECTSLSSPFDQLEERV SVMEDQMNEMKREEKFREKRI KRNEQSLKEIWDYVKRPNLPLI GVPESDRENGNKLENTLQDIIQ ENFPNLARHANIQIQEIQRMPQ RYSSKRATPRYIIVRFTKVEMK EKMLRAARDKSLVTHKGKLIR LTAGKFIALIAHKGNQERSKIDT LTSQLKELEKQEQTHSKPSRRQ EITKIRAELKEIETQTTLQKINES RSWFFEKINKIDRLLARLIKKKR EKNQIDAIKNDKGDITTDPTEIQ TTIREYYKHHYANKLENLKEM NKFLDTYTLPRLKQEEVESLNR PIKALKLRQ
7488	37856	A	7542	1	1082	MLSSVGLLLTHRRKKKSTDTIN DESLNKERDMTGNPHIFPRYQE IWQVFVSSGNNYITTATGPTAV PPLLIPRQTGSGVDLQQTPTDLQ LRLLTVGRKTNKQKGHPHQNPI CTSPSSKTKEIRTTIREYYKHLY ANKLENLEEMDKF/H*HIHPPKT KPGRS*ISA*TNNRL*N*GNN** LTNQKKSRTRWIHSRILPEVQG GADKQRAKHE*TPIHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQM/DRTFHAHG*E ESIS*KWPYCPR*FIDSPSPSSYQ *LSSQN\GKNYFKVHMEPKKSP YCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMVLVPKQRYRP MEQSPQK
7489	37857	A	7543	1	2012	MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQQEELTILNIY

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7490	37858	A	7544	402	675	QGYPGTELSSAPSGPNRHLQNF PPQINRIYILLSTTSHLFQN*PHS WK*STPQQM*KRRNYNKNQ\L ELRIKKQTQNRSTTWKLNNLLL NDY
7491	37859	A	7545	21	428	DKTSRGTIRQQHLLFTNIRCSAA SAADTQANRVWSGPPANSDRP AAEGPDC*KEN*QTERTSTPKS HLYVTIIKDQRNKIPKNPTYKG CEGPLQGELQTTAQQNKRRYK QMQEHSMLMGRKNQYHENGH TAQGNL
7492	37860	B	7546	1	1650	
7493	37861	A	7547	1	946	MAMPPLLIPRQTGSGVDHQQTP TDPQLRILTVRRKTNTQKGHPH QNPNCTSPSSKTKELKEEVGTQ RKEVKNLEKRLDEWLTRIANA EKSLKDLMQLKTMAQELQLDK TTLNFIWNQKRACIAKTILSKK NKAGGIRLPDFKLYYKATVTKT AWYWHQNRYIDQWNRTEASEI MPHIYNHLIFDKPDKKKQWGN DSLF/K*MVLGKLASHMQKTEI GPLPYNFYKN*LKMD*RLKGK T*NHRNHRRKPKQYHSGHRHG QRLHD*NTKSNGNKGQN*QMG SN*TKELL/RQQKKLPSE*TRNL QNGRKFVQSIYLTKG
7494	37862	A	7548	189	380	QTERTSTQNPICTSPSSKTKGR* NHKDGEKTEQKNWKL*KAERL SSSKGMQLLSSNGTKLDGE
7495	37863	C	7549	1	2805	
7496	37864	A	7550	535	696	
7497	37865	A	7551	214	363	LLEGKLTNRKE*HQHQQKGHP HQNPICTSPSSKTKVT*NHKDG EKT*QKS
7498	37866	A	7552	787	1056	GQKKKLMIIGINSRNHHGPQ*P ALQKMPAS*VTEIMNNHFLFCF RKGKGRIKLVNSRVEHQAGSW GPWFQSLVAGQYFWTCSGPDG SPLP

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7499	37867	A	7553	1	4560	MKHTLIPRIKNACLQMSSLAVP VNSLVCLGKILEYLDKWLVLD GILPFLQQIPSKESAVLMGILGIY KCTFTHKLGITKEQLTGKVLPH LIPLSIENNLNQFNSFISIIKEML NRLESEHKTKLEQLHIMQEQQK SLDIGNQMNVSEETKVTNIGNQ QIDKVFSHIGADLLTGSDSENK EDGALNVPPAGAKPTQQRPTD MSALNNLFGPQKPKVSMNQLS QQKPNQWLNQFVPPQVSPATG SSVMGTQMNMIGQ
7500	37868	C	7554	1	1359	
7501	37869	A	7555	272	915	YPGKQGLEWTSSKLQQTCC*GS *LLEGKRTNRKDINTKNPSVRH HHQRPKMGEKTEQKNRKLKIR APLLLQRNTAPH/HAMEQSWM ENDFDELREEGFRRSNYSELKE EVRTNAKEVKNFEKKLDEWIT RITNAEKSLKDLMELKTTA\EN YVTNAQAPVANATN*KKGYQR WKTK*MK*SEKRSLEKKE*KEK KQSLQEIWDYVKRPNLCLIGVP
7502	37870	A	7556	196	494	HTDGVSVWMSFLFVSFPSNSQD PQLQVCWSLLEVHSRPCLPGYQ QQRIRLEPFKINV/T*ADHEAYR KTAVRRCSQTTQQAWEQSAHQ QHIRH*SCRYPG
7503	37871	B	7557	28	303	
7504	37872	A	7558	1216	1863	HPDITIKRTREARANTFKS*QKA RNN*DERRTEGNRDTKNPSKKS VN/RRSWFFEKFNKIDRRLARLI KKKREKNQIDAIKNDKRDITTD PTEIQTTIREHYKHLYANKLEN LEEMDKFLDTYTLPRLNQEEVE SLNRPITGSEIEAIINSLPTKKSP GPDGLTAKFYQRYKEE/PGTIPS ETIPINRKRGNPP*LIL*GLHHPD TKAWQRHYKKREF
7505	37873	A	7559	166	785	FRATSAADTQANRVWSGPPAN SNRSAAEDPDC*KEN*PT\KGHP HQNPICTSPSSKTKARQANIQIQ EIQRMPQRYSSRRATPRCIIVRF TKVEMKEKMLRAAREKGQVT HKGNPIRLTADLLVKTLQARRE WGPIFNILKEKNFQPRISYPAKL SFISEGEIKSFTDKQMLRDFGTT RPALKELLKEALNMERNNQYQ PLQKHVRL
7506	37874	A	7560	1	1164	

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7507	37875	A	7561	770	2670	RRARCSCAPSSTTTLGRTGPSLA RRRACPSSAGRSWRW*ARTTPR GGRPSESGTPTFEPASSPPRGSR RDFQEGQSWVRGWQL/WTSTV GCSPHIFWCVDCETCDCEGYLK GHYVAGLRRSFRLGCRERLGGS QEGKMSSGAESPELLTYEEVAR YQHQPGERPRLVVLIGSLGARL HELKQKVVAENPQHFGVAVPR APWDVKLQWAEDPGSECDKE DEEEENEGARFLEHGEYKENLY GTSLEAIQAVMAKNKVCLVDV EPEALKQLRTSEFKPYIIFVKPAI QEKRKTPPMSPACEDTAAPFDE QQQEMAASAAFIDRHYGHLVD AVLVKEDLQGAYSQLKVVLEK LSKDTHWPPLVIPRQTGSGVDL QQTPTDLQLRVLTVRRKTKKQ KGHPHQNPTCTSPSSKTKVGER VSVIEDQMKEMKREKKFREKR VKRNEQSLQEIWDYVKRPNLR LIGVPESDGENGTKLENTLQDI MRENFPNRARQANIQIQEIQRM PQRYSSRRATPRHIIIRFTKVEM KEKMLRAAREKGWVTHKGKPI RLTADLLAETLQARREWEPIFNI LKGKNFQPRISYPAKLNFISEGE IKSFTDKQMLRDFVITRPALQEL LKEALNLERNNWYQPLQKHAK
7508	37876	A	7562	181	690	QHAIVTGDAVGMDDIPQEARQ* YRHNQAYAYSIQGDGAEDDDE RIVRFHTRCLNGRVLL*DK/IFQ RNDQAATFAAHQYPLFCSLHC* YPGTQGLEWTSSKHQQTCS*GS *LLWPGDERLWPSWEEQKKLS LPTDPDTWL*GSPQAAQGPRCV PPPGAQPLSSVTASLCHCA

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7509	37877	A	7563	2	2233	SSENILTVHEQANVESLKETKQ NCKDLDEDANGITDEGKEINEK SSQLKNLSELQDTSLQHDDEEE STVISVSEDMNSEGNVDFECDT KLYTFLSSDESQQSENSENEED TLCFVENSGQRESLSGDTGSLS CDNALFVIDTTPGMSADKNFYL EEEDKASEVAIEEEKEEEEDEKS EEDSSDHDENEDEFSDEEDFLN STKAKLGRLTPHMAGYSSETKL PEERPGSNICCSPISAVLQPPLLI PRQTGSGVDLQQTPTDLQLRVL TVIKKTNKQKGHPHQNPICTSP SSKTKDRSTRQKVNKDIQELNS ALHQADLIDIYRTLHPKSTEYTF FAAPHCTYSKIDHIVGSKALLS KCKRTEIITNCLLDHSAIKLELRI KKFTQNCSTTWKLNNLLLNDY WAHNEIKAEIKMFFETNENKDT TYQNFWDTFKAVCRGKFIALN AHKRKQERSKIDTLTSQLKELE KQEQTHSKASRRQEITKITAEL KEIETQKTLQKINESRSWFFEKI NKIETASKTNKKREKNPIDAIK NDKGDITTNPTEIQTTIREYYKH LYANKLENLEEMNKFLDTNTIP RLNQEEVESLNRPITGSEIEAIIN SLPTKKSPGPHGFTARFYQEYK EE/PGTIPSETIPINRKRGNPP*LI L*GQHHPDTKAWQRHNKKREF *TNIPDDHQCKNPQ*NTGKPNP AAHQEAYPP*SSGLHPWDARL
7510	37878	A	7564	3	377	DHNCATVLQPG*QSEIL*KEERE REREKKERKKERKKERKKERK KEGKQ*RKGGRKKERKEKEIK KERRKGKKEKKEEEKRRKERK KERERKKRRKEGRKKEYTRKA KRIHRPFEGNGSPLPAP
7511	37879	B	7565	1	834	
7512	37880	B	7566	1	915	
7513	37881	B	7567	1	666	
7514	37882	A	7568	330	793	SCWLCPGPCCPAQPQNTAPFIPE A*TPAMAERGPATAAGQLEFT GGALQTLFAWVSAAAAAEQWI LVNRKCCCLIVPLEVLSQRSTW PCIGLVMPVLPGLLRDIVHSDSI ASHYGVLLALYALMQFLCAPV LGALSDRFGRRPGLLASLLGAT

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7515	37883	A	7569	991	1842	IQCHPHQATKNFLHRIGKNYFK VHMEPKKGPHCQVNPKPKEQS WRYVKQSKKIAVYAERSRCSP GTEFAGTLILDFPSSRTAPSSRG R/P/GRLTRPGTPLRQSFQRNDQ AATFAVQQYSLFCSLCC*YPGK QGLEWTSSKLQQ/YLQLRERSS SPATEQSWMENDFDELREGFR RSNYSKLKEEVQTHCKEAKNL EKRLDEWITRITNVEKSLNDLM ELKNMAKELRDERTSFSSEFNQ LEERVSVIENQMNEMKREEKFR EKRVKRNEQSLQEIWDYVKRP
7516	37884	B	7570	1	2448	
7517	37885	B	7571	2379	4476	
7518	37886	A	7572	1	570	
7519	37887	A	7573	1	1404	
7520	37888	A	7574	1	474	
7521	37889	A	7575	746	1215	PNINRFLKHYREPVPKKRERNY STLWPLCPSTLNKIYTIMSYLSP ATKEYPFFLLLLEQEC*AE*LLA LAVSQPLLSSTTNCLKN*MVTW NGSLIPWSPCKINLTP*/PAVVL QNRRALDLLTAESGGTFLFLEE KCCCYVNQSGIITEKVKEIQGRI
7522	37890	A	7576	1	1178	MPESPTPLLGRDILAKAGAIIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQQGLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCLPLRNQQECHQATQV LLNVLATCGYKVSKQKAQLCS QQVKYLGVKLSKGTRAL/QQ*R TDRT*LSTSNCSNLRHSRGPSRG SLD*SQPQLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIRRRKKGL IRIYMLPLILSAPYDHLH
7523	37891	A	7577	1	1338	
7524	37892	C	7578	109	231	
7525	37893	A	7579	279	346	LLRLALLLQ*QKEEWVLFCCGA
7526	37894	A	7580	260	393	VEVVILPMPVPNLPSIPARITKG RMGTLLLRGLGTT*LYKSCSV

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7527	37895	A	7581	3	2677	TKETCFIRGPKTPVPVTDWEGS LPLVFNHCRDTSVIIHPRFKGVR PRRDACLGPSPLAASPAFLGKG QAELGPNSSSASAPPPYNLFIAS PPHTWSGLQFRSVTSPPPPAQQF TLKKVAGAKGIVKRLKTDTAR SPWKTPRPSRTPSFRKAERTKG LLKIHLTKLSHQLKKDWTILLP LSLLRIQACPRNATRLATGQLG YPFISQSYVLVNGFQTVEDLCE AADLRVSVADLRVSVTALKVA RLELFVPPGGLVVSLASAVKLQ TFAVLQLIKAKRWDWGTLEQG AALIGEARDAQEPTEGVGGSG MAGCRSRDLPRGKAAKARREI ERSAGLTIKKERCIRNGYSKEK MKLIVVSHGLHVNDLQHKLTL FTKETYTYLARDSEKQKQGYL AGLEGAHANRVNQQISDNLVV KTGALPPPYRTKGEKLYFYMSR QNCLFSVSGQLLQGFFPNGGQA APNPYALLSQIPEEAEWFTVLD LKDDFFCIP/VHPDSQFFFAFEDP SNPTSQLTWTVLPQGFR\HLFG QALAQDLSQFSYLDTLVLCGVL KSPIIIVWELNQIDTIKNDKGDIT TDPTEIQTTIREYYKHLYTNKLE NLEEMDKFLNTYTLPRLNQEEV ESLNRPITGAEIEAIINSLPTKKS PGPDGFTAEFYQRVADVKLREE KDENMLLVPLSDLLYQVHAPIP QLPEVLAANSPTCHLDPPTITES
7528	37896	A	7582	1	459	MAVRYTDENVLRKGTREAGT MMRLRGTTECCADFAAWDVT HDALRATGGELPGAQVMLTTT ECGRHVDFCDRAVWLPRMWG YPLALPGEMRKLYTVRMAGRD ILAKAGAIIHLNIGEGTPVRCPL L/EGINPEVWKTEGQYRQAKNA RPVQVKL

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7529	37897	A	7583	3	910	YFSQPLSY\DWGALFFSHAFLIM LESPTTLLGRDILAKAGAIIHLNI GEGTPVCCPLLEEGINPEVWAT EGQYGRAK\NARPVQVKLKDS ASFPYQRQYPLRPEA/LTKGFQ KIVKDLKAQGLVKPCNSPCSTPI LGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCLPLRNQQECHQATQV LLNVLATCGYKVSKQKAQLCS QQVKYLGVKLSKGTRAL
7530	37898	A	7584	158	1272	NPAARTPFFVIKKGGKRGRDIL AKAGAIIHLNIG/GTPVCCPLLE EGINLEDWATEGQYGRAKNAR PVQVKLKDSASFPHQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGVQKPSGQWRLV QDLRIINEVTVPLYLAVPNPYIL LSQIPEEAEWFTDLDLKDAFFCI PVHPDSQFLFAFEDPSNPMSQL TWTVSPQGFRDSPHLFGQALA QDLSRFSYLGTLVLWPCISI/LCT *TMEQLQHRNKHHFRFSRTSCF QSGNNPYLKPHLCKI*QYCRHN QLPMHQCPHDHLH*TRFI/PIML YLSPTTKEYSFFLLLSEQEC*VD *VLALAVPQPLLSSTTNYLKNS MVTWNGLPTPWSPCKINLTS

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7531	37899	A	7585	1	2083	MPLLQMIATPLQQSLISTEDEM DELTEVGFERWVITNFTEEPSPA LGFTPEHKGNVGHAGKGPLESS SPDPFLCGQEKQEKGAGLLHRQ YPLRLEAKQGLKKIVKDLKAQ GLVTPCSSPCNTPTLAVQKPNG QWRLVQDLRIINEAVVPLYPAV PNPYILLSQIPEEAEWFTVLDLK DAFFCIPVHPDSQFLFAFEDPSN PMSQLTWTVLPQGFRDSLHLFG QALAQDLSQFSYLDTLVLQYM DDLLLVTHSETLCHQATQALFN FLATCGYMVSKPKAQLCSQQ/R YLGLKLSKGTRALSEEHIQPILA YPHPKTLKQLRGFLGVIGFCRK WIPRYGEIARSLNTLIKETQKAN THLVRWTTEVEVAFQALTQAP VLSLPTGQDFCSYVTEKTGIAL GVLTQIRGMSLQPVAHLTKEID VVAKG*PHCLRVVVAVAVLVS EAVKIIQGRDLTVWTSHDVNGI LTAKGDLWLSDNCLLKCQALL LEGPVLRLCTCATLNPATFLPD NEEKIKHNCQQVISQTYATRGD LLEVPLTDPDLNLYTDGSSFVE KGLRKVGYAVVSDNGILESNPL TPGTSAQLAELIALTWALELGE EKRANI/YTDSKYAYLVLHAHA AIWKEREFLTSERTPIKHQEAIR KLLLAVQKPREVAVLHCRGHH KGKEREIQENCQAYIEAKRAAR
7532	37900	A	7586	80	678	LCCNMPAAQHRERASNESRHG GCCPP/PWLLSS/APPHDAFTTPQ EAVLSAPSALPSSAATSLLSLLT PQQMFCSKTAGPKPFSSNPHPR LKAPTSSC/PL*PQAAPSGNAHC Y*GHRRGRTVPEDPGCLSPRAR PHRTSGTSSPPSLQPSRTIPPASS APKQGDAGSPPYQAVPEKNKP GATPRTCAESPKRLPRPGPKSFL

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7533	37901	A	7587	3	804	GLLQATALQPAQQI*IFL*KKEE EEEGGGGEGEEKKKKKKTEEE EEEEEERKK\EEEEGEEEGEEEE EEEEKEERTGAGDSSEDEGFDEI PSPGDSRQKTEGNAANIISGCD QRYEESEMDLGTRGIVSGHRYI FTFRVSPLEAIGELLFPFSVAPA QGGLGFRRVDQLALPMGAQSL ERPFCVDGGSRPPLNYAVSSVE DLLNGNNFKCPTTLRTIEITVGN LIISPRQKQLNANIGKNFNAAEN HENAKTTTRSSTVGADTHLTA
7534	37902	A	7588	3	191	SSHPVFSPRWVLSPHPQSQCYT* GSGAQNLTASPPFCVCRGDRGN HLRKDTKVEVKRKTCWL
7535	37903	A	7589	1	1899	HVGASDPDAGPGWGGLTSRPR LVTPRSAPRGRAFQGATVGLAP VEGMCRAESSGGVSTDHSELPI GAAATMAHEIGHSLGLSHDPD GCCVEAAAESGGCVMAAAT/G VRGWGVGAAAGRLVLGTSSA AFLWSSLSFLFCKMGIMIIVSAS GWFMRLKGKKLRQSGFSTV*R LFSE*PGEVTPTPGGAPSGRDST LGPGLLTIGASSSPVPLVV*LCA GYFPSLGSARLAAVAKPRGGD QRSAGVGGLSLHAQCPPRAGR HPFPRVFSACSRRQLRAFFRKG GGACLSNAPDPGLPVPPALCGN GFVEAGEECYCVS\GQECRDLC CFAHNCSLRPGAQCAHGDCCV RCLLKPAGALCRQAMGDCDLP EFCTGTSSHCPPDVYLLDGSPC ARGSGYCWDGACPTLEQQCQQ LWGPGSHPAPEACFQVVNSAG DAHGNCGQDSEGHFLPCAGRD ALCGKLQCQGGKPSLLAPHMV PVDSTVHLDGQEVTCRGALAL PSAQLDLLGLGLVEPGTQCGPR MVCNSNHNCHCAPGWAPPFCD KPGFGGSMDSGPVQAENHDTF LLAMLLSVLLPLLPGAGLAWC CYRLPGAHLQRCSWGCRQGPC VQWPQRWPTQGPPPGRRSPHG VGPHSHWTALAPGP
7536	37904	A	7590	2	280	
7537	37905	A	7591	1	1266	

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7538	37906	A	7592	1	458	LQQSQIFEIHSQKTIVKKCLDLF FELAEEKENYKNFFEAFSKNL\K LGIHEDSTNRRRLSELLRYHTS QSGDEMTSLSEYVSRMKETQK SIYYITGSPCWCLVFFSLSCPCV EGSKLRVSSPIPSLLLTAGLDVV YCGLFYFLHFVLKLKYAK
7539	37907	A	7593	1	862	
7540	37908	A	7594	3	437	IPEF/LNF/IRGVVTLGLPLNISRE MLQQSKILKVIRKNIV*EC/LFEL LSELAEDKENYKKFYEAFSKNL KLGIHEDSTNRRRLSELLRYHT SQSGDEMTSLSEYVSRMKETQ KSIYYITGESKEQVANSAFVER VPLSHLAPPAGV
7541	37909	B	7595	106	1966	
7542	37910	A	7596	453	719	ARGSKHTGLIAQWAHEQSGHG GRAGGYAWAQQHGLPLTKAD LP\AMATAECPICQQQRPTLSPR YGTIPW/WAWDAPGGRGCWRL QKAGE
7543	37911	A	7597	3	837	PECVIGIDILSSWQNPHIGSLTG RVRAIMVGKAKWKPLELPLPR KIVNQKQYHILGGTVEISATIKD LKDTEAVTPTTSPFNSPIWPVQ KTDGSWRMTVDYCKLNQVVT PIAAAVPDV/VSLLEQINTSPGT WFEWSPK\KALQQVQAAVQAA LPFGPYDPADPMVLEVSVADR DAIWSLWNAAIGESQRRPLGF WSKALLSSADNYSPFERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSGAQQ RSIIKLKWYIHDWVRAGPEGT
7544	37912	A	7598	1	399	
7545	37913	A	7599	126	392	ARGSKHTGLIAQWAHEQSGHG GRAGGYAWAQQHGLPLTKAD LP\AMATAECPICQQQRPTLSPR YGTIPW/WAWDAPGGRGCWRL QKAGE
7546	37914	A	7600	1	1677	
7547	37915	C	7601	37	465	
7548	37916	B	7602	1805	2542	

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7549	37917	A	7603	3	865	VIPTTSQFNFPIWPVQKTDGSW RMTVDYCKLNQEENFNNQVDR MTHSVDTTQPLSPATHVITQWA HEQSGHGGRDGGYTRVQQHGL PLTKADLATAGKVFQKAV*AL N*HSIYGTLSLIARIHRSRNQGV EVEVAPLTISPSDPPAKFLLPVP PTLRSAGLEFLVPEEGMLPSGD TTVPLNWKLRLPPGHFGLLFPL HQQANKGRLSPHSRERGTSVFA SSNSQPVTALNNEPAGPNKRDI GKAKGLKFHHPGPHRQERDML E/SML*PWGYPVGKQWNHLIK KQGRH
7550	37918	A	7604	3	857	VTASLSPVVATSPPQPMLPSDFP PLSEEINPMLPEATVIASPKEIAR QDNVDSPQEPPPTPQFSSRPITR LKSQWAPRGPECVIGIDILSSW QNPHIGSLTGRVREGYMVGKA KWKPLELPLPRKIVNQKQYCIP GEIAEISTTIRDLKDTGVVIPTTS PFNSSIWPVQKTDGSWRMTVD YCKLDQVVTPIAAAVPDMVSL VKQINTSPGTWQHITHLDVLLW RIYQVTQKAASFEWGPEQEKA LQQVQAAVQA\LCHLGHMTQQ IQWCLRRNGEMCDYILIYGL
7551	37919	A	7605	1	608	MAPGMVPIPPPGKYHSPKKLIY STPPKPGTYGISDSLSQYPTSAK AEPVPTHKNPRRESPIPHSSPSSF TDG/PSPNSPGDARPHPQNKTSG RGRPAPRQRVPTTITTPAPPARS PNSAHSPAFRDLPFRAEKGTAA ARVPREPHSPAPPKNKGSLQPP AGELLQRGARTTLPRILGTAPG PHLPGCSAPPGAP*RPAAPIGL
7552	37920	A	7606	179	544	HTRLHSHPQLRGFPSWLFHSVSI RSPASGHLEFPSFARSSGSGSTS PLSFGAMTTEKQALGGRAAFPP KYK*AQGRAACFVLTSQQQPS WQ*GVTVTATGSPMHRGTFWH SCTGTPGSGDR
7553	37921	A	7607	90	653	VPGERPRGQSGPQVLPYGPTWC SSNTPEPQSLRAPQ*LQVPVPLQ SRGQR*QPQPMP/VRSQPKAP*V QMPPTPSSAKGPHLDGVRVPA ANPE*PTAGPTRAAILRATPAPS LPMPGTNRPSPRGNSLQDSAPA SDAGWPPTEAVTCP\PWSRENP PQRNL*AHRPQGPRPVPGTERR NGRGGAGCRQL

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7554	37922	A	7608	1	804	
7555	37923	A	7609	28	682	TTCEMSDLEDDETPQLSAHG/T LAALQEFYAEQKQQIEPGEDDK YNIGIIEENWQLS\QFWYSQETA LQLAQEAIAAVGEGGRIACVGS P*CLPET/HESCAEKTFSIYIFEY DKRFAME*KE\LIFYDYNNPLD LPERIAAHSFDIVI\ADPFPYLSG\ ECLRKTSETVQV\LTRGKILL\CT GAHHGRTGSRTPLE*RCARLFP RHTRNFGKWSFRLVYVNL
7556	37924	A	7610	1	611	MAPKAKMEAPAPPEAEAKVKA LKAKKVVLKGVHSH/KKKKKI RTSPTFR*/PLRLRRQPKYPWES VPRRTSTQISSGERPLENKQPRY PRESSPPPGEQAPKYPPEERSPG ETRLDHLCLSIKFP\LTH*VLPM KKIEDNNTL\VPLVNVKANKH\ QIKQAVKKLYDI\DVAKVNTL\I RPDGEKNGICSDLAP\DYDALG CLPTKFGII
7557	37925	A	7611	1	1035	DKDSLCDSCKTSCSYNCSKPRS SWQDQDISSGTGLHSRLTLANT GKESKTVQASLDQQLGRLLSVS LRLGVEPSLQSSGNLLVSLLLSR FITYKVTIVEWVKTYALGLDLK KSERPGFESELHSHNSCECAVS HLKPVHLRVSPMGHSEYYLVT TADYSEANGSQSAGDEFFQTQS FPSRQQALFRPKIQITIREYYKH LYANKLENLEEMDKFLNTCTL QRLNQEEVESLNRPITGSEIEAII NSLPTKKRPGPDGFTAKFNQRY KEELVIYKKFQIPCIVPELNSTIS ANSTNADTCTPKYVTFNSKGT AQNADSDSAGLE/CEPDVLHI** SLRLGVEPSLQSSGNLLVSLLLS RFITYKVTIVEWVKTYALGLDL KKSERPGFESELHSHNSCECAV SHLKPVHLRVSPMGHSEYYLV TTADYSEANGSQSAGDEFFQTQ SFPSRQQALFRPKIQITIREYYK HLYANKLENLEEMDKFLNTCT LQRLNQEEVESLNRPITGSEIEAI INSLPTKKRPGPDGFTAKFNQR YKEELVIYKKFQIPCIVPELNSTI SANSTNADTCTPKYVTFNSKGT AQNADSDSAGLEWSLMFCISD KVSGDDDADAVDS

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7558	37926	A	7612	3	573	KEETFSAWYVDGRVLVVIVTF GIILPLCLLKNLGYLG\YTSGFSL SCMVFFLIVVIYKKFQIPCIVPEL NSTISANSTNADTCTPKYVTFN SKTVYALPTIAFAFVCHPSVLPI YSELKDP\SQKKMQMVSNISFF AMFVMYFLTAIFGYLTFYDN\V QSDLLHKYQSKDDILILTVRLA VIVAVILTVPVL
7559	37927	A	7613	1	831	MSELEDRLFENTQSEESKGKRI KKNEVCLQDLKYSLKRANLRD TGLKEEVIYKKFQIPCIVPELNS TISANSTNADTCTPKYVTFNSK KKMQMVSNISFFAMFVMYFLT AIFGYLTFYDNVQSDLLHKYQS KDDILILTVRLAVIVAVILTVPV LFFTVRSSLFELGLRKQRFNLW PSIPVVTCILLVVINLVGDLHTP P*RIFFGVVGSYILLNMLIFILP/S IFFILKITDQDGDKGTQRIWAAL FLGLGVLFSLVSIPLVIYDWACS SSSDEGH
7560	37928	A	7614	1	1118	FNCEIFYSF/SYGDEEISKTFALN ERRGEIKIIRKLDFEKIVSYQVDI KASDGAGLSGKCTVIIQVVDIN DNAPELTMASFTSPIRENSPETV AALFSIQDRDS\FALRSLDYEAL QEFEFRVGASDPGF\PALSSE\AL VRVL\VLDANDSSLFVLFPLQN GSAPCTEL\IPGRAAEPGYLVTK QLLKATEPGLFGVWAHNGEVR TARLLSERDATKHRLVVLVKD NGEPPRSATATLHVLLVDGFSQ PYLPLPEAAPAQAQAEADLLTV YLVVALASVSSLFLLSVLLFVA VRLCRRSRAASVGRCSVPEGPF PGHLVDVSDTRTLSQRYKYEVF LTRGSGTNEFKFLKSVIP/QASG RCE*WEEKSNFVNGFGFN
7561	37929	A	7615	1	764	TRPGAHGASLTDLANLSEGVSL AERGSFGAMDDPFKNKALLFS NNTQELHPDPFQTEDPFKSDPF KGADPFKGDPFQNDPFAEQQTT STDPFGGDPFKESDPFRGSATD DFFKKQTKNDPFTSDPFTKNPS LPSKLDPFESSDPFSSSSVSSKGS DPFGTLDPFGSGSFNSAEGFAD FSQMS/KGKSTPVSQLGSADFPE APDPFQPLGADSGDPFQSKKGF GDPFSGKDPFVPSSAAKPSKAS ASGFADFTSVS

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7562	37930	A	7616	1	817	MGFCHVGQASLKLLASDPFGT LDPFGSGSFNSAEGFADFSQMS KTDPQVRSELLK\GTAARLVTR LDPLVSGPH\TR*PELTVALVPD SCRASPDAGSVVGAHL*GLGTT GAADGGTP\NSNRSFVLGVIIVV WSMCQLYLVPPPPSGPFTSSLG GAGFSDDPFKSKQDTPALPPKK PAPPRPKPPS/GHRLPVPDGGGP GPPCSP/DPE*QQMPWDPVWGA RGSPRPSCPGPRKCRMCVVPRV IQHPSLLLPSLVGRRSQPQIWRS HPMPAAPPS
7563	37931	A	7617	3	1039	GSLMFQQVPMVEIDGMKLVQT RAILNYIASKYNLYGKDIKERA LYAMTHDDE\AELRTPAAACKL *SECQFRTRVDAVRTMMIP/AFT QVLKSHRQDYLVGNKLSWADI HLVELFYYVEELDSSLISSFPLL KVKLLASSVKPVPLPSALRWPA HAVAQNIVTSWLTGGRFIELKT VQILDRLELEKPCIDAEDECFNT EWSTEFTLLKAWDEYLKAWFA LHLLEAMFQPSDSGKSFIFNMS VGYNLEGQPLNPKNYPSQGVP RVLKSHRQDYLVGNKLSWADI HLVELFYYVEELDSSLISSFPLL KPHTHVDNTKKGSHPHMCAYT DYVNNPNDRMPQREITFVS
7564	37932	A	7618	2	698	NQKTVTMAGKPKLHYFNGRGR MEPIRWLLAAAGVEFEEKFIGS AEDLGKLRNDGSLMFQQVPMV EIDGMKLVQTRAILNYIASKYN LYGKDIKERALIDMYTEGMAD LNEMILLLPLCPAEEKDAKIALI KEKIKSRYFP\AFEKVLQSHGQD YLVGNKLSRADISL\VELLYYV EELDSSLIS\NFP\LLKALKTQNP ATLPHG*RSFLQP\GSPRKPPAD AKALEEARKIFRF
7565	37933	A	7619	102	825	RNLQETAIMAEKPKLHYFNAR GRME\PPRWLLAAAGVEFEEKF IKSAEDLDKLRNDGYLMFQQV PMVEIDGMKLVQTKAILNLHLP ANYNLLMGKDIKGREP*FDYVF *EGFSQILGLN*SSFLPVC\PPE\E KDAQALPLIQEKTKNRYFPAFE KVLKSHG\QDYLVGPTSLSRGW TFIWWELLYYVEGAWTPRLISS FPLLKALKTRISNLPTVKKFLQP GSPRKPPMDEKSLEEARKIFRF

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7566	37934	A	7620	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL\PIYRV SRKAANFEWSPEQEKALQQVQ AAVQAAWPLGPYDPADPMVLE VSVADRDADWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGQRRWWQLAE RQDSRDREAAIGERQETAVGKT ARDGEAVCD
7567	37935	A	7621	1	518	MTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIGSTIKWVVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG
7568	37936	A	7622	1	696	
7569	37937	B	7623	1	1014	
7570	37938	B	7624	1	837	

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7571	37939	A	7625	1	2592	MVRKAKWKPLQLPLPRKIVNQ KQHRIPGGTVEISAITKDLKDA GVVIPTTSPFNSPIWSVQKTDGC WRMTVDYCKLTQVMTPIAAV VPDVVSLLKQINTYPGTCK\FLG VQWCGACRDI/PSKVKDKLLHL APPTTKKEAQHLVGLFGFWRE HIPHLGVLLQPMYQVTRKAASF EWGLEQEKALQQVQAAVQAA LPFGPYDSADPTVLEMSVADRV AVWSLWQAPIGESQWRPLGLW SKALPFSADNYSPFERRLLACY WALMETEGLTMGHQVTMQPE LPIMNWVLSDPSRHKVGHAQQ HSIIKLKWYICDQARAVPEGTC\ *LNKEVAQMP/MGTTRKWTAA ALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGT WKKHDWKTGDNEIWGRGIWM DCSEWSKTVKIFVSHAHEPSGH GGRDGGYAWAQEHELSFTKAD LATGIVECPICQQQRPTLSPRYG TIPQGQTFILTGINTYSIYGFAYP AHNASAKITIRGLTECLIHHHGI PHS/IVSD*GTHFTAKDV\ETRIH RPRNQGVEVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLLE GGTLPPGDPTTIPLNWKLRLPR GHFGLPLPLSQQAKKGVSVLA GVTDLDYQDEFSLLLHNRVTA AFPSLLHSSFAYLDNMIEKANK CHVEGVDHVSDPAQRRECDRH
7572	37940	A	7626	20	238	
7573	37941	A	7627	3	229	
7574	37942	A	7628	1086	1369	ETGMLPLRLLKPFLSDFAGPLH TSIMPTRRFCSKSPT*HTLATAL SQGLS*GT*NEASLTKEKVGKN RCRYSPSYPPSGIREGKAQLCFY THWK

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7575	37943	A	7629	1	1805	MSGRSRGRKSSRAKNRGKGRA KARVRPAPDDAPRDPDPSQYQS LGEDTQAAQVQAGAGWGGLE AAASAQLLRLGEEAACRLPLDC GLALRARAAGDHGQAAARPGP GKAASLSERLAADSVFVGTAG TVGRPKNAPRVGNRRGPAGKK APETCSTAGRGPQVIAGGRQKK GAAGENTSVSAGEEKKEERDA GSGPPATEGSMDTLENVQLKLE NMNAQADRAYLRLSRKFGQLR LQHLERRNHLIQNIPG\FSGQAF *NHVLLASFLNSQEKEVLSYLN SLEVEELGLARLGYKIKFYFDR NPYFQNKVLIKEYGCGPSGQVV SRSTPIQWLPGHDLQSLSQGNP ENNRSFFGWFSNHSSIESDKIVE IINEELWPNPLQFYLLSEGARVE KGKEKEGRQGPGKQPMETTQP GPLSFVWVAVSPSWLPGQQGP QELPVDRGPLPVHETHTYPPQL SRNPTGCQTDGRAGLPVTPCDK KALPCAQCFVSHLLYCMGLQP RQKEKINPEVSSITNVAPKDME KVHAGALDKPMCGRQGKESQ GATHHATPSAISPAPSHPLGSSE TLDIDGLAHFLEHSQINPSLLSR VLIQRQHLRHVAVTNG
7576	37944	C	7630	66	206	

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7577	37945	A	7631	3	1643	VQASQAEADQQQTCLKQLQ\S\ QLSRL*KQAIELREAVEQHKVK NNDLREKNWKAMEALAT\AEQ \ACKEKLHSWTQ\AKEES/ERNQ LCLIEAQT\MEALLALLP\ELSVL AQQN\YTE\WLQDLKEKGPTL\L KHPPAPAEPSFGTWAFQV*GEA E\ETQSTICRAEF\DQYRSILGGD GRALLRDLQKSVEEEEQV\W\R AKVGAAEEELQKSRVTVKHLE EIVEKLKGELES\SD\QVREHTL HLEAELEKHMAAASAECQNYA L\EVAG\LRQLLLE\SQSQLRLPP KNRNPQKTEPMSFALGQASS*V KLKSHVED\GDIAGAPA\SSPEA APQPSRDPRSA*RTQLELDQKPI PWRMRQTTSRQKLHGPSFE\EA SDLRACSVYKEGFWEKLPHSA APPRSFFRNRREAFTA*RRDLEK RGRSLTSD\LGRARPRRLQELSE RRTQEQLGKGRRTRVKKLQE\Q L\EKAEDGSS\SKEGTSVLSFLFG KKKLLFQLYQNALTHSFTIKPT NLHSVYPGPNFPVLREKAHEET SLFRRPQEVRTFPGGPILLNGTC
7578	37946	A	7632	3	247	
7579	37947	A	7633	3	389	GQEFSPKVY/FVNQTMGN/SCG PIGLFNAVANNQDKLGFEY\GP LLNQFLF*NR*KCPPKDRAKCF ER\NEAIRAAH\DAVDKEG\QCR VDDQGEFPFLFCLQNVDGPPSM NLDG\RMPFPRGPMAPSFRRTP

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7580	37948	A	7634	1506	3135	RGLGGGLAEQELQPWSPERSPV HNN/RM/QEKSLKDLMELKTM AQELRDECTSLSSRFDQLEEKV SVMEDEINEMKQEEKVREKRIK RNEQSLQEIWDYVKRPNLHLIG VPESDRENGTKLENTLQDIIQEN FPNLARQANIQIQEIQRMPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKEIQTTIREYYKHLYT NKLENLEEMDKFLDTYSLPRLN QEEVESLKRPITGSEIGAIINSLP TKKSPGPDGFTAEFYQRYKKEL VPFLLKLFQSTEKERILPNSFYE ASIILIPKPGRDTTKKENFRPISL MNINAKILNKILANQIQQHIEKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTNEKNHMIISIDAEK AFDKIQQPFMLKTLNKLGIDGT YLKIVRAIYDKLTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEQ VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI
7581	37949	B	7635	1	594	
7582	37950	A	7636	434	744	TLACLARLGKFSWIISCRVFSNL VPFSPSLSGTPIRRRFGLENRVT ATRILRFSDRLKKRRTTRLYPTP GSEGPTPTESR*LLAQQSEIKLQ GGSEAGGGAPA
7583	37951	A	7637	1	1077	
7584	37952	A	7638	1	348	
7585	37953	A	7639	1	831	
7586	37954	A	7640	275	457	LIAYQPK*AQDYMDSQLNSTRG TKKSC*GRL*GSGVIHIGSMPVP TRTAGPLPFFAGPCR
7587	37955	A	7641	341	504	ILRFSDRLKKRRTTRLYPTPGSQ GPTPRESR*LLAQQSEIKLQGGN EAGGGAPA
7588	37956	B	7642	1	627	
7589	37957	A	7643	121	375	DGQQLIALHRLALRELQQAVH AGLPQQAKILFDGGSEIGKIH*L RCAHCPLSSRETCRASCINESAT RGERPFAYWAPGWFFFHQ
7590	37958	A	7644	3	479	
7591	37959	A	7645	382	642	
7592	37960	A	7646	273	1464	

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7593	37961	A	7647	76	1763	IFGITRFLPFIYQKIHIFSKEQLPD LHSHFSDLNLEAHMYASQWFL TLFTAKFPLCMVFHIIDLLLCEG LNIIFHVALALLKTSKEDLLQA DFEGALKFFRVQLPKRYRAEEN ARRLMEQACNIKVGVYTGTEL Q*DFSLDSLVWSWDSSCCCGK ASWQDDGRNLHYGSL*RPCFQ PAAR*RLPH*SGGHQQAQVYG TN\KKLKKYEKEYQTMRESQL QQEDPMDRYKFVYL*VTPAVA FILGIFIRS*EKERGKRKWLSTF KNETKRKNGKVLF*LCMSYPQ RLLAGELFQD*HKDVSNLPLSV ENVKNTNSLGRKNKNHK\REN RRLQEASMRLEQENDDLAHEL VTSKIALRNDLDQAEDKADVL NKELLLTKQRLVETEEEKRKQE EETAQLKEVFRKQLEKAEYEIK KTTAIIAEYKQICSQLSTRLEKQ QAASKEELEVVKGKMMACKH CSDIFSKEGALKLAATGREDQG IETDDEKDSLKKQLREMELELA QTKLQLVEAKCKIQELEHQRG ALMNEIQAAKNSWFSKTLNSIK TATGTQPLQPAPVTQPPKEST
7594	37962	B	7648	1	618	

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7595	37963	A	7649	1	2375	MAGAPPPASLPPCSLISDCCAIN QRDSVGVRPSKPGAGYNLVVR RFLSLLEKRSIPVGVTRFSRCRP SPLSLTRKGNSLTPCASRIINMH FQAFWLCLGLLFISINAEFMDD DVETEDFEENSEEIDVNESELSS EIKYKTPQPIGEVYFAETFDSGR LAGWVLSKAKKDDMDEEISIY DGRWEIEELKENQVPGDRGLV LKSRAKHHAISAVLAKPFIFAD KPLIVQYEVNFQDGIDCGGAYI KLLADTDDLILENFYDKTSYIIM FGPDKCGEDYKLHFIFRHKHPK TGVFEEKHAKPPDVDLKKFFTD RKTHLYTLVMNPDDTFEVLVD QTVVNKGSLLEDVVPPIKPPKEI EDPNDKKPEEWDERAKIPDPSA VKPEDCALGLELWSMTSDIYFD NFIICSEKEVADHWAADGWRW KIMIANANKKKHKDTEYKKTDI CIPQTKGVLEQEEKEEKAALEK PMDLEEEKKQNDGEMLEKEEE SEPEEKSEEEIEIIEGQEESNQSN KSGSEDEALAEQPREGPGVPGP IPPKRPSRSPIPEPRAAKRLPTQE LRGESYTMSASGTARGPSPKER LGLTTKTGEKEVAQGFCREPGL RRPPNAQARDRSSRAPATHRKE LKPEREHISCSRSHIRYQEWSVL RDTVHRNLVLDTKRHPALILVE YKERTSSPATEQSCMENDFDEL REEGFRRSVITNFSELKEDVQT
7596	37964	A	7650	914	2786	
7597	37965	B	7651	1	2369	
7598	37966	A	7652	333	752	MSYVSRYGCGGRKNVATVSKG WAGSLAWPGGFPRKVKGGGS WRPSGGV/DVAAPVRARLALLL SGPIASESPLTTNPHSHSARRPR TYI/GHAPALRVTN/PESFSYWG TRGPSATMACDGLTRTGHSSPS RARSPPLLCARSL
7599	37967	A	7653	1	177	RPLPSRPHAAPPGHHTISSGPCG HRKFSPKAGDSNTPRTRSRPRV SCALPPDVRGSWLS*KWNQIW YHTLPQPQENTPKSQENKPKSK PQPTQR*TRGPW\PSSRCRVRSG /THRRPGLFLS*KQ/PSESIGHSR ALSAFTPAEMISTLPPPPTSKSPL AARAAPPGNG*SPKAGDSNTPR TRSRPRVSCALPPDVRGSWLS

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7600	37968	A	7654	1	1430	MQDTCSEIISPADFPTFSSSLKIR FSTDSPSQIFKKHCIQKIVLILLP KNSYTRRLLVSNQMYLESFEH QCRKTHILCKRTAGSGPFCSCPT GQPRHNSSASKCPASERGLCLK/ PKSKREKREPGPVAPAPLHAAP SSPGLGAPQLR*PGRTRSFGRD HVGSPGPPRAGPRLFAPRPVLS RCSANPSGSPHTQSPKQSSTGQI SGRADQVCGCWIRKRGVPGAA RGSPGCARTCHSRGHPHAAPFP QCNSLAPSAPAGLWRTQNAGP SG/HAQPSCPPPVPL*PPHPHP*G LSFSSCSRSWVPNTPP/EPREGE GQVPGRRAASAPGASFSAPGT/P RAPQPLPHPFPVAQSPPAAVAA SSESCKREAARRSPGASALHLPP KSARPRQAPCPTLTDGGHIFPAS AARP*HKGHQTAEGKNPGRAD TSTSPFATFPFISGGEEKSRSPVL PERTRQREEAPGPPSSPLRGLW LTFWFVFL
7601	37969	A	7655	1	609	
7602	37970	A	7656	3	649	AKD/ELHIVEQGHDIRGRSIKIT/ LATLKMS/VQPTFS/LGGFEIQPT VV*GLKCVSGPCHISGQHLVA/ VEEDAESEDEEEENVKLLSISER RSAPGVVSMVPQKKVK\LAAD EDDDDDDEEDDDEDDDDDDFD DEEAEEKAPVKKSIRDTPAKNA QKSNQNGK\DSNPYSHPRSQG\ QDPFRKQEKT\PKTPKGP\SSVE DIKAKMQASIGKKRIEPVLGTY
7603	37971	A	7657	1	1013	PWCDSVLRGCSLEQRSFISVRLL SYLSACRHPMEDSMDMDMSPL RPQNYLFGCELKADKDYHFKV DNDENEHQLSLRTVSLGAGAK DELHIVEAEAMNYEGSPIKVTL\ ATLKMSVQPT\VSLGG\FEITPPV V\LRLKCGSGPVHISGQHLVAV\ EEDAESEDEEEEDVK\LLSISGK RSAP\GGG\SKVPQKKSKTCML MKDDDD\DDEED\DDEDD\DDD DF\DDEE\AEEKAPSERNLYRDT PS/AKNAQKSNQNGK\D\SKPSS TPR\SKGTRIPSKKQEKTPKTPK\ GPSSVEDIKAKMQASIEK\GGSL PKVETKFINYVKN\CSRMT\DQE AI\QDLW\QW\RKSL

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7604	37972	A	7658	9	271	GRVCKALWHSDWHTARVLCIN STTTITASCNP/RHTARRSLTTPT *MCRLENWTKNLLFNGPVPVL VMSLLFIASVFMLHIWGKYTRS
7605	37973	C	7659	189	500	
7606	37974	A	7660	5	291	ATPSPPSPPG/VPT*RPELLGPRR ERLLGPEGS/PGGGALPGVPPSR FVRTASSTLFLPPSPRPAFPPSSIP LVPSPPRHCARSRETWPRTLRIG SAP
7607	37975	A	7661	1	431	LALQFSFLQNRQGLNLLIAEKG RLCIFLNEECCFYLNQSGLVYD NIKKLKDRVQKLANQANNYAE PPWALS\NWMSWVLPILSPLIPV FLLLLFGPCVFCLVSQFIQNRIQ AIANNSI*QMLLLTTPQYQPLPQ NLSSVESLPL
7608	37976	B	7662	41	1547	
7609	37977	B	7663	74	298	
7610	37978	A	7664	3	647	ELWTRGPRKRQNGSSKPLWLL YGESGAQKSVVEVTKPRLLWP QWIQHRARRPCLQQAPCSSRPH APAS\LPPSSSPTARDTKHRAQV KTTDSGARRRDGRVLGVLEVS RSIADGQYKRCG\VTSVPD\IRR C\QLTPQ*PGSILLACDGLF\KVF TPEEAVNFIL\SCLEDEKIQTREG KSAADVR\YEAA\CNMLANKA VAAGARPDNVTV\MVVR\IGH
7611	37979	B	7665	1	1302	
7612	37980	A	7666	3	1268	SCARVAAWGGKLRRGLAVSRQ AVRSPGPLAAAVAGAALAGAG AAWHHSRVSVAARDGSFTVSA QKNVEHGIIYIGKPSLRKQRFM QFSSLEHEGEYYMTPRD\FLFSV MFEQMERK\IQSRS*QKRFIEDT LSGIPTAGCGSSFFQRPWAIKGL I\SYNRVIFFFALQSSLNPIPGFH VAFKMLDTDGNEMIEKK/ENFL SCRRS*VNKMT*LTVKTNETWI SGSNK*KNLKL/DTTLQMRFFG KRGPRKLHYKEFRRF\WENLQT EIQGN/VEFLQFSKGLSFMRKRR TLQSGYFFSTNTENKDIYWKNV REKLSAGESISLDEVKAFCHCT RQIGTLCY/SAMQMFTLAHRPV RLAEFKRAVKVATGQELSNNIL DTVFKIFDLDGDECLSHEEFLG VLKNRMHRGLVGTTTSEYTRIL EVCEERKH

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7613	37981	A	7667	2	342	QNRGPGRT*DFLPNS/VGEKILS FCNCSLGSIGALGPACCRVLSEL SEEQVFHVNYLDVEELSLSRLC QCLVELSFQLATAYHGSATTRE AARGEAACRAHLMFWCLCIWQ FCRL
7614	37982	A	7668	1	1166	VGCVLGRVEAAVTVAPAGTEE GMSEEEQGSGTTTGCGLPSIEQ MLAANPGKTPISLLQEYGTRIG KTPVYDLLKAEGQAHQPNFTF RVTVGDTSCTGQGPSKKAAKH KAAEVALKHLKGGSMLEPALE DSSSFSPLDSSLPEDIPVFTAAA AATPVPSVVLTRSPAMELQPPV SPQQSECNPVGALQELVVQKG WRLPEYTVTQESGPAHRKEFT MTCRVERFIEIGSGTSKKLAKR NAAAKMLLRVHTVPLDARDG NEVEPDDDHFSIGVGFRL\DVL QNRGPGCTWDSLRNSVGEKILS LRSCSLGSLGALGPACCRVLSE LSEEQAFHVSYLDIEELSLSGLC QCLVELSTQPATVCHGSATTRE AARGEAARRALQYLKIMAGSK
7615	37983	A	7669	2	328	
7616	37984	A	7670	181	1271	LEASLDQH*ASVHSFRSHIHVIS RTHRK\SQRDPSELDAEHAQKV LEMEHTQQMKLKERQKFFEEA FQQDMEQQYLSTGYLQIAERR GEWGLGLLVWGLTGCAGCHD SSWGLVRWYKCYSFKFVDEPC LQFERNCKPIGSMSSMEVNVD MLEQMDLMDISDQEALDVFLN SGGEENTVLSPALGRVDKLALA EPGQYRCHSPPKLQQWCGSVM NSSQRFDMLHSGNFEIHLSLLL VVKDWRLQGGADSPAGLTGNS SLFVRQAFRGVPAMGKAMGSS QVLQAPGPESSTCQNEITLQVP NPSELRAKPPSSSSTCTDSATRD ISEGGESPVVQSDEEEVQVDTA LATSHTDREATPDGGEDSDS

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7617	37985	A	7671	60	965	QRGVGGVGPRGRQRQQQPEA* GEET\AAAAMLETLRERLLSVQ QDFTSGLKTLSDKSREAKVKSK PRTVPFLPKYSAGLELLSRYED TWAALHRRAKDCASAGELVDS EVVMLSAHWEKKKTSLVELQE QLQQLPALIADLESMTANLTHL EASFEEVENNLLHLEDLCGQCE LKRCKHMQSQQLENYKKNKR KELETFKAELDAEHAQKVLEM EHTQQMKLKERQKFFEEAFQQ DMEQYLSTGYLQIAERREPIGS MSSMEVNVDMLEQMDLMDIS DQEALDGLPELWRRREHCAVP
7618	37986	A	7672	1	124	
7619	37987	A	7673	3416	3920	CCLIKNDIKEKLHYSDCRLNVG QPCILPRNAFEFDLLIFYLGNLH FYISEIGLLGYCTFFFFFEMESC SLTQAGVQ*CNLGPLQPLPPGL E*F/SCLSLPSSWDYRHVPPHWL IFVFLVEMGFCYVGQAGLEFLT SGDPPTSASQSARITGVSHHAQ PGYCILILGFC
7620	37988	A	7674	1	387	

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7621	37989	A	7675	1	1827	MKKVGGRVFWAKERASAEAL RHELAGLLKKCKGSAADADQG GLGQGCRRHSKRWEGFTRGAS RAARLGNEEQDAASAGPGPNG CGHLGAEEPSAAASGMDQCVT VERELEKVLHKFSGYGQLCER GLEELIDYTGGLKHEILQSHETC LSVVLLSLPMVMAGSGNLKVL QLCRFLHMKTGGEMNYGFHLA HHM\ALGTSIFGEEGRYSL\STS NSSIAALLCALYPHFPGFTALD NRYHLQ\ALR\HLYVL\AAEPRA FLVPVGCGTQTRPCY\ALLGSLP YKGTQWY\EQTKE\DLMAPTLL PELHLLKQIKVKGPRYWELLID LSKGTQHLKSILSK\DGVLYVK LRAGQLSYKEDPMGWQSLLAQ TVANRNSEARAFKPETISAFTSD PALLSFAEYF\CKPTVNMGQKQ E\ILDLFS\SVLYECVYPRETP\E ML\PAYIAMDQLIRRLGEREMS ETSELW\QIKLVLEFFSSRSHQE RLQNPPLKRGALLMELGNSPPF CKCT\INNTL\DTW\LQVRGDIC VNAYLTGQPL\EESQL\DMLACF LVFHFVPSSTALPTL*D*KGSTS FA\ELLFKFKASLKMPSAELCLR LAPLPSLEIPQPNGDVTVSGGEP
7622	37990	B	7676	374	515	
7623	37991	A	7677	102	1237	HSHRAACPDTNRLVPGASR*HY LHRCRSRHSSS/NIGKNI/HSLRA GAVNNQSRPQSHSSGEFSLLHD HEAWSSSGSSPIQYLKRQTRSSP VLQHKISETLESRHHKIKTGSPG SEVVTLQQFLEESNKLTSVQIKS SSQENLLDEVMKS\LSVSSDFLG KDKPVSCGLARSVSGKTPGDFY DRRTTKPEFLRPGPRKTEDTYFI SSAGKPTPGTQGKIKLVKESSLS RQSKDSNPYATLPRASSVISTAE GTTRRTSIHDFLTKDSRLPISVD SPPAAADSNTTAASSEYHLHQ WSSHILDIPTHTIGSCAQNDLAI DMPEPLYAQARNSRTGRSHFL NQTFATIRMPSDAFGMLAKDK HRTIYCGPFISAILIPEYRIS

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7624	37992	A	7678	1256	1971	HNCALHADSTMRGKAPLFRPT YKLMEQLLLRIFRWISQKCQNV EVTSICWF/CTCTYSGWVEAYP TRTEKPYKKGKNDPSCTKGQC NPLELVITNPLNPHWKKGERVT LGIDRARLDPRVNILVRGGEVY ERSPEPVFQTFYDELNVPVPEIP GKTRNLFLQLAECVAQPLNVTS CYVCGGTVTGYQWPWKAREL VPVDPVPDEFLAQKNYPDNFW VLKPSITGQYCIAREGKKFTHP
7625	37993	A	7679	1	1710	
7626	37994	A	7680	1	561	
7627	37995	B	7681	1	642	
7628	37996	A	7682	2	611	
7629	37997	A	7683	1	1718	MLSIQSTHAEKELENFFQNTED WYFHTSHHLSSLRFFSARESNC SMKLYEEAYMERYRDFLPATM WSAHTEVDVPGQATWIKQKSE KDPVHLQKGKNGPSCTKGQCN PLELVITNPLDPCWKKEERVTL GIDGAGLDPQVHILVRGEVYKH SPEPVFQTFCDELNVPVPEIPGK TRNLFLQLAWHVAQCLNVTSC YVCGRTIIGDQWPQEAQELVPT DPVPDEFLAQKNHPDNFWVLK A\SIIGQYCIAREGKEFTHPIG*L SCRRQKLYNGTTKTIT/W/RGSS NHTERNPFSKFPKLQTVWTHLG VP\RAWEQPPLGFLLGYVRAWS LLTGLLDHWAGSCCLLGTI\KPS FFPTAP*KQGKLLGFPVYASRE KRIIAIENWKDDEWPPPERIIQY YGPVTWAQDGLWGYQTPIYVL NRIIRLQAALEIITDKISRALTIL AWQETQMRNAISQNRLALDYL LAAEGGVYGKFNLTNCCLHVD DQGQVVEDIVRDRTKLAHVPV QVWHEFDPGAMFGKWFPALG GFKTLIIGVLIVIGTCLLLPCLLP VLLQMIKSFIATLVHQNASAQV
7630	37998	A	7684	3	406	TLISFIYPAQNPELLNKLSQRKT TVLAMDQVPRVTIAQGYDALS SMANIAG/YLIVGGGVAGLASA GAAKSMGAIVRGFDTRAAALE QFKSLGAEPLEVDLKESGEGQG GYAKEMSKEFIEAEMKLFAQQ CKEVDI
7631	37999	A	7685	1	236	
7632	38000	A	7686	1	978	
7633	38001	C	7687	415	453	

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7634	38002	A	7688	3	408	
7635	38003	B	7689	1	2137	
7636	38004	A	7690	112	3688	GNWGARKLGTHINMANLLKTV ATGCSCPLLNNLGSCKGLRVK KDFLRTFYTHQELWCKAPVKP GIPYKQLTVGVPKEIFQNEKRV ALSPAGVQNLVKQGFNVVVES GAGEASKFSDDHYRVAGAQIQ GAKEVLASDLVVKVRAPMVNP TLGVHEADLLKTSGTLISFIYPA QNPELLNKLSQRKTTVLAMDQ VPRVTIAQGYDALSSMANIAGY KAVVLAANHFGRFFTGQITAA GKVPPAKILIVGGGVAGLAS
7637	38005	A	7691	2	288	EFPATIQSNRARGAKPGRRVDR GPQARCFDVGGCPRSAPSNGLR NSEPSP*GR/CGRSPVSPALSSSR DVNLPCMLSSGTDSGACSEVLV GTLYRPL
7638	38006	A	7692	54	522	RFHMSSLSASPPPRRLWTQMNT QCLVFSASHLPRCQEMLFQGTV *EKPHSPRCFSPAKKPRPAGAPA ASHKCR/CTP*PGPPSEPTV/PSD KAPLVGNAESQRVASPSGPPAP CSPV\GWPGTYKAIPASGTVAP TPLSAGTTDMTRLCPLSLEFLL ND
7639	38007	A	7693	3	57	RAGAGRSERAVAEES*GGLSGS CGRHNPGQSRLQRRPSQDVELE DCCRGC*SGSLWLRTLRPKRPA PFGGFSVPASSAASIPTGSAVVQ PGPLPGPTGKSPPVFAGSGPSSN PQPAFS\NMRTRDGSKPGSA/SF APLTPPLEPPAGLRAPSSGVSPL LPATIQSNRARARSPGDA*AAP PRPGVLTSAVPLPRRVT/CLRNS RAFAPAVRTNAVTP*PGGVSGP SQRRAEAA
7640	38008	A	7694	3	237	
7641	38009	A	7695	114	186	

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7642	38010	A	7696	73	904	FGGFLANLSYQEALSDTQVAIV NILSSTSGLFTLILAAVFPSNSGD RFTLS*ELLAVILSIGGVGLVNL AGSEKPAGRDTVGSIWSLAGA MLYAVYIVMIKRKVDREDKLD IPMF\FGFAGLFNLLLLWPGFFL LHYTGFEDFEFPNKVVLMCIIIN GLIGTVLSE\FLWLWGCFLTSSL IGTLALSLTIPLSIIADMCMQKV QFSWLFFAGAIPVFFSFFIVTLL CHYNNWDPVMVGIRRIFAFICR KHRIQRVPEDSEQCESLISMHSV SQEDGAS
7643	38011	A	7697	1	308	
7644	38012	A	7698	3	397	
7645	38013	B	7699	1	963	
7646	38014	A	7700	3	1433	KIRVTSKALELGKAQGQTGTD GSGRGWGRPNSGGKEGHFYYN ISE*VGGGASRSGAGPRRWRRG PRMLQITNASLGLRFRRQLLYW FL*GPSTLRGVESGSGGLEVLW GSRDPAGRMKVSNVSCQASVS RMHAAFGGTFK*APAPTPAHPF RAPQLICLAQVWAATGRRVAR VGMLSL*EGPGELVAGESGCA AVMQHLRAGPFRALLFTSNLD MDFRVSCLGWCMTSDFLTRPL SLLSLQEEERMVYVAFSEFFFD SAMESYFRAGALQLLLVGDKV CHGLFVGWAREGL*QSSLPHC AGGGRDRATCTPVRPRRGAAIK PSGTTISVTASVTIALVPPDQPE VQLSSMTMVRVPEWGLLAGG QGKMGCGLLSR*AGALPCTSVI GGQSHLSTGMGWAGFVRS*PS PSPRKA/RGVRMEEER\GVNWA GPD*ATNHAVSGGRMGKEGGP SPLSIAPQCHRPADVRASTAPTP
7647	38015	A	7701	2	391	MALRGKALRTTSDLRRFRIYSN HSATWKSLA/L*IPLQAPLK\TM LPELG*MPQCSNERT\WRG\VQ DPHYPEGIKLCAMKVVTNPCGI PSPIGA*SPTFAKGLREVIEKNR P\ADVRAS\TAPTPSHSSCLSP
7648	38016	A	7702	1	189	
7649	38017	A	7703	202	455	KCDILPTALDSIHH/SSHRVHLA HSPHSLQ**HPHPLAQPSQQDRP SVPL**MSLADPESHLSESHSHF HL*PACRV*AYDLLPL
7650	38018	A	7704	313	378	

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7651	38019	A	7705	126	1246	PNGLRPPCPSPASETPGNAPVCD PGSSSQGAQGKLNAWWAPGM A/ASRSLHSLHPVR/RACALPAQ SLLGPLRSFRCHLSDPVFRTGAP PGQGSWQYKVLVHAQERELTQ LREKLREGRDASRSLNEHLQAL LTPDEPDKSQGQDLQEQLAEGC RLAQHLVQKLSPENDNDDDED VQVELAEKVQKSSAPREMQKA EEKEVPEDSQEECAITYSNSHGP YDSNQPHRKTKITFEEDKVDST LIGSSSHVEWEDAV/HHYSRK* K***GRGRKRASVSQKPEETPS\ PRPEPPPRGSGEAERSVGSWDA SSRSLRRLHPLREPVPTLPSRFR GRCGASAAIFGSCVPHGGSTRA GMMGSKEVGKGGDPGEETSPV ALFS
7652	38020	A	7706	3	5665	LLEKLRQRIHDKAVALERAIDE KFSALEEKEKELRQLRLAVRER DHDLERLRDVLSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ WLKEEMETKFSRWQKEQESIIQ QLQTSLHDRNKEVEDLSATLLC KLGPGQSEIAEELCQRLQRKER MLQDLLSDRNKQVLEHEMEIQ GLLQSVSTREQESQAAAEKLVQ ALMERNSELQALRQYLGGRDS LMSQAPISNQQAEVTPTGRLGK QTDQGSMQIPSRDDST
7653	38021	B	7707	1	1098	
7654	38022	A	7708	193	5850	HCQRNTTGEHCEKCLDGYMIK S*DSLFGDVWN*LPIFASNFSFA EL*K*GFVRDYHK*TFVCS/CLL NP*GPEFVGKKIKRKKNHDAK YLNV*YS/CFRCAPGYYGNPLLI GSTCKKCDCSGNSDPNLIFEDC DEVTGQCRNCLRNTPGKYCHIL SIKKCISRLLFLFPTVCNCGGGP CELH*EQNFWFKNYFNSRHPLP QTDVSWCSAKTACL*HAFDL*F *RNVSPPGCDKCVWDLTDALR LAALSIEEGKSG

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7655	38023	A	7709	1	713	TPCFESPN/ETGTYFSTKAGYVL LN/ESSN/IGIEFEIAFKVRPRSSS GTLVHGHSVNGEYLNVHMKN GQVIVKVNNGIRDISTSV\TPKQ SLCDGRWHRIT\VIRDSNVVQL DVDSEVN\HVVGPLGIQKPIDH REPVL\VGGVPRILY*HPRFCPP QNPFTG\CIR\HFVIDGPPQWSFQ VKAAPGQAGARKASNSLSQQP GHGQKHSCPKYKVPLRALEKE HKASPGGTVTLSFGVGSFSSS
7656	38024	A	7710	3	322	DGVSHCRPGWSAVA*SQLTAT STSWVQMIACFTLPSSWDYRCT PPCLTNFCVCIFSRDRVWAMLA GW\LKNS*PQAIRPPQPPKVLGI TGHEPRAPGQKILTFHILT
7657	38025	A	7711	2	480	YSPPECPFCGKIEEHSEDMETH VKTKHANLLDIPLEDCDQPLYD CPMCGLICTNYHILQEHVDLHL EEN\TFSKAWIESSVLVIYNWLT SFSKKKTERGD/PEESRQEIEEF QKLQRQYGLDNSGGYKQQQLR NMEIEVNRGRMPPSEFHRRKA DMMESLA
7658	38026	A	7712	187	468	
7659	38027	A	7713	1	1110	MHCIETGVERRILGLLLFRGSLA SVIRPGEVLDAAHALVCQRGPK GKPSGAQCGSCWPLGRPKALT QLVPASFVCLACAFGAERLGDS ALRSSDLTHHLLVNTMLSCNIC GETVTSEPDMKAHLIVHMESEII CPFCKLSGVNYDEMCFHIETAH FEQNTLERNFERINTVQYGTSD NKKDNTLQCGMEVNSSILSGC ASNHPKNSAQNLTKDSTLKHE GFYSENLTESRKFLKSREKQSSL TEIKGSVYETTYSPPECPFCGKI EEHSEDMETHVKTKHANLLDIP LEGMDRVQCSGDLQLAHQLQQ EEDRKRRSEESRQEIEEFQKLQR QYGLDNSGGYKQ\NNYEIWR* K*IGEECLHLNFIGEKLI
7660	38028	A	7714	2	303	
7661	38029	A	7715	97	233	RTVTCYHRNSRACHPQQITSCP *HRALPCLPLWSPKCPSRWPWF G
7662	38030	A	7716	229	359	MKWVYCSVTGMGKGQHRMP\ SKG*GWVQRYNRDGIPSPRVLE LF

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7663	38031	A	7717	1	1185	MSTIDDPRLQGRRMCLMLRGT PEQKALVIGGEACMWGEYVDN TNLVPRLWLCPPSTQDLANEGI REMTILHRHIPDRGKGVMRSCS FRTPRPFTLACGPEKSLMDPQS QSNSEGASSSLVVKLADTDRER ALRRMQQMAGHLGAFHPAPLP LGACGAYTTAILQHQAALLAA AQGPGLGPVAAVAAQMQHVA AFSLVAAPLLPAAAANSPPGSG PGTLPGLPAPIGVNGFGPLTPQT NGQP\APTRSTITGSPLI/SGWSQ SRPILRIMKYAEQRIPTLNEYCV VCDEQHVFQNGSMLKIQPDTII QVWREDIPVNYMKELELVTKA GFRALLSAPWYLNRISYGPDW KDFYIVEPLSFEGTPEQKALVIG GEACMWGEYVDNTNLVPRLW AHRIQL
7664	38032	B	7718	1	1196	
7665	38033	B	7719	184	1689	
7666	38034	A	7720	228	407	
7667	38035	A	7721	1	725	MQRGALSPVLMLSAAPEPPPRP PPGLSPPGSGPGSGSRHGSARPG PTPEPSGSLGAALDSSLRAAVA FKAEGQRCYREKKFREAIGKY HRALLQLKAA/LGGPP*RPARP RPPGPTSSPGPARLSEEQRRLVE STEVECYDSSPA\CLLQSELVNY ERVREYCLKVLEKQQGNFRPP YRAG\IAFYPLGDYARALRFLQ EAPSREPPDTNVLRYI\QLTQLK MNRCSLQREDSGAGSQTRDVI
7668	38036	A	7722	1	262	NGKEPGRYTFEDAQEHIYKLM KSDSYPRFIRTSAYQELLQAKK KGRNIPIFPCHKNCTPTLRASTN LL*KEGKSLTSKRLTSLAQSY
7669	38037	A	7723	1	1392	

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7670	38038	A	7724	1	1544	MAQGNNYGQTSNGVADESPN MLVYRKMEDVIARMQDEKNGI PIRTVKSFLSKIPSVFSGSDIVQ WLIKNLTIEDPVEALHLGTLMA AHGYFFPISDHVLTLKDDGTFY RFQTPYFWPSNCWEPENTDYA VYLCKRTMQNK\ARL\ELADYE AESWA/RGLQRAFAPKW\EFIF M\QAGAQAKVDKKRDKIERKIL DSQERAFWDVHRPVPGCVNTT EVDIKKSSRMRNPHKTRKSVY GLQNDIRSHSPTHTPTPETKPPT EDELQQQIKYWQIQLDRHRLK MSKVADSLLSYTEQYLEYDPFL LPPDPSNPW\LSDDTTFWELE\A SKEPSQQRVKRWGFWAWDEGI GKTQLGRRNSFLKIF*EFRISGS GNFKVLGWASGRTLKKRPF\KE VPSRVQEIWQEFLAPGAPSAINL DSKSYDKTTQNVKEPGRYTFE DAQEHIYKLMKSDSYPRFIRSS AYQELLQAKKKGKSLTSKRLTS LAQSYLNGSSCSMNADWSHCT HFVAQCCDLEQRTLEQDVA
7671	38039	C	7725	81	439	
7672	38040	A	7726	531	686	GWQWLHRPPGATQHCGGNLP AEESLPARATN*ARPAAHTRGG RGQDLPPGG
7673	38041	A	7727	93	428	LHCQVHLSLIDLPLLI\SFLLLLF *D*VSLLLPRLECSGAISSHCSL H/LGPGSRDSPASAS*VAGITGT CHHVQLIFVFLLETGFHRVSQD GLDLL/NLVIRLPRPPKVLGLQA
7674	38042	B	7728	99	425	
7675	38043	A	7729	35	861	
7676	38044	B	7730	141	586	
7677	38045	A	7731	116	926	AEIVAQEVSEEGGKSRKGPQFG KSQYQELIRRSECGLNRGEGESI KANMQQVIYIFPITLAEVVLRP HSYPSKKTGLTLLAAASIAYISR *EWLYFETGTWVYPVFAKLSLL GLAAFFSLSYVFIASIYLLGEKL NHWKW\VSVRNSTLILYIRMAK SHTQSPTSLAHMPFCSIKIEMAE VPSSAQSMNWCEKLLVFPPR*C CFLRPRDSVSPPVFAWFILMHF NTRLFQEAFPGQPQILQRWRLE SVGICFQWPDWKSPAKHQLVK

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7678	38046	A	7732	32	394	GKAVLPIMRETLGDFHYQIHCC PDLPGTDLGHPGSPDLGEVKFL SQT*EVTSLQVSGKVWR*WTAI CTHTSQSLSISLL\FCLRSASATS LTLSHCVNVVKGLLDFKKRRG HSIGGAPEQR
7679	38047	A	7733	1	765	
7680	38048	A	7734	3	1295	QARVSQELKKAAKRTVSISEGP DTLGDGMRERRETLALAPEPEP LEKEACEKWKRPFRSASATSLT LSHCVDVVKALLDFKKRRGHSI GGAPEQRYQIIPVCVAARLPTR AQDVLDAHLSEVQCCSF\GPNS SLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDFDPF G/SNQVLAATYNQAAQLWKVG EAQSKETLSGHKDKVTAAKFK LTRHQAVT\GSRDRTVKEWDL GRAYFSR\TIQCSFSYCNDVVCG DHIIISGHNDQKIRFWDSRGPHC TQVIPVQGRVTSLSLSHDQLHL LSCSRDNTLKVIDLRVSN\TARG FRADGFKCGSDWTKAVFSP\DR SYALATLPVMGPF*IWECGTPG KNWKKQELTGTPIALPVQTPW PWCLLPGSPHGETWTQGRKGC AFGSRAHDLPALGWRLLPEA
7681	38049	A	7735	123	463	DVEVGLISQLQDCELGGCIPLK VFPAVFRLPLSLHTFLPLPLSRT LASGGDGATSASCCRCPGAVSI S*L*QTVASP*VLVFVHSRKE\T GKTARAIRDMCLEKDTLGLFLR
7682	38050	A	7736	1	489	
7683	38051	A	7737	1	423	
7684	38052	B	7738	1	900	
7685	38053	A	7739	1	1824	
7686	38054	B	7740	400	969	
7687	38055	A	7741	3	4781	EISATQIIVCTPEKWDIITRKGGE RTYTQLVRLIILDEIHLLHDDRG PVLEALVARAI\RNIEMTQEDVR LIGLSATLPNYEDVATFLRVDP AKVLFYFDNSFRPVPLEQTYVG ITEKKAIKRFQIMNEIVYEKIME HAGK\NQVLVFVHSRKETGKT ARAIRDMCLEKDTLGLFLREGS ASTEVLRTEAEQCKNL*LKDLL PYGFAIHHAGMTRVDRTLVED LFA\DKHIQVLVSTATLAWGVN LP*H\TALFK
7688	38056	A	7742	2	518	

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7689	38057	A	7743	18	1108	CSGIPRFRDSQSTRAACFFPAWT RMRAPSMDRAAVARVGAVAS ASVCALVAGVVLAQYIFTLKR KTGRKTKIIEMMPEFQKSSVRIK NPTRVEEIICGLIKGGAAKLQIIT DFDMTLSRFSYKGKRCPTCHNI IDNCK\RLQMNVEKSYCQLKEK YYAIEVDPVLTVEEKYPYMVE WYTKSHGLLVQQALPKAKLKE IVAESDVMLKEGYENFFDKLQ QHSIPVFIFSAGIGDVLEEVIRQA GVYHPNVKVVSNFMDFDETGV LKGFKGELI\HVFNKHDGALRN TEYFQSN*KTNSNIILLG\DSQG DLRMADGVANVEHILKIGYLN DRSGMSF*EKYMDSYDIVL\VQ DESLEVANSILQKIL
7690	38058	A	7744	105	548	PQTPRLKQSYHVSLPSSWWDHP VAGKRA*HAH*FYIMAQLFLPA ASPGPTPASQQPLWTQCLPISW RPWSAHSFLKPSSPGPGPTPASQ QGLWTQLPRSFQRPWPKSSSSR PGNGPGRAASRPPRAQLRPLGG LSRFNDGHGNFLAQ
7691	38059	A	7745	186	650	RCPGCPTTASARESREAESRGR GSSGASWGAVQWEEPQPRRLL RGTDDCMIFWAPHGSSTWRRR CVHSRSTAADPVLTPSPA/STPS SNCSGSGTSLAALPLPLPQTLGP *QPGWKGTPQPCLNTWGVSITS TGRWATPKIPGLTVPPENMDS MWG
7692	38060	C	7746	212	556	
7693	38061	A	7747	2	312	PDLK*STCLGLPKCWDYRW/RA TMPGWENIFSSMNHTLNALTG AVTSTRDNS*LHRVSCISSPWCC CLSPCPCRVSAGTGRVPSCLCH SGAWNRLDQDINRNNSC
7694	38062	A	7748	2	366	FLHTKYLLFCGIKAPHKYFIRSII FFFFLRQS/LYSIAQGGVQWGN LGSLQPPSPGFKQLSCLSLPSSW NYRCAPPCPANFVFLVEMGFH WIKPG*SRN*PRDPPASASQSAG ITGVSHHAQP
7695	38063	A	7749	1	446	MPILFTTVSSALSGAQHIADAQ CDRKGHRTTIQGSRVNLVQPSV GPKVEETQCWGPGRGMPGAPE APRERRVRSGSRSGDPGVA/PR AASGVGGRYAITRGRASAAVP CRSGGARRGGAGGQAADCGPG H*KESESRGPEGPAEGSQPL

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7696	38064	A	7750	1	744	GGLIPRAQRESKRRSRGRARAA SGV/VWALCYHPRQSECCGTL* KWRSSPRRCWRTSG\DCGPGH* KESESRGPEGPAEGISASLKM* WFASGTCLSRCLTLRQRK*LKK IKIIWIKK/SEK/PAEAT*SEGQPP F*GPRQTGAEGF*LEPPQPGMSL KLFKVILKG*DSRTKMGDQQPP RVHGRTHGPLQPLTPVKGQGS CPVKGPSPSGIWP*KPLL*CLAT L*WQEGTFSLSGLLGPGTPGAS VGHKIY
7697	38065	A	7751	316	650	SYNTHGITFHVPTANVLVVDL MCHLEKLAKYDDIKKMVKQA LEGPL\KGILDYTEQQVVSSNFT SDTHSFTFDAGAGTAFNNHFFK LIF*YDNEFGYSNRVVELMFHP ASKG
7698	38066	A	7752	2	775	QARRARSRNSRGLSQSAARPLA AKTAWRTVAPPQPWAAAPR*R SSCPHSSCSATSPGPARACQSSA HSPSPRLQAPPPPTSS\SGSSVPE AATAPLAASARRGTPRPRTGRP SWAGTRQGSWAGTQRPWVWA PAPAGPPRAAAAAAR*GRDKS QLTCPPRHSTPPGSAAGASRHR RRGLAGPAPSPPGCRAARPPWP SAAAALGLGGRGPDLVALHCEI HWPLEFQSLCCCLLTSRGGEAS CHPEFHLFMHDFLPGSF
7699	38067	A	7753	1	552	MQTLFTLLQPSSQTPGIPQPIVC CVYAESGARDSGQP/PSKVPVPS FCTPAATQRG*REPGCSHPAGD CSAPQQCS*PGQ/RIS/RGDKVL ASNTYLPGPPGLPGGQGPPGTW MKVETITQQTNTGTENRVFSLS LYMTISKQYLSEEQGSHWLSCL INALQAFFSNAAIWLVTWFELS RVLDGAEND
7700	38068	A	7754	2	538	LGKYITGDKVLASNTYLPGPPG LPGGQGPPGSPGPKGSPGFPRY A\GLLGQPGSRGSIGTHGTIS*S/ G/LPTKQGRRGPVGPPGPPERD GSKGERGAPGPRGSPGPPGSFD FLLLMLADIRNDITELQEKVFG HRTHSSAEEFPLPQEFPSYPETM DLGSGDDHPRRTETRDLRAPRD
7701	38069	A	7755	146	373	

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7702	38070	A	7756	678	1582	CQGNSPLSGVWPSGDWEDKHS Q*CPVVCSPQNILSQTSRHNDR DYRLPRAETHSSSYAQYSTPSN LVVHPTATPSTVPSSPFTLQSD\ YQPKKSFDANGASTLSKLPTPT SSVPAQKTERKESTSGDKPVSH SCTTPSTSSASATE/S/TTSAPPTS ASAGPCFSCSTARQYLPYFRDP NLLRTIAVLLCKATVAALINS*C GTYLKIK*SSYSSCDTSLTAVYN S*VSYCWTICFQHNVSDFSSCSA \PTQAQPSNQSPMSLTSDASSPR IICFSKE*GTPQT\NTVPIQTFGFS TPPVSSQAKG
7703	38071	A	7757	1	1365	MHLIPPATNCDTLVECCLPGKL TRDLVCTAFTGFGTSYSPQENS HNHSALHSSNSHSSNPSNNPSK TSDANILSQTSRHNDRDYRLPR AETHSSSTPVQHPIKPVVHPTAT PSTVPSSPFTLQSDHQPKKSFDA NGASTLSKLPTPTSSVPAQKTE RKVLQQLSKHNRKVMIRSALIT SIILDLLYIEKDLRYQKNIESTSG DKPVSHSCTTPSTSSASGLNPTS APPTSASAVPVSPVPQSPI/PSLT SGPKSS*TIA\PALQATLQLNNS NVDISKINEAQPSNQSPMSLTSD ASSPRSYVSPRISTPQTNTVPIKP LISTPPCFITAKG*LLQ*LSQGTS VHSQPHTAACNC*/PSSK/SHEP VSPRSLQRSSSQRSPSPGSQFILL NSSNGIQMATVVPQEFFLARFH VFHLTPGTRRPPFQWKISLKHV SRDGPADSWQEEGRASRFTAE GRRH

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7704	38072	A	7758	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL\PIYRV SRKAANFEWSPEQEKALQQVQ AAVQAAWPLGPYDPADPMVLE VSVADRDADWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGQRRWWQLAE RQDSRDREAAIGERQETAVGKT ARDGEAVCD
7705	38073	B	7759	56	3476	
7706	38074	A	7760	3	591	DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLTM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEEKSSQW
7707	38075	A	7761	1	558	
7708	38076	B	7762	1	1189	
7709	38077	A	7763	604	1760	NSWCRWFNFRY*YPTFYWES* NT*IPLREWFG*NHDASCP*TLD SKSFSFETRTGSPCSSSLQTAYC GTLWIVQGV
7710	38078	B	7764	1	474	
7711	38079	C	7765	1	3384	
7712	38080	C	7766	1	333	
7713	38081	A	7767	1	390	
7714	38082	A	7768	3	728	
7715	38083	C	7769	184	529	

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7716	38084	A	7770	2	837	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL
7717	38085	A	7771	2	469	
7718	38086	A	7772	3	587	YPASAGLMLQNFGVIGLRYHF AIHSPAAGGLLDGLHAVAAIQG ITKIETTPNHQRAPAHWTLLTQ QAHLQPSPLHFNLPLTLCLMHC PTAIPHCFADARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVG\AYGAQLL
7719	38087	A	7773	1	633	MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAF\LPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPSS GDIKEYFPNAFVLLTTASLQGQ DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
7720	38088	B	7774	1	1431	
7721	38089	B	7775	75	947	
7722	38090	A	7776	6107	6706	MVVVFLHKCLHYFHSTQLVISR YNSPTSEYFQALDLTWRALGT VGSAPPILPDLGGTNRRQPFPIL SHSGLHRNVLQPETDSQSEDRL PVTWLAVSACCQQQMVGGNP TRSKL*RTGSHYHLPG\WEP*RP HFPHAGSLAWQWLLCSSLEHSF GA*ELPCNPCKGWCLCPCHFIF YIFFNSFLSNCPIQLCNWHSSYFI

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7723	38091	A	7777	1	3179	MAEGKEEQVLSYTDGSRQREN EEDAKAETPDKTIRSHETYSLPR EWYEGNRPHDSITSQWVPPTTR GNYGSTIQDEIWVGDHSGYVRP VPVPRSLNSDISYFGVGGKQAV FFVGQSARMISKPADSQDVHEL VLSKEDFEKKEKNKEAIYSGYI RNRKDDYDNHTGIDLVGTIIATI KGSNEEDTDTPLFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP
7724	38092	A	7778	281	1531	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLTAMGVI GSHGARGQVVALNRQRQGDL QPFTRVTVHWGKG/NMQIFGGL LDTGSELTLIPGDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKQYCIP GGTEEISATIKELKDAGEVIPIPT TFPLNSPIWPVRKTDGCWRMT VDYCELNQVVTPTAATVPDVV SLLEQINTSPGTWYADIDLANA VFSIPVHKAHQKQFAFSWQGQ QYTFTVLPQEYINSLGLCHNLI WRDLDGFLLLQNITLLVHYVD DIMLIGSSEQEVANALDLLVSM ASSRVPYDQLTEEEKARFTDGS ARYAGTTRKWTAAALQPLSRIS

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7725	38093	A	7779	332	2159	RGYVFCSWKKTDGS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQGQQYTF TVLPQWYINSPALCHNLIRRDL DCFSLPLDITLVHYIDDIMLIG\P RQLLACYWALVETECLTLGHQ VTI*PELPIMNWVLSDPSSHKVG HEQQHSIIKWKWYVHDWARA GPEGTTTPVISQWPHEQCGHGG RDGGYAWAQQCRLPLTKADL NTATAKRPICQQQRPTLSPQYG TIPQGDQPATWWWVDYMGSL PSWKGQRFVLTGIDTYSGYGFA YPACNASAKTAICGLTECLIHH HDIPHSIASDQGTHFMAKEVRQ WAHDHGIHWSYHVSHHPEAA GLIEWWNGLLKSQLQCQLGDN TWQGWGKVLQKVVYALNQHP IYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLLPFPATLQSA GLEVLVPEEGTLPPGDTMIPLN WKLRLPPRHFGLLLPLNQQAK KGVTVLAGVTDLDYKDEITLLL HNGGKEEYAWNTGDPLGLLLI LPCPMIKVNGKLQQLKPEALVP KGVVFPPGDTTMLSLSWKLRLP SGHVGLLMPLSQQVQKGVTVL
7726	38094	A	7780	84	202	
7727	38095	A	7781	1	551	RWGSHTVAQAGVQWCDHGSL QPRSPGVK*SSHLSLLGSWNHR HATTTPG*FCFFSRIRSHCVAQA GL*LLTSNHPPALASQT\VGITG VSHWTWPNTGFSVLTATNKNL KFFHYAISKCLVRAKLSSRLLKI EERNKALSAPVVSVSIFDRVLR LLGYSASDWQPEFVETAVSNFV IYGIFRGQ
7728	38096	A	7782	1	678	MPACRLGLLATALIISLLLFGFTI VSGTGAEKTGVCPELQADQNC TQECVSDSECADNLKCCSAGC ATFCSLPNGQLAE*FEESEESSL DTVSPFVVFQSISSTLRIE*ARA GDSSQ\DKEGSCPPGVTI*LFPSS GLC\RDQVPGGTAQCPGQ\M\K CCR\NGCGKVSCVTAQFLSSSH HQAEQVRRDSFLPGPASGFQAH LPSPFFGTLYSLFGLTTSFSLSQP

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7729	38097	A	7783	1	1972	MAVNGCLEGPSSNFLSCLFIVA LVGSESTHPLCLEQPATQETRY QLLQLRPAQRASWIGYAIAYHL LEDYEMAAKILEEFRKTQQTSP DKVDYEYSELLLYQNQVLREA GLYREALEHLCTYEKQICDKLA VEETKGELLLQLCRLEDAADV YRGLQERNPENWAYYKGLEKA LKPANMLERLKIYEEAWTKYP RGLVPRRLPLNFLSGEKFKECL DKFLRMNFSKGCPPVFNTLRSL\ YQDKEKC\AIIEKLVVGYETSLK SCRLFNPNDDGKEEPPTTLLWV QYYLAQHYDKIGQPSIALEYIN TAIESTPTLIELFLVKAKIYKHA GNIKEAARWMDEAQALDTAD RFINSQCAKYMLKANLIKEAED MSSKFTRGGTSAVENLNEIQCM WFHTECAQAYKAMNKFGEAL QKCHEIERHFIEITDDQFDFHTY CMRKITLRSYVDLLKLEDVLRQ HPFYFK/EQARIAIEIYLKAS*QP PYR*GIKGTRRLDTAK\LSDKEL KKLRNKQRRAQKKAQIEEEKK NAEKEKQQRNQKKKKDDDDE EIGGPKEELIPEKLAKVETPLEE AIKFLTPLKNLVKNKIETHLFAF EIYFRKAAKMVYYLDPSSQKR AIELATTLDESLTNRNLQTCME VLEALYDGSLGDCKEAAEIYRA
7730	38098	A	7784	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEETLFSN
7731	38099	A	7785	1	681	
7732	38100	A	7786	415	692	
7733	38101	B	7787	1	2204	
7734	38102	A	7788	1	615	MPVDHPPIKAFSEKRTSQSVNM LAKTHPYNPLWAQLEWFKLLEI SPKSPINTDKFLLKRLSVPGSDS CRVRMENVLASQVLHPG\QLM M*EGSGWAEARIT/V/CS*AANP *KWHPASLPLPW*CRVRMENV LASQVLHPGHADDVGGKWLG RSKDHRAPEQQTRESGIRLPSLF PGSAEQPWRGNAQWHLSWKA LRGVFGMIPDSLLYEFHQSAKK SSHFKPPQPLLYWTLVNFLIPFS LHSSTWFMWSSNQGIMCKEEV

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7735	38103	A	7789	3129	3197	TQNRRACSPDTEQLARQSGTYP VSLGQATVLEDSKAALPGLGPT LMAVTVVTTEAAVAIGCEAAH SSREDFTNHQLWRRTVEGKKG EGKNKFMSGGVNTTVPLLKTS RKGSPDSPHLREKPSLEKVTFQI GSFASPESDFESRMKKMEERVK ACGPSLEASEAADVAQDPQVS RSPFKPGFQENVCCPQNRLSEG DEGESDKGFAEDRGSRNDMAA DIAGQLSHAADLGTASHDDVT YAIKPTCWPGLDIIPSCL
7736	38104	A	7790	1	1069	MAEKEAGMSYMVAEVLGFVA VIIEAESLKRIRFFENFTVAEERS TDETFSLAEETCSSNPAMVRRK KIAISIIFSLCEKEEAQRNFQDFF FSHFPLFESHMNRLKSAIEKAMI SCRKIAESSLRVQFYVSRLMEA LGEFRGTIWNLYSVPRIAEPVW LTMMSGTLEKNQLCQRFLKEF TLLIEQINKNQFFAALLTAVLTY HLAWVPTVMPVDHPPIKAFSEK RTSQSVNMLAKTHPYNPLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTYFLRCSELQ E/IPADLEWQSW*R*PAMVRRK KIAISIIFSLCEKEEAQRNFQDFF FSHFPLFESHMNRLKSAIEKAMI SCRKIAESSLRVQFYVSRLMEA LGEFRGTIWNLYSVPRIAEPVW LTMMSGTLEKNQLCQRFLKEF TLLIEQINKNQFFAALLTAVLTY HLAWVPTVMPVDHPPIKAFSEK RTSQSVNMLAKTHPYNPLWAQ LGDLYGAIGSPVRLTRTVVVGK QKDLVQRILYVLTYFLRCSELQ ENQLTWSGNHGEGDQVLNGSK IITALEKGEVEESEYVVITVRNE PALVPPHPTTNSSRETQPLADR
7737	38105	A	7791	118	273	FSLSNLVQFFRVCNDHLYTKLH FCFLQAEVKASNFCIYDSLGHA LGSHHTVECIATDEHTLHLTSP MG*SQGKQFLHLRFSWACPGIP PHS

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7738	38106	A	7792	1	551	MQPELPIMNWVLSEPSSHKVG HGQQHSIIKWRWYICDWAVVG RESTTNGLA\GWS\GTWKKHD WKI\NDNEIWGK\SMWIDLSEW SKTVKIFVSHESAHHIT*KSSAE EDFNNQWDGMTCSVDTTHPLS LTTSVIAKWAHEQSDHGGRYG GYAGAQQHGLPLTKADLAMTT AECPICQQQRPSLSP
7739	38107	A	7793	1	782	MTKIQEPSTSVKFLGVQWSGA YQDIPSKVKDKLLHLAPPTTTK EAYLGL/FGFWRQHIPH/LGTEQ EKTLQHVQAAVQVALFLEPYD PADPMVLEVSVADRDAIWSLW QAPISESQWRPQGFWSKALPSS AANYSPFERQLLAYYWALVET EHLTMGHQVTKQPELPIMNWV LSDPSSHKVGCAQQHSIIKWKW YICDRARAGPEGTTTPVITQWA HEQSGHGGRDGGYTWAQQQG LPLTKADLATATAECPICQQQR PTLSP
7740	38108	A	7794	65	230	
7741	38109	B	7795	1	2115	
7742	38110	A	7796	1	246	
7743	38111	A	7797	1	1293	MAAAACLDASGEARPGLRPPW SQQGRKQAGALPPTKLAGLLA QLQPAEAPDLGIPVLSATREDPL SPQARKCLLPLPGLSPCSQHLL WCRASCGRAWGPSRPSRVCTG LDTAVTPAPCRLSPLWTSGADK RGREASRGEGSSKWACRHPSA QTAWAVEGDRHRFLSRKGQIT GKTPPSSQGQPEAWGLSCSCPH TLHTSFFLDTGPLNGGTEKAVT QTGPKHAPCSPGCGQQGGKGC GPSGTPDLGALRARAVTVGLCS SWHLQASGHHCIPQYLQQKLL VVHLVQPQPCTKPVPVPSFRLQ MTIENMNHLKFIPHKDYTANRL VSGLLQLPSNTSLVIDETLL\EQ GQLDTPGVHNVTALSNLITWQ KVDYDFSYHQMEFPCNI\KVFIT SEGRSLLPADVPDSLTAPANST KHGGST*TAFSQRCCLPC

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7744	38112	A	7798	1	2555	MPSHLNQHQIIHTKEKSYKCEE CGKSFKRSSNCTTHKRIHTGEK PYRCEECGKAFRWPSNLTRHK RIHTGEKPYTCEECGQAFRRSS TLTNHKRIHTGERPYKCEECGK AFSVSSTLNDHKRIHTGEKPYT CEECGRAFNCSSTLKTHKRIHT GEKPYKCEECDKAFKRHSSLA KHKIIHTGEKPYKTGS\CILLQR YCWSTT*TIHFKK*S*EN/PGSC DLNTLRLKKDYQRVGNCKGQK SSYNGIHQCLSATRSKTCQYNK CGKAFGLCSIFTEHKKIFSREKC YKCEECGKDCRLSDFTIQKRIH TADRSYKCEECGKACKKFSNL TEHNRVHTGKKPYKCEECGKT FTCSSALTKHKRNHTGDRPYKC EECHKAFRWCSDLTKHKRIHT GEKPYKCKECHKAFRCCSDLT KHKRIHTGEKPYKCNECGKAF MWISALSQHNRIHTGEKPYICE ECGKAFTYSSTLISHKRIHMELR PYKCEECGKTFKWFSDLTNHK RIHTGEKPYKCEECGKSFTCSS NLIKHKRIHMEVRPYKCEECGK TFKWFPDLTNHKRIHTGEKPYK CEECGKTFTCSSSLIKHKRSHTG DR/PYKCKECGKAFRWFS\ALL NISKHKRIHTGEKPYICEECGKA FIRSSTLTSHKRIHMEERPYKCE ECGKTCIIHIGEKPYKCNECGK GFMWISALRKHKRIHTGETPYI
7745	38113	A	7799	212	461	TEEHLYSPHWKGCGRKVKRLF QVRRGRGWIQTRQPGSMVKEP PLSEAGAESHVSC/RQGDCSRPP SFPLSPERVTPWLPDSHTW

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7746	38114	A	7800	1	1398	AAAERELELLRASLEHQRGVSE LLRGRLRELEEAREAAEEAAAG ARAQLRE\ATTQTPWSCAEKAA QTESPAE\GPP*LRRARPDPWTE TRAVAPAG\ILKSIMKKRDGTP GAQPSSGPKSLQFVGVLNGEYE SSSSEDT\NDSDGDSENGGAEPP GSSSGSGDDSGGGSDSGTPGPP SGGDIRDPEPEAEAEPQQVAQG RCELSPRLREACVALQRQLSRP RGVASDGGAVRLVAQEWFRVS SQRRSQAEPVARMLEGVRRLG PELLAHVVNLADGNGNTALHY SVSHGNLAIASLLLDTGACEVN RQNRAGYSALMLAALTSVRQE EEDMAVVQRLFCMGDVNAKA SQTGQTALMLAISHGRQDMV\A TLLACGADVNAQDADGATAL MCASEYGRLDT\VRLLLTQPG\C DP\SILDNEGTSALA\IALE\AETG MKVAALL\HAHLSSGHPDTQSG VTPLAPQTANTW
7747	38115	A	7801	3	408	
7748	38116	C	7802	141	251	
7749	38117	A	7803	1	1173	
7750	38118	A	7804	451	853	LQMHRLCGGHSLSGCGWHTAR GQELVGQCFL*GGGQLLGLQH PL/AENPTFQEYSLITSEAGLLEG RKKKNKTSRGPSGPATCPLGLP RTSPGATRPGPVS/HAAIASQRD SSRTRFSSSLDAAIIARPYTTPSA
7751	38119	A	7805	1	2950	MAASRLELNLVRLLSRCEAMA AEKRDPDEWRLEKVGVTYSVA SGRVLFQDFTEQFQVLLPKDAQ PCREVISTLLEKMKIDKRNYQIG KTKVEPGV/EAWPLRRVRRQPD QRQGLGAHRAGEAPGTRGDAR PVHRGPLPQVGCCQPHSGAPAG AADRPRSSQAGELPHPRHHRGA EAVAAGAARAPHDLRTVRRLP PSRRAAGEAGAAGCH/RMPSW STFQKPTTTPWRDSSSTLSSNHP LTASGCAGWPCSRMST
7752	38120	C	7806	398	415	
7753	38121	C	7807	13	81	
7754	38122	B	7808	1	972	
7755	38123	B	7809	1	1803	

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7756	38124	A	7810	1	929	IAAAPELLERSGSPGGGGGAEE EAGGGPGGSPPDGARPGPSREL AVVARPRAAPTPGPSAAAMAR PLVPSSHKALLLELKGLQEEPV EGFRVTLVDEGDLYNWEVAIF GPPNTYYEGGYFKARLKFPIDY PYSPPAFRFL\TKMWHPNIYETG YVCISILHPPV/DTDPQSGELPSE RW\NPT\QNVRDHSS*V*SSLLE RRPNTFLRPANVGRLPWMLQG SWEREQGGRIRELHRTSFRKQV LGTKVDAERDGVKVPTTLP\EY CVKDQGRRAPDEGSDLFYDDY YE\DARVE\EEADSCFGDDEDDS
7757	38125	A	7811	2	296	LSLSFFFVKAHFYVKSMLHSKD ASGISGMDFYVVQ*FSWQTAY AGEVGRWLSPALTERGSGQTL* TWCWRVFCVCLE\GHMWVTEA YVTVKH*NYSKVK
7758	38126	A	7812	397	410	SPGEI*G*VPPLLG*GVLLYQPP LFKIWEAPLLPDLLQQ*KLYSL WLNKALGK
7759	38127	A	7813	2	739	ELCALVFGVNTFFATIVKTIITFI VSDVRGLGLPVRKQDSVVVFL DCPSIW*LRYIDLLILRVHLQIH LWGLRGRRAEFKHI/RSAEEKK LTRIPSVNGE*TGKSPAPANS\PP RGARDMWRTGRPAPRRPLVGG PSPSDRGPASTTSPELAVGAVN GGPSSANISRGFWQQSFHGNMC WFCAEPGVAGVPFTANIAGTEP GGLGQGRQCSLATQCHKPELK LQAKPAFPFSFSLSLFFFLLKHIL

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7760	38128	A	7814	594	2868	CWTSRNRRPIPGSCHPMELPRPF RGKAKVQNHQLVH\HNKALIN RGSLTFWLDDGAIQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSWLNEDPFVCEYQ GQSSDLPQPPVNAGGGSGGGS GGGSEGGGSEGGGSEGGGSEG GGSEGGGSGGGSGSGDFDYEK MANANKGAMTENADENALQS DAKGKLDSVATDYGAAIDGFIG DVSGLANGNGATGDFAGSNSQ MAQVGDGDNSPLMNNFRQYLP SLPQSVECRPYVLSAGSEIGAA CASRSGYDNKGVRDIGYTDCK RSEDLDPLRHQILGGKKAIQFTL QGFPTLPEGAPAGNSGSLAVHK TAQSSYRHHALLILTPMSGTRF PPIPGPVVNIRVFPFAPSSECRIC YSWSWVPGSPVHCQSDGSVPIP SYAPLASQYSSSFLFFRNRQPYA PYDYLSVMTPSRTLREQIRIRYA PSAPRLPPPEVYCSNSTIVYVRN NPSGPTPGFAGGTLLEGRSGGP FRFYAKRAKGDVLKPFSLNLPL QTLIRFMVDIACGMEYLSSRNFI HRDLAARKCMYEFWRTRGWE TAAAYYGGGTTFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGYVSNSLT GPYKPLNKTGLVLQMGLDPND
7761	38129	A	7815	2	474	RRFVSADNCRSLRWKSLYTPLD ADASVLISTGIDATQTNHGRQH LDETQVRVFGQHLMQGSYTTQ DGRSDVAISCSCKLEMCAQQSY DQLLAASTENWRQWWQKRRIT VNGG/GSSPASDADQTPAPGFR RDVGDRDWFAWRQCLLKSALT RRRPVAYIVISSAMSGSCLPKQS D
7762	38130	A	7816	302	409 .	
7763	38131	A	7817	199	359	ARRQQVSVKSYRWEEEDQHCG ELQGSE*VSDGLFKPP*S*HGW VEEERQKEQN
7764	38132	A	7818	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLKSILVLIRIVVMMVSMLP QLALSGWGRFRVLPG

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7765	38133	A	7819	118	445	AAGGEPGDAPWVPGVWEPPES VCRGPPPSSTFPHPVLSTFGASG PENSRDCSWLSPQH*AA*VASG NNGPQAAQGSLSGIPDAATLSG I*RASILHVSVVEIISSPGFR
7766	38134	A	7820	1	770	MRVLGIETSCDETGIAIYDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCWKIPAPNFR CALLGSAAYAVNHGTGLSKKP TTLGSDHSKTPAQLAKRAGEA RRNGWQGALFPWESARSGEEE TP/VICRH*HSHRAAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVLD
7767	38135	A	7821	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRRPFRGKAKVQNH QLVHLQQSSHQPWLPHFLAG* WGDSGLGGGS\EGGGSEGGGSE GGGSEGGGSGGGSGSGDFDYE KMANANKGAMTENADENALQ SDAKGKLDSVATDYGAAIDGFI GDVSGLANGNGATGDFAGSNS QMAQVGDGDNSPLMNNFRQY LPSLPQSVECRPYVFGAVRHDV RRIRVTGVTRVTPPEEVDTSVH SRGAHRIRSGFAPKRSVRVTTD TCIKRNSTCGVKSLSLWDGGGF
7768	38136	A	7822	1	1044	

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7769	38137	A	7823	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRPVPPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCRTSGSVYITLKKCKQREGS RAMLPGFPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQGQSSDLPQPPVNAGGGSG GGSGGGSEGGGSEGGGSEGGG SEGDGSEGDGSGGGSGSGDFD YEKMANANKGAMTENADENA LQSDAKGKLDSVATDYGAAID GFIGDVSGLANGNGATGDFAG SNSQMAQVGDGDNSPLMNNFR QYLPSLPQSVECRPYVFGAGKP YEFSIDCDKIKILRGVFAFLLYV ATFMLPVIANIAIPQKRPFMQQT RCEVQCREDIEVQKLKSYDKLL ASINKKPGVNGWQKRRITVNA GEAHDQQALDYALYHLRIMTP AHDERSSIAAKGLTGEGYKGH VFWDTEVFLLPFHLFSDPTVAR SLLRYRWHNLPGRARRKRDGN GWAGGAPISVGKARAAAKK
7770	38138	A	7824	601	853	
7771	38139	A	7825	2	644	MAQGQ/RKFQAHKPAKSKTAA/ A/ASEKNRGPRKGGRVIAPKKA RVVQQQKLKKVSLCCSGWS*T PGLKASSRLCLPKCWDYRRDTL WLFLSATFICRWNLRKSESGKK IEHDVVMKA\SSSLP\RKLALLK APSPRRNGAAAA\TSSKTPSLRT AGPQLQGQHPTPLPSIWGPLQV NSHRLSLFRMRTLSPSDWASPR HSSGGPKGAENPGNDQGRYSH
7772	38140	A	7826	1	2616	
7773	38141	A	7827	1	504	

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7774	38142	A	7828	1	1068	MAEIQHKTIRPLLEGRDLLAAV KTGSGKTLAVLIPAIELVVKLKF MPRNGTGVLILSPTRQLAMQTF GVLKELMTHHVHTYGLIIGGSN RSAEAQKLANGINIIVVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPKKEPLYVGVDEDKANATVD GLEQGHFVCPSEKRYLLLFTFL KKNQKKKLMVFFSACMSVKYP YGLLKYIDL/PVLAIHGKQKQN KHTTTFF*YCNADSGTLLF\QLE KLIEKNYFLHKSAQETYKSYIR AYDSYSLKQIFNINNLNLPHIAL SFGFKLPPFVDLNMNSNEGKQK KQGGFGYQKTKKVEKSIIFKHIS KKSSAAGSSLTQEMPVFILNNF
7775	38143	A	7829	3	1851	
7776	38144	A	7830	1	905	MVFDAKYLTGWRFEDTVVQSN MKHQPFIVVNKHNVQVEYKGE TKSFYPEEVFFMVLIKMKEIAET YLGKTVTNAVVTVPAYFNDSQ HQATKDAGTIVSLNVLRIISKPT AAATAYRQKGIDFNTSIFHALF EELNAYLFHGTLDSVEKALGN AKLDKSQIHDIVL/GPFEQGRH* MYGPGS*EIQS*R*EAEGQDVIQ EFS*KLCIRYESSC*R*ETSRQD* R*GQTEDS**GY*NYQLAG*ES DSEEGRISTSKSGESLQPHNYQP VPEYRRHTRRNAWGIP*WWSS LCWSFPRAPIEEAD
7777	38145	A	7831	2	886	ARGACSSWVFCGFLRYWSQAY TPATMSKGPAVGIDLGTTYSCV GVFQHGKVEIIAN\DQGNRTTPS YVAFTDT\ERLIGDAAKNQVAM NPTNTVF\DAKRLIGR\RFDDAV VQSDMKHWPFMVVNDAGRPK VQVEYKGETKSFYPDEV\SSMV LTKMKEI\AEAYLG\KTVTNA\V VTVPS\YFNDSQRQATKDAGTI AGLNVLRIINEPTAAAIAYGLD KKVGAERNVLIFDLGGGTFDVS ILTIEDGIFEVKSTAGDTHLGGE DFDNRMVNHFIAEFKRKHKKDI SENKRAVRRLRTTK
7778	38146	A	7832	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTLDPVEKALRDA KLDKSQIHDIVLVGGSTRIPKIQ KLLQDFYEAVAYGAAVQAAIL SGDKS\ENV\QDLLSL\DVT\PFP LGIETAGG\VMTVPH

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7779	38147	A	7833	1	218	
7780	38148	A	7834	508	883	YYHSYQADT/HLGGEDFDNRM VNHFIAEYKRKHKKDISENKRA VRRLRTACERAKSTVSSSTHAS TEIDSLSEGIDIYTSSTCASFEEL NADLFLSTLDPVEKALRDAKLD KSQIHDIALSINPDEAVAYGAA VQAAILSGDKSENVQDLLLLDV TPLSLGIETAGRVITDLIKHNTTI PTKQTQTFTTYSDNQPGVLIQL YEGEHTMTKDDNLLDKFELTGI PPAPRGVPQIEVTFDTNSNGILN VSAVDKSTRKKNKITITNDKGH LSKEDIEYMVQEAEKYKAEDQ KQR/D/KVSSKNSL
7781	38149	A	7835	1	194	
7782	38150	A	7836	1	1482	MVFDAKRLIAHRFDDAVVQSE MKHWPFMVVNDAGRPKVQVE YKGESKSFYPEKVSSMVLTNM KEIAEAYLGKTVTHAVVAVPA YFNDSQRQATKDAGTIVGLNV LRIINEPTAAAYGLDKRHRSSLP ILTASL\GAGSGL*STQA/SIEIDC LYEGINFCTSITHARFEELNADL FRGTLDPVEKALRDAKFDKSQI HDIVLAGGSTRIPKIQKLLQDFF NGKELNKGINADEAVAYGIAV QAAILSGDKSENVQDLLLFDVT PLSLGIETAGGTQILTTYSDSQP GVLIQAYEGKHAMTKDNNLLG KFELMGIPPAPRGVPQTEVTFD SDANGILNVSAVDKSTGKENKI TITNDKGCLSKEDIERMVQEAE KYKAEDEKQRDKVSSKNSLES YAFNMKATVEDEKLQGKINDE DKEKILDKCNEIIIWLNENETAK KEEFEHQQKELEKVCNPIITKLY QSAGGMPGRMPGGFPGGGAPP SGGASSGPTIEEVD

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7783	38151	A	7837	2	2221	PRVRPRVRSPAALGFFVASFVIG ARPTPQQPWSKGPAVGIDLGTT YSCVGVFQHGKVEIIAN\DQGN RTTPSYVAFTDT\ERLIGDAAKN \QVAMNPTNTVFDCQTV*LDGR FDDAVVQSDMKHWPFMVVND AGRPKVQVEYKGETKSL\YPEE\ VSS\MVLTKMK\EICRSLTLGKT VTNA\VVTVPS\YFND\SQRQAT KDAGTIAGLNVLRI\INE\PTAAA IALQKFRQKRFGAERNVLIFDL GGGTFDVSILTIEDGIFEVKSTA GDTHLGGEDFDNRMVNHFIAE FKRKHKKDISE\NKRAVRRLRT ACERAKRTLSSSTQG\SIKIDSL* EGIDFYTSITRARFEELNADLFR G\TLDPGEKAL\RDAKLDKSQIS *YLSWVGGSTSYSPRLQKSCCQ DFFQWEKELELRSINPGWKAV/ AFIGAAVPGQPFLSGRQVLENV\ QDLLLL\DVTPLSPWVLKTAGG VHDCPPSKRNTTIPTKQTQTFTT YFWTTQPGCGLFRFYEGRALP WTKDNQPALASFELTGIPP\APR GV\PQI\EVTFDIDANGYTPWSL AVDKKYGKKRTKITITN*QGPF *AREDIGTYGSREAEEVTKLEG GGRQEGTRVSSNDFT*GPMPFN MKSTLLKDEKL\QG\RINDEGQ NRRFLDQV*LKLSNWL**ESRL LEKEEFEHQQ\KELE*VCNP\IIT QAGTQSARRHCQGGNPWGAFL
7784	38152	A	7838	3	757	PFPGGRVVRLHPVILASTVDSY ERRNKGAARVIGTLLGTVNKH SVEVTSCFSVSHNESDEVAVDM EFAKNMYEL/H*KVSPNELILG W\HDITEHSVLIHEYYSREAPNP IHLTVDTSLQNGHMSIKAYVST LMGVPGRIVGVFTPLTVKYAFY DTECIRVDLIMKTCFSPNRVVG LSSDLQQVGGASARIQDTLSIVL QYAEDILSGKVSADNTIRKVGH FLMSLVNQVPKIVPDDFETMLH SNINDLLMVT
7785	38153	A	7839	1	1821	
7786	38154	B	7840	16	1305	
7787	38155	A	7841	1	359	

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7788	38156	A	7842	2	1085	GVAPWGRGRAAPRCASATVGG SGIGRLR\GITSSGL\KMDNKKR LAYAIIQFLHDQLRHGGLSSD\A QESL\EVAIQCLETAFGVTVEDS DLALPQTLPEIFEAAATGK\EMP QDLRSPARTPPSEE\DSAEAERL KTEGKPKQMK\VENF\EAAVHF LTEKPFELNPSQRPSYFCNRAA AYSKLGNYAGAVQDCERAICID PAYSKAYGRMGLALSSLQQHL\ EAVAYYKKALELDPDNETYKS NLKIAELK\LREAPSPTGGVGSF DIAGLLNNPG\FMSMASNLMNN PQIQQL\MSG\MISGGNNPLETP GT\SPS\QNDLASLIQ\AGQQFAQ QMQSVGIPRVV**SAQESSIRSR TPSASNDDQQE
7789	38157	A	7843	225	398	FIIDYTNSCIFHQNICLICSNRNF RQSNVVMICHY*TLQEIKTFC* MNSSLWSIIIF
7790	38158	C	7844	162	269	
7791	38159	A	7845	273	501	HKDQPIQTENDHPSTNFSFVLK LHDPLLNEMDLIVWVSF*Q*SC FYLVHPNCCSPLV*HP*SENPKF SNEYFLRVS
7792	38160	A	7846	1	867	
7793	38161	A	7847	185	1325	EEQQTNLASKKKSCIMLEKTEN KIRLVIVSEEEKKKVLKRMP*K MTVRAHHGISRTPHSWVESN\Y YWDICDQWMS/EPVGYMPCQH CQVAKNTVIVAPKQHLLQGGKI PWSLVTVDLMGAFSYKPQKS/N VYAIIMTDLFTKWIVILPLCDVS ASEVSKAIINIFFLYGPPQKIIMD QRDEFIQQINIELYRLFGIKQIVI SHTSGTVNPTESTPNTIKAFLSK HCADHPNNWDDHLSAVSFAFN VTHLEPTKNTPYFQMFKVEKNP LYYLPETSDSLHEVDGDNTSMF AKILDAIKEADKIMENKTTSLG QMENNNLDELNKSKIIVKKKPK QLNPFHLKVGHGSFKTKEKLV GRMVVFQSWNGVGPLCHRLY YRKWMCCP
7794	38162	A	7848	2	455	MADRLTQL\QDAVNSLADQFC NAIG\VLQQCVPPASFNNIQTAI NKDQPANPTEEYAQLFAA\LIA\ RTAKDIDVLIDSLPSEESTAALQ AASLYKL\EEENH\EAATCLGG MLFIEGDMLLGGRYKGALA\DI\ AQSQLEGQGSGYP*ASLFPDS

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7795	38163	A	7849	229	560	
7796	38164	A	7850	1	1077	
7797	38165	A	7851	25	690	WPSDEAEGYSEHFVEFVKDVR KRFPQHTIMAGNVVTGEMVEE LILSGADIIKVGIGPGSVCTTRK KTGVGYPQ\LSAVMECANAAH GLKGHIISDGGCSCPGDVAKAF GAGADFVMLGGMLAGHSESG GELIERDGKKYKLFYG\MSSEM AMEEVLLGGVAEYRTS\EGKT\ VEVPF*REMLEHTIPRHP*GGIR S\TCTYVGA\AKLKRR*ARTNYL HPEVHPAR
7798	38166	A	7852	768	1857	EGGHHFGGQGADSAAPFGSASI LPIKLDVHPHDGRRRAEKSKPG GNPQRQLYCQPPAGCLPGAVY RPRRSRGARMYSRYSPAERRNP DQRAGYCQAPDRLRFSRADDC RSRWRHVFHGTSRHCAGDRAV RPPPHSAAEALPVALPVFQ*PTA DQ\VLFPSLIAACYNNHQNKIIL EQEMSCVLLATFIQTRAQQRKY KRRNNRGIPRESTAREQARHNA NKAQQPRKHARNGASPAQQRK NRAAARDKDEKPAQQKDKAR QSAPEKKNRAIRGTNSREQAAK AERNRRQRGGQKGAQGGQHR EEAGEPTYVDEKAQAATSPPPQ TPHPAPDHDDAEDHRTRDTNR NAHQPKVYTHKDTPTNESR
7799	38167	A	7853	1403	2028	RRIQTNGRTFHAHGGPSRGLPE ELGKDHREKETSSRTL*QFQPN AKSPGQNLRESMNPVC/MTQQ ARRLQRLAKDLLKQVQVQDSG SWANNKVSALDRTLGEITRILE KERSRRGKGPSKEDLEGAAN/G VRRTM/WMSGNLVKESQPHPT HRPNILT*YPSIFP*RSTLLTLWL KVQLQQKL*KMEKSGKKIKKK PKR*KPG*TSGTLNTL
7800	38168	A	7854	1	675	

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7801	38169	A	7855	2	1110	AQEEEAKVNEIAFINTLEAQNK RHDVLSKLKEYEQRLNELQEER QRRQEEKQARDEAVQERKRAL EAERQARVEELLMKRKEQEARI EQQRQEKEKAREGAARERARD REERLAALTAAQPRSYGRVTEK NSAQA**KYSKAH/RNRLNKEK KKLLS*AVGDMQILIMPPN*PL YERKKQCSLCNVLISSEVYLFS HVKGRKHQQAVRENTSIQGRE LSDEEVEHLSLKKYIIDIVVEST APAEALKDGEERQKNKKKAKK IKARMNFRAKEYESLMETKNS GSDSPYKAKLQRLAKDLLKQV QVQDSGSWANNKVSALDRTLG EITRILEKENVADQIAFQAAGGL TALEHILQAVVPATNVNTVLRN
7802	38170	C	7856	65	425	
7803	38171	A	7857	1	1131	
7804	38172	A	7858	953	1311	FLFFIFFNYFFFGGRKCPLLVAP RLEVQMAVILGSLQ\PSPPGFK* FSLPQPSPSSWDYRHAPTHAQP NFVFLVETGFHHIGQAGLELQT SGDPPTSASQTAGITGVSHRAW PGTILFLK
7805	38173	A	7859	2	857	FVDIFQRWKECRGKSPAQAELS YLNKAKWLEMYGVDMHVVR GRDGCEYSLGLTPTGILIFEGAN KIGLFFWPKITKMDFKKSKLTL VVVEDDDQGREQEHTFVFRLD SARTCKHLWKCAVEHHAFFRL RTPGNSKSNRSDFIRLGSRFKFS GRTEYQATHGSRLRRTSTFERK P**TLSIPETFNVQSKQPSDSSPA LLLKQIQKS/NNYQPPISILISIPS PAPGGILT\PQMSGHPFQDDRSH WKASASGDDSHFELCPTTQNPE GTLGGMPKYDVSEINVMTAL

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7806	38174	A	7860	1	936	MELTHLQPHEPQEDVHAVGLL LGLREQHHMVSEGPRQQSWQE ERTELAAVSRLLFNMYPLLIHK NHASPGIPNLLLHPRGLRAITIA VFGKQNTYIRLEPFKINVLEQIT KHIEKLQCGEHNFPEQEIQEGK SHQNQHEAHFVVELCKYFLCQ EYLPSQITILTTYTGQLFCLRKL MPAKTFAGVRVHVVDKYQGE ENDIILLSLISNRICVALSRAKKG MYCIGNMQMLAKVSLWSKIIH TLRENNQIGPMLRLCCQNHPET HTLVSKASDFQKVTEEGC/MLP CEFRLGCGHVCTRAWHPYDSS
7807	38175	A	7861	218	580	
7808	38176	A	7862	3	1636	
7809	38177	A	7864	24	386	
7810	38178	A	7865	2	999	GRVGFFFAGNPGSDSFGGLLLG LTPVLRWVADGGTIPKRHE\LV KGPKKVEKVDK\ETELVAQWN YCTLSQE\KLRRPIVAL/CNFAD FYNK\EPVIEFLLDKSAEKGS/SG RQASHIKTH*RIVDRAESFPDNP CPGKGIKGN/D*KVDKHDDLQA GASSSSPVGGPGRWNGRHRFLL PSGGCGLCCFS*AEPWKEIKAG V\CHTCGAGLSRRMMIIVLNGT KEDVDLLKTMMEERRL*SEAG KENKENPRQQSLFQNQDVSERS PRAIKS*DRGSLKKPAFDSREK KTNLAPKSTAMNESSSGKAGK PPCGATKRSIADSEESEAYKSLF ITHSSAKR
7811	38179	A	7866	1	559	MGCDGGTIPKRHELVKGPKKV EKVDKDAELVAQWNYCTLSQE ILRRPIVACELGRLYNKDAVIEF LLDKSAEKALGKAASHIKSIKN VTELKLSERALKEIKAEVCHTC GAAFQEDDVIMLNGTKEDVDV LKTR\WRREG*ERRGKKKTKKP KAAEVCFQNPDVSGRKPQGPS KVKTREALKKPSP
7812	38180	A	7867	188	368	YVACMPAWPNVTVANQLFNV YFPARDMTVPSSPG/QPVVDQL STQGQARRDALEVVGYEDS
7813	38181	A	7868	179	554	LRPADPRSLVPGWALGLGPGAI LGPGRVTFPGGRPPPTHPPSLSF PPGGRQPLWVPALPAEEGRE/R LGREREEGRGKAGAGMA*AGL VL*CLQLQVQGQPLGGSWLST RLRSPRCHPWLLRRHLP

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7814	38182	A	7869	2	131	YKSELEEQLTSVAEEMRARLSK ELQA*KDRLGENMEKVRGRLV KYRGEVQAMLGESIEELRVRLA LY\LRKLCTGFLRDADHL*RPA GREYGESKRTLG
7815	38183	B	7870	1	3639	
7816	38184	A	7871	279	1077	IQHPRLSADDFRVNCETEPAM/* HAVENDIHGLCELQLETEIQAF KEELL/FMKKNHEEEVKGLQAQ IASSGLTVVVDAPISQDFAKIMA DIWAQYDEVAQKNREELDNNR SQQIEESTTVVTTQSTEVGAAK AMLTELTRTVQFLEINLDSMRN LKASLENSLREVVARYALQME QLNGILLHLESELAQTWAEGQC QAQEYQALLNIKVKLEAAIATY RRLLEDGKDFNLGDTLDCSNS MQTIQKTTTRQRMDGKVLSET NDTKLRH
7817	38185	A	7872	712	855	
7818	38186	B	7873	50	788	
7819	38187	A	7874	201	372	ICQMILKRRVLS*TQKHQATHG WNSAYSLTAPFPVSCQDHLC*P L*AEAQISIKEEP
7820	38188	A	7875	3	323	FFFETEFHSVAQTGVQWHDPSS PQPPPPRFK*LSRPSLPSSWDYR HVPSHPGNFLHFQ*KRGSTNQA GLELPTSGDLAAFA\SPSARITG VSHCARPNYQCFLEFKY
7821	38189	A	7876	1	911	MLLTLAGGALFFPGLFALCTW ALRRSQPGWSRTDCVMISTRLV SSVHAVLATGSGIVIIRSCDDVI TGRHWLAREYVWFLIPYMIYD SYAMYLCEWCRTRDQNRAPSL TLRNFLSRNRLMITHHAVILFVL VPVAQRLRGDLGDFFVGCIFTA ELSTPFVSLGRVLIQACMNEMT ESLKQQHTLLYKVNGILTLGNF\ FPCR\ILLFPFMV\WSYGRKKGL SLVPSTLQHPILTATWANAFPR* APQIYWFCLLLQ\KAVRLFDTP QAKKDG*MLLGVRRSLTPAAS STQHSMDQIVPWVASDFGY
7822	38190	A	7877	2	283	SCHCTPAWILALSPRLECSGAIL AHCNLHLWG*SDSPASASRVA GTAGAHCRAWLIFCVLVEMGF HRVAP/GLVLNS*AQTIRLPRPP KVLGLQA

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7823	38191	A	7878	1	1042	PKVRSPRIKRLAPAPAF\VRKQE LKKIVDP\LL*KKS*EFGHLDRDI QPQKRPPPLL*KWPR\YIRV\QG RRAILYK\RLKGPFCDYPGFTQG PGTPQTS*SSLLKL\AHKYRPRD KAQRSKQR\LLA\RAEKKAAAK GAVPQERAHPVLRAGV\NPVSP PLVGEQEKLSLVVIA\HDRGSPS ELVVFLPALG/RVKMGVPYCIIK GKGKTGDGLVHQKALHPLSAF TQ\VNS\EDKGAF/ALKLVGSYQ GPNYNDRYDEVRGSFTQNTVIH KSFSQITGWLNL*EVLSDDQLG TAKQN*RN**P*KSQKTVSQAN CLFLSFQIRRHWGGNVLGPKSV ARIAKLEKAKAKELATKLG
7824	38192	A	7879	3	472	GRGVAYRGPSPRGTGPGRGDE RLQHGGG\SREGPPAAPAAAAP GYGQSCCLIEDGERCVRPAGNA SFSKRVQKSISQKKLKLDIDKSV DLFQLQVNTLRRYKRHYKLQT RPGFNKAQLAETVSRHFRNIPV NEKETLAYFIYMVKSNKSRLDQ
7825	38193	A	7880	3	638	GRGVAYRGPSPRGTGPGRVR*T ASARRRTAAKGPPPPQLPPPRA TAKSCCLN\EDGERCVRPAGNA SFSKR\VRKSISQKKLKLDIDKS VRHLYI\CDFHK\NFIQ\SVRNKR KKEDQVYDGRENS/SPSTDTDIP EVD\LFPACQVNT\LR\RYKRH* QVARPRPGFNKAPVSRQL*VDT FRNIPVD*KETLALLSSSMVKSN KSRLDQKSGGWQAA
7826	38194	A	7881	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL\DPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
7827	38195	B	7882,	446	625	
7828	38196	A	7883	1	1875	

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7829	38197	A	7884	31	809	KPRLENYVKNAEASGADAINW KKGY/LVMEDEMNEMKREGKF REKRIKRNEQSLQEIWDYVKRP TLHLIDVPETLNAHKRKQERSK TDTLTSQLKELEKQEQTHSKAS RRQEITKIRAELKEIETEKTLQKI NESRSWFFERINKIDRPLARLIK KKREKNQIDAIKNDKGDITSDP TEIQTTIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVES LNRPITGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
7830	38198	A	7885	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM

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7831	38199	A	7886	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
7832	38200	B	7887	1	3570	
7833	38201	A	7888	2	1624	
7834	38202	B	7889	67	3156	
7835	38203	A	7890	1	1416	MIILIDAEKAFDKIQQPFMLKTL SKLGTDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILP\R DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFHKWC WENWLAVCRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLKSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL
7836	38204	A	7891	1	1932	

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7837	38205	A	7892	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQHFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSL*RRI/W KRLQRTLSIPVLDAV*PPMF*AS
7838	38206	B	7893	1	1710	
7839	38207	B	7894	1	2265	
7840	38208	B	7895	1	2142	
7841	38209	A	7896	1	1791	
7842	38210	A	7897	1	1878	
7843	38211	A	7898	1	2091	

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7844	38212	A	7899	1	1751	MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIMKMAILP KVIYRFNAIPIKLPMPFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTKDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK IFTTYSSDNGLISRIYNELKQIYK KKTNNPIKQWAKDMNRHFSIE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAIIKKSG NNRNHLDFKHIRILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA

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7845	38213	A	7900	1	2540	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLIDIYGTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITSYLSDHSAI KLELRIQNLTQNHSTTWKLNNL LLNDYWLHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKTNTLT SINKIDRPLARLIKKKREKTQID AIKNDKGDITTDPTEMQTTIRE YYKHLYANKLENLEEMDKFLN TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAEFY /HEL\LKENKIPRNPTY/RGCEGP LQGELQTTAQ*NKRGYKQMEE HSMLMDRKNQYRENGHTAQG NLQIQCHPHKATNDFLHRSGKN YFKVHMEPKKSPHRQVNPKPK EQSWRHHAI*LQTILQGYSNQN SMVLVPKQRYRSMEKNRALRN NAAYLQLSNL*QT*EKQAMGK GFLI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RLKH*T* NHKNPRRKPRHYHSGHRHGQG LHV*NTKSNGNKSQN*QMGSN *TKELLHSKRNYHQSEQATYKL GENFCNLPI*PRANNQNLQ*TQ TNLQEKNKQPHQKVGKGHEQT LLKRRHLCSQKTHEKMLSITGH QRNANQNHNEIPSHTS*NGNH* KVRK*QVLNGLDDVQLFR*NK QPCCSHKACLVVSSYRRA*SLV

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7846	38214	A	7901	1	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKRIKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIIQENFPNLARINKI DRPLARLIKKKREKNQIDTIKN DKGDITTNPTEIQTTIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPITGAEIVAIINS LPTKKSPGPDGSIAEFYQRYKE E/PADKQLQQSLSIQNQCTKITSI LIHQQQTNREPNHE*TPIHNCFK ENKIPRNPTYKGCEGLLPGELQ TTAQGNKRGYKQTEEHSMLM GRKNQYRENGHTAQGNF*IQC HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKPKEQSWR HHTT*LQTILQGYSNQNSMVLV PKQGYRSMEQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
7847	38215	B	7902	1	2337	
7848	38216	B	7903	1	1677	

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7849	38217	A	7904	1	1722	MAGYPSEMKLPEELSGSNICCS AVFTVLQPLLLIPRQTGSGVDL RQTPTDLQLRVLTVRRKNNKQ KRTSTPKPHLYVTIIKDQRSKKL TQNHSTTWKLNNLLLNDYWV NNEMKAEIKMFFETSENKGTIY QNLWDTFKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAIKN DKGDITADPTEIQSTIREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEDESLNRPITGSEIEAIINS LPAKKSPGPDRFTAEFYQRYKE ELHINRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKQEVKLSL FADDVIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYS NNRQTESQIMNELSFTIASKRIK YLGIQLTRDVKDLFKENYKPLL NEIKDDTNKWKNIPCSWVGRIN IVKMGILPKVVYRFNAIPIKLPM TFFTELEK\TTLKFIWNQKRARI AMTILS*KNKAGGITLP
7850	38218	A	7905	1	2310	
7851	38219	A	7906	195	791	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTLLHCWLDCKLVQPL WKSVWRFLRDLELEIPFDPAIPL LGIYPNEYKSCCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/IYTRDTMRPKNDEVQ SLVG/TWVNWETTFSVTIAVQK PTRLSH
7852	38220	A	7907	1	984	
7853	38221	A	7908	1	2076	
7854	38222	A	7909	1	1872	
7855	38223	B	7910	1	3309	
7856	38224	B	7911	133	3213	
7857	38225	A	7912	1	1364	
7858	38226	A	7913	1	3249	
7859	38227	A	7914	1	2757	

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7860	38228	A	7915	1	2268	MAGYPSETKPPEERSDSNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDLQLRVLTVKRKTNKQKG HPHQNPIRTSPSSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFIKEVLRDLQ RDLDSHTIIMGEFNTRLSTLDRS MRQKVNKDIQELNSALHQADL IDISRNLHPKSTEYTFFSAPHRT YSKIDHIVGSKALLSKCKRTEII TKCLSDHSAIKLELRIKNLTQNC STTWKLNNLLLNDYWVHNEM KAEIKMFFETSENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKTDTLTSQLKELEKQEQT HSKASRRQEITKIRAELQEIETQ RTLQKISESRSWFFEKINKIDRS LARLIKKKREKNQIEAIKNDKG DITTNPTETQTTIKEYYKHLYK NKLENLEEMDKFLNTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRCKEEL VTFLLKLFQSIEKEGILPNSFYE ASINLIPKPGRDTTKKENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSQIVPVCR*H DCVSRKPHHLSPQSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE*TPIHNCFKENKIPRNPT YKGCEGPLQGELQTTAQ*NKR GHKQMEEHSMLMDRKNQHRE NRHTAQGNL*IQCHSHQATNDF
7861	38229	A	7916	1	4729	

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7862	38230	A	7917	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD
7863	38231	A	7918	1	1205	
7864	38232	A	7919	1	2274	
7865	38233	A	7920	1	2307	

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7866	38234	A	7921	569	3030	RKH*TWKRTSSTSHHKNMPN* LEKQEQTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKKREKNQI DTIKNDEGDITTHPTEIHTIIREY YKHLYANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLKLFQSIEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLLNINAKILNKILANRIQQHIK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIISID AEKAFDKIQQPFMLKTLNKLGI DGTYHKIIRANYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLARAIRQEKETEGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQVFLYTDNRQTESQIISEL P\FTIASKRIKYLGIQLTRYVKDL FKER/YNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIWNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPDKNKQWGNDSLFNKWC WENWLAICKKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLEEN LGNNIQDIGMGKDFTSKTPKA MATKDKIDKWDLMKLKSFCTA
7867	38235	B	7922	1	3171	
7868	38236	A	7923	1	2646	

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7869	38237	A	7924	321	2211	CCQFSMARRGHLPRSVQVSIPG QSPVPRAAYQDSGRYKEPTAD C/VGPRQT*CMAPHCHLGGWH MLALSLGKGAGAGGKESTWEP SPGIRMTKTYSTRREQSHPRTI/ KGQIKQMNLRETCSWTFHKKF LKTVAFQISHPHKNTCLAMAVS ANRSMRQKFNKDTQELNSALH QVDLIDIYRTLHPKSTEYTFFSA PHHTYSKIDHILGSKALLSKCK RTEIITNYLSDHSAIKLELRIKNL TQNRSTTWKLNKLLLNDYWV HNEMKAEIKMFFETNENKDTIY QNLWDAFKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKASRRQEITKIRAELKEI ETQKTRQKINESSSWFFEGINKI DRPLARLIKKKREKNQIDTIKN YKGDITTDPTEIQTTIREYYKHL YANKLENLEEMDKFLDTYTLP RLNQEEVECLNRPITGAEIVAII NTLPTKKSPGPDGFTAEFYQRC SRWIKDLNVRPKTIKTLEENLGI TIQDIGTGKDIMSKTPKAMATK DKIDKWDLIKLKSFCTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKSNNPIKKW AKDMNRHFSKEDIYAAKKHM KKRSSLAIREMQIKTTMR
7870	38238	A	7925	1	3057	
7871	38239	A	7926	1	1830	
7872	38240	B	7927	1	3192	
7873	38241	A	7928	1	3484	MGTSEVQNGEERAGTSGQGSV EQLSGSSVQLPPGLKLCFEPYFS SCASDCILHASPLSLMAASGSQ NPNLWASWLCCKWVQCPERQ LGCHLTSSVIYGLRYYPQAKRS ELELRDCEGLCNQTSPLSSLDG MGWKAAAEESNSGIRNIWIPIP AFATHKQYNVRQVISPSPPYWS HRGNGNNSLCVTRLSGGLKQP VAGTGRGLEGGSGTRDLMPFL SAAPKEQPPILAPARRSWFFEKI NKIDRLLARLIKKKRE

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7874	38242	A	7929	1	1946	NLTQNRSTTWKLNNLLLNDYW VHNKMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRKQERSKIDTLTSQLKELE KQEQTHSKASRRQEITKIRAEL KEIETQKTFQKVNESSSWFFERI NKIDRPLARLIKKKREKNQIDAI KNDKGYITTDPTEIHTTIREYYK HLYANKLENLEEMDKFVGTYT LPRLNQEEVESLNRPITGSEIVAI INSLPTKKSPGPDGFTAEFYQRY KEELAGRDTTKKENFRPISLMN IDAKILNKILANRIQQHIKKLIH HDQVGFIPGMQGWFNICKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLVLEVLAR AISQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKLLSK EIKEDTNKWKNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKATLKFIWNQKRARIA KSILSQKNKAGGITLPDFELYY KTTVTKTAWYSYQNRD\IDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK
7875	38243	A	7930	1	4801	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVNNEMKAEIKMFF ETK\ENK\DTTYQNLWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDTIKN

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7876	38244	A	7931	1	3146	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
7877	38245	A	7932	1	2669	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNREHGKKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTLTSQLKELEKQEQ THSKAGRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIK\NDK GNITTDPTEIQTTIREHYKHLYA NKLENLEGMDKFLDTYTLPRL NQKEVESLNRPITGSEIVAIINSL PTKKSPGPDGFTAEFYQRYKEE LHINRAKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLL SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKHLFKENYKPLL KEIKEDTNKWKNIPCSWVERIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYSYQNRDIDQW NRTEPSEILPRIYNYLIFDKPEKN KQWGKDSLFNKWCWENWLAI CRKLKLDPFLKPYTKIKSGWIK DLNVRPKTIKTLEENLGITIQDI GMGKDFMSKTPKAMATKAKID

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7878	38246	A	7933	1	2962	MNNSIKEKVKLSLTKWEMQTK PNNNTVDLKDAQEVNLTSTDY RKQHVMLPTEINSDDSLLKIGVI RLANWIKSQDPSVCCNQETHLT CRDTHRLKIKGWRKIYQANGK QKKAGVAILVSDKTDFKPTKIK RDKEGHYIMVKGSIQQEELTIL NTYAPNTGAPRFIKQVLSDLQR DLDSYTLIMGDFNTPLSTLDRS TRQKVNKDTQELNSALHQVDL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHILGSKALLS
7879	38247	A	7934	1	4220	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKTSRRQEITKIRAELKEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKRE
7880	38248	A	7935	1	3229	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLRDIIQENFPNLARQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKDRSTRQ KVNKDTQELNSA
7881	38249	A	7936	1	3227	MGDFNTPLSTLDRSTRQKANK DTQELNSALHQVDLIDIYRTLH PKSTEYTFFSAPHHTYSTTDHIL GSKALLSKCRRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYGVHNEMKAEIKMFF ETNENKDTTYQNL\WDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKSLQK\INE SRSWFFERINKIDRPLARLIKKK REKNQIDTIKN
7882	38250	B	7937	1	2089	

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7883	38251	A	7938	1	3527	MELKTKARELREECRSLRSPCN QLEERVSAMEDEMNEMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSDHSAIKLELRIKNLTQNHST TWKLNSLLLNDYWVHNEMKA EIKMFFETNENKDTTYQNLWD TFKAVCRGKFIALN
7884	38252	B	7939	1	5238	
7885	38253	A	7940	1	3587	MENDFDELREEGFRRSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRSLRSRCDQLEERVSAM EDEMNEMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLARQANVQIQEIQRMPQRYSS RRATPRHIIVRFTKVEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDLIDLIYRTLHPKS T\EYTFFSAPHHT
7886	38254	A	7941	1	6202	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH LKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNEN\KDTTYQNLWDAFKAV CRGKFIALYAHWRKQ\ERSKM DTLTSQLEELEKLEQTHSKASR RHEIAKIRAELKEIE
7887	38255	A	7942	2	3134	WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPTFI QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSDHSAIKLELM IKNLTQNHSTIWKLNNLLLNDY WVHKEMKAEIKMFFETNENKD TTYQNLWDTFKAVCRGKFIAK\ NAHKRKQERS

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7888	38256	A	7943	1	4455	MELKTKARELREECRSLRSRRN QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSSRRATPRHIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DL\IDIYRTLHP\KS
7889	38257	A	7944	1	6108	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVV\CIQETH LTCRDTHRLEIKGWRNIYQANG KQKKAGVAILVSDKTDFKPTKI KRDKEGHYIMAKGSIQEEELTI LNIYAP\NTGAPRFIKQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKKLTQN RSTTWKLN
7890	38258	A	7945	2	788	CGLAIYNCTIVDLHFPLALYKK LLKKKPSLDDLKELMPDVGRS MQQLLDYPEDDIEETFCLNFTIT VENFGATEVKELVLNGADTAV NKQNRQEFVDAYVDYIFNTSV ASLFRCFS\SGFHKVCGGKGL\R LFQPNELQAMVIGNTHF*WKG TGKDYRNTKGNIWAEHP\TIKIF WEVFH\ELPLEKKK\RFLLFLTG S\DRIPILGMKSLK\LVIQSTGGG E\EYLPVSHTCFNLL\DLPKYT\K KETLRS*T*SQAIDHNEGFSLI
7891	38259	A	7946	1	1647	
7892	38260	B	7947	363	550	
7893	38261	B	7948	1	1123	
7894	38262	A	7949	1	3136	MVTHQQPAARKPNMTSKKPKP MGPKAHGIFSGTRKNNLEIYMD QTRTGIAKTKLSKNNKSGGMT LPDFKLYYKAIVAKIACGGSMY NSDTDEDEETEPSSSGQQIIENSI TMNKMKLLKAKMKNMNLSKK HITQVSDEEEDDDGCDLFADSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDAVGRVDEEPTT VSYEDDRRGKNQDAYTEGGLS TIKTVNCSSSLTLRRSKTSEDTQ EKKERRTPSDDEED

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7895	38263	B	7950	303	1010	
7896	38264	A	7951	3	280	
7897	38265	A	7952	3	514	FYLKELDPAEHSYVLIRKIDPAL VWGLTGDQGTPKTRLLMITLD SIFMQASCVPEEVVWEVLRVLE AH\SSKKHFVFGESMKLITKAS VQQEYLVHK*VSHSNPTLYVFL WGLSKETRQMEVPEFVAKVND THPSSFSVGSK*GI*EKEGGRYP VPEMGSCRLVTVTSASV
7898	38266	A	7953	2	351	
7899	38267	A	7954	2	529	EKGERPHWSNKPSNLKRTHEL DIDENPASDFDDSGSLLGFKYG SGQKYGGIPYFSHRQVR**EKN VKLKAKYLNMRGQIKMKNKHI FFTKETEKPFFKKSKILSKVEKF LTWVNKPMDEEASQESSSHDN GHDASTSCDSEEQDMSVKKGD DLLETNNPEPEKCQSVSSAGEL
7900	38268	A	7955	1	1370	MPVGTSNFLLLGLLENPNLPLT RPSPFPSQREASWGIQKATTGP GEGECTRLGFSLLLDVFCALHG PREKCVEILRSGHLLAISPGGVR EALISDETYNIVWGHRRGFAQV AIDAKVVEKFLTWVNKPMDEE ASQESSSHDNVHDASTSSDSEE QDMSVKKGDDLLETNNPEPEK CQSVSSAGELETENYERDSLLA TVPDEQDCVTQEVPDSRQAETE AEVKKKKNKKKNKKVNGLPPE IAAVPELAKYWAQRYRLFSRFD DGIKLDREGWFSVTPEKIAEHIA GRVSQSFKCDVVVDAFCGVGG NTIQFALTGMRVIAIDIDPVKIA LARNNAEVYGIADKIEFICGDFL LLASF*KADVVFLSPPWGGPDY ATAETFDIRTMMSPDGFEIFRLS KKITK\NIVYFLPRNADIDQVAS LAGPGGQVEIEQNFLNNKLKTI TAYFGDLIRRPASET
7901	38269	A	7956	3	560	RIHTGEKPYDCKDCGKAFGRTS ELILHQRLHTGVKPYECKECGK TFRQHSQLILHQRTHTGEKPYV CKDCGKAFIRGL\QLTVHRRIHT GARPYGVLKECGESLLDSTHS* LLHQ\RIHTG\EEPYECKECGKG FIHSSEVTRHQRIHSGEKPYECK ECGKAFRQHAQLTRHQRVHTG DRPYESAED

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7902	38270	A	7957	155	1288	HTTASQTTMSQAVR/RRRSDYL SSARR/RRDPARSKPTQGGPPPN PPPTRQGRPTALTNPSQPRPRHR AHPHQHATPKPRTNEEQEGRR HTKQPNPTRTEPRPPNRRGRPN PQTRRTKQQNTTPQAHTSTRKN ARTPGLCP*CVKGKTEGGYDA RASARGPYMAGVSWPGEHEDP GAPEARRGRRALPG\GSAFPEM STHTESTPKTTAHTSNDRRNRE QRVKKKTYKTTRSRGANRNST ERHEDGYFYGSLTTGPLPWHSA IHSVSAGQPWSLKFVTGLQQAS EGYFSQSQERSLPNRKSSVPRLR LLFLQQASRLSELPLGTEGPGSL LLRPREELACTGKRRKTGGAIM GEVSVCELSLPAPAFQSPVQLC GCQPEKA
7903	38271	A	7958	1	2045	REAAAATPSFPPSSSVRPSVRAS VRSARSGPKHGRRQLQRPPPGA /RWRLTRR*SERRARPTGLCTH MKMAPMTSSLQHQEKGACRSF RDTLRTRR*CTASAVSRTPK\RS AKIRAHQLGGRRCA*CPQVRLC QPRG*GGRVLPGCRRDRERQQ RGRHRRGCHRAAAL*RAGATL QPCAAPTAAARG*ER/SSPWAPP TRRRMQLWK*SGLTESSSGSRP RRKKSCGRRRSGRRPWMRGSG SSRSGWSRSGRSKRSASGATGS GSSRSRSTGGNSRL*KRKRPRG G*RSSLSLVTIGMRRKRPT*RSQ SRRWRRQQLLLPSGLTTQGSSS SSRKESHRPLRAAVMYPRPSTI DQAATWTATGGWRPLPSPRGA RLTPAPPPPLSLSR*SGPWMRSP P/PQPPPLPPPPPP\PKRPRSPAPS* TVRRPEQQPLRPGPAPWRSPLR HRRLPGGQAALQRT*CSWSLQS RLSWLLPWSLPQLTPRRSTMQL TPLKLTLPLLTPLLPTTYPPPPPA SLTYGLATGKGPPHSRVSPGPP RHPRVLRSPWQRCPCWMRWL RSHCCQQAKAVPPFSTLMSCLS RQPPSVTQRKWKGSPWLPPRPQ LCPQPLRSWSKSRSRSPTC*PM ARPPRRRGPRPSEGYFSQSQEEE FAQSEELCAKAPPPVFYNKASE NVIHMLGCRPSSRRGGGLRGW
7904	38272	A	7959	3	174	

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7905	38273	A	7960	3	862	GVMASRTLLLLLLGALALTET WAGTHSIRYFSTAVSRPGRGEP RYIAVGYVDDTQF\DAATPRM* PQSPWLEQEGPEYWDRSTRNIR PAHRLTRVNLPMPRRYYHQS* AGTGIFHGIRR/YIPDTCVQTHM IHHSVSDYKATLRCWALGFYP VEITLAWQ\QDEEDQTRDHE\L VETRPAGDGTFQKWAAVVVPS GQEQRYTCHVQHEGLPKPLTL RWEPSSQPTIPIVGIIAGLVLFGA VITGAVVAAVM/WQEEELRTFS SHR*SELTSERASSDHAQGSDV SLTACKV
7906	38274	A	7961	1	591	MVTDYAIELFLQASLILLSSTLP YNEREMGLSIFALLTLTVFLLLL ADKVPETSLSVPIIIKYLMFTMV LVTFSVILSVVVLTLHHRSPHTH QMPLLVPSDLHSQTSAVPASKK AQTRERPDAGAPSLFFSRKWLG YIARQLQEQEDHD/VAEGGLAV CGHGSGPPLPVDFHHLHQRWD PSHLPGRHVPLAPSRPLSL
7907	38275	A	7962	1519	1888	ILKHPTLDKELILTYLFIYLFIFL RRNFTLVA*ARVQWCDLAPPQ PLSPGFKPFSCLRFPSSWDYRYA PPYLANFVFLVGTGF\SMLVRL VSNSRPQ/CDPPASASQSAGITG VNHHA\RITFNF
7908	38276	B	7963	280	1977	
7909	38277	A	7964	994	1651	CRGSQPAPPLTPHPPNAPLGPSD LHSQTSAVPASKKAQTR\GDLM PEPPHCSSPGSGWGRGTDEYFIR KPPSDFLFPKPNRFQPELSAPDL RRFID/VSKPGCGPASGATGG\V SSISYIARQLQEQEDHD/VAEGG LAVCGHGSGPPLPVDFHHLHQ RWDPRSSSW\SHVPLAPSRPLSL KTGGLRPGPLPVEVREFGDTVK PYPSLPLNSFTRNLGLLFRSG

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7910	38278	A	7965	10	533	DEVSLCCQAGVQLHDVGSLQT ASQVQAILLPQPPEVAEISGACH HACLIFVFLVEMGFHHIGQAGL KLPTSGDLPASASQSAGITGVS HRARPASSYLFFF*DEVSLCCQ AGVQLHDVGSLQ\LPPRFKRFS C\PASRSS*DFRRLPPRLPNFCIF/ M*RWGFTILARLVSNSRPQ/CD LPASASQSAGITGVSHRARPASS Y/CIFFLRWRLTIAQAGV**CNL SSLQPPTPGFKWVSCLSLPSSW DYRSLPPLPANFCIFSRDGVSLC SLSWSRTPDFK
7911	38279	C	7966	312	467	
7912	38280	A	7967	31	678	TGLYFLFLFCLRRSLA/SVAQPG VQWRDLGSLQPAPPGLRRFSFL SLQSSWEYRCPLPRPADFLYF*S RRGFSTLVRLVSNSRPQ/CDPPA SASQSAGITGVSHCAR\LFFSFE MEFRS\VAQAGVQWRDLDSLQ PLPPG\LT*FSCLSLPRLGAA/WD YRRVPPCPAIFC/IFFFFSRDRVS PCWSGWSQTPDPQVIRPPRPSQ SAGITGVSHRARPSHIS
7913	38281	A	7968	23	99	YTMTGPGCWRPL*TGPHPPHT WPGGSSSHPQIPHRPPCVFG
7914	38282	A	7969	144	1239	ERTEPDH/TTTLT*P/ELPADTTA TVEDMLPSVTSVTTNSDTITETF ATAQYILTSETTTLTSSIAPPAT ATPDSNSVPAGQATPSKGPSAS APSPAPASAPKVAPLVDLSDTP TSTPAASNLSSSVLANQGAVLS PSAPAGVGEASKAPPASKPTPA PVPTPTGAASPLAAAAAPATEA PQAKQEAPSTKGPDPEPTQPGA AKSPAEAATALASPKSEAASVS TTNPSQGEDFKMDEGNFKTPDI DLAKDVFAALGSPAPAAGASG QAPELAPSTADSSVSPAPAKTE YGLSLSAVIGLCPVVSGWEDSG LPSIKWLLGLKVQEKGLNLSGK NTASGINLGLEEERTRSSDSVLL NYGCTLESLGCF
7915	38283	A	7970	3	375	ARQAMKSCLHQCFLTLPRQAL EASSCNSTGWGGEGTGKSGLQ RGP*NQCWEPSPAQQAAFTSS* AVATAAGQGEEELPLLPPSTTP GKNTASGINLWLEEERTRSSDS VLLNYGCTLKSLACF

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7916	38284	A	7971	1	2230	MFEASVGWFMRLEERTRLHDI QAQDEAVTADLEAAAGYPDLA KIIDEGGYTKQQIFSVDDTAFS WKKMTLRTFIAKEGTNTDGAS SATSSLVSLCLELCFLRAHHDV GFYCDLDVYQSAVYAPTCPTG YSLPQAKEESDFIPLEYEKGRIT STAGQGQDVEPEMEQLEKGSIK GVTETRTGPLGCSNYDNLDSVS SVLVQSPENKVQLLGLQVLLPE YLRERFVAAALSYITCSSEGEL VCKENDCWCKCSPTFPECNCPD ADIQAMEDSLLQIQDSWATHN RQFEESEEFQALLKRLPDDRFL NSTAISQFWAMDTSLQHRYQQ LGSWL*KVLF\KKTHRILRRLFN LCKRCHRQPRFRLPKERSLSYW WNRIQSLLYCGESTFPGTFLEQS HSCTCPYDQSSCQGPIPCALGE GPACAHCAPDNSTRCGSCNPG YVLAQGLCRPEVAESLENFLGL ETDLQDLELKYLLQKQDSRIEV HSIFISNDMRLGSWFDPSWRKR MLLTLKSNKYKPGLVHVMLAL SLQICLTKNSTL\EPVMAIYVNP FGG\SHSES\WFMPV\NEGQFSL TW\ERTNVDAAA\Q\CQNWTM HLGGIRWKTFF\ETV\HVYLRSR IKSLDDSSNET\IYYEPLEDDWIP LRNLG\YMKINTL\QVFGYSLPF DPD\AIRDLILQLDYPYTQGSQD SALLQLIELRDRVNQLSPPGKV
7917	38285	B	7972	62	232	
7918	38286	A	7973	3	258	KLSPPPPPLPPSPPLPRPGPA\GPP SRLPSP/PASASPQGVP*LGPAA AELPGIRSR*PQVAAPEAETHP WCCC*RSSPQQQRISH

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7919	38287	A	7974	1	1048	MAHSQNSLELPININATQITTAY GHRALPKLKEELQSEDLQTRQK ALMALCDLMHDPECIYKAMNI GCMENLKALLKDSNSMVRIKT TEVLHITASHSVGRYAFLEHDI VLALSFLLNDPSPVCRGNLYKA YMQLVQVPRGAQEIISKGLISSL VWKLQVEVEEEEFQEFILDTLV LCLQEDATEALGSNVVLVLKQ KLLSANQNIRSKAARALLNVSI SREGKKQVCHFDVIPILVHLLK DPVEHVKSNAAGALMFATVIT EGKYAALEAQAIGLLLELLHSP MTIARLNATK\ALTMLAEAPEG RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7920	38288	A	7975	1	782	MAVTAAACWSLRPLARRDVCV GVALASPFVKPTHWFCKTLLEP CRPTGMGAQEIISKGLISSLVW KLQVEVEEEEFQEFILDTLVLCL QEDATEALGSNVVLVLKQKLL SANQNIRSKAARALLNVSISRE GKKQVC\HFDVIPNPWSHLLKD P\VEHVKV*RCRLPLMFA\TVIT EG\KYAALEAQAIGLLLELLHSP MTIARLNATKALTMLAEAPEG RKALQTHVPTFRAMEVETYEK PQVAEALQRAARIAISVIEFKP
7921	38289	A	7976	1	300	VEQTGRGE/RAYDIYSRLLRNA FLCVMGPIDDSVASLVIAQLLFL QSESNKKPIHMYINSPGGVVTA GLAIYDTMQYILNPICTLPRTVR MSPRWCRRSL
7922	38290	A	7977	2	470	RPPQRTLQNGLALQRCLHATAT RALPLIPIVVEQTGRGEASYDIY SRLLRERIVCVMGPIDDSVASL VIAQLLFLQSESNKKPIHMYI/N QPSGGARGQATDIAIQAEEIMK LKKQLYNIYAKHTKQSLQVIES AMERDRYMSPMEAQEFGILDK

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7923	38291	A	7978	3	864	SCRYPALGPRLAAHFPAQRPPQ RRPPRTACSLQRCLHA\TATRAL PLIPIVVEQTGRGERAY\DIYSRL LRERI\VCVMGPIDD\SVA\SLVI AQLLF\LQSR\SNMKPIHMYIN\S PGWVWVTAGLGHLTDTIAVTF LQPDFCTW/CSLGPGAASMGSL AFFAAGTPGMRHFAPQLPVFMI QPALQEGAGGQSPPDI\AIQAEE NP*KL\KKQL\YNI*RQRTTQTRS LQGDRVPPMAEGTA*HEAPME GPQEFG\ILKTRFLVPPSPQDGE\ DEAPRLVQKEP\VEAAPAAEPV
7924	38292	B	7979	1	2088	
7925	38293	A	7980	412	812	FQSLFTCVLFHFKFSLTIHHMNS QPF*RIRSTFFFLKQSL/DSVTQA GVQWRDLGSLQPPPPGFKQFSC LSLPSSWDYRRAPPHPANFFYF F**QTG\FTHVGRMVPI*PRDPP ALASQSPGITGMSHCTRPRIR
7926	38294	A	7981	2	178	
7927	38295	C	7982	279	322	
7928	38296	A	7983	2	760	GVRRSGGGR\GRPGGGPRKARR GKAEDKE*MPVTKLGHLVKDM KIKYLEDV/YFSLPIKESETIDFF LGSSLKEEGLKIMPVQKQTRAG QRTRFKAFVATGDYNGHVGLC VKCSKEVATAIRGSVILTKHSIV PVRRGY/WGNKMDK/PHTVPCK VTGRCGSVLVHLIVSAPVPKKL LMMAGIDDCHTSARGCTAT/LG NFAKATFDTISKTYSYLTLDLW KETIFTKSPYQEFTDHLVKTHT RVSVQRTRAPAVATT
7929	38297	B	7984	318	406	
7930	38298	C	7985	333	439	
7931	38299	A	7986	2	171	
7932	38300	A	7987	1	668	MGGLFWRSALRGLRCGPRAPG PSLLVRHGSGTIMGVFVAVGTI PVPSRVPCIEADTLKPGGPSWT RERTLVAVKPDGVQRRLVGDV IQRFERRGFTL\VGMKMLQAPE SVLAEHYQ\DLRRKPFPPCPSSR YMSSGPVVAMVWEGYNVVRA SRAMIGHTDS\AEAAPG\TIKGV DFSVHISRNVIHASDSV\EGAQR RIQ\LWFQEQ*SWVSWA\D\GGQ HSSIHPA
7933	38301	A	7988	1	897	

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7934	38302	A	7989	1	142	MEYYAATKNDEVMSFV/GT/W MKLETIILSKLTQEQKTKHHMF SLISGS
7935	38303	A	7990	287	1086	EPWREMFISVYTLQKLGALFTI AKTWNQPKCPSMIDWIKKMW H/IYTMEYYAAIKKDEFMSFER TWMKLETIILSNLTQEQKTKHR MFSLISGSRTMRIHGHREGNITC QGLLGGECVHTVATRGSPSATE DESCRMNVNDYGGNSPSTLQV KTSPQGRAEKGNNVRTWLYSN LVCWPSLGSLMGKLRDRVIKR VIYTHTAGDVSMHEEGFQFPLK QVSLLLCAIAFQPSLVVAAALV HITMEAYTYLEVTLLQIHSPLFC FLPKCHF
7936	38304	A	7991	1550	1835	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKK\MW HIHTMEYYAAIKRNEFMSFAGT WMKLETIILSKLTQEQKTK\HH MFSLIRGS
7937	38305	A	7992	164	647	DLPVEPHIGKMILFEALVL/HCL DPVLTIAASLSFKDP\FVIPLGKE KIADARRKELAKDTRSDHLTV VNAFEGWEEARRRGFRYEKDY CWEYFLSSNTLQIM/MKIIKAVI CAGLYPKVAKIRLNLGKKKK\K VKVYTKTDGLVAVHPKSVNVE QTDFHYNWLI
7938	38306	A	7993	66	345	

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7939	38307	A	7994	1	2367	HRVTVISGETGCGKTTQVTQFI LDNYIERGKGSACRIVCTQPRRI SAHSSCGKSSCRKGQNLVASGN STGY\QIRLPESVAQGNRVLSYT VPTRNHPSSGSQSDPYLSSVSHI VLDEIHERNLQSDVLMTVVKD LLNFRSDLKVILMSATLNAEKF SEYFGNCPMIHIPGFTFPVVEYL LEDVIEKIRYVPEQKEHRCQFK RGFMQGHVNSQEKEEKEAIYK ERWPDYVRELRRRYSASTVDVI EMMEDDKVDLNLIVALIRYIVL EEEDGAILVFLPGWDNISTLHD LLMSQVMFKSDKFLIIPLHSLM PTVNQTQVFKRTPPGVRKIVIA TNIAETSITIDDVVYVIDGGKIK ETHFDTQNNISTMSAEWVSKA NAKQRKGRAG\RVQPGSLLFICI NGS*EASLLGWTIQLPEIFEE\PF WEGTLFTK*RFLRLGEIAYFLSR *MDPPSNEPVLLSIRHL\RSLNA LDKQEELTPLGS\HLARLPVEPH IGKMILF\GALFCCLDPVLTIAAS LKFQ\SPFVIPLGKEKIADARRK ELAKDTRSDHLTVVNAFEGWE EARRRGFRYEKD\FCWEYFLSS NTLQMLHNMKGQFAEHLLGA GFVSSRNPKDPESNINSDNEKII KAVICAGLYPKVAKIRLNLGKK RKMVKVYTKTDGLVAVHPKS VNVEQTDFHYNWLIYHLKMR\ TSSIYLY\DCTEVSP\YCLLFFG\G
7940	38308	A	7995	25	312	WLIYVITDARMYRQRGRYYFL VSSSLDKVLMISFLLGWRRSSR RLRAFLVLHLRASPWAPRSFVR PVSAFSVGMCHMKTRVFENTF PFTLGHTVRYVGREIF/CRRVFT RYRESIKISLPTYLTVCPRVKGN VFSNTRVFMWHIPTLKADTGRT KLLGAQGEARRCKTKKARKRR EERLQPNKKEIIKTLSKEEETKK
7941	38309	A	7996	2	417	QQIRKLIKVGLIIHKPVIVHSQV GCQKSTFS/RTRKGRHMGTG*R KSTANFQMPEKVTWMRRMRIL HWLFGRYHESKKTDHHMYHSL YLKVQGNMFTNKQILMEHNHK LKADKAHKKFLADQAEARSSK TNKASKLREER
7942	38310	A	7997	3	124	KKRPELRDLLNQARKETL/ARK EDRSASSGAEGDVSSEREP

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7943	38311	A	7998	911	1497	SQRKARDQRRKRNKRASSIAK HKEPKRPILPSGKNSQEGVATH TKPLAQGKVWLDP/NETNEIPN ANFRQQIRKLIKDGLILRHRKPV TVHSRAQGWKSTLARRKGRHL GIESKKIDRHMYHSLYLKLKGN VFKHKRILTEHSHKLKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEEIIKTLSQEEKAK
7944	38312	A	7999	34	279	EVIHAAIGEKKGSY/NA**PWVE EQLTRQPLIHHQPASLHSVY/RC RYHSLYLKVKGNVFKNKRILM EHIHKLKADKARKKLLA
7945	38313	C	8000	351	530	
7946	38314	A	8001	356	921	WRATACTYPSWAPPRILVATGP AAVSAGLPSLHGTRAGPQAPCT AAVPPAPLPPHRPAS*G/MPAGP VQKGAPT/AAAAG*RLLKHGQS RRQGRGGAERTEGCQHAVTFQ DCFLRCFFG*C*CLSG/ERAIALE QGASHAAEQLPRLQAFKRPGPL /QVNPDAPQKSAASSSLKVLSG LPKHQRPRRFCQNTGS*SGP**T TGRRSAAGAA/GKPENPGSPPA PHNFKSGTNPAVTTHHPVGSKP RPEPHGNSEA
7947	38315	A	8002	495	653	MTLTSIDPVLTTFFNLECPL/VFT ATASSGLGEVE*AIALN
7948	38316	A	8003	1	1433	MPESNCSLTWRHSVGRAVAAQ GGEHSSQGASLVLGEPRGGSS WLLGLEGDTGLWGGLLKEGRL TDGKGKTIDCKDAIFIMTSNVA SDEIAQHALQLRQEALEMSRNR IAEN\LGDVQISDKITISKNFKEN VIRPILKVRGLSWHFLLEPKAHF RRDEFLGR\IGEIVYFLPFCHSEL IQLVNKELNFWA\KRAKQRHN\I TLLWD\REVADVLVDG\YNVH YGARS\IKHEVER\RVVN\QLAA AL*SRTLLP\GGCTLRITVEDSD KQLLKSPELPSPQAEKRLPKLR LEIIDKDSKTRRLDIRAPLHPEK GRLTDGKGKTIDCKDAIFIMTS NVASDEIAQHALQLRQEALEM SRNRIAENLGDVQISDKITISKN FKENVIRPILKVRGLSWHFLLEP KVLTTFFNLSVLYLHGNSIQRL GEVNKLAVLPRLRSLTLHGNP MEEEKGYRRARGHSLHQGIEK YICESDDIFRKYCNNQFL
7949	38317	A	8004	1	789	

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7950	38318	A	8005	1	409	LRLELSFCSSCLLEPPWS/TTVV CLYCRPATDFHPSGSGRVSAVL LIQ*G/RPLPLLIRLKACHCSHTA KCPGSSPSSMSPTAEEQKSGTA EERREGASEHGEEFGWGRLERS AVEWPNSRGRSSSHSIPFPAPRP
7951	38319	A	8006	1	1787	MSKGESRKCNEENVSKSSKVV KVFIVLTPQFLSRDKDQLTKEL QKHVKSVTVSCKSPRKLLSHIT RLHPPSKGQGENLTHLVDSIKA TIWCQPVWETVEGQRRRVGNC IDFTNGCDLVGSSSLHNMLVCS SYDINRQDTFQKDRTSEKHLLD SVFTALQDSAGQQWPARLHPQ RGEEVADPRGAPSRHVEPENSS PCQGNGEQAGKAGARALCGQ ARRSPATMPPPLTTRSLCEFAVF LLHWLFPELFHYRKLGEQDSCY GDGGKQELDPQRLQIICNFTEV YFPHMQEEEAWRQAGPGPAEA AD/TSATSRRSTSPTCRRRRPGC SGAPSASTTSFRAWGWTQAAK ASPPRDNCYNSSSLPDDISLFTH DNLHKQHSCSDSLGKKQLDPS CIKLIRH*VHLLYLCTKNNRVW TLEFMGNLHWNRNRGAPTSSS ARSTCWPRV*RHEELCNQS*EV QRGV*GSPAAPERSSKDFCKIPL DEVVVPH*/DFPVRSPYLLSDKE VCKIVQQSLSVGNFAAGLL/LPP RTSSCSTTIFGL/DNKKQLDPTQ LRLICH*VEAVYPVEKVEEVWH CECIPSNDEQCHCPNRKKCNIL

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7952	38320	A	8007	1	1475	MAVDFSLAVLMIVSSYDINRQD TFQKDRTSEKHLLDSVFTALQD SAGQQWPARLHPQRGEEVADP RGAPSRHVEPENSSPCQGNGEQ AGKAGARALCGQARRSPATMP PPLTTRSLCEFAVFLLHWLFPEL FHYRKLGEQDSCYGDGGKQEL DPQRLQIICNFTEVYFPHMQEEE AWRQAGPGPAEAAD/TSATSRR STSPTCRRRRPGLQRCAQCIND KLQGLGLDAGSEGEPPTRQLLQ LLQPAR*HLSNQGGG*LQGRAL FTHDNLHKQHSCSDSLGKKQL DPSCIKLIRH*VHLLYLCTKNNR VWTLEFMGNLHWNRNRGAPT SSSARSTCWPRV*RHEELCNQS *EVQRGV*GSPAAPERSSKDFC KIPLDEVVVPH*/DFPVRSPYLL SDKEVCKIVQQSLSVGNFAAGL L/LPPRTSSCSTTIFGL/DNKKQL DPTQLRLICH*VEAVYPVEKVE EVWHCECIPSNDEQCHCPNRKK CNILKKAKKVEK
7953	38321	A	8008	1	3524	MCNNLIHLSLANNKITTINGLN KLPIKILCLSNNQIEMITGLEDL KALQNLDLSHNQISSLQGLENH DLLEVINLEDNKIAELREIEYIK NLPILRVLNLLENPIQEKSEYWF FVIFMLLRLTELDQKKIKVEEK VSAVNKYDPPPEVVAAQDHLT HVVNSVMQPQRIFDRYLLEIQR PEFRLVLKLVGNESLPIASADSL ALTSDMVRNGLGDLFYDFRAC HTTRPPYFGEGDRVDYHFISQD VFDEMVNMGKF
7954	38322	A	8009	258	719	MTPPSVLP*PSLSY*HPDYSLPF PFSPPVLCFPHPVQGLYSVLFVN TAAEPREKSAMAILPLSGHACS HVCLGSHQSLFQRACGRCPRPL SGSLRSHCHWLLILGVKKCSPP EAGKAILLTTDRTETMNISWKP RNPSHTVPHPHHICCHWRI
7955	38323	B	8010	1	1953	
7956	38324	A	8011	32	533	GRERPLLSPYMETLYRVPFLVL ECPNLKLKKPPWLHMPSAMTV YALVVVSYFLITGGIIYDVIVEP PSVGSMTDEHGHQRPVAFLGL QSKMDNNINGKGLCIQAS*FTM GGFRFS*ILDPIECTKYPKTSI\DS FFCSIGISSVVLLEFFPWARSNS MRNGNCPGLI

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7957	38325	A	8012	670	1052	TRRDSRCKGTWLLSVKTLAISA VKSQKSKASECRFTNRSSSTAVI RVLLPGILLSSKLRCSMVLATA LERDDSDVGVTISSINPQDSHFS CLLLLRISSNSC*IC/CNFFAIRV HLAEVCI*QTSLLL
7958	38326	C	8013	40	186	
7959	38327	A	8014	1	1216	
7960	38328	B	8015	1	1032	
7961	38329	B	8016	1	1761	
7962	38330	A	8017	108	708	LTNQKKSRTRRIHSRILPEVQGG AAADRHCPIDRLGSLQDHHRRS RLLSQWSP*KSTHD*HGFS\YQS AEDIRRKLQQQAEFAGMNTSEL LQIANQAFVNRDAVSRKENHR DNERQAQRNTDLLAAAIRGVPP KRQGKGGPGKETQPGCQSLQR NQCAYCKEIGHWKNKCPQLKR KPGDSEQEAPDKDEGALLNLA EGLLD
7963	38331	A	8018	1	512	LSRSSPLLPLVWHQAMVGSMD VEPAAWVLMTFCWDTPRQSGV PRERMPHTGTWRTVGIRCPKK KLRSANSSMMRGKVQPFRP/DI QAYGAAPFEDLQVDFREMPKC GGNKYVLVLGRTYSGWVEAYP TRTEKTREVTPVLLRDLIRRFRP PLWIGSDNGPAFLAALVQKTA
7964	38332	A	8019	3	764	KQVLVNGDAVSREEKRKENER QARRNADLLVSCSNQSGPPKEA REELWTKDYRPGQDLRLLSQA TLTFHPTVPSPSTLLGLLPAEDS WFTCLDLKDAFFPIRSAPESQK LFAFQWEDPESALAKTVRQRC VSCRQHHA\GKVQPFRP/DIQAY GAAAFEDLQVDFTEMPECGGN KYLPVLGRTYSGWVETYPTRA EKAREVTRVLLRDLIPRLELPFR IGSDNGPAFVADLLQKTATVLG ITRKLHAASRPQSSGK

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7965	38333	A	8020	19	1548	CIYGAQLCTGPSAPVWYCPLGT MAPTGLPGHPAVATATEPHRE RGSPL/IDSTVLVPPQDKHILRPP TVDKRGGEASGETPPLAARLRH KTGIQMPLREQQYTGIDEYGHV VERRVFGYQPFTSAHLLNWKS NTPSYTEKPQALIDLLQTIIQTH NPTRADCHQLLMFLFNTDERR RVLQAATKWLEEHAPTDYKNP QEDVRTQLLGTYPQWDPNERQ DMQRLNRYREALLEGLKRGAQ KATNINKVSEVIQRKEESPAQF YERLCEAYRMYTPFDPNSPENQ CMINMALVIQSTEDIRRKLQKQ AGFARMNTSQLLEIANQVFVN RDAVSRKENQKENGGWPPCLR ALAATALLVQEANKLTLGQNL NIKASRAVVTLMNTKGHHWLT DARLTKYQTLLCENPRITTEVC NTLHPATLLPVSESPVEPDCVE VLDSVDSSRPDLRDQAWASVD WELYVDGSSFFNPQGERGAGY AVVTLDTVVEARSLPQATSAQ KAELVAFIRALELSE
7966	38334	A	8021	1	895	MDGAGICYLHQTNAGTEIQTPH VLTYKRELNNENMWAHRGDN THWGPEGSTNSPASASGVADV SRVGSLQWVLGLADFKNEAKE LRLYKQEKREKAKRWKETEKG FNGDYGVTMTPGKWRTYFEID WSKLEVGWPSEGNLERSLVSK VWHKVTGKSGHSDQFPYIATW LQLVLDPPQWLRGQAAAVLVA KGQI\PRKDPTPPGRGKSTPEVL FDPTSEDPLQEME/PSDPSGALP LPGKDAPHS*AHSPCASTRQTY P*ATRSRQERR*SLERNPYIGSS FKTQNWDTNAPERAVVYWDR

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7967	38335	A	8022	1	1959	MLKNFKKGFNGDYGVTMTPG KLRTLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIQMPLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWKNNTPSCTEKPQALIDLL QTIIQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGEHAP ADYQNPQEYGKEESPAQFYER LCEAYHMYTPFDPDSPENQRMI NMALVSQSAEDIRRKLQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHSVVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTW LPQGFKNSPTIFGEALARDLQK FPTRDLGCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSKKK\AQICQQQVRYLGFTI RQAERTLGSGRKQVICNLPEPK TRRQVREFLGAAGFCRLWIPNF AVLAKPLYEVTK*GDREPFEW
7968	38336	A	8023	2	367	
7969	38337	A	8024	3	687	GGRRQRRSKVTSTWWQARESS CRGTLLYKTIRSCDTYSLSQEQ HGPNLH\LIGVPESDGQNGTKL ENTLQDIIQENFPNLARQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKGRVT HKGKPIRLPADLLVETLQARRE WGPIFNILKEKNFQPRISYPAKL SFISEGEIKYFTDKQMLRDFVTT RPALQELLKEALNMERNNWYQ PLQNHAKL
7970	38338	A	8025	1	993	

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7971	38339	A	8026	1	842	MAEQEQLQSAVPSPLLVIPRQK GSGVDFQQSPTDLQLRDLTDRR KTNKQKGIASTLTKRTSTPKPH LYVTNIKDQRPNPRLIGVPESD GEKGTKLENTLQDIIQENFPNL ARQANIQIREIQRTPQRYSSRRA TP\RHLIVRFTKVEMK\EKILRA A\REKGR\VTHKGKPIRLTTADL SAETSTSQKTEWGPIFNIL\KEK NF\QPRIS\YPAK\LSFFISEGEIK\ YFTDKQMLRDFCHHQTCLP*KS TRPALKELLERKHLNM/EKGNN WYQPLQ\NHAQICKDH
7972	38340	C	8027	320	433	
7973	38341	A	8028	9	189	
7974	38342	A	8029	26	738	VAASSFDTCADHLCALHLLQV LHYLAIQKPADLARHLLPCVIH AAVLKVKEEESLENISSVKKIIK QIISHSSKVLHFPNPEDKKLEEII HQITNVEALIARARSLKAKFGT EKCEQEEEKEDLERFVSCLLEQ PEVLVTGAGRGHAGRIIHKLFV NAQNVA\AMTPP\EEELKRMGS PEER\RQNS\VSDFP\PPAGREFIL RTTVPRPAPYSKALPQRMYSVL TKEDFRLAVKIIDGDV
7975	38343	A	8030	3	2961	MAADSEPESEVFEITDFTTASE WERFISKVEEVLNDWKLIGNSL GKPLEKGIFTSGTWEEKSDEISF ADFKFSVTHHYLVQESTDKEG KDELLEDVVPQSMQDLLGMNN DFPPRAHCLVRWYGLREFVVIA PAAHSDAVLSESKCNLLLSSVSI ALGNTGCQVPLFVQIHHKWRR MYVGECQGPGVRTDFEMVHLR KVPNQYTHLSGLLDIFKSKIGCP LTPLPPVSIAIRFTYVLQDWQQ YFWPQQPPDIDALV

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7976	38344	A	8031	1	1688	MREKPCQSNECGKAFNYSSLLR RHHITHSREREYKCDVCGKIFN QKQYIVYHHRCHTGEKTYKCN ECGKTFTQMSSLVCHRRLHTGE KPYKCNECGKTFSEKSSLRCHR RLHTGEKPYKCNECGKTFGRN SALVIHKAIHTGEKPYKCNECG KTFSQKSSLQCHHILHTGEKPY KCEECDNVYIRRSHLERHRKIH TGEGSYKCKVCDKVFRSDSYL AEHQRVHTGEKPYKCNKCGRS FSRKSSLQYHHTLHTGEKPYTC NECGKVFSRRENLARHHRLHA GEKPYKCEECDKVFSRRSHLER HRRIHTGEKPYKCKVCDKAFRS DSCLANHTESSILGEKPYKCY\K CCGGFLIQKGSLPQHQRVHTGE KPYECNECGKVFNQKASLAKH QRVHTAKKPYKCNDCGKPLPD QSTLFHHQSNPIGVGKRYQ\CN DCHKVFSNATTIANHYRIHIEE/ KIYKCNKCGKFFRRHS*LVVHQ *THTGEKPYKYHDCDKVFSQA SSYAKHRIHTGEKPHKCDDCG KAFTSCSHLIRHQRIHTGQMPY KCKGGKVFTLWSFHAEHQKIH
7977	38345	A	8032	25	1091	IHIYSDSCSLSLQDSGDEKEFNL DDNVSFRASLWDLAAGPGQGG GGGREKWRAVISRTMNRKMG KMMVKALSEEMVRPADIGDGV SRGPGDRSGRM*AEKMALAFS EQEEHELPVLSRQASTGE*GMR GTPAESGGKDWVTAVLVAGPF CGRARVHTDFTPSPYDHDSLKL QVRSASGLLWSLAGCAQKGSW TEPVGSFKFIYVDVLPEEAVGH ARPSRRQSKGKRPKPKTLHELL ERIGLEV*AWSSLVSSIREAQLP QGWGPGHLNELNIMDPQHRAK LLTAAELLLDYDSEWL*ERPGE GAESSQEPG\GEACPKVDIPRDS GCFEGSESGRDDAELAGTEEQL QGLSLAGAP
7978	38346	A	8033	35	437	
7979	38347	A	8034	1	1845	
7980	38348	A	8035	1	212	
7981	38349	A	8036	371	915	
7982	38350	A	8037	1	2460	
7983	38351	B	8038	10	1510	

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7984	38352	A	8039	1	188	SASTTLWGLLIFLIHRLGTALRA VSSWGTHLTAKEVQWGH/DCG THWSYHHLHQPRAAGHKEC
7985	38353	A	8040	3	2332	FFFMWDPQHF/TFI/VLPQGYYN SPGLYSTVLRDLENLDIL*NIKF LYFIDNIMLTGMDE*EEDGTLE ALVKHLLSRGVKINKPYRDSEV ATAVK/FLQV*WLGASRG\VPS NVKDKLLHLCI\PCKGREAHCL G*ALF*VS*HH\IPTCKVVSGFDP HF*VT*EECPAFEWSL/QQERTL QQIPGHGAVTILQDPLVLKVPV GGVRFGVELNQAPVGESQWKG LGIWSKAMSSTAQKYAP/FQSR EICWKQLLACY/W*ALI/EIECLT MGHKTTM*FQ\MPLRN*HLCNS *SHTLDMPQQHPIMRWKSFL*/ D*A*IPMLTSPRKHPNLKWP*TT KQKH/WKL/GQPSPWVSPGRVG WVHKWSKHSGRD/GGYLWVQ QY*LPPTKVDPDTATSKCPTHQ HLNPMIFP/R*GSISLGDQPDPK* GVDYIALFPS*KGQRFMFTGIGT YSIVGFSCRVVIPSVSTTFWGLL IFVIHRLGTASPCS\SSWGTHLT AKEVQWGH/DCGTHW\SYHHL HQPRAPGP*RMLKRASIGTAQR QLAGST/LCGWEGAIFQDMVHF KNQRHLYSSVISVGRTRGSRYQ GVEVDVAPYPIPSTHLSWDFAL LSQNHHSAG*KVLDSKGGYP*K ETNECPLNYTLQLP/PGE/FGQY VSRDQRVRRGVPSSPGT\VIDPD PQEEAWLLSHN/GG*EEFVWNP /GDPLGGLLV/LPCPIVSVRRIVQ
7986	38354	A	8041	1	1296	

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7987	38355	A	8042	498	2219	KSVKTST*DTLRTKAKTGQGHI TGLQPWLGLRIRQEP/SAKTEK KAAIQAKAGAEREATGVVRPV AKTRAKAKAKTGSKTDAVAE MKAVSKNKVVAETKEGALSEP KTLGKAMGDFTPKAGNESTSST CKNEAGTDAWFWAGEEATINS WFWNGEEAGNSFSTKNDKPEI GAQVCAEELEPAAGADCKPRS GAEEEEEENVIGNWFWEGDDT SFDPNPKPVSRIVKPQPVYEINE KNRPKDWSEVTIWPNAPAVTP AVLGFRSQAPSEASP/LFIYCSG LR*RKCLFFACGNSLPPF*E\PRS CSQPIPECRFDSDPCIQTIDEIRR QIRIREVNGIKPFACPCKMECY MDSEEFEKLVSLLKSTTDPLIHK IARIAMGVHNVHPFAQEFINEV GVVTLIESLLSFPSPEMRKKTVI TLNPPSGDERQRKIELHVKHMC KETMSFPLNSPGQQSGLKILGQ LTTDFVHHYIVANYFSELFHLL SSGNCKTRNLVLKLLLNMSENP TAARDMINMKALAALKLIFNQ KEAKANLVSGVAIFINIKEHIRK GSIVVVDHLSYNTLMAIFREVK
7988	38356	A	8043	1	453	MEKLDELKIKIDNINGALICARH FSKCSSNAQSHLCPYLQAFPGG PG/VRGLPGWPGRTGSRELGHG WRGCG/EGLVSGCQTMLSGA\P AGSPQ\PTGGTRAHAVRGRP*V PARSQGSRPLARPGQED*GAAP\ DFDPGAAGVPGVPALQEAAQI
7989	38357	A	8044	3	690	SLSLPSSWDYRRAPPRPANFVF LVETGFTMLTTIVLIS*PHHPPA SASQNAGIV/GVSHSPRPGIACLI TRLDF/HQGTQSRVPALGSS*PIP HARPRGHTLKALPYRLYTQTA RGFGQPRVRIPLLSLLGSLKPSE LRGQVGHAFASAIFASAISLCVF TLLVEGKLKPPGASVRRCLQSN RDLGFRATFPTSHRGHGALGLN YISQRATGTPNLWLPFRFRVVL LQAACG
7990	38358	A	8045	106	299	
7991	38359	A	8046	306	445	
7992	38360	C	8047	570	926	

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7993	38361	A	8048	47	988	ASRPGSRVSLMFGAAGRQPDRS SSSPGTSWPFPVEPMEELVHDL VSALERELQSKPRGGFAEPGDP FSEVY/PCPLKRPARKRRGRKR RFV*CASPVGGLVT\A*SEGSDS SFRRTKSKKRKLKIIRQGPKIQD EGVVLESEETNQTNKDKMECE EQKVSDELMSESDSSSLSSTDA GLFTNDEGRQGDDEQSDWFYE KESGGACGITGVVPWWEKEDP TELDKNVPDPVFESILTGSFPLM SHPSRRGFPTKTQSAFMECLQRI LKNLEGLQLQWYPFLAQWVTR EWFIFPRILITMTIGLALGLGQS MTSISF
7994	38362	A	8049	3	476	LTRPVD*RPGTIHLGRGVRARP ANRRRQRARRGAAISPPGPCSV AGFLRGRLG/PEPGDNGQHLGE PWLGCGSLFA*RA*CSRSTRCT* RRRAPGDRELPRAPATWAPPIK LVPRVFSSKVGQGVSGLVEAM CLGQDSILNQSNKHNSVASSNT ITVIG
7995	38363	A	8050	2	143	
7996	38364	A	8051	1	161	
7997	38365	A	8052	3	1189	ESPLLGHHSSSDAARRRSVSSFP VPQDNVDAHPGSGKEVRVPAT ALCVFDAHDGEVNAVQFSPGS RLLATGGMDRRVKLWEVFGEK CEFKGSLSGSNAGITSIEFDSAG SYLLAASNDFASRIWTVDDYRL RHTLTGHSGKVLSAKFLLDNA RIVSGSHDRTLKLWDLRSKVCI KTVFAGSSCNDIVCTEQCVMSG HFDKKIRFWDIRSESIVREMELL GKITALDLNPERTELLSCSRDDL LKVIDLRTNAIKQTFSAPGFKC GSDWTRVVFSPDGSY\VAAGSC *RALLYIW\DVLTGKVEKVLSK A\HSSSHQCGWPWSPSWART\F VSVDKGCKAVLWGTVLTGLSG LGGPQCPPHEEAHGLLQPWSW QVNVLGYSMDLPEKLKANVGH

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7998	38366	A	8053	116	921	LSKSNRCW*GCEEKGTLIHCW WEC/KFNPLLKAI*RFLKELKVE LPLDPAIPSLGLSKIGTGKKVW QRLPNCPTISLFSFFHKNRHTGT YRRRFLDSLAVRCPCNPATFGS KSDVCNFWVMPSTGKKCALPS HPLFPNGLNADVVCLSDSENLS QKILLILEVSDSVILGKLSHKNII QHDCIEEPLTLLRNTQQFRFLCI ACHGCTSQYSTFLVKASWTRS QGLIQRQPSAGSGYPEKLFSEG AGDEGVDLLPLLAKPASPDEQL
7999	38367	A	8054	35	422	SCSEVTEASWGSVPELRDAQLG VGLHSPTYRHPHRETLTCCPAG TLQAWPFCGRIRVRVPVSWLGE PGRGLIPGSGSAASSECLPGLHG RAPLGTSCRPGRPLP/WNQPPPR LAQPGHRDPDADAATERPGLQ RPSRTACERFPMGVSVRRRVEA HSQLGVPELRD
8000	38368	A	8055	3	277	GPPRPPA*RGHGGRPENT\PAPP RWPPPP\PRSPAPLPPRRACADV THPPVPTPGKRTPPPIGGAPAAR AAPRRPAPSCFSAPTPGCSLTTG
8001	38369	A	8056	3	179	PPPHPQGPPPPGRPPGC*RPI/QG RQVFSMKPGRTPERTAWS/PPY PGCLGSRPRRPSAPA*SGAHCV VAPYPGCLGSRPRRPSAPA
8002	38370	A	8057	3246	4682	ENTLSFASFFFFEMLSLCRPGW SAAAPCQLTAASTYWVKRFSC LRLPSSWDYRRAPQHPANSFCI FSRDRAL/TMLVRLVSNS*PQVI RLPQPPKVLGL*ACCGFCSGSS GMAPGCGRVVSHAGAPGGGTR PP
8003	38371	A	8058	3	718	LTRLVLSPDAPD/RATHLIAA/R AGTEKVLQ/AQE/CGHFHVVNP DWLWSCLERWDKIEEQLFPLR DDHTKAQRENSPTPLPDREGIPP TALSHPMPILPKAQPSPEVRIYD SNTGKLIRTGARGPPAPSSSLPI RQEPSSF/RVDDILGEGSDDSDS EKRRPEEQEEEPQPRKPGTRRA RTLGAPASSERSAAG/SRG/PRG HKRKLNEEDAASESSRESGNEY EGSSSEADEMAKALEAELNDL
8004	38372	A	8059	273	468	NVKGTAANGD*G*RGEAAPA\G RSRARVPEDAASESSRESSNED EGSSSEADEMAKALEAELNDL M

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8005	38373	A	8060	1	2886	MEVPAAGRVPAEGAPTAAVAE VRCPGPAPLRLLEWRVAAGAA VRIGSVLAVFEAAASAQSAGAS QSRVASGGCVRPARPERRLRSE RAGVVRELCAQPGQVVAPGAV LVRLEGCSHPVVMKGLCAECG QDLTQLQSKNGKQQVPLSTAT VSMVHSVPELMVSSEQAEQLG REDQQRLHRNRKLVLMVDLDQ TLIHTTEQHCQQMSNKGIFHFQ LGRGEPMLHTRLRPHCKDFLEK IAKLYELHVFTFGSRLYAHT
8006	38374	A	8061	2	680	
8007	38375	A	8062	658	1657	PGILSLRNALLTGVDCKVVVPV PPGHTHPQLRLFHFHPKTCSGW GEWGDHGVVWAGPAPA\YHL HRDVQALWTNDHALAW\P*AM TSERTLWPGHELSARPGRSWRI SCPTGL\PQGGDDRTRGHWVTA TCCSADGLRLCRYGD\GVRGGL PTVAWP*LTGSCSLRYGSGQQC CYTADGTQLLTADSSGGSTPDR GHDWGAPPFRTPPRVPSMSHW LYDVLSFYYCCLWAAPDPGKD RAGLGCTPT*PSTLTLASAFGDP HFVTFDGTNFTFNGRGEYVGM G*NQGGRLEPSGSRSAPTTAGT ETRGTGLTAVAVQEGNSDVVE VRLANRTGPER
8008	38376	A	8063	873	1791	RCAGCPHSSSFFERGQ*AAVGP CCHGGTYRKASSV*RVSV*HPP HDRGSRK/QSLSGR*STGLS*MP SGVASSASV*FVNVFSLSSSN*L AQSTARFPPGSVRGLGQGRAG GG*APGHGADHPTGRQHS*GSP APVTWLWWPPPRHQAALAPAP STTPYDNSPLHCRPSGPSQSSHP HSALPGT/SVPGSSPLEIVPGSSL YVS*SLIRALAAPISSSSVGKNC RCTERLAIKPAAESCRTRSSSAG QSVFSRFTSL*AFTG*AR*PSAS AADLLVKASILLAQLLILESLAS STRMYSFRDCTSSFSA

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8009	38377	A	8064	2	935	YSPARGSGRGDLSRRPGAGRRA GQGPQVGAPKPGGAEYVRWA AGGMKGAGGSSGSGSGSGSRE AG*PGVPRGRRGWRTPAEPPG WGPGRRQACGA*G/EGRAAAQ VGGAPAAAGGGVAREEAPS*P GDAAGGSGTPGAASVQVSAPP AQPQINLSAGARAGVARRCVCP RGAES*GPGPDPGPGSRR*PPAA QSGPPPCPSALFLHPSGFLCRRP QPSRAQGGEVSGALRAVPRLSG GAGNLAALPCQLPGSGGLTPGC /QASQGLGVLGLVRAGPAWSPL DGPLDQKVFSPQTSLWNQRCFS LAAAGPVIIR
8010	38378	A	8065	3	367	
8011	38379	A	8066	2	1246	TPAWSREILAEELCTPPDPGAAF VVVECPDESFIQPICENATFQRY QGKADAPVALVVHMAPASVL VDSRYQQWMERFGPDTQHLVL NENCASVHNLRSHKIQTQLNLI HPDIFP/AAHQFPL*EGGPHPQC AHGSG*MPPQVPAPFQE/WSAR GMPLLLAILRNS*LRRCSFPTSS RALQEYRRSAQDGPAPAEKRS QYPEIIFLGTGSAIPMKIR\NVSA TLVK\QSPDTSLLLDCGEGTFGQ LCRHYGDQVDRVLGTLAAVFV SHLHADHHTGLPSILLQRERAL ASLGKPLHPLLVVAPNQLKAW LQQYHNQCQEVLHHISMIPAKL PSGRWLRSPVLQWKD*FSSLLR T\WIWEEFQTCLVRHCKHAFGC ALVHTSGL\KVVYSGDTMPCEA LVRMGKDATRKQADELISFQG
8012	38380	A	8067	121	880	GAAASQLPAVPQPVPGGPAPH QYDSCQMPSGRG*DLQSCSGKI DQFA/AWTTCDLEEFQTCLVRH CKHAFGCALVHTSGWKVVYSG DTMPCE\LLVRMGKDATLLIHE ATL\EDGFRKREA\LEKTHSTTS QGHSAWGMRMNAEFHY/VLN HFQARRY\SKVPLFSPNFSEKVG VAFDHMKVCFGDFPTMPKLIPP LKALFAGDIEEM\EERREKRELR AGAGRPSCSRGAGRRPLEDGEP QQKRAHTEEPQAKKVRAQ

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8013	38381	A	8068	1	607	SPGSWETRLWVWSFYRSCKHS LCPCLVGEFLVFNSPMQSGSAG EPPRLQF/GAPLPGAAPGNYRRT GRGREGPWPPPLAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRGRPRRAA*TGPSAQ/PP RSLSTLSPAPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLAKRPKRLAQMH WGH
8014	38382	A	8069	1	290	QFLDAESGSAGEPPR/LAVPAPF PGGAPGNYGRTGRGREERSWP PPLAPSLFALSDFGSSPGRTSRR PLAVSRRLGPTFPPPPLPPAPGR GRPRAAP
8015	38383	A	8070	1	565	SPGSWETRLWVWSFYRSCKHS LCPCLVGEFLVFNSPMQSGSAG EPPRLQF/GAPLPGAAPGNYRRT GRGREGPWPPPLAPSLFAFSDL GSSPGRTSWRPPAVSRRLGPTFP PPAPGRGRPRRAA*TGPSAQ/PP RSLSTLSPAPAAPAVRTAPPVAS PRAAPAPLRAITLLATKSEELPV VSFFSSRLVLA
8016	38384	B	8071	475	913	
8017	38385	A	8072	145	275	
8018	38386	A	8073	1	310	VEELTARTGGGAPPGCQADAK RMPQFPPQRTPWGHGFAGAPFP ISKPHGPPAGQL*PG/PSCEQT/E PPSPVNVTVTHLRANSATVSW DVPEGNIVIGYSISQQV
8019	38387	A	8074	1	483	GSHRVGRWAALCDRAAPRGLT NRETGGGAPPGCQADAKRMPQ FPSQRTPRGHGFAGAPFPISKPH GPPAGQL*PG/PSCEQT/EPPSPV NVTVTHLRANSATVSWDVPEG NIVIGYSISQQRQNGPGQRVIRE VNTTTRACALWGLAEDSDYTV QVRSIGLRL

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8020	38388	A	8075	2	854	RPPAARARRWLPKPSPARRSRR PAHRCSRRRRTCTPQATRPGMR *APAAACGPTGRRS/RLPALKL ALEYIVPCMNKHGICVVDDFLG KETGQQIGDEVRALHDTGKFT DGQLVSQKSDSSKDIRGDKITW IEGKEPGCETIGLLMSSMDDLIR HCNGKLGSYKINGRTKAMVAC YPGNGTGYVRHVDNPNGDGRC VTCIYYLNKDWDAKVSGGILRI FPEGKAQFADIEPKFDRLLFFW SDRRNPHEVQPAYATRYAITV WYFDADERARAKVKY/RNR*K RCEG
8021	38389	B	8076	1	205	
8022	38390	B	8077	1	806	
8023	38391	A	8078	1	2279	MKVGLDQIIEVVPSHSVTSGAA AGECGGVHCDSVCAEGRWGPN CSLPCYCKNGASCSPDDGICEC APGFRGTTCQRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNEAYSQ/SCPSGR FGKNCAGICTCTNNGTCNPIDR SCQCYPGWIGSDCSQPHCADKC VHGRCIAPNTCQCEPGWGGTN CSSVKKQSTVCES*KCEPWEER PCGGLHWDIAG*/P/GKHGGYL NELGAFGLDRSYMGKSLKDLG KNSEYNSSNCSLSSSENPYATIK /GPTCTYPEKLRVWLCGDEIAG TKRFPICRDQ*LNFSQQECL*S* TYSECCPRSIQQ*WASFPGSI*PP KNSHIPCHYDLLPVRDSSSSLK QEDSGGSSSNSSSSSE*/APKDR LGLLV**RS*SM*TNRLAKHPK QPGRKGPKI**HGTWKSSQEK/ HAEEQSGKLAATLCGKDWLIQ REGWPYILSRMFL/CFISTDGRE SESLWRKSNGNSKFKF*WGRPG KCGL*EGQREEVWGLGNSLYC LAGQL*CLDCECHH/GFQECCP VLGHSWGYKS/CLNRNPLKGLS SRCAGLAVRDSLAPNSQGWKA TFDFPSLECPSGTYGYGCRQICD CLNNSTCDHITGTCYCSPGWKG ARCDQA/GCYHSWKSEQLKPN QYCSPC*FLPDRGHCRHHHSCP SCSLPTGIVHYL*TQAEGKGIKH
8024	38392	B	8079	1	2909	

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8025	38393	A	8080	332	602	NSLNSRWLKGLPGAPGIQEIKE MWRCMSSICQKEGWRMTAGS LGHHRSLLHVGQ/AGNDVDRT GSLPASVR/QHAYYTASSVEGR VSYKLYT
8026	38394	A	8081	2	422	FNISLGFACPLRIDFFGWFFFVFF LSWSFTLFAQAGVLWCDLGSL QPPPLGFK\KFSCLSLPSSLDYRC LPPRLTNF*FLVEMGFHHVGQ AGLELLTSGDPPASASQSAGITG MSHRAQSAALSFK*SGISKNRY FIFWA
8027	38395	A	8082	1	951	
8028	38396	A	8083	1	924	
8029	38397	C	8084	271	738	
8030	38398	A	8085	1	575	
8031	38399	A	8086	2	332	
8032	38400	A	8087	1	897	
8033	38401	C	8088	181	804	
8034	38402	A	8089	1	1923	
8035	38403	A	8090	294	2340	EKCRHNCSSRVWQSLVSQSVW ATEGQYGRTKNARPVQVK\DS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINEAI VPLYPAVPNPYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLLLAAHLETLCH QATQKKTGIALGVLTQVQGTSF QPVAHLSKEIDVVAKGWPHCL WVVAAVAVLVSEAVKIIQGRE LTVWTSHDVSGTLTAKGDLWL SDNLLLNQALLFKRPVLRLHTC ATLNPATFLPNNKEKIEHNHQQ VIVQTYTIQGDLLEVPLTDPDL NLYTNGSSFVEKGLRKAGIHPS RQWTPLWPKAGPEMLSKRQVL ESGILKAFLVPYLLVAVLGSIDF NGKPPVAVFSLSQAHRFLCAT WLLLGYGEVWIHSHTAIKTYQ RRRSQDGRIGTAPVYSSQRERR RRRVISAFPSEGIPTDLQLRVLS VRRKTNKQKGHPHQKPICTSPS SRPKVDKTTKMGKKQNRKTGN SKTQSASPPPKERSSSPATEQSW MENDFDELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSQCDQLEERVSAMED

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8036	38404	A	8091	158	865	NPAARTPFFVIKKGGKRGEGCL AKAGAIIHLNIG/GTPVCCPLLE EGINLEDWATEGQYGRAKNAR PVQVKLKDSASFPHQRQYPLRP EAQQGLQKIKDLKAQGLVKAC NSPYNNPTLGVQKPSGQWRLV QDLRIINEVTVPLYLAVPNPYIL LSQIPEEAEWFTDLDLKDAFFCI PVHPDSQFLFAFEDPSNPMSQL TWTVSPQGFRDSPHLFGQALA QDLSRFSYLGTLVLWYVD
8037	38405	A	8092	1	748	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYLGLKLSKGTRDLTTFLP VNEEKIE/P*LSTSNCSKLRCSRG TSRGSLG
8038	38406	A	8093	194	1377	NPAAQTPFFVVKKGGKRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSSPCNTPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEAEWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDTLVLQ YMDDLLLVTHSETLCHQATQV LLNFLATCGYKVSKLKAQICSQ QVKYLGLKLSKGTRALSEERIQ PILAYPHPKTRKQLRGLLGITGF CQIWIPRYSEIARPLHTLIKKTQ KANTHLVRWTPEAEAAFQVLK KALTQAPVLSLPTGQDF\SLYVT EKTGIALGVLTQHYGEERNS*L PTEYLSNIRKPLGDYYWLYRNL KRWQSYTARVIRKERKGK
8039	38407	A	8094	3	521	

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8040	38408	A	8095	1	3203	DSPLSTKAMLGMLVKDHWSPA AQTPFFVIKEGGKRGAGLLHGQ LILKDKFITQSAADIKEKLQKST LGPERNLKTLLNLATSVFYNRD QEEQAERDKRGKKKATTLVMA LGQADFGGSGTRKAWANRMP NRAYFQCGLQGHFKKDCPSRK PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGVLGQ PVTRYFFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAII HLNIGEGTPICRLL
8041	38409	A	8096	13	183	VHLHPQGHVPVKHTPTGLGYS SCRHLLLGRACY*KGEVGAKA GMQVSDALPRLGGVS
8042	38410	A	8097	1	2427	MSKFSCASLTATESDGTPLMEQ YVPCPVCETAWAQHTDPSEKS EDVQYFDMEDCVLTAIERDFIS CPRHPDLPVPLQELVPELFMTD FPARLFLENSKLEHSEDEGSVL GQGGSGTVIYRARYQGQPVAV KRFHIKKFKNFANVPADTMLR HLRATDAMKNFSEFRQEASML HALQHPCIVALIGISIHPLCFALE LAPLSSLNTVLSENARDSSFIPL GHMLTQKIAYQIASGLAYLHK KNIIFCDLKSDNILVWSLDVKE HINIKLSDYGISRQSFHEGALGV EGTPGYQAPEIRPRIVYDEKVD MFSYGMVLYELLSGQRPALGH HQLQIAKKLSKGIRPVLGQPEE VQFRRLQALMMECWDTKPEK RPLALSVVSQMK/APDFCHLHV *TVLWEADSLLLIPGPGVHRGV LGWKRGVQELHGG\NTEKGLM EVQRMCCPGMKVSCQLQVQRS LWTATEDQKIYIYTLKGMCPLN TPQQALDTPAVVTCFLAVPVIK KNSYLVLAGLADGLVAVFPVV RGTPKDSCSYLCSHTANRSKFSI ADEDARQNPYPVKAMEVVNSG SEVWYSNGPGLLVIDCASLEIC RRLEPYMAPSMVTSVVCSSEGR GEEVVWCLDDKANSLVMYHS TTYQLCARYFCGVPSPLRDMFP VRPLDTEPPAASHTANPKVPEG DSIADVSIMYSEELGTQILIHQE
8043	38411	A	8098	1	1641	

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8044	38412	A	8099	1	1075	VLHKFPYRMVPALPPKRMLGA DREFIEARRRALKRFVNLVARH PLFSEDVVLKLFLSFSGSDVQN KLKESAQCVGDEFLNCKLATR AKDFLPADIQAQFAI\SRE\LIRNI YNSFHKLRNRAERIAS/RAIDNA ADLLIFGKELSAIGSDTTPLPSW AALNS\STWG\SLKQALKGLSV E\FALL\ADKAAQQGKQ\EENDV \VEKLNLFLDLL\QSY\KDLCE/R GHEKGVF/HTKHQRALAQSTA* LKRPD*LSATGAEPRSPEVRGS KLKSRIRGARENAI\QTMELRN Y\FSLYCLH\QETQLIHVYLPLTS \HILR\AFVNSQIQGHKEMSKVW NDLRPKLSCLFAGPHRT\LTPPC SPPEDG\LCPH
8045	38413	A	8100	1	974	MPQVPAP/PLPSITSGHPGEP/PA RPSCSCLFSPQPCNSITPSSLLLR QLAVAAAGGCGGHGAPALSST GWQQVCKSPQVRSVPDNPTTA DSTASLAWKFGEVLRSHINCGY K*KQQPLLPVHAQRRAQVSAP/ APPAGLSCGQHSLPQPPRCSDLS LGLHPGRLPCDRGHCPPLPPVT PTPDKAGPILDPAQSCPFCSPIPA PPKQPSPPARFPEMKRKKTLM MPPSEGSLSLASGMEASVFQRL LSRCTCLDQATVIWGFCYMQV QASQGIPCRGKDELLRLAPLPV KEARRTKPRSPGKHAKAPPSSS ACSPHLCCSSPILQALD
8046	38414	A	8101	1	460	SLQAPRRNSRAEHTRTLNSECP RRRRCCIKGCTYT*LDAVP\PPP VLDWLVQPKPRWLGGNGWLL DGPEEVLQAEACSTTEDGAEPL LCPSGYECHILSPG\DVAEGIPN RGQCVKQRRQADGRILRHKLY KEYPEGDSKNVAEPGKG\QQRH
8047	38415	A	8102	3	219	NNHRLDRTLPRDYCHAATAYT THELAFGDFRLPTEGHQELCHN SHLIYFRRDK*THCTWRSVDSL TGVTHR
8048	38416	A	8103	230	555	NVRPS*ALQAPWGRHHLCVTP MQLRMTLVVSSLGKGTCGLSL AQ/CAPVQEGTHGGSPPVEGWL AATRTCEGCRRENTMKNVGSR KYAFNSLQLKAFPKHYRPPEDL RKS

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8049	38417	A	8104	23	304	KGFYLFNKQTIEQTNNGSKSFA KRNTEGHDDLLLQGFQGSQTPS FLSSSGRCYSWGAIGP\QFGALS G\FSPFPHSAANRQSSALDFWIT TSISF
8050	38418	A	8105	99	375	VLEFGALSGSLSISPLCTIPALVE PPCGPQPSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSPQGVQ LPLGPR\RLKMNTEPPTRP
8051	38419	C	8106	5	376	
8052	38420	A	8107	545	990	GLCHVLQPCDPCLPGTMQEAQ PPEVLKTAGKAGGQEPG*L*RIP *GSLCPPCPVAFGAAAELPLPSS DPVSRTGAPPGQG*WLGFGYFS SNEGPSQAGG
8053	38421	B	8108	252	801	
8054	38422	A	8109	169	1226	PNGLRPPCPSPASETPGNAPVCD PGSSSQGAQGKL\KPGGLPGWL FPFFAQPSPSEG/GLCPPCPVAFG AAAELPLPSSDPVFRTGAPPGQ GSW/PI*SPGSRSGTRADPVKGE VAGRERCLPLIE*ASPGPPHSG* AGQVPGAGPPRTAG*GV*TGTA PCPKAQPRK*QR*R*RCSS*VG* ESAEIVCPQGDAEG*RKGSP*G/ SHRRNVPS/RYSNSHGPYDSNQ PHRKTKITFEEDKVDSTLIGSSS HVEWEDAVHIIPENESDDEEEE EKGPVSPRSPRKRP/PSATRAAA SRLRGS*TLGGLLGCIFAFFAPP SPTEGACAHPAQSLSGPLRSFRC HLRILCPARGLHQGRDDG
8055	38423	C	8110	58	504	
8056	38424	C	8111	203	1874	
8057	38425	A	8112	32	1026	KLLEQCLHSVSTWETPQYRRPP SPS*RGSREQPCSFSSPRDTPGE NHWLSLPQRD*AGPPVR/PSAG GFMTP/PPRGVPTVEVPPDPTC/S PNHTRPFRPFPSKNPCFRFPEPL RAPTLVPGPLPPTHPGRVPHLE RNLSALGLGKSEGLKRNPCVEP /PAPTPIRFPKITGTLPLR/PAADH ALLGMRDQSLSGQSPGPKSPDA DDQLQNRDHTETEQRISSGRSS ALAPESQLQQGCAGIHFRGRFC KAPPLASGPA/RPPCLSLPPPPW APVRPKPPR*APPPAP/PVPSPIN HPRAEECGRTARDWQAAPLAA LVRDPLDEASWAPESGGDVEN LYV

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8058	38426	A	8113	3	909	TEGGASHRAHPVGPAPRG\KRH SGATEPANGTWARRRGPGRDS SNQSSGGGERSQLRHRGWRRL SRPLLPPGAASPLAGEDPERNA G\GWRGGAAPMRPKRGPMNGG GCGPGAGSGAGGEALGRGRGA VSGCRPAPPVRPPPPPPPPPGG WLRRTAGSGPEYV/GSRCARGS GQVSAGGGLCARAARGGKLAP RLRALRGRPSPWPAPLGRSPAR APARVPAGRCGPGA*RGRCAL GGQGEEGPAGSEGAGRPLPGRP GCPGTSPRLLPRRPVRKTDVGN RSSFFPRAPGRAPHAQCPTQFLII
8059	38427	A	8114	1	454	
8060	38428	A	8115	2	172	MFIYTSAFI*QFTNSINIPI*TSFC *TASVHLSCIVAVFCFHPCQCSS SFIQCTTN
8061	38429	A	8116	1	594	LAPVFKLIPMPVS/YGIFLYMG WAALSSIQFTNRVKLLLMPAK HQPDLLLLRHVPLTRVHLFTAI QLACLGLLWIIKSTPAAIIFPLM LLGLVGVRKALERVFSPQELLG LDELMPEEERSIPEKGLEPEHSF SGSDSEDSELMYQPKAPEINISV N*LE*ESGSGDPRKQHEVLTQE VRTFLAFGLTSRCSVGLGKD
8062	38430	B	8117	1	3402	
8063	38431	B	8118	1	4614	
8064	38432	A	8119	3	435	DHAKLGTRTSGMRPHSLSLCFF SSSYDILMRITKDRVKNLTCITY TILPTDLQPGCGLPRSFYPSSKP TSFWLWACKLFPPLPISFNPSPA HSKTAHGHSGKHTEAGM*WS* TGEGITGRCCFVSIKAPPLPSSG PVGGPVGG
8065	38433	A	8120	1	525	MALLPTVLCLWAQAQFLVDLG QSNSKHQEHQLAPDVAFAKMK GACVCAAGFRGWRCEELCAPG THGKGCQLPCQCRHGASCDPR AGECLCAPGYTGVYCEELCPPG SHGAHCELRCPCQNGGTCHHIT GECACPPGW/IG/TV*GPPSPGSL LGCLPRETSISLIISSIQLCLYLLL

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8066	38434	A	8121	1	1050	MLIMTFHGLLPCMQMACKWQ LRVLVAGIRCDSTCPPGRWGPN CSVSCSCENGGSCSPKDGSCEC APGFRGPLCQRTVHILYPRGCGI RDVGESGNRKQKAVEQYREH WTVSPEVQCSASHFSSVRPKSA CPPGFWGPACFHACSCHNGAS CSAEDGACHCTPGWTGLFCTQ RCAPGTFGYGCQQKCECMNNS TCDHVTGTCYCSPGFKGIRCDQ GIMLLL/CPHCGAAGPICLASAA AEREGPRPGSPCLLHTCHEDDQ HRLLPLSGANSIPTYR*SGRPDS PLRTEALILPQ\CQKFSGSQGEV CAVSCAAGTYGPNCSSICSCNN GGTCSPVDGSCTCKEGRIICLQ
8067	38435	A	8122	3	732	IRCDSTCPPGRWGPNCSVSCSC ENGGSCSPEDGSCECAPGFRGP LCQRICPPGFYGHCCAQPCPLC VHSSRPCHHIIGICECLPGFSGAF CNQG\QAPTGNPSPGWYRS*EM TDPRCSCR/CLSGESTRHTSPVL LGTDASETQVIGFVNLAQFLIIC PRKLHYKAQNSKKSNGSDASS DWKDWGIWDRESCEELCPPGS HGAHCELRCPCQNGGTCHHIT GECACPPGWTVGA/HC*ALCCP
8068	38436	A	8123	77	864	PAVPEL*VFQAKPERKSRYWQL HFPPHSSSPTSWRKSLEPMYRC TCPPLTPYGCTCPPLSPYRRTCP PLTMYRRICPPLTPYRCTCPPLT PYRMFSSPLHKEITSAQRSPEPS SRPHSSKAAALR*QPRIMEKQRI YGPSPTSVQPASPPPCLDDPRKK AERPDHRATGKRHLPETSL/YA ELVRRAVENPEDSEAPAPAPAA LSPASEHRTDPIQETKKARKSSD NDGSTPLAQTPTRRSSQWPRLG QFQQQEDDSSGLYSTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8069	38437	A	8124	314	1188	KHFLNFCLPYMILNKYRNQYCT FNDDIQGNKIFTAYGSITCLKLV HNCIKKIWLVDSKGLIVKVRIC HF*PE*R*LCHSGWPSNLEAIVQ EIKPTALIGKHFLLSLLPYPLF*P DCFFNERPIIFALSNPTSKAECS AEQCYKITKVK*NYNRYFNNQI FIHYREATLYPGQGNNSYVFPG VALGVVACGLRQITDNIFLTTA EVL*NPLSLPRV*NTKCAQPRN TIRDVSLKIAEKVKPLLFKLHYF SFLFLLNMQEAFVRSQMYSTD YDQI\LPD\CYSWPEEVQKIQPQ
8070	38438	A	8125	1	1115	SPAQVMFQCLWKSCGKVLSTA SAMQRHIRLVHLGRQAEPEQSD GEEDFYYTELDVGVDTLTDGLS SLTPVSPTAS/IAACLPPPGAAR AAGAPSPA*SPAAACPAPAPAP CPEHRC*PPVLSQ*PCLPRAA*R PPAWSRMPRRLEPAHPPCPPGS ESS*GSPAATRISAGM*YGMEA PGPPGAQPAAGRKP\PAVPGLK SGSFKNIKLPPSPSPPPPGPGAET ARRNKPQGAGPSPAAGSAFNW VGVPDLTLEPFPPPGPGEGSPPT QS/SPLKKPSFLH*SPNPHPLSPF TPKGPGGSHPSRLSARRFIKGV MGPALGGQSRCTLRGVGEGTP PLALNSTALGPWGCFYPCLFLK LQVSHVWAATRRREKLKI
8071	38439	A	8126	116	333	KLRDRCLSH*K*NGASPPRPTN VSIMRPSLV/SLVHHSGL*FPQM LRALS*LRVFGVAVSSP*MVPL NPCIISH
8072	38440	A	8127	5	829	KPSPQPPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVRGRPPAGG ARRRAASLG/PWVRRRLQARPG /LFRPRDFYLRSPRSYGTRP*KSP QSSPRGSARPDP\GPA\PPPEPPV KRRARGVLESSRHAAPRRVFHL GREREQSQEGPAWPKRGRPAPS PQRTATWRPAAGGGK*GSAAT S*ARAGPARRGKRRG*EPRENR RAGRPATRGRPPGRRCCPPA*S PRPSKRSSPLCSPRPSWPPTRPS KSSYGASLARTTTLQWKFSVNL IRKQIRDAQ

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8073	38441	A	8128	5	844	KPSPQPPCPRPGPPRARFLRRSP DVEKIPFA*RPCDVRGRPPAGG ARRRAASLG/PWVRRRLQARPG RFAPGTFTCGAPRSYGTRP*KSP QSSPRGSARPDP\GPAASARATR EAQSARGLGELAARGSQAGLP LGKGARTEPGGSS/CSQGPAWP KRGRPAPSPQRTATWRPAAGG GK*GSAATS*ARAGPARRGKRR G*EPRENRRAGRPATRGRPPGR RCCPPA*SPRPSKRSSPLCSPRPS WPPTRPSKSSYGASLARTTTLQ WKFSMNLIRKQIRDAQ
8074	38442	A	8129	795	914	RGIRLASEMYPLTCFWRS*LYR RGSLARIALVNCRRNAL
8075	38443	A	8130	4073	5350	YSLKSGSVTPLALFFLLKIDLA MQALFWFHVNFKVVFPNSVKK AIGSLMGMTLNL*ITLGSMAIFT ILILPTHEHGMFFHLFVSSFISLS NGL*FSLKRSFTSLVSWIPRYFIL FEAIVNGSSLMIWVSVCLLLVY KNACDFCTLILYPKTLLKLLISL RRFWA\GQWGFLDIQSCHVQTG TI*LPLFLIEYPLFP\LLPNCPGQN FQHYVE*QW*ERTSLS\LPVFKG NTSSFCPFSMILAVGLS*IALIIL RYVPSIPNLLRVFSMKGC*ILSK AFSASIE/YNHVVFVFGSVYMQ FLLVPLVEFGCESIWSWTFFGW *AIDYCHNFRSCYWSIQRFNFFL V*S\GRVYVLRNLSISSRFSSLFA *RCL*YSLMVVCISVGLVVISPL SFFIASI*FLSLFFFTSLASSLSILL IFSKNQLLDSLIF

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8076	38444	A	8131	1	1715	MDGISGGKRALRERHSKSKAL GRCFPWTNITPPALPGITNDTTI QQGISGLIDSLNARDISVKIFEDF AQSWYWILVALGVALVLSLLFI LLLRLVAGPLVLVLILGVLGVL AYGIYYCWEEYRVLRDKGASIS QLGFTTNLSAYQSVQETWLAA LIVLAVLEAILLLVLIFLRQRIRI AIALLKEASKAVGQMMSTMFY PLVTFVLLLICIAYWAMTALYL ATSGQPQYVLWASNISSPGCEK VPINI\SCNPTAHLVNSSCPGLM CVFQGYSSKGLIQRSVFNLQIY GVLGLFWTLNWVLALGQCVL AGAFASFYWAFHKPQDIPTFPLI SAFIRTLRYHTGSLAFGALILTL VQIARVILEYIDHKLRGVQNPV ARCIMC*FKCCLWCLEKFIKFL NRNAYIMIAIYG\KNFCVSAKN AFMLLMRNIVRVVVLDKVTDL LLFFGKLLVVGGVGVLSFFFF\S GRIPGLGKDFKSPHLNYYWLPI MRNPITPTGHVFQTSILGAYVIA SGFFSVFGHVCGTRSFLCFLGK DLGSVNNGFPGDRPYY/MVPRA FLKILG\KKNE\APPDNKKRKK
8077	38445	A	8132	1	208	GTRASSPAPCPSSSAPAHSFEAC CCRMSLWGSCGGSGDGSSACG SGWNLSMAGTSCSSPAMCSPSR APS*RSASRPRTWRATTSAASS WAPRRCWCGWA*SAT*PSSTTT ISSSPHCGWPCPASCASAAAWL SSTWATASVAGSCWGPIM*SSA PAHSFEACCCRMSLWGSCGGS GDGSSACGSGWNLSMAGTSCS SPAMCSPSRAPS

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8078	38446	A	8133	28	1956	SRAARERGRSDSGGRSDPGCPA VPACVPRSRPSMTAPAGPRGSE TERFLTPNPGYGTQAGPSPAPPT PPEE/VRPSPSS/TNTFS*VPATSF EPRAASPAS*CCKWSRSWWSR CSSSCLGSVISWL*HSGKRTPSP SDTSSCWATRTERMTPSQPTRG SSCTRPSSMLWT\SAGGRAGAG GQAGAVPGVA/WTCHWAGLLS ASGTTTEATWTRPTTHLTLIRW WLLTASRWIPPSGPLRPPATISP SWKAAPVTRTSRSNSTSTACSL EGGPGVSTWQGTLALGAGRDP KTPLTLTRASCLGWSMSPSTSG *RPLTSRASSIMRSRTAIPSAS*S RLTTKHTVGGSPSAWRPRPTSR SVSTPVSSSTGGQQLPGSCLTW WSYSPAPCTSSS\SPLTPSRLPAA EQSLWGSCGGSGDGSSACGSG WNLSMAGTSCFVTSDVLHHLG HHS*RSASRPRTWRSLRRFAAS SWAPRRCWCGWA*SAT*PSSTT TISAHSPWCLSACSRSSMGTTC L*RSPPCRRSRAAAAWCGSSPS STFTPSSSLFILHGAQPLHRAHH RAPTYTIKHSRRRRRKRRASCR PYIAQCPGQPHLRQVPPRERAR PIAILLLLRKGPLGGAFAAGELI RPDCRWTVGPGLQRPPPPTPLIY L
8079	38447	A	8134	1	2994	MQRPCLCVEPMRLCFDSFLLLV NQGEEEEGVVPCLEENGRAAA DPGPQDQDCLLPTLTPSLSGDE APDRTQSSGDPRERCGYLSVTC EEGDNRFAAFCLCGSWRLNHG HADWCDQRRSQISNRLPASLGII VGTRGSRHLLAALRGVKEDRQ TKGCVQTPASLSPWLPGLSSET RAQKTCSVLLIDYATFLKLAND DDDGCLDCLQPGVRTAWASSQ HGIRAPRKSVQGSASSPSLRTW ALTCTQNWFCCVLLVK
8080	38448	A	8135	215	418	

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8081	38449	A	8136	767	1458	WREHLTKFNVWGKQHLESLNS QQKNMRCPVRSQTRPPTDVKP VSRSGRREDRRAAGGEGGADR QGPGTARARAPGSPQRGG*GR NLR\QAGPPGKHGRGIPPPQTRG RSRGAPPGTPEGPRHPPRPASRA PGPATGAPKRPQPQTQRQGHIA RDSRPSSDPVPLRETGAPPPWD A\SQGQAARPRATQTPSSAPVA TRQGSGRRADSRRRGVTRRTER CAQPSLAVSRVPTR
8082	38450	A	8137	3	424	
8083	38451	A	8138	1	813	MVQKELEEEGRKSTPQSWGRE NMEKALNSSLKASLGSGGVMI CASVKALLTVVIAKVLGRLL\ES LFLLLQTQTAL*QTL/RHTNRNI SHQYQDEIIILDGSDLPRMSPRR KYEPPVFPGRKTYKISIRGKAN KKCEEARQEKEAMVMKYVRG EKESLDLRKEKETLEKKLRDAN KELEKNTNKIKQLSQEKGRLHQ LYETKEGETTRLIREIDKLKEDI NSHVIKVKWAQNKLKAEMDS HKSFKNPLVRCNFAATFGYYK KLIPEIKTGSSH
8084	38452	A	8139	3	808	NVRVEPTDSSFMEAIEFAQKGA FDAYVAVGGGSTMDTCKA\AN LYASSPHSDFLDYVSAPIGKGK PVSVPLKPLIAVPTTSGTGSETT GVAIFDYEHLKVKIGITSRAIKP TLGLIDPLHTLHMPARVVANSG FDVLCHALESYTTLPYHLRSPC PSNPITRPAYQG\RNPISDIWGYS TRWGFVG*VS*RRAVQEIPMDL *KARSHMHLASAFAGIGFGNA GVHLCHGMSYPISGLVKMYKA KDYNVDHPLVPHGLSVVLTSP AVFTFT

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8085	38453	A	8140	2	1154	IDPLHTLHMPARVVANSGFDVL CHALESYTTLPYHLRSPCPSNPI TRPAYQGSNPISDIWAIHALRIV AKYLKRAVNSTDK*RRRMSLR APSWEWPSPSRGPARCLPRRFY IT*GS*QRYLLWPLLETVDEKY VSLQFSFRRQGVV*ITCLIFLPTE *HFFFFHHIFP*GSSLFCRNCQC* CVIVRYLYHSQGWQKSR*S*RQ GLIWHLGKCFLLGIGFGKCWVF ICGHGNV/SYPISGFRWKDVIKG KGIYNVGIHPTGWPPWAFSVVP HVPQRCFTFHGPRCFPERTPWR WQEILGADTRTAQ/RSQDAGLV LADTLRKFLFRSG/IVDDGLAA VGYSKADIPALVKGTLPP/QER VTSFAPRPQSEEDLAALFEASN ETVLNVHLN
8086	38454	A	8141	2	990	WENWISIC*RMKL/DPYFSPYTK IKSKWIKDINVKPQTMKLLQEN IRETLQDIGLGEDFSQAQATKA KVDKLDHVKFKNFCTAKETIN KVKRKPKEWEKILIFADYPSDK GLITRILFIDHSWVFLGEGNLAG SSDNSGGKAWKHLLPLLASRCS GTHSNLRAKLRLSQGTVATWP VLKREGEKSCGPSESPDLGAPQ ARDVTPCLGICSSWLLQASGHH HIPWCQLWKLFVVYLVQLQPH REVALVPAPGAAHPTTASVPVC AQWLDPMVIHSHTLCCSEPDSP LAGMGFRPVAQAKHNPARPSG WNESSRPEQNLDKGATSHRGF WLAR
8087	38455	A	8142	1	196	GQYPWPLETNPRFLRE*TLPKS LQKSLL*DSPVPE*SLCGTCQQA RSLSEEVDESSISQQVCCPT
8088	38456	A	8143	3	413	ITLGKDCIMHGYML/KLGNPFL TQWQRRYFTLFPKNI*WRRRGE S\RQNLLTMEQILSVEETQIKDK KCILFRIKGGKQFVLQCESDPEF VQWKKELNETFKEAQRLLRRA PKFLNKPRSGTVELPKPSLCHR NSNGL

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8089	38457	A	8144	705	1983	EIKVDSSLLKSFLDLMNGKQNL ENLNALKDFAMMLNLSYATEII LGLEHMHNRFVVYRDLKVRTI DRLILHSRYCVNGPLEDKVTEK DFPGNPEIKPS\GKWLGCPS*KS PTLSQRGLMTLPCQTLGSG*LSF PE/VLDLP*WTNAHFADWFSLG CMLFKLLRG*VEMHPSSAVLM AAGAWMKTTVVRGFKTVFLSV W*LSCFIPSKRDVSKRLGCHGG G*AIVPAFRYLYQKSKIVILNFQ YPPPLIPPRGEVNAADAFDIGSF DEEDTKGIKVHM\CHLFLYFYF WM/VMISVGKQEVTETVYEAV NADTDKIEARKRAKNKQLGHE EGKIAHVSQNISNAVNFQNFLY LTQWQRRYFYLFPNRLEWRGE GESRVSLRQPHRACFPVRTMAY GYWLLRRAPKFLNKPRSGTVE LPKPSLCHRNSNGL
8090	38458	B	8145	156	281	
8091	38459	A	8146	2	181	VWCCSRTATLRTRNCARRRCS RGSRTWKRSGRSSSRRRAH/SQ YDLERLRAAQKQLEREQE
8092	38460	A	8147	3	670	ETGLKNEGRVLVRHSAWCPLL WGREGSRSSLSSWPELQGSPLC ASQGVVLQQDSYIEDQKLVLSE RALTRSLSRPSSLIEQEKQRSLE KQRQDLANLQKQQAQYLEEKR RREREWEDRERELR\DGRPSWP SARRRCSRGSRTWKRSGRSSSR RRAH/SQYDLERLRAAQKQLER EQ\EQLRREAERLSQRQTERDL CQVMGLPAESNLMMILIKTPCV LSKVRK
8093	38461	B	8148	47	699	
8094	38462	A	8149	1	242	MNRGGFAVKILALLDALSTVCS QRVQKAKKQQHLQNKEHFKA LLKQKEKLKQQEDL/RKKLF*IQ GIRCPQATPHHGQCSL

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8095	38463	A	8150	3	929	ASSCVVRAVPPG/SGVWGFRCG LCGPDCESGLLISGSRMFAGPQ G/PPGAGTAVTLLAAGEEGLES STAQHGSGLCSEEPP\VPRRHA WQGKSYSRNWLPPARPRPALA MSSDTRGQAQLSPSWQLEKKG LSSSTAQRGCRALQGRAASARR \QRGKANPTAGTGWLRLAPGLP LLCPQTPGGRHSCHPPG/K/PGK EGLEQFYSSARLQGFAGKSRQV PDVTRGKANPTAGTGWLR/HR GPRGGEACAMAVRGPRSHEQR CPWSAGADSVS*GHCEGTDGR VASGACLQVDSRGSAGQNLPL DPEHWHVFCFDFP
8096	38464	A	8151	2	1749	WVQGASLCVRASRAPLPLARP* VQGAELTHPWGPAAHP*TRNQ KPALGSSGPHSPH\GNPQTPTQA GQP*PHTARHGPVQEHGRGQR GPHLHKTETPQEATP*EVGSIAT EQAWLPHLCL*RPPPFHQGLFP RGPCMEGAQQRVEGSSSAQGT QVCMGPKTAGDWDGPWLVCW FH*GEAAARILRPGLG\GLSGHP LWPQGGGQMTVGYGGASEAC GAGELLMRRAPPQSPGKARGL PA/HYWHQGQTGPRKAEI
8097	38465	A	8152	1	583	MAAVVAATALKGRGARNARV LRGKERDPGEGRTAEDPFSFTS SPTIAGGIL\AGATA\NKAS\HNR TRALQN/HTASPEGKEEP*/DPLS PELENTFPRKEGQRTPMESCGN LPWA\IGFPLWLFLPLSSFTQAG KWDK/VTVLKAD*RLRAEHCG FSNTGRV*RARRFRAFLPEVAPF PLMFGSGVSGGADLRSVCDPP
8098	38466	A	8153	141	341	GTRGSPSKKGERVRRDAQQTA TW*TRSPASGCFQICEGNKQDE ACDVRGLQHCERHSLAGPREY
8099	38467	A	8154	1	521	MKNRSRNKGNVEWQAEGIRSK RSVGKQRPSKAKIPSGDKNGVS LTHNEVINNDNPLESNDEKEGQ EATCSRPQIVP/EFQQ**LFRPE* WRRASGNLQLIPKKRVSA*GTR GSPSKKGERVRRDAQQTATW* TRSPASGCFQICEGNKQDEACD VRGLQHCERHSLAGPREYMP

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8100	38468	A	8155	1	619	PEAELHNHGIQINSCSVRLVDIK KEKPFSNSKVECQAQARTHHN QASDIIVISSEDSEGSTDVDEPLE VFISAPRSEPVINRATPCELKC* KEG\QEAIC/SRPRDVPRALGFR KF\SPFEESFRKGLLGQDPDFPD SIEKKPPAEASSG\ALRSKHGEK APMTSRSTSTWRIPSRKR\RFSSS DFSDLSNGKELQETCSSSLRRG SGKE
8101	38469	A	8156	362	1043	PTTPPSAGSSWTTASPPS*GKA WLGTGRPPSPWRRMSASMRT\S EEDGRLQPQLPL*AHPSESSGQ DRGNQVSVGREADCGQD/SPVS TMTRSHPGRPCAEGC**PCCSSR P*PCPCGSGSLVTSPLSLPAPSF WLPLRPS\SPPGLPPLQSSLSFPP PPPPVPQPPAPPALQWGLHLPG VPQPGVPAGRRVVRLSAKHLPR LPDHSV*GAPGRRSLREHLPQH RPGDQ
8102	38470	B	8157	52	633	
8103	38471	A	8158	15	3054	AGPDGLAAPASCQGARGQTRV PGAFSWLAPGSHHASEGLAPG VPPAGGVSAQELTAPPQEGWG LGAPPAAPRPESDEKRAGSDAV RSFSRGARDSLGQRRLGGTRGA GPAGKGAQRTMGPASGFHSFPP RPHQEPSPRSSCWQHLLWHCP WPQPSRLPRLTPAQLLQGPGVL AAPPGP*HVPGFLAQSPWPLPS GPRSP*DPLHQGALVPLPQGGS PHTAPHCLPSVLSPAIQQPLLPT AST/SSRSPPASTMAP
8104	38472	B	8159	748	3111	
8105	38473	A	8160	1	463	GGGGGRGQRGRPSRPRYLCPGP GPTG/GPGACAAGGVTVGPSED NGRPLLPPQRHPPVGDFSRRRC RFRLPKHKERSPDARFKEGPGG AA/GPGARGQ*DSARTPDS\ALK LVRPPLPIPTGRPSCASGGR*PA GKRGHLSAPPRPGRSSPGPSQP

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8106	38474	A	8161	1	2733	MALRRAGAGRTGCFIAIDTML DMAENEGVVDIFNCVRE/LRAQ /RVNLV/QTEEQYVFVHDAILEA CLC/GNTAIPV/CKLQNLFQNTK CTAMSNYTLTQGLLQHWLS*T T*FIWLAGTMRLCLSLCVDAAS APWVLKTLNIVT/PRVRPEDCSI ARPNHDKNRSMDVLPLDRCLP FLISVDGESSNYINAALMDSHK QPAAFVVTQHPLPNTVADFWR LVFDYNCSSVVMLNEMDTAQR GQSFVGPLEFGGAQL
8107	38475	A	8162	1	307	
8108	38476	A	8163	3	969	GLFCSRKTPPSK*\KHNVIASDK AAEKSVVHEHEHSHDHTQLHA YIGVSLVLGFVFMLLVDQIGNS HVHSTDDPEAARSSNSKITTTL GLVVHAAVFYVSLFPNIADGV ALGAAASTSQTSVQLIVFVAIM LHKAPAAFGLVSFLMHAGLER NRIRKHLLVFALAAPVMSMVT YLGLSKSSKEALSEVNATGVA MLFSAGTFLYVATVHVLPEERL KLVTVLGAGLLCGTALAVIVPE GVHALYEDILEVVPSFYYCHLY VYEYLMFSSHFCSPDPWQDQL LTLRVCSSTSASLGEGCLGVSSI RKGMELSVQAQHHVEVAKA
8109	38477	A	8164	164	240	
8110	38478	A	8165	2	417	QQIRKLIKVGLIIHKPVIVHSQV GCQKSTFS/RTRKGRHMGTG*R KSTANFQMPEKVTWMRRMRIL HWLFGRYHESKKTDHHMYHSL YLKVQGNMFTNKQILMEHNHK LKADKAHKKFLADQAEARSSK TNKASKLREER
8111	38479	A	8166	1	86	RTRGCLSHHNHH*HLHRHHLH HHYPYSY*HHHCLNYH/APYLF HWLYH/APHHLNQHAHYLHLY YHHHYNHHHHLHHHHRSHCH HHHHHLTIHLLCQHHHHHFHPT KHLLLAHPQALQTHH\NHHDM/ HHHYPYSY

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8112	38480	A	8167	50	1156	LLLQFSRATFILFQPPANTFTSA FSQTRARRGGSGRGGGQESAEE TSEFGDRHAPEAAAATRGSAR APEPKHASSCGTRGQCACARRE VEAQVRAKGDTVAERARRGGR WLTRSGMEHLERCEWLLRGTL VRAAVRRYLPWALVASMLAGS LLKELSPLPESYLSNKRNVLNV YFVKVAWAWTFCLLLPFIALTN YH/HDRQGWLGPAA/D*/CTLLV GTAIWYICTSIFSNIEHYTGSCY QSPALEGVRKEHQSKQQCHQE GGFWHGFDISGHSFLLTFCALH DCKKRCLCLQ*R*KTDRSHCLH TAITTLVVALGILTFIWVLMFLC TAVYFHNLSQKVFGTLFGLLS WYGTYGFWYPKAFSPRTSSPEL
8113	38481	A	8168	2	926	
8114	38482	A	8169	2	1053	TRERFSVANRVTGSETVPKAEA GPESAAGGQEEEEGEDEEELSG TKVSAPYYSFWGTLEYHNAMV AGTEEARDGSAGVRVLYLYPT HKSLKPRPVSLEGKCRFKENCR FSHGQVVSLDELRPFQDPDLSS LQAGSACLAKHQGWPLERQHA SPMWDNGYLHSQV*LAAA\RE AVVGGGRHPAPTAHKRPQESD SDS\EVRVTPAMPEWWGQMLW TLGPAALPLLGWEVHTRGIGSR LLTKMGYEFGKGLGRHAEGRV EPIHAVVLPRGKSLDQCVETLQ KQTRVGKAGTNKPPRCRGRGA RPGGRPAPRNVFDFLNEKLQGQ APGALEAGAAPAGRRSKDMYH CQQECQAGP
8115	38483	C	8170	166	419	

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8116	38484	A	8171	55	1157	ALDEPHGAGASEERAGDVFGPP RRVPGPSLWPLEAWPTSSQKV MPQVRCLHLHQVWGQRGGPPR \KRWAWAARGHTGLGPTPHGP S\WTHSNFLKEKIF*KMFA\KQV GPEAKQSLPNGFPGVATAWSP VRSSVCPLFIKARPSC*QLQDSC WDPGGTETADPGHTGLELRFPE PPKPTLPLALSEAPVPQREEKTQ GRGHYPAPQCLPGDPCSPHHPA PQPHQPHPAR/HN*PPPPRPSSHP PTTVPPTRPQPWQPGCCAQPPR PCLH*RGGN*VY*GMQLHQKS VSWPHSQWPQKREGNGSSHEI HPSCPPSGFHGPSPEGRMPTQA GALHSWVPGLSLSHGSGPHPPP RWTATVQAARPRVPPLTNL
8117	38485	A	8172	1	362	LFDNTVYCPRTERLLKNDTKH QRHAQSACQLSTTLVCSQHRK VSDFIFQHKHSAPLPQKSKRKQ NQQSFMLKTLNKLGIDEMY\RA IYDKPTANIILNGQKLEAFPLKT GTRQGFSLSPLL
8118	38486	A	8173	1	655	MIISTDAEKAFDKIQQPFMLKTL DKQGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPF SQLLFNLMLEVLTRAVREEKEI K\GIKYLGIQLTRDVKDLFKRN* KPLLNEIKEDTKKWKNIPCSWI GRTNTVKMAILPKFR*WTR*RQ FSTVHKD*KLSETVSHSYLKIKF WKLKRPFLLHSEPLKERQQDSV SLMNWVCMSSKTGQY

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8119	38487	A	8174	2	1936	DKPTANIILNGQKLQAFPLKTG TRQGCPLSPLLFNIVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNL\LKLIS NVS\KV*GYKINVQKSQAFLYT TNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL N\EIKEDTNKWKNIPCSWIGRIN IVKMAIL\PKVIYRFNAIPIKLPM TFFTELEK\TTLKFIWNQKRARI AKSILRQKNKAGGITLPDFKLY YKATVTKTA\WYWYQNRDIDQ WNRTEPSEIMPHIYTILI\F\DKPE KNKHGGKASL\FIKW\CW\ENW LA\ICRKLKLDPFLTPYTKINSR WIKDLNVRPKTIKTLEENLGITI EDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRCWRGCGEIGT LLHCWWDCKLVQPLWKSVWR FLRDLELEIPFDPAIPLLGIYPND YKSCCYKDTCTRMFIAALFTIA KTWNQPKCPTMIDWIKKMWHI YTMEYYAAIKNDEFMSFVGTW MKLETIILSKLSQEQKTKHRIFS LIGGN
8120	38488	A	8175	2	1105	LPTKKSPGPDGITAEFYQRYKE ELVPVLLKLFQSIEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLMNIDAKIP**KY*QN*IPAAH QKSLSHHD\KVGFHPPGMQDW F\NIHKSIN\LIQHINRAKDKNHM IISIDAEKAFDKIQQPFMLKTLN KLGIGGTYFKIIRAIYDKPTANII LNGQKLEAIPFEMLKVMYRAF RQNKQIKGIILEKEEVKLSLFAD DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNNT QTESQIMSELPF\TIASKRRKYL GIQLTRDVKDLFKKNYKPLLKE IKQDTNKWKNIPCS*VGRINIVK MAILPK*DVLASPSPFTMTVTC RKQVQVL
8121	38489	B	8176	120	2036	
8122	38490	A	8177	3	316	

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8123	38491	A	8178	1	1447	MSIRVTQKSYKVSTSGPWFFSS CSYLSGPSAHISSLSFSRAGSSSF QGGLGRGYGGASGMEVITAVM VNQSLLSPINLEVDLNIQAMHT *EKEQIKTLNKFASFIDKVQFLE QQNKMLENKWSLLQQQKMAQ SNLDNMFESYINNLRWQLETLG RKKLKLEAELGNMQGLVEDFK NKYEDEINKYTEMENEFVLIKK DVDEAYMNKVELEYRLEGPTD EINFLRKLYEQEIRELQSQILDM SVVLSMDNSHSLDMDSIIAEVK VQYEEIANRSWAEAERMYQN* YEELQMLAGEHGDDLLSTKTEI STINQNISWLQAEIEGLKGQRA/ SLESTITDVEQRGELVIKDANA KLSQLEAALQRAKQDMALQLH EYQELMNFKLAQDIVITTYRKL LESEGSWLESGMQSMSIHMKT TSGYAGSLSSAYGGLTSPSLSYS LGSSFGSGAGSSSFSHTSSTRAA VVKKIEAQNGKLVSKSSDVLPK
8124	38492	A	8179	272	1813	KCGLRSRSSFSAPSRISAWFGPP ASTPASTMSIRVTQKSYKVSTS GPRAFSSRSYTSGPGSRISSSSFS RVGSSNFRGGLGGGYGGASGM GGITAVTVNQS\LLSPLVLEVDP NIQAVRTQEKEQIKTLNNKFAS FIDKVRFLEQQNKMLETKWSLL QQQKTARSNMDNMFESYINNL RRQLETLGQEKLKLEAELGNM QGLVEDFKNKYEDEINKRTEM ENEFVLIKKDVDEAYMNKVEL ESRLEGLTDEINFLRQLYEEEIR ELQSQISDTSVVLSMDNSRSLD MDSIIAEVKAQYEDIANRSRAE AESMYQIKYEELQSLAGKHGD DLRRTKTEISEMNRNISRLQAEI EGLKGQRASLEAAIADAEQRGE LAIKDANAKLSELEAALQRAK QDMARQLREYQELMNVKLAL DIEIATYRKLLEGEESRLESGMQ NMSIHTKTTGGYAGGLSSAYG GLTSPGLS\YSLGSSFGSGAGSS SFSRTSSSRAVVVKKIETRDGK LVSESSDVLPK

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8125	38493	A	8180	1	3519	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDSDDSVDR DIEEAIQEYLKVGSSKDQGSASP VSMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSVEKKPDTHE NSAKSLSKSHQEPATKVVHRQ GLMGVQKEFAFCRPP\RLAKTN VQPRSLRSKVTTTTTQEKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8126	38494	A	8181	208	445	AACVWRERHHRAEECGCPGVH LPPLLHP*KSKWPGRC/RLRGN AAHHPPWGQGQATPALCGGLQ QPESSQ*GLSSLGGSR
8127	38495	A	8182	1	1607	MDMFRSGIRRDGGLGDGIVRA RRRRQGALAGSSQPIQAAAVPR GP\GPAPRDPRSWPSCQGSSGEA *PYWKLEGAGLE/RKRGTEIRA VGEQLESWRSWRKDVAGCSSP TPIPEFGAAAPTKS/GPAGPSSTQ QPSSRIWAAPRKRLAG*DTAHK NHP/SAAP*PAPQDRARPK*PPR ADPQRSVTPPRSPKGS*GSPFFP KQ/PRIPKSGAASEASNPLLAITS QVVGGSESETRVEGLMKEESV REGNAAFSRFLRKSV/ACKPPAS EKDRGSRAAEGDEHASSNLQEP IPHLP*TALGERPEARGQPIRFRP PGEPCSHPRSVNELGTGEPHTF QLGCLQRHPGAVDQAGPRGPG AGSRARETGKTGTNSEAAVRQ EPKQRILSKIHTSSTPGHRL/EPT AFRTRSARSPELASGHQAGKVV AGPRVRARGA\PPTGRPGLAAR PTEAERASRAPCP\PPQTDARLFI TARPRGKSGCRLPAHSPPDPPSR LPGPRSRSR/LSPAVRVVAAGEK EASGAETAFPAWGTMALFWSL QPRALQAL

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8128	38496	A	8183	3	683	ERGITAGPPGVHPPTARSAGAA LPVWDSSACVEGVRPAPAMDP *EHQLR\SGLGCQDTLMLIESGP QVSLVLSKGCTEAKDQEPRVTE HRMGPGLSLISYTFVCRQEDFC NNLVNSLPLWAPQPPADPGSLR CPVCLSMEGCLEGTTEEICPKG TTHCYDGLLRLRGGGIFSNLRV QGCMPQPVCNLLNGTQEIGPV GMTENCNRKDFLTCHRGTTIM THGNLAACI
8129	38497	B	8184	230	252	
8130	38498	A	8185	29	316	GRVSRCLPFKLVTPVLCFCLWH RSY*EYRNF*MNQISKTQLKQR PTRFTG**QPWPRWW/PAPPRPS QGRLAGREWSTQAHPRDSQGP RLCGEGRGA
8131	38499	A	8186	1	57	SRPVQAGPKATGTPQPPPS*PEP VERPLSMASSGTHAQGPSPPSW PQLTGAVAQDSPSPGLLPPRDT APAPSMPTADGVQRCARQSGN TGPRVAT*PVAPTSFPAGPDSGE MG/ESCRRRPGT*PTPFQSRLFR RRPSASRIYGLLGPCVISL/HKK QKSLPPLAPPGTITVDILFTWAS SLFSLNATEGHTVRHV*CSRRN YQKANAPRTPTASPNTRSHSLG NAKTPPQTVPHRDHPTPQEHTG DTSSCVAVLSANTRERAAVEC GVTVLNLD*LK*TARSYSMSSA STGVAGSVQGKR/LRTSALSSG G*GPKATGTPQPPPS
8132	38500	A	8187	1	3564	
8133	38501	A	8188	154	256	
8134	38502	B	8189	1	1206	
8135	38503	B	8190	1	1311	

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8136	38504	A	8191	2	2491	EAGEWEEGPSQNGLVLQGEKL PPDFMPKLVKNLLGEMPLWVC QSCRKSMEEDERQTGREHAVAI SLSHTSCKSQSCGDDSHSSSSSS SSSSSSSSSCPGNFGDWDPSSF LAEHKRLGLWNSPHSIGAMPGS SLGSPPTIPGEAFPVSEHHQHSD LTAPPNSPTGHHPQPA/LSNP/AL TPAPLAP/APHPHLLPTTPAAPFP AQASECPVAAATAPHTPGPCQS SHLPSTSMPLLKMPPPFSGCSHP CSGHCGGHCSGPLLPPPSSQPLP STHRDPGCKGHKFAHSGLACQ LPQPCEANEGLGEEEDSSSERSS CTSSSTHQRDGKFCDCCYCEFF GHNAPPAAPTSRNYTEIREKLR SRLTRRKEELPMKGGTLGGIPG EPAVDHRDVDELLEFINSTEPK VPNSARAAKRARHKLKKKEKE KAQLAAEALKQANRVSGSREP RPARERLLEWPDRELDRVNSFL SSRLQEIKNTVKDSIRASFSVCE LSMDSNGFSKEGAAEPEPQSLA PSKLSGSSEQQPDINLDLSPLTL GSPQNHTLQAPGEPAPPWAEM RGPHPPWTEVRGPSPVFVPENG LVRR/HEHRAQPIPGDLGQDTQ AG\HPSSEEASSKEVPSCKQELP EPVSSGGKPQKGKRQGSQAKK SEASPAPRP/TSQPRGSQCQGPG RWP/TSSQAGS*SLPK*AAVLKL ERGAGGAGQDQVGLAVPKLRR
8137	38505	A	8192	277	434	
8138	38506	A	8193	4	168	
8139	38507	A	8194	26	219	PRLQCIGQPRLTLPPGFK*FLCP SLPSSWDHRQTPT*LANF*KNY F**IWGFTMLGMGSGTCNP
8140	38508	A	8195	1	498	
8141	38509	C	8196	105	251	

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8142	38510	A	8197	1	1620	MWGVGKITDPKDVDTLIPGTC GCVTLHGERHFVDVIKAGPTRS VQGNPKLGSKKMEVSIMKTQE SIKLTVKATTQRRNRNESNGPT TEFHQSTMTNTHSDTWMVVLD PMKPGGPFEVMAQQTLEKINFT LRVHDVLFGDVWLCSGQSNM QMTVLQTLSCGVVTVIFIMTLA GAHGSTLSSGIFSIYQSDSLKCK SGRKAPVGPRVLRTGYTWSQE NSTGNPDLFVQDHTWQFCTKH SGSYVASMETVDETAFILSTHT SFRTDWELKCFITVRRQLGRQY ERTCYLSFRPVANTVEYCIGFRF ASYINNDMVLQKEPAGAVIWG FGTPGATVTVTLRQGQETIMKK VTSVKGLISLLVCLSQFEIVPED DPQNAIVSSSADACHAELLRTIS TTMGKLMPNLLPAGADFFGFS HPAIHNLIQSCPGARKCINLPAS RPVGLSIGPLSPLDSYQWVKFD VCKPGDGQLPEGLPENDAAMS FEAFQRQIFDEDQNDPLL*SSL* PWLVHMVPL/WSSGIFS/TISK*L FEV*VGSEGSSGSPCAEDRLHM VSRKFHRKSRPVCSGSYLAVLH *ALRILCCFHGNSG*NCFHSLHP H*/HSALTGNSSASSQ*DASLGG SMREHATCLLDPLLTL*STVLV FALLHTSIMIWCCRRSLLGQ*Y GASVHLEPQ*P*PCAKVRKPS*R K*PV/CKGLISLLVCLSQFEIVPE
8143	38511	A	8198	1	900	
8144	38512	A	8199	915	986	IITDRPGFHDESAIYPVGYCSTRI YASMKCPDQKCLYTCQIKDGG VQPQFEIVPEDDP\RNAIVSFFW QMLVMQN\SQDYKALLWGKL MPNLLPAGADFFGFSHPAIHNLI QSCPGARKCINYQWVKFDVCQ TLEMGQLPEGLPENDAA\RALK PFQRQIL**RIDKRNLLLKIKQL KVFPGKTITTRTFHDEIPLVSSLP SELLPSFIYPKILV
8145	38513	A	8200	3	414	
8146	38514	A	8201	1	2445	
8147	38515	A	8202	1	248	ENGNLGPIQAEVKGATGECNIS ERKSPGVEIKSLRELDSGLEVH KIAEGFSESKKRSSEDENENKIE FRK/KGGF*GGGFLRRK
8148	38516	C	8203	70	324	
8149	38517	A	8204	1	675	

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8150	38518	A	8205	692	808	
8151	38519	A	8206	1	1954	PGTGEETVRLGFPVDPRKVLIV AGHHNWIVAAYAHFAVWYRI KESS*WQQVFTSPYLDWTIERV ALNAKVVGGPHGDKDKMVAV ASESSIILWSVQDGGSGSEIGVF SLGVPVDALFFIGNQLVATSHT GKVGVWNAVTQHWQVQDVV PITSYDTAGSFLLLGCNNGSIYY IDMQKFPLRMKDNDLLVTELY HDPSNDAITALSVYLTPKTSVS GNWIEIAYGTSSGPVR\VIVQHP ETVGSGPQLFQTFTVHRSPVTKI MLSEKHLVSVCADNNHVRTWT VTRFRG\MISTQPG\STPLASFKI LSLEETESHGSYSSGNDIGPFGE RDDQQVFIQKVVPITNKLFVRL SSTGKRICEIQAVDCTTISSFTVR ECEGSSRMGSRPRRYLFTGHTN GSI\QMWGSGPLLWDMVNKSE DKDVSGPT\EEELLKLLDQCDL STSRCATPNISPATSVVQHSHLR ESNSSLQLQHHDTTHESATYGS MRPYRESPLLARARRTESFHSY RDFQTINLNRNVERAVPENGNL GPIQAEVKGATGECNISERKSP GVEIKSLRELDSGLEVHKIAEGF SESKKRSSEDENENKIEFRKKG GFEGGGFLGRKKVPYLASSPST S\DGGTDSPGTASPSPTKTTPSP RHKKSDS\SGQEYSL
8152	38520	A	8207	2	383	
8153	38521	A	8208	13	332	SKGFIVLLKCLQILKTPSLGPGN QGLNAGKESRGGGLSVKA*RA RPDSWRPGPPLSISITLRRLKEG RRHHRALPLCCIITLLASSPNCI AP/TSVP*IPRLHPFWL
8154	38522	A	8209	1	1839	
8155	38523	A	8210	1	364	
8156	38524	A	8211	3	3723	MIPAGGRAPGPPYSPVPAESESL VNGNHTPQTATRGPSACASHSS LVSSIEKDLQEIMDSLVLEEPGA AGKKPAATSPLSPMANGGRYL LSPPTSPGAMSVGSSYENTSPAF SPLSSPASSGSCASHSPSGQEPG PSVPPLVPARSSSYHLALQPPQS RPSGARSESPRLSRKGGHERPPS PGLRGLLTDSPCTT\VLAEA\RR AT\ETPRLGGQLPVVAISLSEYP ASGALSQPTSIPGSPKFQPPVPA PRNKI

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8157	38525	C	8212	398	415	
8158	38526	A	8213	3	45	
8159	38527	A	8214	1	929	IAAAPELLERSGSPGGGGGAEE EAGGGPGGSPPDGARPGPSREL AVVARPRAAPTPGPSAAAMAR PLVPSSQKALLLELKGLQEEPV EGFRVTLVDEGDLYNWEVAIF GPPNTYYEGGYFKARLKFPIDY PYSPPAFRFL\TKMWHPNIYETG YVCISILHPPV/DTDPQSGELPSE RW\NPT\QNVRDHSS*V*SSLLE RRPNTFLRPANVGRLPWMLQG SWEREQGGRIRELHRTSFRKQV LGTKVDAERDGVKVPTTLP\EY CVKDQGRRAPDEGSDLFYDDY YE\DARVE\EEADSCFGDDEDDS
8160	38528	A	8215	80	430	IAQGPFYPPGWPCSGPGGNTSSP RPPPTGGKGK/PGGPQK/PLAPRI PAVFTRGDSG*RSCPATTPLSA GSPSLPHRIPEPKPPHRIPEHKLH RACAHAPDPGSGGLRIFLTAVH HGKL
8161	38529	A	8216	3	645	FSVSHLLDLEEAGDMVAAQAD ENVGEAGRSL\LESPGLTSGTAT PQQDNDQLNSEEKKKRKQRRN RTTFNSSQLQA\LERVFERTH*T PSSLFFLSFLMPSCLLTILQVWF QNRRAKFRRNERAMLANKNAS LLKSYSGDVTAVEQPTDLQLCE TNACYSPCSLLCPYSAMATYSA TCA\NNSPAQGINMANSIANLR LKAKEYSLQRNQVPTVN
8162	38530	A	8217	3	907	RVDDFVAVQLGRPIGSCFGGRA QLQEGVQKPQAMAVGNINELP ENILLELFTHVPARQLLLNCRL VCSLWRDLIDLVTLWKRKCLR EGFITEDWDQPVANWKIFYFLR SLHRNLLHNPCAEEGFEFWSLD VNGGDEWKVEDLSRDQRKEFP NDQVKKYFVTSYYTCLKSQVV DLKAEGYWEELMDTTRPDIEV KDWFAARPDCGSKYQLCGHLS\ DAAQGPHGTFQPDPATIQQKSD AKWREVSHTFSNYPPGVRYIWF QHGGVDTHYWAGWYGPRVTN SSITIGPPLP*HPLSPHLLNPDW
8163	38531	B	8218	117	398	

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8164	38532	A	8219	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFPVQNCLS LARSDSREQGLVLVMESRNRE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSTFSQFSPISSAEEC GDDEKIKVDDPLTRRTCNQASG SAPQQDYDKLKAFGGENSSKT GLSPSGNMEKNKVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
8165	38533	A	8220	1	1188	MPLDEDPSKLCRHNLKCLECNE IFQDKTSLATHFQQAADMSGQ KTCTICQMLLPNQ/CQRIHQHKS P*TCPECRAICR\SHCEVFYKCPI CPMTFKSAPSTHSHTYTQHPSIK IGESKIIYKCSMCNTVFTLQTLL YRHFDQHIENQKRDVYISHVRK EHGKQMKKQPCCQRDKPFSSS HSLCWHNRIKHKVIRKVYTCSH CSDSRGTFTKQLMLEKHVQLT HGIKDPDLKE/TDRRHQ*GGNR NKRRPQGPQSQVEVERTGSGV QASQ\GAITQPKLEINVFKVHKC AVCGFTTENLLQFHEHIPQHKS DGSFYQCREHLFVAHKLKEPQP VSKQNGAGEDNQQENKPSHED ESPNGAMSDRKCKVCAKTFET EAALKTHMQTHGMAFIKSKRM SSDEK

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8166	38534	A	8221	842	2687	KGECLPSALSLNGNGRESLESL ESLSLEGFTRGRAGLRTCSPPCL SLPAPPWAPVLPEPPRGAPPPAP RRPVPSTTQGLRSAGARRGTGR QLHLRPRC/ADPLGEASWAPES GSAPAILKVRIKTIKMSSGEIKR TVTRVLPEVDLDSGKKSSEQTA SVMASVTFLLSSPASAAILS/SSP QGASPVHGHDQCSFTC/SSSPLN RAPA/GAIIKAANAIQQQTVVVP APSRANAKLVPKTVHLANINLL P/HGSATN/ISRQ*SMQQ/RSQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPPTNAG ITLPTRGYKCLECGDSFAVEKS LTQHYDRQSMRIEAADTRGQK TCTICQMLLPNQCSYASHQRIH QHKSLYTCPECGAICRSVHFQT HVTKNCLHYMRRVGFRCVHCN VVYSDVAALQSHIQGSHCEVFY KCPICPMASNQNKEDTKSMNG KEKLEKKSPSPVKKSVETKKVA SPGWTCWECDRLFIQRDVYISH VRKEQGKQMKKHPCRHLCQH NRIKHKGIRKVYACSHCPDSRR TFTKRLMLEKHVQLMHSLKDP DLKE/TDRCHQ*GGNRNKRRH QVPQSQAPLHCTQVKGTSASV QAKWSWGR
8167	38535	C	8222	1	438	
8168	38536	B	8223	98	463	
8169	38537	A	8224	1	2679	
8170	38538	A	8225	1	1209	AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKSLYTCPECGAI CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGSHCEVFYKCPICPMASNQNK EDTKSMNGKEKLEKKSPSPVK KSVETKKVASPGWTCWECDRL FIQRDVYISHVRKEQGKQMKK QPCCQRDKPFSSSHSLCWHNRI KHKVIRKVYTCSHCSDSRGTFT KQLMLEKHVQLTHGIKDPDLK E/TDRRHQ*GGNRNKRRPQGPQ SQVEVERTGSGVQASQ\GAITQ PKLEINVFKVHKCAVCGFTTEN LLQFHEHIPQHKSDGSFYQCRE HLFVAHKLKEPQPVSKQNGAG EDNQQENKPSHEDESPNGAMS DRKCKVCAKTFETEAALKTHM QTHGMAFIKSKRMSSDEK

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8171	38539	A	8226	58	391	FAKNDGFQLHPCPEPL/PWSQT RTQSAAWA*GCNYLQPTGAAD LLAYFEFLGPEGKTGW*QGLDR DATGAPPSPTARQ/RVGKALGT AASLIPSFIPL*SKKMARETAAW SEW
8172	38540	A	8227	993	2235	NGGPHLWRLPTAHRRACGERH GQAVACGGAVAE\ALVGPAPT VGLRRGCPHSAPGGYACPVSSS TYSGLGQRCVFPHY\SPRAVPN LVPALGAPKP*MGPASGL*GD MLPAASVKRAPTAAGPWMLYP YSPARLDSAA/LQALSTKKVAS DSSKEQVANSRESSSLSKEVND SPRAADKSPESQNLIDGTKKTS LKQLDSPRNISSENSIKGTPASP AGSTPPIPKVRIKTTKTSSGEIKR TVTRVLPEVDLDSGKKPSEQTV SVMASVTSLLSSPASAATLSSPA RVPLQSAVVT\KQFPLQSPPLNR SQSSLWLLLSSQCLL*RQQDPK SLI*SSLTTPR*KPRSYLLPLSRV PAAPSLKLANAIQQQTVMMPA SSLANAKLVPK\MHLANLNLLP QVAPATSELCPVSIKTQPQI
8173	38541	A	8228	1	3370	MIINTIITTTTTTITIIFIITIMSSSPIT ITNIITIIQHHHHHNDQRPSLGK CRGLYIRVRKVPGERATANSRC PINAQGIESCWNGVMALWLGP NSTCSRLPELTDSEDCQIYGDTE RKRRHSRKTCRWEYQVETKDT FLEELLFEPALRTGIQSKQGGPL LQLAANNYNLEPKQHFGSWFG TMKQLGETESIFSFAYEVCLTV YEIFGLPGIAPSKTKSFSNFLSCI TAIAALSTKKVASDSSKEQVAN SRESS
8174	38542	B	8229	1	438	
8175	38543	A	8230	38	597	VPCGPHCRLPSAWRTSPPRLWN DTTSRKWKSGVAKSSCYNL*PS AGMRRKRF*LRAPSTLSGSALL *NRLMRSRRFCATSSCAS**CEQ RTSLSFEGSLWRSTITSRPPPSA ARISSASAPTRRRCASESAACRR STGRAGPGPGGGKQQMKAGR\ RGTAQPSSPHPLGIPTHHPDTRG ASRQTGHL
8176	38544	C	8231	1	1062	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8177	38545	A	8232	3	595	WSSAQPRSASRAASRSSRLHSS RRLCLRCRAPRRPQLVASAKGR ASSARSRRGRSRSRR*RGRARS GGGMSPLAQRRLK*ASSSSGRG AAWSRASRGAARGSGPLTGRR SAPLHSSSTVPCSPRYARPGPPR ATA/RGPTRATCLPSHRSTITSRP PPS\LPVAVQPALPPGAAAPPSP PRAGGALAALGPGLTVGAGR
8178	38546	A	8233	2961	3005	SRLQQTIQADAFAECAKGCWP GGM/DELEAETSSSLFLLAMQV WMCGGRMEDIPCSRVGHIYRK YVPYKVPAGVSLAR/SKNLKRV AEVWMDEYAEYIYQRRPEYRH LSAGDVAVQKKLRSSLNCKSF KWFMTKIAWDLPKFYPPVEPP AAAWGEIRNVGTGLCADTKHG ALGSPLRLEGCVRGRGEAAWN NMQVFTFTWREDIRPGDPQHT KKFCFDAISHTSPVTLYDCHSM KGNQLWKYRKDKTLYHPVSGS CMDCSESDHRIFMNTCNPSSLT QQWLFEHTNSTVLEKFNRN*A ALLFDDESQFDSSNCQHSCYPR
8179	38547	A	8234	203	314	VPASSPALGSTLEFQLCEPINSG FCLNQID*GFGYL*ARFMSWPY WSLLSPFPLIPLH
8180	38548	B	8235	1	1008	

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8181	38549	A	8236	2	1495	CLVVTSTDSIRFQIIPWAGTEMK QE/IIKLKDGSMEEHLKKPLEDY MALFPSVRILRTKKREGLIRTR MLGASVATGDVITFLDSHCEAN VNWLPPLLDRIARNRKTIVCPM IDVIDHDDFRYETQAGDAMRG AFDWEMYYKRIPIPPELQKADP SDPFECQLVRDTLGDADSQQH DVSHLARCQADFLFPWSPVMA GGLFAVDRKWF/WELGGWAFS HGDPQQPWKESLFFPSSCTSPQ VESHWPAGPMPIPEQYCNWSP AVTCPVTAGRVCLGWGWR*RK *WGTKDLLGARWKSKPF*SP*T NQDVKPNPHDLIEQFQRKEHFC TESAWLGCPQNGSWLLQSQRS HRERWNHGIFMTVISAVSCGLH GVVCGGRMEDIPCSRNLKRVA/ EVWMDEYAEYIYQRRPET/GHL SAGDVAVQKKLRSSLNCKSFK WFMTKIAWDLPKFYPPVEPPA AAWGEQKDMPLSQYTSKGAGI KSYLGSCTHHWGHRGRQKQG NILIAHQ
8182	38550	A	8237	1126	1603	TIMKITGRAGDAIMGADICH/N KDRKVRRKEPKSQDIYLRLLVK LYRFLARRTNSTFNQVVLKRLF MSRTNRPPLSLSQMIQK\MKLP GRENKTAVVVGTITDDVRVQE VPKLKVCALRVTSRARSLILRA GGKILTFDQLALDSPKG*GTVL LSGPRKGR
8183	38551	A	8238	504	737	QLCWAGGKILTF\DQLAVDSRK GCITVLLSGPLKGRKVYGHFGK APGTPHSHT\KPYVHSKGRKFE RARG*RAS*GYKN
8184	38552	A	8239	1	360	MLGFALLPAPPGPGLV/GSG*SP DDQ\GRTGPALAPSCLSRPSPAT LNSAGSEIHDRPRSGAPPTPCLR GSAQASTSACSPGANGPEPKPG LGTLRQQLEHIMATNRLDEAG WVACYPTDVR

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8185	38553	A	8240	3	666	MSFRQLFQDLKRYVQDADVR WEYCVRAKRGQTDTSLGRLFQ QGPGVPGRHRAHSATSPDHRFP VADLTGQGVL*GCGPPAAPWG AG*YPGAPLHAGLGTLPAAAG AHHGHQPAG*GGAGSPATRLM SVEGCSQRPWTEAPDRPLEHEA VCSVRPRPRCFLGGVGRAGAFL EEEWQHQSVCVPCQPPWGLGT CSSMSGKLSRPPASSSLLSRGKA WGQEES
8186	38554	A	8241	2	443	RTSLEFFFFFF*DGSFTLVAQA\ GVQWRHLG*LQP\RPPGFK*FS YLSLLSSWDYRHALSHLANFV VYVLFCFYETKSRSVTKAGVQ WCDLGSLQAPPPGFTPFSCFSLL SSWDYRHLPPHLVNF\CIVSRDG VSLCWSGWSRTPDYK
8187	38555	A	8242	1	354	VSLQPVSQEGVSQRTLGQSSRS SGSG/CPGELNSPIFSGVPHRWD AA*EESRAAGVPWPSGQISGMC SKFRI*NW*DVSWAGWSEDLRS *VDLSHGAKSRRTGD*SPKGGP PIRVTAP
8188	38556	A	8243	2	241	WSTGLLRRSGS/NQSSAGKPRR SQSESPGP\GSRSSGSGCQESGT CH*G*RRRG*GVLAPAPGKRDL PPRVKDQVRHPCVV
8189	38557	A	8244	5	282	AKKESVREPWARVPGALGVAA R*VEQSDFQCGPAQMGHGLGG IPGCG/PFLGLVVRFLALVASSC PFPRKAGLAAKGEGPRQASLRG LTPLKRG
8190	38558	A	8245	1	302	LSREGVGQKALGQSSRGSGSVC /LGELNSPISSGVPQRWDTA*EE SWAAGIPWPGGQIDFWHL*QA PCPRKSREGVETRREGVGVLAP SPEKRDLPLRVKD
8191	38559	A	8246	1	200	LSPKGVSQRALGQSSRGSGSG/C PGELNSPISSGVPHRWDTA*EES WAAGIPWPGGQISGTCSKLHS
8192	38560	A	8247	23	187	
8193	38561	C	8248	1	1764	

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8194	38562	A	8249	115	872	LRRGRTYPPP*ELPKARHP*WS TGLLRRSGSISLQPVSQEGVSQR AFGQSSRGSGSG/SPGELNSLISS GVPHRWDMA*EESWAAGIPWP GGQISGTCS/RAPGGGGSGGMP GCCGSGVWKFLCASRKAGKGS GHRDTRSGCGHKGLGRRDMRL GCGNKGSGHRDIRGWGTCPFP RKAGLAAKGEGPRQASLRGLT PDLKLVRC\PWAGWSEDLRS*V DLSHGAKNRRTGD*SPKGGPPI LGRPLRACSAAAVHF
8195	38563	A	8250	85	529	SGSISLQPLSREGVSQRALGQSS RGSGSG/CPGELNSPISSGVPHR WDTA*EESWAAGIPWPGGQISG TCS/RAPVGGGSGGTPGRCGSG VWKFLCAGDVAGVCLTVEAR NCNFFLLLYTLKARLIKSCPCPR KAGLAAKGEGPRQASLQ
8196	38564	A	8251	1	552	MEARETGPWKEGNVERVASVL IKKGTGLPSTVRVTGSSASVMV YGASEAIGQHQSSAAKPRRSQS ESLGPEFQGLWEWLPGPRAVK RLRVIFDEKEPKRYLIWDKEKG ALTLTMPLAPATFLRVNCWAG GGGLVTERNCKP*WSTGLPRRS GSISLQPLSREGVSQRALGQSSR GSGSGCQGLGL*SVLIKKGTGL PSTVRVTGSSASVMVYGASEAI GQHQSSAAKPRRSQSESLGPEF QGLWEWLPGPRAVKRLRVIFD EKEPKRYLIWDKEKGALTLTM PLAPATFLRVNCWAGGGGLVT ERNCKPDQKMKGIEIKRRERLK CGSKIERRKRLRDSEGGWRRVE
8197	38565	A	8252	535	710	KCFPACHHYHNHHHHHYHHH HQHHHHYHHHHHHRITIIIITIIF TIITTIIINIIINIIITNITIVIFMRVR VKRPPNRLCVSNMAVYFTWVQ KKKSSLAFSSVVTSDLKSKKRR LSGKSLETSSASLMVYGASEAT GQRQSSAAKPRRSQSESLGPEF QGLREW*YGDGGDDDNDDGV DGGDDSGGGGGCGSGGKQESI SIFD

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8198	38566	A	8253	54	563	AEKESVREPRARVPGARGVAA RPSA/RPR*GRPLLCSPTYPKH* NCAWHQQAGCWLGTGPAAPA SPPACAAFSWGYGGLPAPIQTA FQAGW\GAPGQRGRSKTTRPGV QSVSNPGEPAPEPRAAASSGLSS GAFPAPATDPGICSWAEGLVM GKGHHHRPSISARIPCFHV
8199	38567	B	8254	232	987	
8200	38568	C	8255	1	1812	
8201	38569	A	8256	1	1035	
8202	38570	A	8257	2	664	SLIKLIPPPRPFGRNRHLPVIRQN ERTQRGKRRG\TRYMFSRPF*/R KHGVVP\LATYLCEIYKQRCDF VDIQGEWGTCSKKGMP/HHKC Y\HG\KTGRSLTIVTPACLLPLFN TTQFRRKILAK\RINV\RIEHI*AL LRARD*LP*NRVKENDQEKERS PKRKGTWGST*SRQP\APPR\EA HFLEEPNGEGALSCWEPFPYWI SLGLLGVKKKNKKDLWATKK
8203	38571	A	8258	1	747	MSESFLKPLPEVDAGAILLVQP AELYSKASRLDDCYQKDSYTH RCQEKRTCHTTGGHSGKHQSL SGASVSPTCSAKTRDKINCFDFS PKSEVITLSSNDDSIVLSDCQEG KPKPCSGPFATFKMQYDRTCE WTALKISNGGKLILISTNVSFIR LIGAFKGVVIHTFGSYANSEAV TLEASFTADSQFVMIGSEDGKI HVWNEESG\KK*LGWMVNTQA QLPVCNSTPSSMTFASACSNMA FWLPTIDD
8204	38572	B	8259	50	260	
8205	38573	A	8260	1	541	EVWGPGLASEGAVGITHGPFPK AKRNPGKVRSKRRDPPIQFQNL RRS*WRSIPRKPGRQTGSRRSL WT/ALHPGAGTAKHPPPAA/CA GRET*CKSKSPAGRKWSFHRSS SRRASE*DASQFAVPAGVTSRE PFGSRRTGAPTGGTGTPTRTAR SRTWSSSWVRLSGRTGAVGYS RSPSCSS
8206	38574	C	8261	177	236	
8207	38575	A	8262	1	417	

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8208	38576	A	8263	2	475	GIHTRLNSELLKEEESNKRLEAE IE\YQSRLTAAISKHSESVKTER NVKLALE*TQDVSVQVKMSSDI SEVEDKNEFLTEQLSKKQIKFN TLKDKFRKKRDTLRKKSLALET L/QNDLSQTQQQIKEMKEMYEN AEAKVNNSTGKWSCVEERICQ LQHEN
8209	38577	A	8264	3	518	IFRAPFRICLGILLSPPNTEQAQY KKQLEQ/FKQGYNTASLNKKEL TLKDVECKFYKMKTAYEEVTT ELEEYKEAFAAALKANSSMLK KLTKSNKKIAMIS/TQLFMEKEQ VKYFLSTLRARRGRESPCDENL TSIGL/NRKYIPQMPVRIPTS/SPQ TSNNCQNYLTEVSHMTVSL
8210	38578	A	8265	1053	3733	NGRSCCERSSTKKECTDIESSEF VNRKSLTSG\LEEEQQRRERSEK KQPQDFHNHEEVKDLMDENCI LKTDIAIPRQEICTMKNDNLEKE NKYLKDIKIAKGTNAALENCIK LNEEMITKTAFRYQQELNDLKA ENTRLNSELLKEKESKKKLEAE IESYQSRLAAAISKHSENVKTER NLKLALERTQDVFEQPAGLEEA ELVLSRLSCGEATEGAARRALA AEEAGRWRRGVG/DSWLAPES RLHVLKTCGSCWWENLELGRH H*LCLWAVKNFQKRFLPGQKK SPFQLMSPQREFQHTL*ITQKQN RVMNNFIKKYLRLMSSV*CMP LT/IKHSIDKEVRSTSARLPCLGS EERICPAALSGKYKKLLEMTIN VLSVFGNEDFDCHGDLKTDQL KMNILIKKLKHKFDDLTAEKEA VSSKCVDLAKDNQVLQQELLS MKKVQQQCEKLEKDKKMLEE EILNLKTHMEDNMVELSKLQE YKSELDERAMTAVEKLEEIHLQ LNKGNTASLNKKELTLKDVEC KFSKMKTTYEEVTTKLEEYKE AFAVALKANNSMSKK\LTKSN KKIAMISTKLLMEKEWVKYFLS TLPTRRGQESPCVENLTSIVLNS KYIPKMTGRIPTSNP*TLNNWQ NYLTEEDMVSGDLISGTWSME EWSLGASSLGTWSAAVGQYLA RWPLCDLSVTVAESPSPLCCGA
8211	38579	A	8266	2	209	

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8212	38580	A	8267	1	1431	MTQKAAASVEHLAIRCHWSQR PAVTGDVLQVYSGSEGTAIIFCE TQRSVTEIAMNPHIKQNAQCLH GDIAQSQREFTLKDFREGSFKV LVATNVAACGLDIPEVDLVIHG SPPQDVE/SYIHRSGRTG\FVTM TLESLEEIQDVSCAWKELNRKL SSNAVSQITRMCLLKGNVRVCF DVPTTKSERLQAEWHDSDWIFS VPAKLPEIEEYYDRNTSSNSRQ RSGWSSGQSGRSGGRSGSRNYF AVDTASAIAIALMTFGTMYPMS VYSGKVLLQTTPPHVIGQLDKL IREVSTLDGVLEVRNEHFWTLG FGSLAGSVHVRIRRDANEQMV LAHVTNRLYTLVSTLTVQIFKD DWIRPALLSGPVAANVLNFSDH HVIPMPLLKGTDDLNPVTSTPA KPSSPPPEFSFNTPGKNVNPVIL LNTQTRPYGFGLNHGHTPYSS MLNQGLGVPGIGATQGLRTGF TNIPSRYGTNNRIGQPRP
8213	38581	B	8268	128	1497	
8214	38582	A	8269	1	618	
8215	38583	A	8270	1	334	LFHSIFGYLPFARQTLLPGSILVF TYTQPPKIQFANGTKGLPDPLM TPK*QK\APLMPLLVSLGLSAST IALGTRIAGISTSVTTFCSLSNDF SASFSPYLHRCFLPWSSL
8216	38584	A	8271	1	2919	
8217	38585	A	8272	1	4192	MRIPVDASTSRRFTPPSTALSPG KMSEALPLGAPDAGAALAGKL RSGDRSMVEVLADHPGELVRT DSPNFLCSVLPTHWRCNKTLPI AFKVVALGDVPDGTLVTVMAG NDENYSAELRNATAAMKNQV ARFNDLRFVGRSGRGKSFTLTI TVFTNPPQVATYHRAIKITVDG PREPRNNECVYGNYPEIPLEEM PDADGVASTPSLNIQEPCSPATS SEAFTPKEGSPYKAPIYIPDDIPI PAEFELRESNMPGA
8218	38586	B	8273	385	3930	
8219	38587	A	8274	830	906	

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8220	38588	A	8275	483	971	ATMPGHFYLFCETGSNSVSQAG VQ*HDFGSLQPPPPGFKQFSCLS LLSSWDYRHMPPRPANF/SVFL VEMGFYHVGQAGLGLLTSGDP PASASQSVGITGMSHHAGPTM KLLNPQSEVIFSPRNSHSTLLTP LSRHLPHPISISTWCIHYAPLHT VSISAEEAP
8221	38589	A	8276	1	2088	
8222	38590	A	8277	1	1822	MMTKDGLVFGLQRGSPILYVQ GLSRFRSFSVASGDSKRTRHRE KLPLLEAGERDHNCYGSPQILA FQAICKIAKPGKEQSCSKLVGH TFDPLLIEARKPEERQKLPDPCV KWGGVGNFPPVKRVGDIRIFVS QGGKFSQAPEGPEVTSGSQGLE SKTLEVYPVFYCTVAELALNHN VQPSHSTLPFPQAEEPHSVATTT GPWGVLPGCCQCSLKAQGLFS QLVMNAACTGIHTSGQWAPLW PSTVPEMPSKSSGLESGTPRTCF VLYPAVAKLLPRGTLAYSGKG CQNSSANHWDGTQIHSPCHAA AAREYGGKSGISDSRLSPTLFSA SFSNMNLKLDFKVFKYGCFECF EATAGANVLIKIIRESKYKNTD DIDILSRQATPVIAQLAHEHSGH VAGMEVVFGFSNTDFHLPRQT WLQPLSHASLLAAETNTESKND TTPQGDQPATWRLNSGYGYAF PACNASAKTIHGLTEVLYTVLV DGNHNLLTKLSLEEENCLIQLK CENLQQKLEQMAA\E*KSLRRK RATQEECLMHSNLKFKEKSAE YTALARQ\LEAALEEGRQKVAE EIEKMSSRESALQIKILDLETEL RKKN\EEQNQLVFKNEQ
8223	38591	A	8278	1	5103	MDESSVHSSVGDRHVDRVSTS QVAERTRCNKMWRIETKSPSG DNEGTGTVIEKKTRLSGQGFCL QLSEGLQNLQAQRRKIKFREME DPSSRPLCSSLDIALCASVKPSA GFPQRPKVKPLCVLGSGAGTG DAERSLQSSDPLKKQQPLARSL RGLCERIVLGGGSGCGARGLRG AGGGTALSVPGASRGFEGMFG LDQFEPQVNSRNAGQGERNFN ETGLSMNTHFKAPAFHTGGPPG PVDPAMSALGEPPILGM
8224	38592	A	8279	1	783	
8225	38593	A	8280	888	4915	

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8226	38594	A	8281	94	757	APTGCLACNLLLCELGQVTSPL *ASAPKCVTVHN*PLCKALPRR *SSAWELS*MRKLRLRGVNFLR TDGLCFCISTRATPPSSARARCV STSLKPASLQLAVS\YHHGSRSQ GCHLPAGREVCTSQSRGVRETS PWGC\EKGSPYAEGFPAVISLNP PSSSTAHDLPANKASASQPGSH LQCLSVHCTDDVGDAKARASV PTWRSLHSDISNRFGTFVAALT
8227	38595	A	8282	2	374	
8228	38596	A	8283	260	500	
8229	38597	A	8284	98	828	RWASVFPHPFPYYLPALLEKKT AERRGGAFSRNKQTAGPCGGT LQEEGSARTVGDSYGEASAGG FSCNKEEGNQRYREG*VTEML\ GVGYHRALLQLRGLDPS/PALS VT*SRTSGPRPSRLNKKTYCIPP RQDCYNNLAACLLQMEPVNYE RVREYSQKVLERQPDNAKALY RG/SGVAFFHLQDYDQARHYLL GCRE*AALKMPNVRRYPPRLTR VRTQQPTHRKEKQLLPWACLV NKEERCSSS
8230	38598	A	8285	396	602	GNCGPEKERTCLRSPSWTPMPS\ PKQAVPVSSWPPGPHHQ\RCVP SRSSNFSKSSKSNSCDGWNSSSS SS
8231	38599	A	8286	3	156	SVVSLSPHR*AIQILSGVAAGW GLSDGPSSSPPSPSGARDTGSPG SSLGL
8232	38600	A	8287	32	515	ARGSWGPGAGARPPGTARRAA RCATGCGSRSRSSHAPVSPRRA APSSVHPGGCHGPALPPPSPRR VTQAADARRAAPPLRAASAAP SRRWSQAPTP/K/RRLGYPPPRP PAHPGPR/PPLRRMVSRSSGEDP PRRLT*TGSETPKSTWRELSSRR RSLQSKAATR
8233	38601	A	8288	30	460	RRCPAQRGEIWQSGH\RALLSC SGLHPFQTSWLPVYTVRVKLPT QALAMVDAPPPTKLECPRLISV CCYAGSENFKPVDLSLLSSIGGS GGVGTRGNLLVCELRRPWDKR SIWAGV\SRFLRLSPSRFPLA*LG LSSYLTTRKT

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8234	38602	A	8289	2	1094	RMSRISDDSRTASQLDEFQECL SKFT\RYNSVRPLATLSYASDLY NGSSIVS\SIEFDRDCDYFAIAGV TKKIKVYEYDTVIQDAVDIHYP EN\EMTCNS\KISC\ISW\SSYHK NLLASSDYEGTVILWDGFTGQR SKVYQEHEKRCWSVDFNLMDP KLLASGSDDAKVKLWSTNLDN SVASIEAKANVCCVKFSPSSRY HLAFG\CSDH\CVHYY\DLRNTK QPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKP\Y CLRSFKGHFNEKNF\VGLASSG DYIACGSENNSLYLYYKALSKT LLTFKFDTVKSVLDKDR\EEDD TNEFVSAVCWRALTQMGES\N VLIAA*QFRVPIKVLELV
8235	38603	A	8290	1	667	MRIKATSEDGTVIAQAEYGSVD IGEEVLKKGFAEKCRLASRTDI CEEKKLDPGQLVLRNLKSPIPL WGHRSNQSTFSRPKGHLSEKM TLDLKDENDAGNLITFPKESLA VGDFNLGSNVSLEKIKQDQKLI EENEKLKTEKDALLESYKALEL KVEQIAQELQQEKAAAVDLTN HLEYTLKTYIDTRMKNLAAKM EILKEMRHVDISVRFGKDLSDAI QVLG/SKGALLLQLL*MD*R*Y GQNTVWLRRILKL/SEYVSEGNI LIAQRNEMQQKLYMSVEDFILE VDESSLNKRLKTLQDLSVSLEA VYGQAKEGANSDEILKKFYDW KCDKREEFTSVRSETDASLH\LL *HGSKEP*RIKVMQTRR*FQIHI VKYCKRFIQRKGSLPQYKLSTR TVLS/SKKQLIEYLKKIPSVDHL LSIK/TDIEKLKSSTQMEIG*KE* FGKSQMILMALKLRK*KKK*LK KGFAEKCRLASRTDICEEKKLD PGQLVLRNLKSPIPLWGHRSNQ STFSRPKGHLSEKMTLDLKDEN DAGNLITFPKESLAVGDFNLGS NVSLEKIKQDQKLIEENEKLKT EKDALLESYKALELKVEQIAQE LQQEKAAAVDLTNHLEYTLKT YIDTRMKNLAAKMEILKEMRH VDISVRFGKDLSDAIQVLG
8236	38604	A	8291	1	325	
8237	38605	A	8292	1	593	
8238	38606	A	8293	1	2013	

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8239	38607	A	8294	2	1427	LLARGAGRTNPAPPLMSCGPW GKFLKCCEVYKSGPYKVQ*EEI TIHSRAEAESTYQIKYEELQTLA GKHGDDLRCAK/T/EISEMNQNI SRLQAETEGLKGQGASLEAAIA DAEQWGELAIKDANTKLSELE AAMQRAKQDMA/RQLGEYQK LALDIEIATYRKLLEGEESRLES GMQNVSIHKKTTSGYAGAPARI VSLLQNELLSLEVGVLKGHPTG KGEELGAPYSECSFGLCRRTVM LTQAPSSVVRSRNSRNHTVNSG GSCLSASTVAIPAINDSSAAMSA CSTISAQKRTCCTACEPARKYK DTASHQEPAVCQPACQLETADP KGGGVLALPQPPSPGMLCWPY CRAHATDYFLANFFSEFPCHFL HRAGAAQTQATGDGMEHGQS RELPKRKAPREESETSEEKSPNK WGPVSKQKKQLLVDILTTIIRPT RGNAYTGLSTRKWKPRSEENA LMQPNKKDEKGTLTQKLGL
8240	38608	A	8295	301	462	
8241	38609	A	8296	2	825	YPPSPPGRSAAHVSCTLYRTTP* WPDQRSAAPPTAWAAS*SPSAR RRPSAESMVPREPL*YRPSAATS AATPAISPARALGAGAPCPLFR RRSGPFGRTSAIRPPSSAGKAVL FPPHGRPVWPVGRLARYATAS GWGAHI*ASSGASE/PAVVSVLP AGSGASPFHSASWDPPAHPAAA ASAAAVIPAL*RSGDRPPVLSFQ PLFWFLIRGDNSVSFWLLRGLP CPSQAVTTRHRSLQKEKLKRNR KSCVNFMQSQVSVSKYSNLVK HHHFCIRPL
8242	38610	A	8297	3	251	
8243	38611	A	8298	208	307	
8244	38612	C	8299	18	197	
8245	38613	A	8300	1	1866	

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8246	38614	A	8301	2	2558	FEVLWSDSSITSVTKSSSEVTEFI SKLCQLYPEENLEKLIPCLAGPD AFYVERNHVDLDSGLRYLASLP SHVLKNDHVRRFLSTSSPPQQL QSPSPGNPSLSKVGTVMGVSGR PVCGVAGIPSSQSGAQHHGQHP AGSAAPLPHCSHAGSAGSALA YRTQMDTSPAILMPSSLQTPQT QEQNGILDWLRKLRLHKYYPV FKQLSMEKFLSLTEEDLNKFES LTMGAKKKLKTQLELEKEKSE RRCLNPSAPPLVTSSGVARVPPT SHVGPVQSGRGSHAAELRVEV EQPHHQLPREGSSSEYSSSSSSP MGVQAREESSDSAEENDRRVEI HLESSDKEKPVMLLNHFTSSSA RPTAQVLPVQNEASSNPSGHHP LPPQMLSAASHITPIRMLNSVH KPERGSADMKLLSSSVHSLLSL EERNKGSGPRSSMKVDKSFGSA MMDVLPASAPHQPVQVLSGLS ESSSMSPTVSFGPRTKVVHAST LDRVLKTAQQPALVVETSTAA TGTPSTVLHAARPPIKLLLSSSV PADSAISGQTSCPNNVQISVPPA IINPRTALYTANTKVAFSAMSS MPMGPLQGGFCANSNTASPSR HPSTSFANMAT\MPSCPAPSSSP ALSSVPESSFYSSSGGGGSTGNI PASNPNHHHHHHHQQPPAPPQP APPPPGCIVCTSCGCSGSCGSSG LTVSYANYFQHPFSGPSVFTFPF
8247	38615	A	8302	2	266	YCGPL*SVWVARNPPGFAFVEF EDPRDAAGVV*ELDGRTLCGP\ PSWGHRP*DDYCRRGLPPRRRP PRRRNLSCSRSRSLYSPWTLSL
8248	38616	A	8303	37	535	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMHRDSCPL\DCKV YVGNLGNNGNKTELERAFGYY GPLRSVWVARNPPGFAFVEFED PRDAADAVRELDGRTLIGC\RV REE\LSNGEKKK/SRNRGPPPS\W GRPPSENDNRKEESFPPR\RRSP R\RRSFS\RSRSRSLF

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8249	38617	A	8304	2	668	EIAERRITQPAPPGPSRPSGPGPA GELGGPGTGRALCPADNGGLC CGCPLAVP/GPLAVPR/ALKPQR TSLSHPTSVTNGGRGVSQPGPR RHPGLPTQASTKPPQSRRDAAP LGGAGRGGPGSMAAARTPRGG GH*GVDGPGRRPRDASRLGRLF RPRSRADPVPG*P\PVAIGRDLPS PDDNGQRP*GAWKVSE/CPERR RVERLAAIGRLVFILPDFAVGRE
8250	38618	C	8305	101	183	
8251	38619	A	8307	329	399	RERET*SSINTTFIPGSVLQPDAS PSKTGTLTSIPVTIPENTSQSQVI GTEGGKNASTSATSRSYSSIILP GVIALIVITLSVFVLVGLYRMC WKAHPGTPENGNDQPQSDKES VKLFTGKTISHESGEHSA*GK
8252	38620	A	8308	192	537	KFPTSTPENGNDQ*\PQSDKESV KLLTVKTISHESVILNQNKMDEI TEIEFRIWMAMKITENQKIETHS EESEEFNKTIQGMKYEIAILRKN KTDLTELKNSPQEFHNTLEVLT AE
8253	38621	A	8309	1	789	
8254	38622	A	8310	1	423	EDIWFDDVDPADIEAAIGPEAA KIARKQLGQSEGSVSLSLVKEQ AF\AGEELEVVQKEVAEMLKG RILVGHALHNDLKVLFLDHPKK KIRDTQKYKPFKSQVKSGRPSL RLLSEKILGLQVQQAEHCSIQD AQAAMRLYVM
8255	38623	A	8311	1	1077	MGKAKVPASKRAPSSPVAKPG PVKTLTRKKNKKKKRFWKSKA REVSKKPASGPGAVVRPPKAPE DFSQNWKALQEMGSKKKPKII QQNKKETSPQVKGEEMPAGKD QEASRGSVPSGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKAK\GQPQPH PPR/IDIWFDDVDPADIEAAIGPE AAKIARKHLTRALALDCEMVG VGPKGEESMAARVSIVNQYGK CVYDKYVKPTEPVTDYRTAVS GIRPENLKQGEELEVVQKEVAE MLKGRILVGHALHNDLKVLFL DHPKKKIRDTQKYKPFKSQVKI QDAQAAMRLYVMVKKEWES MARDRRPLLTAPDHCSDDA
8256	38624	A	8312	3	640	

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8257	38625	A	8313	1	1274	MGKAKVPASKRAPSSPVAKPG PVKTLTRKKNKKKKRFWKSKA REVSKKPASGPGAVVRPPKAPE DFSQNWKALQEMGSKKKPKII QQNKKETSPQVKGEEMPAGKD QEASRGSVPSGSKMDRRAPVPR TKASGTEHNKKGTKERTNGDI VPERGDIEHKKRKAK\GQPQPH PPR/IDIWFDDVDPADIEAAIGPE AAKIARKQLGQSEGSVSLSLVK E\QAFGGLTRALALDCEMVGV GPKGEESMAARVSIVNQYGKC VYDKYVKPTEPVTDYRTAVSGI RPENLKQGEELEVVQKEVAEM LKGRILVGHALHNDLKVLFLD HPKKKIRDTQKYKPFKSQVKSG RPSLRLLSEKILGLQVQQAEHC SIQDAQAAN*GCYVMVKEGVG RAWPETGAPCLTASRPLQ*RRL SSPALLAACPPRLQRQC
8258	38626	A	8314	2	414	
8259	38627	A	8315	1	621	
8260	38628	A	8316	1	885	MGEKPGPLLFSSAKPKNPQEGE HKDEGDHPNNSFSPCSAHDRRC LQKHFAKIRDRSTSGGKMKVN GAPREDARPVNKGTYLVSTGG QTVAFTTGSWDQDDSESSLGC QEDSTALHPTSTSPGPSETVPPS LLPEATKRLLSLDFESFGQTQR NLSCPLCPAGVWQEKTLCEWR DAGGNRQAGVPQAPCMKSNN ALIVILGTVTLDAVGIGLVMPV LPG/SPALLQRQAEESPGRRTQG /RRVTTPTTASAPVAPMTAGAC RSTSPKFETGAPVGAR*RSMGR PGRMPGL*IKAPTWCPQVGRLL PSLLAPGTKTTQSPA/SGCQEDS TALHPTSTSPGPSETVPPSLLPE ATKRLLSLDFESFGQTQRNLSC PLCPAGVWQEKTLCEWRDAGG NRQAGVPQAPCMKSNNALIVIL GTVTLDAVGIGLVMPVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPVLGALSDRFGRRPVLL ASLLGATIDYAIMATTPVLWIY
8261	38629	A	8317	1	396	

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8262	38630	A	8318	186	2123	CPAHCWQEAMLSAWRLVMSP GGPCTQHPAPACHPSVLTTPRK AGEPRP*WPPCPAWGPLADSSK PHRWRPKPPASCRPLVRRPWGP QRTLTPTLTSHWRASIR*SWNW TPPSSCFPQGLGAPRLSWPRAPC Q*ERRRNLKPWT*STSR*PPPDQ GATMAPSTAPAPLSPRPSAPFA VVASSFPETSPERHEAAVRASSS LGTRAGGTSALCPPQRVSP/HRP PNSPSISIPCMGSKASSPHGLGSP LVASPRLEKRLGGLAPQRGSRI SVLSASPVSDVSYMFGRTPHSP PLAKEHA\AAAPHPSPTPWWTY PLC*STAAQN/RGSSPPQRTPGH QNSVQPGAASPSNPCPATRSNS QTLSDAPFTTCPEGPARDMQPT MKFVMDTSKYWFKPNITREQG CPGGAVSISDSRIVPAIELLRKE EPGAFVIRDSSSYRGSFGLALK VQEVPASAQSRPGEDSNDLIRH FLIESSAKGVHLKGADEEPYFG SLSAFVCQHSIMALALPCKLTIP QRGCHTLYLSSVSVETLTGALA VQKAISTTFERDILPTPTVVHFK VTEQGITLTDVQRKVFFRRHYP LTTLRFCGMDPEQRKWQKYCK PSWIFGFVAKSQTEPQENVCHL FAEYDMVQPASQVIGLVTALL QDAERM
8263	38631	A	8319	15	909	LHVSHPGHADARGGLLQPCAA PPLWLCRIQCPPRWFQTPSQVF YHAATEHGGKDVYPGQCLWE GCEPFQRQRFSFITHLQAANCR/ EAQ/RSTPRAQKAIVNHPSAAL MALRRGSRNLVFRDFTDEKEG PITKHIRLTAALILKNIGKYSEC GRSWPRASRYQQGHQDLFILRS DLPSQVFIRDKLMERRNRRTGR TEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSVPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS

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8264	38632	A	8320	189	4419	KPGLFP*RVY*EYVFRLSQSLGE FHQF*FKRGQY/ATTSSPPFSPW ANIIRKATRC*CRWRFRFIMPFV MASMSA/GMLNELQQYCDEW QGGAAVVAQHVAPPPGIVEIDS EKFACQWLNAHFEVNPDCSVS RAEMYSEYLSTCSKLARGGILT STGFYKCLRTVFPNHTVKRVED SSSNGQAHIHVVGVKRRAIPLPI QMYYQQQPVSTSVVRVDSVPD VSPAPSPAGIPHGSQTIGNHFQR TPVANQSSNLTA
8265	38633	A	8321	27	674	GPQNTPMPPSPSVRVQGQPNSS QPSPFSGSSQPGDPMRKPGQNF MCLWQSCKKWFQTPSQVFYHA ATEHGGKDVYPGQCLWEGCEP FQRQRFSFITHLQDKHCSKDAL LAGLKQDEPGQAGSQKSSTKQ PTVGGTSSTPRAQKAIVNHPSA ALMALRRGSRNLVFRDFT\DEK EGP\ITKHTPTNSCP*Y*KISGKY SECGSADWLKETMENNLSSA
8266	38634	A	8322	16	341	PPGRGSAHPAARQLQTPGSAAP LS*HQGPASRGTGPPGPIKARAP SKSRARGLRAAQRARLSARAR AGCA/PP*ARGAARKLGAPGTF QETLPPGTRDRKCCSGDAVVH
8267	38635	A	8323	1	400	MAEGMAMLRWTRLGTWPDDS FDEMDSTLAVQQYTQQNIR/AQ DCSNTDKNLEPPEGQDADCHG F*APRWHCSASYVASSEFAGDD RRI*IPLDPWVKKFCECWCSGPT PFRE/CPRELN*HLKDGCSCRYL RARN
8268	38636	A	8324	3	179	ISWPSPSLLGQTAALCANGAGP AGTPPGRGPVSARFGRRGAAC VCSPPSPSPLAPLSR*RFAVMW WQEA*RRGPRLPLLSSLPAAAG SGRAARAAAELPGGGRAGAR/P L/LLTPAQVQGESARG/AGAEG GRGTPGP/GCPLPAGRSLCQP\G PRSPP*TAALCANGAGPAGTPP GRGPVSARFGRRGAACVCSPPS PSPLAPLSR

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8269	38637	A	8325	1	1744	DFQERLSMKDQLIAQSLLEKQQ IYLEMAEMGGLEDLPQPRGLFR GGDPSETLQGELILKSAMSEIEG IQSLICRRLGSANGQAEDGGSST GPPRRAETFAGYDCTNSPTK\V EAPGTES/DPRLPTVLESELVQRI QT/LSQLLLNLQAVIAHQDSY/V ETQRAAIQEREKQFRL/QSTRGN LLLEQERQRNF/EKQREERAAL EKLQSQL/RHEQQRWERERQW QHQ/ELERAGARLQEREGEAR/ QLRERLEQERAELERQ/RQAYQ HDLERLREAQRAAQPPS/HPPSF NGEGLEGPRVSML/PSGVGPEY AERPEVAR/RDSAPTENRLAKS DVPI/QLLSATNQFQRQAAVQQ/ QIPTKLAASTKGGKD/KGGKSR GSQRWESS/A*AGPPLRLGLEG ATGQALAAAGSQEIRDTCAILW RGNQKAQLASWLRPPHTGPVW SPGPKLR*STLHLLTSTLKTVG WGPGALERARARRQRSLATWD QHSRTGTASFDLKQQLLLNK/L MGKDESTSRNRRSLSPTCPGRH SPAPPPDPGFP/APSPPPADSPSE GFSLK/AGGTALLPGPPAPSPLP/ ATPLSAKEDASKEDVIFSKRAV TQANH
8270	38638	A	8326	147	536	WAQEGSGRNTHQQYKILDVML KGLFKVCAGRGQLMAGPVFDL GTDG*TGVQLKDG\WSALPRPV LRTTRSSLAAPSLLF/YYFDHNS NWNLLIRWGISFCNQTGVFNQ GPHSPILSLVRTGVEVAREPSVG
8271	38639	A	8327	59	339	
8272	38640	A	8328	43	510	LLLWGGLRELTIMVEDEGEQM SIWVLDKDLGAPHLVLVGSML TARSRCWTPWRSSHATAATSE GEGWGVGVLIADRPGWASDEG DGEGGGGGLLTSAEFGELAAV GEAGSAHPMFSFRPRYSTWCLT HIGQGGLELLTL*STRSASQSAG VTGMSH
8273	38641	A	8329	98	493	FFYFLFIYFFETESRSVTLAGVQ WYDLCSLQPLPPRLKRFSCLSLP SSWDYRHPPPHPANFCSFLVVT GFHHLGQAGLELLTS*S/IPSSAS QSAGITGVSHHARPGPLSLANN PRSQTRTSATVCPEQLGLD

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8274	38642	A	8330	3	328	HSAARRPSSRRSSPRPETSCANS VNAGWNQDPTHVIRF\RSMAT AGSTRYR*GLHAAPSPPHPRRP RSPPGAE*A/RREARSLKR*SPPC HPTKKATMCRCIIYVPLIIK
8275	38643	A	8331	24	593	FEQQWGWAAAAAPPGKAHTR *TGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRPPR *GPSRR*VRSARPSRA*RAPPGS HRPGCGAAAPAPAASAPARAP WAGADSSAPPRTAD*SLPTRVC CSLSALHTGSESGDLGPGTQIEG KQNYSVTVWFLAR
8276	38644	A	8332	24	832	FEQQWGWAAAA/CSSRQSTYSL RTGRSPHRPHRTQPR*NPSGTA APGPVPS*AGSSH*AGSG*RAW GPGSSRR*RSCT*RLRSRGRP/TS MRAFSPLSAIRSPKSGRDAHHQ ASHRPGCGAAAPAPAASAPAR APWAGADSKRASSYSRLEVLK VIPEAAAWTSAGSFRT*/PENLPI PVNEIMLLSNCPGRMGSVPLKR RLILGVRVLGERGPG\AWCTCG PPTSMCTGALDLVSWAGRGMP WASQRR/PQGDRVRDKPGTCFL PSAVPVLPCV
8277	38645	C	8333	153	269	
8278	38646	A	8334	615	1275	QKRKTFNTTKCYNKEKGSWPR WPTGSS*CAQLSWRGMEGTSK YRTF/ILKHPGQEIPS\EPTPPGP/S SLTCRATWSLSRAAPQPHMKPR EP*ILSIYVAPSPSTIEKPSIGERF AIFITLLMRNGDLGEASCDAVK ALRQPWGKAQVEKNQLSQTKC PAMWHFESQNPALLIVRECLEG WKAYPQSTKEERLLHPEEGAG FTSSSQEKYVRVRGQRLWPTPF FSLQMIDRKERHLIPPNVIIKKR GVGQDGRLEAVSVHSSHGEEW KGQVNTEPSTETSRSGDPIMNP LHQGLKSDMQSYMESQQSSPS ATHEAQGALDTQASWKKQQQ LRKSRRAISSPQADGVQHGHEA RHCHDVLKRDRQTSWPCKMSS LAEEVVAADTWLLDNGTMQA TGRAAQVREQGKGMDLGQYIS CYLMTLSRAIKQKENKKVCFQ RLGKPRVKTASVQKK

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8279	38647	A	8335	423	998	PPSAVPHDHSSPART*\PQSLSVI TAELEPVRAPSLIAFFHGHSAC MCPFRWRYSRFSLKQQRILAHD PVNTFGIDRRHTIKFCLSAKQRP YPTITIRWQLSDNMVYTEKHIRI ISVTTAAAIHPVIGSFPIPG/PIRA RALSTFLPVHIQRLL*GVHFPSF SCRAGAGVL*SASWRQQVQRQ EQPVLRRRQQ
8280	38648	A	8336	2	218	HPSPSPGLKHRSSLGSV\PNPLL LPSGSFSLLPAGHSHGDGPSAS QMH*FQNQTHPVP*PDPASLPA VQSHQ
8281	38649	A	8337	76	129	
8282	38650	C	8338	1	410	
8283	38651	A	8339	651	741	
8284	38652	A	8340	1	612	
8285	38653	C	8341	1	729	
8286	38654	B	8342	1	313	
8287	38655	A	8343	705	990	TRSSCWGKEASLGDGNRGVVA ALHHFTGAAARQHSGSPLERGP HPQL*SPRS*VEGHWLEI/LQA* S*VLPQKQPHQPARCWQLLSH WLPRPALLC
8288	38656	B	8344	1	588	
8289	38657	A	8345	220	678	MNAIPVASPCMVCSLIVHVLGS RPM*PW*RPPTRFQWSEVQE/V MELTTMRPRQPPPPPPPPP*QQ QQQQQQQQQQE*L*LAATPR APGTLAQGSLTPSQIFSA*RLKT DAAGSP\GSPQTITDAELRVTLT VEGKSVPFWAVLPQSFTDSPH
8290	38658	C	8346	1	411	
8291	38659	C	8347	1	534	
8292	38660	B	8348	1	774	
8293	38661	B	8349	1	705	
8294	38662	A	8350	1	297	MPGHQKAPLRPAVSKK\ESMLE KGKIK*LLKPEGILPISEPPSNRIF ACWGKPAWTACCNSLRARR*R AISCCPSHW*KEKPPWRPIRKPP LPARWPIH
8295	38663	A	8351	616	988	DPQLQAGSGHIPGRNVCPGERI CWRGTPD/SDPSTPTY*PPLEKE VAQGRDLIHASGCLWS*IPLEA LQGPQGCPQFSQVCCIPVIPTVE MKQGRQQLASDFQDQQDLEFY EILSWKPGILIIPP

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8296	38664	A	8352	1	1668	MELVPEEATAVSARAYTGRWP LDAAARTILVTAPGVGHTNIVL CGQASLDAYIKSICLKKEGRKE GKKKGRKERKRDKYGKKEKK RKKGRKKGRRKKEKKKKEREK ERRKEEKEGKKRKKEKERKKE KERKKLSIGKGVVYCLSSNTQK KQVSQTKIRVISTILFILAGCIVF VTIPAVIFKYIEGWTALESIYFV VVTLTTVGFGDFVAAHPSDHL CWVIVTCKGKYLLPDSPQEKAT DFSGVAQKRNEPQKPL/IWC/W ELRSYPTALMMQERVV*KEKP KAAAPNRRGLGTEKLEF*R*EV AAAVEPHAVLSMIGDWLRVLS KKTKEE/VCRPPLFKSPSPNLRL LGVAHHVGEIKAHAAEWKAN VTAEFRETRRRLSVEIHDKLQR AATIRSMERRRLGLDQRAHSLD MLSPEKRSVFAALDTGRFKASS QESINNRPNNLRLKGPEQLNKH GQGASEDNIINKFGSTSRLTKR KNKDLKKTLPEDVQKIYKTFRN YSLDEEKKEEETEKMCNSDNSS TAMLTDCIQQHAELENGMIPTD TKDREPENNSLLEDRN
8297	38665	A	8353	1	418	
8298	38666	A	8354	251	394	GAQVPTLLVGVLTVTISTVQNL AISLLGKAK*GEGILSVSGRMY RVL
8299	38667	A	8355	107	250	EEGHHLLDPRMVDPMAACTM QLEKLQTLNASL*KQLGGGLYL AKPQG
8300	38668	A	8356	331	893	SITENCENKNPIPHVENKDIGTK YNSLKLPEHIRAEVMQPSKLD* VNP/LPSTCKERFVMQSHLART VGSSICNL*MSP/CFGIW*QLAE ANPAKCFP/GCWKTNSCTSSML CSKYVTPNGTVV*ITREGPISDD SILRFLLSMETKRMQGLLV\STA QPKGHQSSYQLHKRGPEHIERS SSQPPVAAFGIH
8301	38669	A	8357	2	416	SGFRYGSDIVPFSKVDEEQMKY KSEGKCFSVLGFCKSSQVQRRF FMGNQVLK\PFMEDLRQYMFSS LKNSKKYAPTEAQLNAADALI DSMSLAKKDEKTDTLEDLFPTT KIPNPRFQRLFQCLLHRALHPLE PLPSIQQ
8302	38670	A	8358	1	2130	
8303	38671	A	8359	1	1152	

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8304	38672	A	8360	1	320	FKGTAAPWPLSFARAAAGRQA GTDTRPSLRVRFPRERSARQKG RGRSVRLSAKSPPAKVETKPSG GSRTA*IFRQRSKQGKMGAKG KQAKWLLILRALICFSLSER
8305	38673	B	8361	1	1231	
8306	38674	A	8362	1	2276	GGRPKRLRTGNMVRSGNKAAV VLCMDVGFTMSNSIPGIESPFEQ AKKVITMFVQRQVFAENKDEIA LVLFGTDGTDNPLSGGDQYQNI TVHRHLMLPDFDLLEDIESKIQP GSQQADFLDALIVSMDVIQHET IGKKFEKRHIEIFTDLSSRFSKSQ LDIIIHSLKKCDISLQFFLPFSLG KEDGSGDRGDGPFRLGGHGPSF PLKGITEQQKEGLEIVKMVMIS LEGEDGLDEIYSFSESLRKLCVF KKIERHSIHWPCRLTIGSNLSIRI AAYKSILQERVKKTWTVVDAK TLKKEDIQKETVYCLNDDDETE VLKEDIIQGFRYGSDIVPFSKVD EEQMKYKSEGKCFSVLGFCKSS QVQRRFFMGNQVLKVFAARDD EAAAVALSSLIHALDDLDMVAI VRYAYDKRANPQVGVAFPHIK HNYECLVYVQLPFMEDLRQY\ MFSSLKNSKKYAPTR/EAQLNA VDALIDSMSL\AKKDEEGQTPL KDLFPTTKIPNPSIFRGLFQCLL AQELLHPR\EAFYPPISGRHIWE YAGILPAEGGQRKSSGFPLS*N* RTLFFL*FEAKEKGFKWTAQGI FQGQPWKVGPTAKKLKTGARG EPTFSVSSLAEGSVTSVGSVNPA ENFRVLVKQKKASFEEASNQLI NHIEQFLDTNETPYFMKSIDCIR AFREEAIKFSEEQRFNNFLKAL QEKVEIKQLNHFWEIVVQDGIT

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8307	38675	A	8363	624	1992	GRKVVVVLPPPLGNQSTPGGIC LSAQLPL*RD**SASARCSSPGS *TSPPSYFLPDPRGPGRALQRFS RSPSSPGGNPA\SAAPSPRSKLLL GPPG\AAAATAAAAGAKPELRH RLPPSSATTASRVRACHFLLAS AAATPAFSPPPPPP\PASPSQRTP KEVQRAGKAAESCPAAPELLGF GGSRDSAGELGGLSSDACV/PD SSEPGVRRPARRRTLAHALTHA STHTRTLPGSCARVAVPVALCK GGFT*PIFSPQYVTNTYPGEEGA RLGVLIGREQTVSAILLGGSRSK APTTTVAVASAPPVTAAGR\TP HASIRIPPRMLSKPSPPPQAL*K GVMAPAQCPPARRGQAGLEGT \GFGKSPTRPHQLTAASSPCNGL IRIRQGQGGGKGRRWRGSSGDP GAWYCFRGRRRGPSCPSLRTAT LIPGLGGHGGGSGDAASPLLGT RDGGPEAHLGKE
8308	38676	A	8364	123	248	
8309	38677	A	8365	1	540	MLEALGALNKPESSRPLIPELHL ASTAAANLGEHPNQQRLKFAS QETPEESANAVPHYHKLCNRVS HVWGNRRGQHIRNTMDNPRP\ GKTTFV*IIVSPLPALLALTHSW DSQVRPAVL/QP/YSHGTGTP*W RSSSPCAASST*KSPYP*CH*QR LSQSPSA\FRPTLRRLSRSTRCRS WRRK

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8310	38678	A	8366	31	1429	RETRSCWAHYHAESSKHQKAK LKDSRKARRSIELIGPGSSQKGG DICSLIHLSSKLGILCYSKTGNM GGWEGGMQLRVSSENSMGKSS RERAAADLPQGSCWHELPGRLI NTRISLKPRHVWNLSSVLCQVV KKVKSMQMFHMPITSAMQGD RLGICVTQFDPKLLERGLVCAP ESLHTVHAALISVEKIPYFRGPL QTKAKFHITVGHETVMGRLMF FSPAPDNFDQEPILDSFNFSQEY LFQEQYLSKDLTPAVTDNDEA DKKAGQATEGHCPRQQWALV EFEKPV/YLPSAVPGDWLQARC GHS\PNTCRLAFHGQSCSTG*RT GTTPTASCPG*RCTS*STSMGLV ERAMDDYSVIGRSLFKKETNIQ LFVGLKVHLSTGELGIIDSAFGQ SGKFKIHIPGGLSPESKKDPDTP PSKTGPGWPVGGQPGRRRSPSG ANPHKMGWLTRPFKRYVFDTH KRMVQSP
8311	38679	A	8367	3	119	RSPREGGGHRGPSSGGGRCRRR PGWAGNEAM*PDRRARVVGIE VPAAEEGGAAVAQDGLGMKR CSLLRDLL
8312	38680	A	8368	3	389	SFATHTAGPQPPAA/PAPKRMA ARASWGRNPPRAPVRTSAAAA RAAGTRRPAPARVACPLPAGPG SPRRPPRAARTRRARRRPGPGR AAQQSAGRRWTPPAPAPSGASF AAPAAGSASPPSHRRSAPGGGS TQSSLLSPSSSALHSSPPSRPWA ARHERSSWS*/PRSALPPTSTEP/ GPGPRRAPVLGTRSCGRGAGQL E*EA*GAA*APPPLGWTP*LLCV HVTLGNAVSHWVSCGAAPPHG GVGVGYRARSPREGGGHRVPA\ RTREVPPSPRMGWNEAM*PFK* VSSRWPPLRLPSRGMAAPRGA AAGGARRVEGWEGASLLSGSA PGSARWPRAAPAPASQVGARC AAGAPCPLRPRVWRRGAVGAE NAPSELAASTPAG/GGRGAGSG SSDLAGRGAVAARFPGG*GHSR QQHGAEKDGGQGFLGSQPPPR SCAHQRRRGACSGNAAPSSSAR RMSASSRSRQPEKATQSRSNSA RSSAARPRSRSTAVSRAQVDTA SSCAFWRVFCSSCRRFCESAEPP TVSTRWW

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8313	38681	A	8369	3	1130	LDFQHHNYKAMRKLMKQVQE QCPNITRIYSIGKSYQGLKLYV MEMSDKPGEHE/LGYWHGEW GEVGTGQGPRHEPAASPHVSPG EPEVRYVAGMHGNEALGRELL LLLMQFLCHEFLRGNPRVTRLL SEMRIHLLPSMNPDGYEIAYHR GSELVGWAEGRWNNQSIDLNH NFADLNTPLWEAQDDGKVPHI VPNHHLPLPTYYTLPNATVSILR AAVEVLWGADPCLCLLPLLTCP IQVAPETRAVIKWMKRIPFVLS ANLHGGELVVSYPFDMTRTPW AARELTPTPDDAVFRWLSTVY AGSNLAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDF SYLHTNCFEVT\VELFCDMFPH ENELPHEWENNTDA
8314	38682	A	8370	1	2229	MWGLLLALAAFAPAVGPALGA PRNSVLGLAQPGTTKVPGSTPA LHSSPAQPPAETANGTSEQHVR IRVIKKKKVIMKKRKKLTLTRP TPLVTAGPLVTPTPAGTLDPAE KQETGCPPLGLESLRVSDSRLE ASSSQSFGLGPHRGRLNIQSGLE DGDLYDGAWCAEEQDADPWF QVDAGHPTRFSGVITQGRNSV WRYDWVTSYKVQFSNDSRTW WGSRNHSSGMDAVFPANSDPE TPVLNLLPEPQVARFIRLLPQT WLQGGAPCLRAEILACPVSDPN DLFLEAPASGSSDPLDFQHHNY KAMRKLMKQVQEQCPNITRIY\ RIGKSYQGLKVYVVEMSDKPG EHELGEPEVRYVAGMHGNEAL GRELLLLLMQFLCHEFLR\GNP RVTRLLSEMRIFLLPSMNPDGY EIALH\RSS*LVGLSEGRWNNQS IDLNHNFADLNTPLWEAQDDG KVPHIVPNHHLPLPTYYTLPNA TVAPETRAVIKWMKRIPFVLSA NLHGGELVVSYPFDMTRTPWA ARELTPTPDDAVFRWLSTVYA GSNLAMQDTSRRPCHSQDFS\L NGNIINGA\DWHTVPG\SMNDFS YLHTNCFEVTVELSCDKFPPEE* ICPKEWE\NNKDALLTYLEQVR MGIAGVVRDKDTELGIADAVIA VDGINHDVTTALGPGIIWRLA* PPGD\YMVDLPSSEGYHSVTRN

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8315	38683	A	8372	409	517	HFRSAGVCW*PPPLSVHGPR*H FRSAGVCWSSTPDPVCLGITSR GCRTAKIAAFSFL
8316	38684	A	8373	957	1230	
8317	38685	A	8374	1	2658	MVEEVLLDNILKSVFRLGSILPI TFSFPSDSQGPLLQVCRSLLEIH SRPCLPGYHQWRLQNSKDCCL FLPLEASSQRGTCQMPAGALFY KVSVDPFWEVSSSQETWGSGIH LRRQSVPYQSSSAVLGDLLFSS EPACKNKSAEAVPTAAPSPRDA LSREEESREAVWPQRLSHAPM GSAQLELPGGFVYTVRRKLPTQ ASVMLDAPPATKLEHPRSSSDC CVGSKNFKPVDLSLLGSMGVG SVELDHLAPWLQPPFQESERFC LSGVPVSPPLSEEINHALPKATV MASLGAVARKDNADSLHVPPP TPLFASRPVTALKYWQAPREDL QPFTRVTLHWGKGNDQTFWGL VDTSSELTLTPNDPKHHYGPPIK VGAYGGQVINGVFAHIQLRVN PMGHWTRPLVIFPVPERKISIDI LSSWQNHIGSLIGRKTDGSWR MTVGYRKLNQVVTPIAAAVPD VVSMLEQINPSPESECLKMSHQI TMRPELPIMNWVLSDPSSHELG YAQQHFIIKWKWYICDRAPAGS ESTTSPFITQWVHEQSGYGDRD GGYTWAQQHRLPLTKNDLAM AT/AECPISQQ/QRPTLSP*HGV/I PRGDQPATWWRVDYIAPLPSW KGQRFFFTRIDTYSGYKFIYPAP NASAKNTICGLMECLIHCHGIP HSIASDEGTHFIAKEVQQWAHA YRIHWSYHVPHHPEGWGKVLQ
8318	38686	B	8375	1	3258	
8319	38687	A	8376	3	196	DWESCQNQC*PQQPRLHGTHW DPC*DME/CPSVCPQSPCPSPLR DQWTIPCPDPLSPQTMAAGRW
8320	38688	A	8377	248	423	
8321	38689	A	8378	407	683	LSSYCVHAGCYPREAAMRMISF SPSQ\RWKPFGESWRPPARRGT CTPGAHPPRPPSPRAAGPAHRP/ PPP/PSSELPRAPQRPGRNRRPG NSGPV

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8322	38690	A	8379	11	888	TGKLHTSVICNSTELTSWDSRR LFLKGKPLLSAGAGVNVMPST APFPAPCKGSLRGNPSRPTHP*S/ RSPQLERDTGGASFRVDEGEER GASSGGS\RDTEGGSGAVPFGE SWRPPARRGTCTPGAHPPRPPS PRAAGPAHRP/PPP/PSSELPRAP Q\GPEAPTLGQPHGRGLFPPLFK LSKLYWPLGETRSRPRPRPYCQ SPGPGVTERGRRWSAPRAPGAP RSPRWRRQSGPGALPRPRVNPC IQHGSEASYAPAL*WALRIPQG GNTSSADEPADFTPNQQADQM PCLHSCSCG
8323	38691	A	8380	1	3135	
8324	38692	A	8381	44	2279	RQTVGDAQPHHHPPQPPRPSFP PFPALPCTPAPQLPPSPSCLREEF PSSPMGQTPGTWSSSGGPWTSP PHSSSRRLASPLAPLSVIPSTSQT MARSSSQSQTTRFSPTPTHSQQ ASQAGTLWPWWLRSGTMLTSP LVGGPHFIRNTRRSMVNTAC*S SRPSLGLERSQTTGATRPGGP*R SRGSMPTPILPSGPSGATPTKPS SPRTGAGPMPCFSTRAVGCSGT WPSAQATRCSWASLVEMAISK TAH*CPSQCGRGIALIDS*IPTQA SKGCSSTGYTGKKGPTTVSSAC SG*RASLGGPAGAGTRSPALVP GSRDDGTYDSNPSA*VAGASA VGSCAASPLGEEACAAATGPGE SFSEGWHEQ/TSLAVGPGTGAT ELVLPLEG/HSPTSVPCTSRGGP TWAVATYRPP\SPPGCSGTPTSP PWMVSVTPSMGWGTSCWSGP KTGTPPSCFRAAPPRLAQPRPPT SSPLRLST/ASSSLGPVTVQWLL EPHDAIRVLLDNQTVTFQPDHE DGGGQETFNATGVLLSRNGS\G SRPASTAGPPSR*SRSPTSSTPPP ASRPSTRTARRGSWGSGITIQRT TSGCPMAPPFPQGALRRCFSTL E*PGRSTGQASLARGMTSCLPT SPLFSTHNCKKTAPGLNI*SPTV TEIAHASMTPWPCATQASDFTR GKSVKTTSRRTPPSISTRPPSMV VV*LKPTRGRPR*FSTPAMLRM

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8325	38693	A	8382	1	2900	MVWGFTCSTTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQTDTLTQMMTSTLFSSPSV HNVMETVTQETAPPDEMTTSFP SSVTNTLMMTSKTITMTTSTDS TLGNTEETSTAGTESSTPVTSAV SITAGQEGQSRTTSWRTSIQDTS ASSQNHWTRSTQTTRESQTSTL THRTTSTPSFSPSVHNVTGTVSQ KTSPSGETATSSLCSVTNTSMM TSEKITVTTSTGSTLGNPGETSS VPVTGSLMP
8326	38694	A	8383	3	468	SSPPLGHPRPISQSCPRPAVSCSR GPSALLCRPLLGPEDAP/P*GSS WP/EGPLWGPRYPSVSVGNGH WSGAGVADE/PAAPSRPAGARR APSGGRPAAARCSRRRASRSSR PGPPAGRAGR*ACPAAARSAVA AAPRPPGAP*CGSASSATAPAA APP
8327	38695	A	8384	3	1319	DSSRLCSRRSSRGHTVGLWGQS PGLGTKGRGGGG*EDPPPGTPR GQQDPSHSAKQ/PPAGLPAGVK WGPS\SSPPSPPP\PAKRELQGRC PKFGRCSEGRRAGDPGPS/GCPR AKQTHSLGTAVPVVVIYYPPVH ALSPAANRTLN*NIISSQPLGTPP MVPGE*HGPRGHA*PRHPLPK DPPQG/PAQR*RGCRSEVQRRP GTLP*GSPP/GNSHNGLPAMPPR *PPTAR/PQFPNPQDPRPLGQSSS EPLPRCPKTLCKTRHPDLRGRG KQPRGWAQVPPGEVFGGGNGA QLEA*EGARMSASP\P*SLESSD TTASPPSQGLFTAQKGLWGPQR RLGALWLGRRESEKTSWRRLQ SQVYWSCREEVEKCSRQGARL GQRRGWENVLGKSGSASECLS CPFCASLLAMPSGCPWELSKVA QCFPLKTGHPGPQEGSNNLKVT QQS

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8328	38696	A	8385	1	771	HSLIHSLTHSLPSPPVQSPAWLR PLCLSAPAT*ATA/CRVCLPGSC DSCSDSWQVDDCPESCCEPPCC APSCCAPAPCLTLVCTPVSCVSS PCCQAACEPSPCQSGCTSSCTPS CCQQSSCQPACCTSSPCQQACC VPVCCKPVCCVPVCCKPVCCKP ICCVPVCSGASSSCCQQSSRQPA CCTTSCCRPSSSVSLLCRPVCRS TCCVPIPSCCAPASTCQPSCCRP ASCVSLLCRPTCSRLSSACCGLS SGQKSSC
8329	38697	A	8386	1	453	AQSLGRARPWRGASSGRVPDS\ RLE*TPTVCLA/PEHGIVAATAS LGTFPLTQWEGHNGCYQRSLFP PQSMPTPPCPASETP/PVFRYRPP PSPGSSPRSITAHPVPLGS\SVNP PHPEVWNLPCTWKRLATSLQQ KFTFGPKLGITNVDSDSLS
8330	38698	A	8387	39	630	IGTWRFGGSDRQEGQSRQGNC EANDWPVSTALA\KPRGATGK NKSPGNDPAAAIATAGAAATA GPGSPCSLQN/RPHLLPFIS*APP EG*TPSTQDRPWYSAGAA*ASV KCRTGAVQKQLLL*NRRRFPGS PAPAQTADPGRGGGRGTGS/GV PSTGSSSDWQERPWPCGGMEPP RLRCLLRCSGSIHSPTALQSLRN HQ
8331	38699	B	8388	1	2673	
8332	38700	A	8389	10	281	TTSDPYHPAPEIGLG*SPN/GGP MQGDLPGASGKEVSFL*GNVN EDIHNSGCVWQPSCDHLARQP KNKAVTMETKKRQKDTGSSLF SSSCS
8333	38701	A	8390	3	416	EYGQQCQCHKRPRGPFGFHSPG PRGGSYISDLSGQESPEAGGGFP PRISALRPKSNCSFLRPRGRGS* YPAAGRPRAPGGPALQLSPR/PH PAAPPCRAAPQPKPPRRDVEPA P/PKLHPPP/GGPAPRRQGQDLP GRLQP

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8334	38702	A	8391	98	1286	TMPPTRFLAHLPDQAYVCFCCV EGKERNLSRSKHTSPHSSTPAH LLSKPPRSSEVVYHSQVLPGTP RPTSQLHLELVLPVFARLPGHR GIEREQSSPYS/RRGHHRGYTEE D*VNS**DGVEPYGKVAAAAG PQRGRGYCCPWRRQRHGRHR/ RRPPIALQRRQ/PARTPSARPPIA LQRRQ/QARTPSPRPPIALQRRQ RHGRHRPRP/RHRSAEKTTART PSPRPPIALQRRQRHGRHRHGH\ HRSAEKTTARTPSPRPPIALQRR QRHGRHRPRPPIALQRRQRHGR HRPRPPIALQRRQRHGRHRPWP PIALQRRQRHGRHRPWPPITLQ RT*RHRCHRHGHPL/PLQRT*Q HGCHRPWPPIALQRT*/PAWTPL AMATHRSTKKITAWTPSPRPPI ALQRT
8335	38703	B	8392	128	457	
8336	38704	A	8393	348	1355	GNEGKAGTSSCWPDKPAAPAV ASSLAS*GASNSTPSPAAGSTVA SASWLVESWSPGVTVVGVTEG SSKLGPMLLSTSTPDEAWSPESS CLLLVAPGVWLLPEAGFLLGIH SQGAAPPSPSSSCFSTSSFSLSSS SSSSSSSSLPMATPCDLGFSKCG SRLSPPAKALLEDALTPRGGA* AWMRDRASIGADPVWLCPSLP SSFLCFSLKAVCTSSA/PPCYTT GFLSPTQKTKPSKQGLGVCSSQ VSRHPALGQLLQDIAEDKSPPH SGSTICSLWLSSSRAPCDRCTSR PSSKVQGYLCQQDSRSRTRAG WKTPTVVGRHVPVKIEKESIRP ANFG
8337	38705	C	8394	154	219	

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8338	38706	A	8395	3	1054	LYLKVCYI*KELFEFSNLYKHPS GEEVWERILRV*DNGGRNI\KL YQAEFIDLGPVSRDSAFNVAAQ GVKKGSNRLFPWLAEIWITRWP TVSELEMPDLPWFNVEEGIKRL REIGMVEWISHFRCTHPSWKGP EDIPLTNALQNRFVRAAPASLK SLVIAL\FCMSDATAGTAVTQL QNLNTMGIIGSRGVRDQVVAL NHQRQVGVANRQGTPR/QRGT KKRTR*PGQAKRPGPKERGTRS HAYAHTSVTTPKNNRHDTRPS QRTPQQKRDAQHQTETPNTTP NTSRPPSHVSFFRSKKRRRRPQ HEERNKRTRTEEEARERNRAN KDDTKRQPPKKTRENRRQLWS
8339	38707	A	8396	140	398	
8340	38708	B	8397	15	192	
8341	38709	A	8398	1	1167	AGTARRAPESSRRRAVAAGHPE TMGKLVALVLLGVGLSLVGEM FLAFRERVNASREVEPV\EPENC HLIEELESGSEDIDILPSGLAFISS GLKYPGMPNFAPDEPGKIFLMD LNEQNPRAQALEISGGFDKELF NPHG\ISIFIDKDNTVYLYVVNH PHMEVHCGRIF*ILREQQRSSGY YL\KTIKTWNFFKSVNDIVVLGP E\QFYATRDHYFTNSLLSFFEMI L\DLRWTYVLFYR\PREVK\VVA KGFCSA\NGI\TVLSQTQKYV\Y V\ADVAA\KNIHIMEKHDNWDL TQLKVIQLGTLVDNLTVDPA\T GDI\LAGCHPNPMKLLNYNPED PP\GSEVLRIQ\NVLSESPRVSTG YANNGS\VLQGTLWASVYHGK ILIGTVFHKTLYCEL

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8342	38710	A	8399	89	1685	KGPLLLSLPCRAGAMAETS\AT GACGEAMAAAEGSSGPAGLTL GRSFSNYRPFEPQAFGASSPS\W\ RLDGAFSGNERAEGCKVPQEG RLLKLLAG\LTRP\DVRPP\LGRG \LVGGQEEASQEAGLPAGAGPS PTFPALGIGMDSCVIPLRHGGLS LVQTTDFFYPLVEDPYMMGRIA CANVLSDLYAMGITECDNMLM LLSVSQSMSEEEREKVTPLMVK GFRDAAEEGGTAVTVGQTVVN PWDLLIGGVATCSIANQFEFI\M PDSAVVGDVL\VLTKPFRNPGL LFNAHQWLG*FLERWD*S*RW WFSREE\VEL\AYQEA\MFNMA TLNQNCCRV*MHTFNAHAATD IT\GFG\ILGHSQNL\AKQQRNEV SFVIHNLPIIAKMAAVSKRASGT VWGFFQGTSA\ETSGGITGFCLP R\EQGGLAFCS\EIQILPKYGRGS PKAW\IVGIVEKGNRTAPDPLTS PRVIEV\LPRG\ATAAVLAP\DSS NALLLSLAREIERTEVVWTLEP LSTITDGSQELIVKKFPKKAACI VVPAALSR

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8343	38711	A	8400	30	2391	ARGRPLLAARSSRPCGPRLPFK RAGPAPAAPHRGDQEARWFSG AAPSRLPPAPRFSGPAAIFLSAQ GPPSGAMQPTLLLSLLGAVGLA AVNSMPVDNRNHNEGMVTRCI IEVLSNALSKSSAPPITPECRQV LKTSRKDVKDKETTENENTKFE VRLLRDPADASEAHESSSRGEA GAPGEEDIQGPTKADTEKWAE GGGHSRERADEPQWSLYPSDS QVSEEVKTRHSEKSQREDEEEE EGENYQKGERGEDSSEEKHLEE PGETQNAFLNERKQASAIKKEE LVARSETHAAGHSQEKTHSRE KSS/QFSAA*EAGSQENRPQESK GQPRSQEKSEEGDEDATSEVDK RRTRPRHHHGRSRPDRSS\QGG SFPS\EEKGHPQ\EESEESNVSM ASLGEKRDHHSTHYRASEEEPD YGEEIKGYPGVQAPEDLEWER YRGRGSEEYRAPRPQSEESWDE EDKRNYPSLELDKMAHGYGEE SEEERGLEPGKGRHHRGRGGEP RAYFMSDTREEKRFLGEGHHR VQENQMDKARRHPQGAWKEL DRNYLNYGEEGAPG\KWQQQG VLQDTK\ENRVEARFQDKQYSS HHTAEKRKRLGELFNPYYDPL QWKSSHLERRDNMIDNFLEGE EENELTLNEKNFFPEYNYDWW EKKPFSEDVNWGYEKRNLARV PKLDLKRQYDRVAQLDQLLHY

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8344	38712	A	8401	73	1922	ILPVPIIP/CRQVLKTSKCPTRQA DLGHCSDPCSYSLHITFPADASE AHESSSRGEAGAPGEEDIQGPT KADTEKWAEGGGHSRERADEP QWSLYPSDSQVSEEVKTRHSEK SQREDEEEEEGENYQKGERGE DSSEEKHLEEPGETQNAFLNER KQASAIKKEELVARSETHAAGH SQEKTHSREKSSQESGEETGSQ ENHPQESKGQPRSQEESEEGEE DATSEVDKRRTRPRHHHP\RSR PDRSSQGGSLPSEEKGLPQEESE ESNVSMAS\LGEKRDHHSTHYR ASEEEPEYGEGNKRGYPGVQA PEDLEWERYRGRGSEEYRAPRP QSEESWDEEDKRNYPSLELDK MAHGYGEESEEERGLEPGKGR HHRGRGGEPRAYFMS\DTREEK RFFGEGHHRVQ\ENQMDKARR HPQGAW\KELDRNFLNYGEEG APGKWQQQGDLQDT\KENREE A*VFKINHFS\SHHTAEKRKRLG ELFNPYYDPLQWKSSHFERRDN MNDNFLEGEEENELTLNEKNFF PEYNYDWWEKKPFSEDVNWG YEKRNLAR\VPKMDLKRQYDR VAQLDQLLHYRKKSA\EFPDFY DSEEPVSTHQEAENEKDRADQT
8345	38713	A	8402	1	381	
8346	38714	A	8403	1	444	MKLIVGIGGMTNGGKTTLTNSL LRALPNCCVIHQDDFFKVPALA RGVLESLDMEAMLDTVQAWLS SPQKFARAHGVSVQPEASDTHI LLLEGFLLYSYKPLVDLYSRRY FLTVPYEECKW/KEKYPQLHSP *SPRPLRWPRVAHVPEV
8347	38715	A	8404	3	421	
8348	38716	A	8405	3	4065	SAPPDVTTYTSEHSIQVERPQGS TGSRTAPKYGNAELMETGDGV PVSSRVSAKIQQLVNTLKRPKR PPLREFFVDDFEELLEVQQPDP NQPKPEGAQMLAMRGEQLGV VTNWPPSLEAALQRWGTISPKA PCLTTMDTNGKPLYILTYGKL WTRSMKVAYSILHKLGTKQEP MVRPGDRVALVFPNNDPAAFM AAFYGCLLAEVVPVPIEVPLTR KDAGSQQIGFLLGSCGVTVALT SDACHKGLPKSPTGEIPQ

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8349	38717	A	8406	10	580	KQCALLTFICSLPMSFGFAPAIT VTVVN/PRHPLIRDMLRRIKEDE DDKTVLDLAVVLFETATLRSG YLLPDTKAYGDRIERMLRLSLN IDPDAKVEEEPEEEPEETAEDTT EDTEQDEDEEMDVGTDEEEET AKMS*ALLTFICSLPMSFGFAPA ITVTVVNHFVLCSKTGSQVFRS ENWKVWAESSRGDHDDCLDL CSVLCWGRTATGAFSCPAQLIF AVSSSSSVPTSISSSSSCSVSSVV SSAVSSGSSSGSSSTFASGSMFK LRRSILSILSPYALVSGKRYPDR SVAVSNKTTARSKTVLSSSSSLI RRSMSLISGCRD
8350	38718	A	8407	1	1967	MTMAAAAVVARGAGARAATA AALRGGCGTAARGRPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGTKKYTTSLNARHY YTHFTEENEDEINSSSSYASQKK TFEINPRHPLIRDMLRRIKEDED DKTVLDLAVVLFETATLRSGYL LPDTKAYGDRIERMLRLSLNID PDAKVEEEPEEEPEETAEDTTE DTEPDEDEEMDVGTDEEEETG KESDDPMAYIHFTAEGEVTFKS ILFVPTSAPRGLFDEYGSKKSDY IKLYVRRVFITDDFHDMMPKYL NFVKGVVIRKKLVRKTLDMIK KIADDKYNDTFWKEFGPTTKL\ GVIEDHSNRT\RLAKLLRIQSSH HPTDITSLDQYVEK\MKEKQDK IYFMAGSS\RKEAESSPFVERLL\ KKGYEVIYLTEPVD\EYCIQALP \EFD\GKRF\QNVVQGKECKFHE S*ENLRK**CKSVEQRISALCLN W\MKDKALKDKI*K/ALWVSSA ALTESPVLLLVAQPVRDWSWP TLGE/RSMKAQAYQTGQGHLL QIYYAESERKHFEINPQTPRLIR D\MLRRIKEDEDDKTV\LDLA\V VLV*NRQRLGSGYLFTQTLKAY GDW/RLERMLRLSLNI*PLMPK VEEEPR/EEEPEETAEDTT\EDTE \QDED\EEMDVG\TDEKGRTSKG
8351	38719	A	8408	181	462	GMASASDSSKTGFRGKQVVAG AVGDSAKESQGQPPGAPPRRA AGL/WRRHHCSF*AD*TTNAPG GKNPRPGKGAGGEQGTAGDFT CQMPRTQNTL

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8352	38720	A	8409	3	228	STGVPVSQQNLP\LEKASVLFNT GALYTQIGTRCDRQTQAGLESA IDAFQRAADMSPPGLTRRSLGP TRWHQGTPH
8353	38721	A	8410	129	311	RCFQPDCSHSTPGTGPRRSGCL LSSAAPW*KPPAAPRTPHSRSH NRGPRRQQHARHQDDP
8354	38722	B	8411	1	789	
8355	38723	A	8412	1	933	TVVLKDFILEHYSEDGYLYEDE IADLMDLRQARRTPSRDEAGVE LLMTYFIQLGFVESRFFPPTRQ MGLLFTWYDSLTGVPVSQQNL LLEKASVLFNTGALYTQIGTRC DRQTQAGLESAIDAFQRAA\GP TRGGRASTYEMTPAAS/PEIPGA SLQREE/QWTGAWTHQQIYPQP GTTP*SPPQAQPSRFLFAMDFA ATTSAIGSARPSTNQS*GYFHTG RSWQPVA**ECHILRGNAENVL HDLLSH***RQN**NQENLQEAF LPELGHQQEQTEVSQHLVPPIG RGCTASGQEEAALPFQPSQLRQ FLVL
8356	38724	A	8413	1	389	
8357	38725	A	8414	1	506	
8358	38726	B	8415	125	700	
8359	38727	B	8416	19	338	
8360	38728	A	8417	1	3335	MAALWNTCGAWKNMLIPECH SQLLRVAANPKVREQVRLELSF VNSDLQMLKEELEGLNISVGVY QNTDEDGYLYEDEITDLMDLR QACRTPSRDEARVELLMTYFIQ LGFVENRLFPPTWQMGFLFTW YDSLTGVLVSQQNLLLEKASVL FNTGVLYTQIGTRRYRHTQAGL QSAIDAFQRAAGVLNYLKETFT HNPSYDMIPAMLSVLVKMMLA QTQESVFEKISLPGIWNEFFMLV KVAQEAAKVGEVYQQLH
8361	38729	B	8418	1	1689	
8362	38730	A	8419	2	722	CPGGSERGQRQPCGCRSRGRTE PGFSPC*KSAPRPQAVSLKSASP RPSSSS\GPAGISSPGRESRSCGT QNILGPFQLVSG*PL*GR*CQFP AAAEPPAVPL*AEDISA/GPPAV *AP/SGLAHLASG/PGPLPPLGG AGLV*QSI**GGHQGADEGP*G EMDAKEAGPAAQNCDLHVCPG ARGAEGAPGEGCIS*QPHAPDA L*AASELPKDELLRQCSGG*RC SPAGSAAPRAGSSAVLEPQ

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8363	38731	C	8420	144	439	
8364	38732	B	8421	1	4747	
8365	38733	A	8422	1019	1880	YCCLPRGGNAGCQTRQDPSCRP GPGSQGLSLPPGR\PGAAVECG ARSRGWGQQDGPGPPSPGKAQ VPAEPAPPQT\PGPPEDPCLGPR NEVPDGG/GARQSHHPGPPPRSP GPEGGSPQAAARLVDWRVSRP QNQLPNPGP*DQPPRPAIPTATP SGCNGPGFPRAPRPRLSSEEEAP SRAGPEEEAPPTYTPRLRRGRP ARGPVCR/PPAGPPAV*PEFRRF ALPRASVSGFQSS\PVAAGGAP DPGPGRLLGYTDAHGDLLPLTN TTACTGPWPAGPRHCASGAEA
8366	38734	A	8423	240	763	VLVARRPQRPGHEPAVLQQ/PA AGP/PVPRKPNPSPPSRSPAGLRP PGRAGPLTSPRCPGLPAFTGHR T/PVGPVRPKAAGPRRRTYQGR GMGPRPRPRRPVVPVGGERSHS HPSGPPLRSPGPEWGLTSSSCPA RGLEGVSA/TQNQLPNPGP*DQ PPRTCHPHGYTQRI/PSGPPLRSP GPEWGLTSSSCPARGLEGVSAP RISSRIQGRRTSLPEPAIPTATPN GYIGSGFPAG
8367	38735	A	8424	2	609	PYSISIVSTGPSADSVYTKVRLL EGETLSVQCSYKGYKNRVEGK VWCKIRKKKCEPGFARVWVKG PRYLLQDDAQAKVVNITMVAL KLQDSGRYWCMRNTSGILYPL MGFQLDVSPAPQTERNIPFTHL DNILKSGTVTTGQAPTSGPDAP FTTGVMVFTPGLITLPR\P*PPPD LPPRQATASLLPAPPARDPGGP WGPRQ
8368	38736	A	8425	1	252	

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8369	38737	A	8426	3	1581	ALHCAIRHEDKWPTAVRANGH LLLNSEKMSKSTGNFLTLTQAI DKFSADGMRLALADAGDTVED ANFVEAMADAGIL\RLYTWVE WVKEMVANWDSLRSGPASTFN DRVFASELNAGIIKTDQNYEKM MFKEALKTGFFEFQAAKDKYR ELAVGRDAQ\KLVFRFIEVQTLL LAPFCPHLCEAHLGHSWGKPG LQLWNCFPWACGRVPV*WKFL IHSSQYLMEVTHDLRLRLKNY MMPAKGKKTDKQPLQKPSHCT IYV\AKE\YPPWATLPPCLFLTV KHFEGQLTGKTGLDNK\AIASE LGSMPELKKYMKKVMPFVAMI KENLEKMGPRILDLQLEFDEKA VLMENIVYLTNSLELEHIEVKF ASEAEDKIREDCCPGKPLNVFRI EPGVSRFLLVN/RPQPIPMAHFL NPKLEIRQGD\TVIPIIRRLMKM NRGI*RPFPKVKPGWRI**SHCW GPRRSSCPWEKEYTREDPPFPE ACLFS/DVDLMSKKIHLTENGIR VDIGDTINLSGSLNSCTLEIYPG FLGILLL
8370	38738	A	8427	1	1052	MIKNIGPQYLTPSFLGEQEGDEE EEGHIVDAEAEEGDADASDAK RKEKQEEEVDYESEEEEEREGE ENDDEDMQEERNPHRRGARKT QEQDEEVGL/GH*GGPVPSRPP DAAPETHPQPGAPGA\EAVERR VQAVREIHPFIDDYQYD\TEESL\ WGQVTVKLPLMKINFDMSSLV VSLAHGAVIYATKGITRCLL\NE TTNN\KNEKELVLNTEGINLPEL FKYAEVLDLRRLYSNDIHAIAN TYGIEAALRVIEKEIKDVFAVY GIAVDPRHLSLVADYMCFEGV YKPLNRFGI\RSNSSPLQQMTFE TSFQFLKQATMLGSHDELRSPS ACLVVGKVVRGGTGLF\ELKQP
8371	38739	C	8428	154	219	
8372	38740	A	8429	1	1584	
8373	38741	A	8430	200	277	

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8374	38742	A	8431	3	877	LYLKVCYI*KELFEFSNLYKQPS GEEVWERILRV*DNGGRNI\KL YQAEFIDLGPVSRDSAFNVAAQ GVKKGSNRLFPWLAEIWIKKW PTVREVEIPDLPLFNVEEGIQKL REIGMG*WISHFRPTHLSWEGP EDIPLTRPSQNIFVRAAPASLKS PVIALLYMSDLMVRTAVTQLQ NLNTMGIIGSQGGRDRVAPLNH QRQSGHGYHNGQQRESGNQNS LTGVELWHWLINHVVSRSEVD RKPTTFLLNLYKQKTSRSNGRK TSLNYKNRESRPLNQFPDLSQF
8375	38743	A	8432	1	282	
8376	38744	A	8433	1	281	SVHTGHHHYHHRHHHHHHHHQ HQLHQHQHQGGGHHHHHHHH HHH/HYFQ*ATWEMLLWVGHS HL*RQP*KQHEHRDDVSQAGS VCPCASRGFHIR
8377	38745	A	8434	64	302	
8378	38746	C	8435	133	262	
8379	38747	A	8436	1	1962	MFSIPTGQLRAAASGARRHRGR GSIGGPFHAIQGPVETDTTAQH ETVAPPDLAHPSPASRGPRPY/G RHLALDEPFLHISGALF*DSLAV *EPPESRLDARPGARNSNSRCPI TA/RPPDTDMGTPSAQGAKSSA\ FAQLPPPHNSTRRAPAGDMPPS MPGATELLACSVPAG*TSELRG GGFASSLSGSPCSKFGSPASSDA WPRLQPRWPVTFPEAQPLEVPG GTEHGCSPWEPLSNSAAQTPFF PPLHPTAPSCPLGLPGSPPGPTSS TGDYIPT*DQSGTSKLYCPLQQ GGAEAAHCV/PA/PEQPETNSKR KGETPTPN/DKEGETPTPNEKKE KHQQQTKRRNTNTKRKEGETP TPNEKKEKHQHQTKRRRNTNT KRKEGETEPAQGGTNPGRVQQ SPAAL*CFSY*SECGQACPSDES AGARFTAGSAPDKGL/PPGPSS WAPSS*HLILATTVHLLVTRPC* PPSCTGPSGHLVVGGPRPSAHH HSDLLF*SSAGKPDSWPCWTMS AMGILRPRGRASGAPGSATPFP GEFQEAH\APPVQPSTAQSLPAP CLPLGASGGPRQHPPDV\SRGG DRGLQQSVLSDAAP*PGVRGNP PRGARWGARAAWPAGPSAPHS PCPQP\PGPRDPLVYPSPGTEAQ MSCLTPQFLQILLCDFE

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8380	38748	A	8437	438	699	LLEGKLTNRKDIHTKTPSVCHH HRGPKVDKTTKMGKKQSRKAE NYKNQSASPPPKDRSS\YQQRN KAGHRMTLMS*EKKASENQTS PS
8381	38749	A	8438	1	1334	MDGRLYSVTIQPSSVLNLQLLL SGPKSAVLVVTILMCSETNLSF NEFSESFKTTSPEKMSIRKPQEK SADGKQFLQNDRKNPKLGNTQ TLLRNDVSGLLSRTKRNIVPPG WYSVYVTNNYVFKKSPKAKK VSESTTKNDPVKNIHIESSHNID LNKIAMNSNLQVVVKRLEDTIS IAKKSWNNQPLSEGYKASKKLI EIDGKDQHADRNMTLTLNRMT CKEQSLSKSVVASGNIINSHCM PTVDLNNKRLENLKKSSILDMG RLISSVENVPAKYEGTESSSVSN YSSPIKLMFLSEVKSSEGVKYTL TSVGTSHSNVVLPSEKPTTHHV TEEKTETNEDISNANSENYHSS HYDTDTFQRELNKFSHAKETA GSSTMFIGDINSDKPQEEPKDNS SSATDPSF/NKKTR*TKKNRSPS CETD*ATNWKTTKA*N*SNKH
8382	38750	A	8439	115	523	QFFFSLSQALKLDQAIHISMDAF HSVSELFASQSRRGLDPAMDLL VLSQGHQTNILDIVHIHKEALT KVTENRQHVAEGKTE/SAEADD VRIT/VNRNSFTTSLEIHHFHPI*I RDMKSQMQHFLQQEILFFQKSS RN
8383	38751	A	8440	1	461	
8384	38752	A	8441	3	319	
8385	38753	A	8442	112	480	IFSSLNVAYPWIPEKKVDGSKC PIQQQLERKIKNFVLYLK/RLQL TKCEFKN*RLENFIRVNKNEKY VCT/SYHTKLLFNNLHMALILIV FKYQSFFSLHSCNQQPHAKVLE PALELQDEDGMVH
8386	38754	A	8443	1	528	

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8387	38755	A	8444	2	811	GIHTRLNSELLKEEESNKRLEAE IE\YQSRLTAAISKHSESVKTER NVKLALE*TQDVSVQVKMSSDI SEVEDKNEFLTEQLSKKQIKFN TLKDKFRKKRDTLRKKSLALET VHNNLSQTQQQIKEMKEMYEN AEAKENNSTGKWSCVEERICQL QHENPCIEQQLDDVHQKECLPS RKEKFKSEPPAFLSGNQVKSSS CSLQTLFPPDDLILYLENPKDST KKLLELINKFRVTGYKIKLQKS VAFLNDKNEQSKEENQECNPIY
8388	38756	B	8445	1	1581	
8389	38757	A	8446	617	2972	EQNKPYQWLQRKNSKRRERSE KKQPQVKEGNNTNKSEKIQLSE NICDSTSSAAAGRLTQQRKIGK TYPQQFPKKLKEEHDRCTLKQE NEEKTNVNMLYKKNREELERK EKQYKKEVEAKQLEPTLQSLE MKSKTARNTPNRDFHNHEEMK GLMDENCILKADIAILRQEICTM KNDNLEKENKYLKDIKIVKETN AALEKYIKLNEEMITETAFRYQ QELNDLKAENTRLNAELLKEK ESKKRLEADIESYQSRLAAAISK HSESVKTERNLKLALERTRDVS VQVEMSSAISKVKAENEFLTEQ LSETQIKFNTLKDKFRKTRDSL RKKSLALETVQNDLTQTQQQT QEMKEMYQNAEAKVNNSTGK WNCVEERICHL\QRENPWLVQQ \LDDVHQKEDHKE\K*LISQRGF IESGKKDLVLEEKSKKLTNECD HLKESLFQYEREKTEGVPKKEN EELRKLFELISSLKYNVNRIRKK NDELEEEATGYKKLLEMTINM LNVFGNEDFDCHGDLKTDQLK MDILIKKLKQKFDDLTAEKEAL SSKCVNLAKDNQVLQQEFLSM KKVQQQCEKLEEDKKMLKEEI LNLKTHMENNRVELSKLQEYK LELDEKAMQAVEKLEEIHLQEQ AQYEKQLEQ/FKQGYNTASLNK KELTLKDVECKFYKMKTAYEE VTTELEEYKEAFAAALKANSS

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8390	38758	A	8447	1	2794	AVYLSRGCVCCIRCISSLLKEPH EEGVMCSFRSVATQKNDIRPDF QLGKMDSKIKELEPQLTILYQN PKTLKFQGKKSVKFALSPSMAL RK*PFKMFSI*SIFIALQFLHGYY KPILFEPNQTWPGHVAVWQDT CSIVAI/SANITQKVHPVI/W/SSIP PYGVALSSLTTGTAAFPLCTQL GV*IPLDCAQATFISHDKMVISL KGYLFLSSCLGNSLLLKYTEKL QEPPASAICEAADKEEPPSQKK RVDT/S
8391	38759	A	8448	184	427	WAIAIQRHVVYDQEWQIADPC NM**VENAETLPPGPFLNISLES SARRRATSRDDNRRFRPHRSRR SRRSRSDNALHLASE
8392	38760	A	8449	1	903	MAQKFMAPNRARTLRDICTDR EAYPVQESMGSGTRGQRKEDM GGAALSTGEGGARDVKAPLPE ATLCSQMGPTGRPSGSLCDLAG STLAGRWMHQSFDFDGGMEAS KLPGQEGVRIQPMSERTRRRAT SRDDNRRFRPHRSRRSRRSRSD FSLHLASEREAISRLKDRPPLRA REDYDQFMRQRSFQESMGHGS RRDLYGQCPRTVSDLALQNAF GDRWGPYFAEYDWCSTCSSSS ESDNEGYFLGEPIPQPARLRYV TSD\DCCTNTAPTASPNLPH*VA EDSCTAGKDQRAKTCIISLY
8393	38761	B	8450	1	322	

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8394	38762	A	8451	1	2460	MEEKSKRRGVLWSLLILALKFG DEPPLGSPNSCKYKLTTLKELG WREVFSSLQFCLCTSVASQMLS QYFEYTQPHPGDICHPETCALQ KVFLTSSGQSSSTSSSSQQFVLQ INAIQTILEKTPTHISTPTPTPTLA NPTAVGLEEDREQDVGTSSRG GAWDTRIKRELEKMSEKCGGQ INGGDIAVFASRAGHGVCWHPP CFVCTVCNELLVDLIYFYQDGK IYCGRHHAECLKPRCAACDEIIF ADECTEAEGRHWHMKHFCCFE CETVLGGQRYIMKEGRPYCCH CFESLYAEYCDTCAQHIGEAIF GSQ/HWSFC/RCGHLCFGEWG* PQLLWMLC*LELTKGPRDAIMS SLHSWHLRKGVRRRRRKKEDK SPEVLP*KS\SSGTLSH*R*RPH* SLFLGSRVSL\PSGECRGPGPPYS HSLRLYSQQALPTGRGPSSSQFP FCQFYCCYKKSLLCDCLSKSPA LEKAMRGIDQGQMTYDGQHW HATETCFCCAHCKKSLLGRPFL PKQGQIFCSRACSAGEDPNGSD SSDSAFQNARAKESRRSAKIGK NKGKTEEPMLNQHSQLQVSSN RLSADVDPLSLQMDMLSLSSQT PSLNRDPIWRSREEPYHYGNKM EQNQTQSPLQLLSQCNIRTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGHAGSFIKECREDY YPGRLRSQESYSDMSSQSFSET
8395	38763	A	8452	2	942	NKNPKNHYPESYVSLKNDFTK LTSRRHRGVEQALVQLCHVFV CEHGHVIVTLSSGFIVYRTRAN YSSSAQGVGIAAAALDAVLIRA HQRTQGCHHELSALLAFEKGSE KKEEEEGGQVSRSSSLKVQAQE LSATEDKGHISPFFWEAVYHYA SGECRGPGPPYSHSLRLYSQQA LPTGRGPSSSQFPFCQFYCCYK KSLLCDCLSKSPALEKAMRGID QGQMTYDGQHWHATETCFCC AHCKKSLLGRPFLPKQGQIFCS RACSAGEDPNGSDSSDSAFQNA RAKESRRSAKIGKNKGKTEEP\ C*TSTASCK

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8396	38764	A	8453	1	937	VHQYYSCLPEEKVPYVNSPGEK LRIKQLLHQLPPHDNEVRYCNS LDEEEKRELKLFSSQRKRENLG RGNVRPFPVTMTGAICEQCGG QINGGDIAVFASRAGHGVCWH PPCFVCTVCNELLVDLIYFYQD GKIYCGRHHAECLKPRCAACD EIIFADECTEAEGRHWHMKHFC CFECETVLGGQRYIMKEGRPYC CHCFESLYAEYCDTCAQHIGID QGQMTYDGQHWHATETCFCC AHCKKSLLGRPFLPKQGQIFCS RACSAGEDPNGSDSSDSAFQNA RAKESRRSAKIGKNKGKTEEP\
8397	38765	B	8454	214	551	
8398	38766	A	8455	1	1140	
8399	38767	A	8456	1	2525	MLNIQSVPGIGQGHYSRYLHSN PMHSGDFISNIHMRKPKFREIIF ADECTEAEGRHWHMKHFCCFE CETVLGGQRYIMKEGRPYCCH CFESLYAEYCDTCAQHIGEAIF GSQ/HWSFC/RCGHLCFGEWG* PQLLWMLC*LELTKGPRDAIMS SLHSWHLRKGVRRRRRKKEDK SPEVLP*KS\SSGTLSH*R*RPH* SLFLGSRVSL\PSGECRGPGPPYS HSLRLYSQQALPTGRGPSSSQFP FCQFYCCYKKSLLCDCLSKSPA LEKAMRGIDQGQMTYDGQHW HATETCFCCAHCKKSLLGRPFL PKQGQIFCSRACSAGEDPNGSD SSDSAFQNARAKESRRSAKIGK NKGKTEEPMLNQHSQLQVSSN RLSADVDPLSLQMDMLSLSSQT PSLNRDPIWRSREEPYHYGNKM EQNQTQSPLQLLSQCNIRTSYSP GGQGAGAQPEMWGKHFSNPK RSSSLAMTGHAGSFIKECREDY YPGRLRSQESYSDMSSQSFSET RGSIQVPKYEEEEEEEGGLSTQ QCRTRHPISSLKYTEDMTPTEQ TPRGSMESLALSNATENQDDCS FVNRLKGSNNRPGRRQELMVT WNFIQERNGSGMDQCDDGGG KILDPVYILTVELTGFAKGWKM FSVKDQSVNVLGFAGCLSADG GAKRQEHLSRFSMPDLSKDSG MNVSEKLSNMGTLNSSMQFRS

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8400	38768	A	8457	7	302	PLPSSPEQPAGRKGT\GLPCALT EIYFRVT\IY\FYVEIEK\LLIIVAK QEGLSGN\HKP\VERKYMTYLS AQD\HELIQVVQNGHLQMCGK SETGNEASPVS
8401	38769	A	8458	1	241	MTYLSAQDHELIQVVQNGHLQ MCGKSETGNEASP/G*GRGVNP WP/RHARSRMRALTRSSASCCR CSGASSICTGTSLSTGG
8402	38770	A	8459	31	454	QRSAWRSQIWSASRSV*SVFVR RASSRCLRNTGSGPGHPDR*DC RT/ARRCGWTRRRMASPSAAC GRSRCCSACVI/LNIVELKEVVV GNHLESIFLVMGYCEQDLASLL ENMPTPFSEAQVKCIVLQVLRG LQYLHRNFIIHR
8403	38771	A	8460	1	914	SYHHLRHHHHHLPHHCF/HHN NHYHHYHHYYHHHHHCHHYH YHHLHHHHHHHHHHDHCYYH NNNNNCHHHHHHYHHHHH*Y HHYHPHHHHHHHYHHHHYHH HHHHHHHRHHYYHHHHHQHH HYHHLHHHHYHHYYHNNY\HR HHRYSCNNNHHYHHHHPHHY HHHHC*HHHYLYHHHHHHNH HHHYHHHHHYYHYHYH/HHH HH\HHHHYHHYCHDHNYHYH HHHHYH/AHFHHHYHHYHYHY HHHHRHHHHLHHHYCHRPHH YHYLSCCETSHTLFPQNAISSFD CKYLDGQDDEDFVVYKLCTLY
8404	38772	A	8461	102	420	DTGPGEGAAGGCGG\GVGEGV AAPAAPGHS*VG/GNQPYLSPV CSRGSPGTGRAAARGLSGCWP WWSPRSGSAPSQCSSASWSAW SAGAPRFAPSAPGHPEGRRCPA
8405	38773	B	8462	121	215	

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8406	38774	A	8463	44	1584	AVLDRGPRVGSSSPSPGGMSTC LSSPLFATAAELGG\GLCSAGRD GPRRKVYLSVDEKKLRCCQPKS GRSVAERAAGH\SAEGWRPVH VGPGLLGLAL*GP*AWGFQGR KGGI*KGAYTAKCMMGSDKAQ ASGIATGGGHSGAEAVG/PQQ/ QGTVLSFEGGGGLSFRRMPGSL \GPSVPCKCGHPGPRCPPHHAV E\GTDTVATVAAT/GPPLAPSHG TSWQSGSLQ*DTGPGEGAA\AA AVVGVGEGAELPAAPGHS*VG VISHICHPFVAGGSPGTGRAAA RGLSGCWPWWSPRSGSAPSQC SSASWSAWSAGAPRSAPSAPGH PEGRRCPA*GWNPQGSKSSLKS SELWTPIPYVPYAVP*HTCGYA AGPAPVQTPCRGGWNGAQVGL DP\GGHGDGTPHGS/APRLPGRV GGAP*AAVAAISTDPPATASLG PAPGGPACCPSL*AACPASSASP APARSSWPPAPASCGSAAPWW HQTGHGSLWWPEHSCRLSHRS PSPGAPCWPFPFRASPDRGTA
8407	38775	A	8464	1	541	MKSLEEKIGCLLKFLGDLDDQT CKEDLHILFSNHGEIKWIDFIRG AKEGIILFKEKAKETLGKAKDA NNGNLQLRSKEVTWEVLEGEL EKEALKKITEDQQESLNKWKS KGCRFKGKRKGSKAAQPGSGK GKVQFQDKKTKFASDDAHDEN GSTGP\IKRGREETDKE*PASKQ PKTENA

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8408	38776	A	8465	1	1326	PAALGGGVVAVAVCEPVARLL WAGTLKIAVMAENGDNEKMA ALEAKICHQIEYYFGDFNLPRD KFLKEQIKLDEGWVPLEIMIKF NRLNRLTTDFNVIVEALSKSKA ELMEISEDKTKIRRSPSKPLPEV TDEYKNDVKNRSVYIKGFPTD ATLDDIKEWLEDKGQVLNIQM RRTLHKAFKGSIFVVFDSIESAK KFVETPGQKYKETDLLILFKDD YFAKKNEERKQNKVEAKLRAK QEQEAKQKLEEDAEMKSLEEKI GCLLKFSGDLDDQTCREDLHIL FSNHGEIKWI\DFVRGAKEGIILF KEKAKEALGKAKDANNGNLQ L\RNKEV\TW\EVLEGEVEKEAL KKIIEDQQES\LNKWKSKGRRF KGKGKGNKSCPSPGSGKGKVQ FQGKKTKFASDDEHDEHDENG ATGPVKRAREETDKEEPASKQ QKTENGAGDQ
8409	38777	A	8466	2	331	CSTSLMIREMQVKTTMRYHLTP ARMAIIKKSRPGVCGPQFTASY CSSWNRGLSRAMAQSLTPRPLS TLQ/PLLAVDRGS/PVLGASHRL PAQC/CMTDSSSSTLGSAAGSW QQ
8410	38778	A	8467	1	209	MNSHFLKEDIQMANKHMEKCS \PLLMIREMQIKPTVRYHLTSAR MPIIKKSK\NSRCWHGCGEHGT LLHC
8411	38779	A	8468	2	370	CSTSLIIREMQIETTMRYHLIPA RMAIIKK\SRCWQGCGEQETLL HSWKPQP/LWRSSSGTARERQF LHPLLLKARIEITPPESLAVLKIP MEGTWMELEAVILSKLTQKQK TKH*MLSLTSGS
8412	38780	A	8469	2	194	CSTSLMIREMQIKTTVRYRLTS ARMAIIKKSK\NSRCWHGCGEH RTLLHCCNLWKERNVSYVSA
8413	38781	A	8470	341	496	

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8414	38782	A	8471	46	711	SLIHLELIFCIGLDVRLGKDFMT NNLKGNAIKTKINFWDLIKLKN FCKAKRNSQ\RANR*QTEWEKT FIICTSDKGLTSRIYNKLKQISKK KTNNPIIKWAKDMNRQFSKEDI QMANKHMKKCSTSLMIREMQI KTTVRYHLTSARMAIIKKSK\NS RCWHGCGEHGTLLHCWK/SKS LYEKDTCTRMFIAAQLAIAKTW NQPKGPSINAWIKDWCQSKTN HNK
8415	38783	B	8472	36	1199	
8416	38784	A	8473	3	184	FFFFFLRRSL/DSVAQAGVQWR DLSSLQAPPPGFTPFSCLSLLSS WDYRRLPPRPANFLYF**RRGF TMLARMVSIS*PRDPLASASQS AGIQKNSFFFLETRVSAFVAQA GVQWCDLGSPQPPPPGFK*FSC LSLLSSWDYRRLPPRPANFLYF
8417	38785	A	8474	3	295	AAAFFVFFETEFRSVAQAGVQ WRDLDSLQAPPPGFTPFSCLSLP CSWDYRRVPPCPANFCIFSRDG VSPC*PGWSRSPDLVIHPSRPPK VLGLQAMS
8418	38786	A	8475	1501	1879	IRNTHAKIIELCLLPLFTEL*CNF FFFFLRRSL/DSVAQAGVQW\RY LGSLQAPPPGFTPFSCLSLLSSW GYRRLPPCPA/NFFVFLV\ERGFT VLARMVLMS*PRDPPASASQSA GITGVSHHARPTLK
8419	38787	A	8476	1550	2469	FFPFFFFLRRSSPLPPRLQCSGMI LAYCNLRLLGSSNSVASASGVA GITGTCHHTQ*IFVFLVETGFHH VGQAGLEFLTSGDLPTSASQSA/ RDYRRDDHTRPEKCF/C*KTHIL WHSPSWSS/EERGSQFFSQDS*K SSRYPKKLLGMWVIAINIYGTR T*K*EKFKTREYIGTHSIHRGNH GVNTYHVASEKLH/*YTYRMK KAKNFFFFFLRRELAS\VAQAG VQWRDLG\SLQSPPPGFTPFSC\P ASLRSWDYR/RVLPPCLANFFL YFFS/MRRGFTVFSR\MVSIS*PR DQ\PASASQ\SAGITGVSHRAR\L KIIFLFFFFSETESRSVAQAGVQ WHDLGSRHRPPPGFTPFSCLSFP SSWDYRGPPPRPANF\CVFSRD GVSPC*PGWSRSPDLVIRPASAS QKCWDYRREPPRPA
8420	38788	A	8477	1	2268	

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8421	38789	A	8478	1	2312	MAGPPSGPGRPEVCGAGRTRV AKARFRRRRAFASLGWSSGRE VVTFGDVAVHFSREEWQCLDP GQRALYREVMLENHSSVAGIG EDAPWGPFPCIISQHPPSQASIR GPCVYTVADVPVTGIAVIPPAA VCFSRLKDCDTRTEDKEFLHKE DIHEDLESQAEISENYAGDVSQ VPELGDLCDDVSERDWGVPEG RRLPQSLSQEGDFTPAAMGLLR GPLGEKDLDCNGFDSRFSLSPN LMACQEIPTEERPHPYDMGGQS FQHSVDLTGHEGVPTAESPLIC NECGKTFQGNP\TLFSVKQSHT GEA\SFMCDDCGKTFSQNSVLK NRHRSHMSEKAYQCSECGKAF RGHSDFSRHQSHHSSERPYMCN ECGKAFSQNSSLKKHQKV\HMS EKPYECNECGKAFRA\SSNLIQH QRIHSGEK\PYVCSECGKAFRRS SNLIKHHRTHTGEKPFECG*CG KAFSQSAHLRKHQRVHTGEKP YECNDCGKPFSRVSNLIKHHRV HTGEKP*KSSACGKAFSQSSSLI QHRRIHTG\EKPHVCNVCGK\AF SY*LQCSESTRFIHTGRGRPYRC SVCGKAFSHSSALIQHQGVHTG DKPYACHECGKTFGRSSNLILH QRVHTGEKPYECTECGKTFSQS STLIQHQRIHNGAEAP/YKCNQC GKAFN\QSSKFSIHPQKVHIGEK\ PSPCVECGKGFSQSSHFFQH\RY
8422	38790	C	8479	194	458	
8423	38791	C	8480	214	378	
8424	38792	A	8481	107	345	GPLTCRYWEIHSQEPGPPRSLE MVLFSPSQN*SPVWSKEKNL*P *RDMR*/YAKPPGRCK*K*IQQ MTQMRGRNIQEKASP

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8425	38793	A	8482	1	1454	MHEEEGESGDSRVYMSTQCTH VTLNKFLGFIVSESVSGLNIQES MKEVLRGQSLKHNPIREAGLET LQSGRQLERRGRLSGMARPLSL AAAGAPDLLFTALCSLLIEAQP LRPFDLQTTLTAAECHYTGKKF SLNEGKPVLRKNSQTNTWEPG TIITWGRGYACVSPGDQSPVWV PTERLKLRVNSDKESHREKTSK SETAFIPAQDLAYNRFYLIILLLT LSVSPVSPQTDLPAT*NYSYWA YVPFPPLIRPLTWMDAPAEIYT NDSVYMPGATDDHCPTRPREE GTAFNVTMGYKYPPLCLGHAH VDGCIHLQAQIWAAYLPERLAT REQGHLISSLSLSPLRQMKGGVI GDTPNFQYKPVGKPCPKNFEGP SKILIWEDCVNSHVVVLKNDA YGLVIGWAPKGYFK\NNCSSGG RECLEATYFISHWEDKDHHPTL HRRVSSFFPL*WEDKGITPPRPH MIFPILSLEHSELWKLAIAMSGL
8426	38794	A	8483	49	1393	AEPAPTHLPPPPSTAPQPERNSC CISQQSFSVP*S/SPDSDRPRGRH /SPPPP/SPCPPPPCLPPPKSTTAM PTRCQCPPPPIPTVAAFPLPPSHF LRTLPAPRPPTQPPPLSH/TTHPP EQRTLGPKFRLFSTPSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPQTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRRACLPQCRDKELLITK RKYRKKKDFAAGLEDVTEFQG REENPRHTFIYSLPLGLQKHQV LTVDIGFGGTAIMTGIARVPLA GAAGGPGVGRAAGRGVPAGVP IPQAPAGLAGPVRGVGGPSQQV MTPQGRGTVAAAAVAATASIM APPPGMRPPMGPPIGLPPARGTP IGMPPPGMRPPPPGIRDCGGSLT PLGDVCLKGSLARVLCRAIVQI YSICVLLTTSEQQLSIRIHPQNA V

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8427	38795	A	8484	49	752	AEPAPTHLPPPPSTAPQPERNSC CISQQSFSVP*S/SPDSDRPRGRH /SPPPP/SPCPPPPCLPPPKSTTAM PTRCQCPPPPIPTVAAFPLPPSHF LRTLPAPRPPTQPPPLSH/TTHPP EQRTLGPKFRLFSTPSPKNLEYL MNKSGRSPGCLLREATGTADL ARSIASLTAPQTDASGISGGRST LRQTRCSSGRLRTHPRLSMRAS LPLRPRRRACLPQCRDKELLITK RKYRKKKD
8428	38796	B	8485	511	1349	
8429	38797	A	8486	3	431	ADAVGGPGGPGMAGCDGLPG GFGSDIRPRLWLWLGPRLWSS* RGT\NIILASVPKKLLLM/DCYA LARDRTATLG\TFDAISKTASN WIPDLWKETVFTKFPYQEFTDH L/VKTHTRVSKQKTQVPAVATT AARQTMEGQAPVEYI
8430	38798	A	8487	1	470	
8431	38799	A	8488	3	314	
8432	38800	A	8489	1	458	
8433	38801	A	8490	1	855	PTRPLVLRVGATARALPRPSRS CSPSAVVPSAPSSCPPQPR\RTPK PEPEPEQVIKNYTEELKVPPDED CII\SMEKLSTASGYSDVTDSKAI GSLAVGHLTKCSHAFHLLCLLA MYCNGNKDGSLQCPSCKTIYG EKTGTQPQGKMEVLRFQMSLP GHEDCGTILIVYSIPP\GIQGP\EH PNPGKAVSLPEGFPAQCYLPEQ RPGPAKSLRAP*RWAWK\RRLI FTVGHVPAPTGETDTVVWNEI\ HHKTEMDRNITGHGYPDPNYL QNVLAELAAQGVTEDCLEQQ
8434	38802	A	8491	1	3797	MEYYAAIENDEFMSFVGTWMK LEIIILSKLSQEQKTKHRMFSLID FGFSNLFTPGQLLKTWCGSPPY AAPELFEGKEYDGPKVDIWSLG VVLYVLVCGALPFDGSTLQNL RARVLSGKFRIPFFMSTGLVPEL DKRLKAGCLSIAECEHLIRHML VLDPNKRLSMEQICKHKWMKL GDADPNFDRLIAECQQLKEERQ VDPLNEDVLLAMEDMGLDKEQ TLQSLRSDAYDHYSAIYSLLCD RHKRHKTLRLGALP

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8435	38803	A	8492	1	2563	MGDFNTPLSTVDRSMRQKVDK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDNIIG SKALLSKCKGTEIITNSLSDHSA IKLELRIKKLTQNHSTTEKLNNL LLNDYWVHNEMKAEIKMFSET NENKDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKLNQEEVESLNRPITG AEIVAIINSLPTKKSPGPDGFTA KFYWRYKEELVPFLLKLFQSIE KEGILPNSCYEASIILIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNICKSINVIQHINRTKD KNHMIISIDAEKAFDKIQQPFML KTLNKLAQNLLKLISN/SQQSLR IQNQCTKITSILIHQ*QTNREPNH E*TPIHNCFKENKIPRNPTYKGC EGPLQGELQTTAQGNKRGYKQ MEEHSMLMGRKNQYLENGHT AQGNL*I/QMPSPSSY**LSSQN WKKLL*SSYGTKK\GPHSQVNP KPKEQSWRHHTT*LQTILQGYS NQNSMVLAPKQR*RPMEQNRA LRNNAAYLQLSDL*QT*QKQA MGNGFPI**MVLGKLASHMEK AETGSLPYTLYKN*FKMD*RLT H*S*NHKNPRRKPRQYHSVHRH GQGLHV*NTKSNGNKSQN*RM GSN*TKELLHSERNYHQSEQAT HKMGENFRNLLI*QRANIQNLQ

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8436	38804	A	8493	1	1839	MPRALAFQAPVNIQAEQAGTA MNISVPQVQLINPENQIVEASSN LWELSAETTFFAISLLPFLLISNS MPDGTLNLDSDEGEEPSPEALV RYLSMRRHTVGVADPRTEVME DLQKLLPGFPGVNPQAPFLQVA PNVNFMHNLLPMQNLQPTGQL EYKMSGLPLSPRLPLISWSVLPT LFLA\EQSLLQPPTLQLLNGMGP LGRRASDGGANIQLHAQQLLK/ RPRGPSPLVTMTPAVPAVTPVD EESSDGEPDQEAVQRYLANRSK RHTLAMTNPTAEIPPDLQRQLG QQPFRSRVWPPHLVPDQHRSTY KDSNTLHLPTERFSPVRRFSDG AASIQAFKAHLEKMGNNSSIKQ LQQECEQLQKMYGGQIDERTL EKTQQQHMLYQQEQHHQILQQ QIQQPAQSQQVTIQVQEPVDML SNMPGTAAGSSGRGISISPSAGQ MQMQHRTNLMATLSYGHRPLS KQLSADSAEAHRLKWETREKG LEDDSSVSSNTGGDVTNEGKST ESADFGFSNLFTPGQLLKTWCG SPPYAAPELFEGKEYDGPKVDI WSLGVVLYVLVCGALPFDGST LQNLRARVLSGKFRIPFFMSTG YFHLLGSHCNVVLNAKDKVGF
8437	38805	B	8494	1	3879	
8438	38806	A	8495	1	4065	MGKKQSRKTGNSKKQSASPPP KKRSSSPATEQSWTENDFDELR EEGFRRSNYSELREEIQTKGKE VENYEKSLEECITRITNTENCLK ELMEPKTKARELRKECRSLRSR CYQLVERVSAMEDEVNEMKDT HRLKVKGWRKIYQGNGKQKK AGVAILVSDKTDFKPTKIKRDK EGHYMMVKGSIQQEELTILNIY APNTGAPRFIKQVLSDLQRDLD SHTLIMGDFNTPLSTLDRSTRQ KVNNNTQELNSALHQA
8439	38807	A	8496	1490	1813	TGNLQNGRKFLQPTHLTKG*YP ESMMNSNKFTRKKQTTPSKSG RRT*TDTSQKKTFMQPKNT*KN AHHHWPSEKCKSKPL*DTISHQ LEWQSLKSQETTGAGEDVDK

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8440	38808	A	8497	1614	3085	AGEGNKADKQLQQSLRIQNQC TKITSILIHQQQTNREPNHESTPI HNCFKENKIPRNPTYKGCEGPL QGELQTTAQGNKRGYKQMEE HSMLMGRKNQYHENGHTAQG NLQI/QMPSPSSYQ*LSSQNWKK LLSSSYGTKK\GLHHQVNPKPK EQSWRHHAT*LQTILQGYSNQN SMVLVPKQRYRSMEQNRALRN NAAYLQLSDL*QT*EKQAMGK GFPI**MVLGKLASHM*KAETG SLPYTLYKNQFKMD*RFKR*T* NHKNPRRKPRHYHSGHRHGQG L/LCPKHQKQW/HTKAKIDKWD LIKL/IELLHSKRNYHQSEQATY KMGENFRNLLI*QRANIQNLQ* TQTNLQEKNKQPHQKVGEGHE QTLLKRRHLCSQETHEKMLIIT GHQRNANQNHNEIPSHTS*NGN /QLKSQETTGAGEDVEK*EHFY TVGGTVN*FNHCGSQCGDSSGI *N*KYHLTQPSHYWVYTQRTIN HAAIKTHAHVCLLRHYSQ

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8441	38809	A	8498	2	2013	LNQEEVESLNRPITGAEIVAIINS LPTKKSPGPDGFTAKFYWRYK EELVPFLLKLFQSIEKEGILPNSC YEASIILIPKPGRDTTKKENFRPI SLMNIDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIISIDAE KAFDKIQQPFMLKTLNKLAQN LLKLISN/SQQSLRIQNQCTKITS ILIHQ*QTNREPNHE*TPIHNCFK ENKIPRNPTYKGCEGPLQGELQ TTAQGNKRGYKQMEEHSMLM GRKNQYLENGHTAQGNL*I/QM PSPSSY**LSSQNWKKLL*SSYG TKK\GPHSQVNPKPKEQSWRHH TT*LQTILQGYSNQNSMVLAPK QR*RPMEQNRALRNNAAYLQL SDL*QT*QKQAMGNGFPI**MV LGKLASHMEKAETGSLPYTLY KN*FKMD*RLTH*S*NHKNPRR KPRQYHSVHRHGQGLHV*NTK SNGNKSQN*RMGSN*TKELLHS ERNYHQSEQATHKMGENFRNL LI*QRANIQNLQ*TQTNLQEKN KQPHQKMGKGHEQTLLKRRHL CSQKTHEKMLIITGHQRNANQN HNEIPSHTSQNGD/QLKSQETTG AGEDVEK*EHFYTVGGTVN*FN HCGSQCGDSSGI*N*KYHLTQP SHYWVYTQRTINHAATKTHAH VCLLRHYSQ
8442	38810	B	8499	1	2860	

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8443	38811	A	8500	3	2202	EGRNKDVI*NQREQRHNIPESL GHIQSSV*REI*NTKCPQEKAGK IQN*HPNITIKRTRKARANTFKS *QKARNN*NQSRIEGNRDTKNP SKN**IQTTIREYYKHLHANNLE NLEEMDKFLDTYTLPRLNQEEV ESLNRPITGSEIVAIINSLPTKKS PGPDGFTAKFYQRYKEELRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWVGRINI VKMAILPKVIYRFNGIPIKLPITF FTELEKTTLKFIWNQKRARVAK SILSQKNKAGGIMLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEIMPHIYNYLIFDKPEKN KQWGKDSLFNKWCWENWLAI CRKLKMDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMATKAKID KWDLIKLKSFCTAKETTIGVNR QPTKWEKIFATYSSDKGLIFRIY NELKQIYKKKTNNPIKKWAKD MNRQFSKEDIYAAKRHMKKCS TSLAIREMQIKTTMRYHLTPVR TAIIKKSGNNRCWRGCGEIGTL LHCCWDCKLVQPLWKSVWRF LRDLELEIPFDPAIPLLGIYPKDY KSCCYKDTCTRMFTAALLTIAK TWNQPKCPTMIDWIKKMWHIY TMESYAAIKNDEFMSFVGTWM KLEIIILSKLSQGQKTKQRIFSLI DGN

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8444	38812	A	8501	437	2163	KQKCNISHLWNAVKVERIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVEESIP*K WPYCPR*FTDSMPSPSSYQ*LSS QNWKKLL*SSYGTKKEPASPSQ S*AKRTKLEASHYLTSNYSTRL Q*PPGKRGPPEVQGHNADENN HTEDRQGNRRHEHSIDQLAVT DVHSTTAEYTFLSTRGGFSKID HMLGCKTNLNKYKEIEIIQSIFS NHNEIKQEINSRRKTRKSTNLW ELSSALLMNGSEKKTQVNLDNI WKLMKAKMQHITLMECSESRK NKIPRNPTYKGREGPLQGELQT TAQGNKRGYKQMEEHPMLMG GRINTVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RARIAKSILSQKNKAGGLTLPD FKLFYKATVTKTAWYWYQNR DIDQWNRTEPSEIMPHIYNYVIF DKPEKNKQWGKDSLFNKWCW ENWLAICRKLKLDPFLTPYTKI NSRWIKDLTVRPKTIKTLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLKSFCTGKET TIRVNRQPTKWKKIFATYSSDK GLISRIYNELKQIYKKKTNNPIK KWVKDMNRHFSKEDIYAAKK HMKKCSPSLAVREMQIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTLLHCWWDCKLVQPL WKSVWQFLRDLELEIPFDPAIPL
8445	38813	A	8502	1	2001	MPHIQVMLMQEMDSHSLGKLC PYGFAEYSPTSSCFHGFVLSVC GSSRDKATQRVDALVRQVIVN GGIVLDQFAVHDRVALADLIDL LVDLSAMMLCGVPTTGDPFVA FALGHPDDFDHLILPKHLVDRY LLLEPLLGPVQLLSHSASVHLD LHQFCSDFSYGIQLTRDVKDLF KENYKPLLKEIKEDTNKWKNIP CSWVGRINIMKMAM\RPR*FID SMPSPSSYQ*LSSQNWKKLL*SS YGTKKEPVSPSQALA
8446	38814	B	8503	152	3166	

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8447	38815	A	8504	15	2745	HPTVNIRQINETESQQGYPGIEL SSAPSGPNRHLQNSP/PPNQQNI HFFQHHTTPIPKLTT*LSTLDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEII TNYLSDHSAIKLELRIKNLTQSH STTWKLNNLLLNDYWVHNEM KSEIKMFFETNENKDTTYQNL WDAFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITK
8448	38816	A	8505	2853	3925	AVGPSVRTPRPYLCVRKDVHD VVPILRPSATSLFMPRAAGQGG QKAGGTEKSSGP*KDDV*RLQP PNGFRIIH*VQ*TCRKGCPHLSK RNTFQFQN*R*NLLYPALPNIPH SSVEEGVGSI*ARSEDLEGAQLP *LLARLFTCRSNTYRGLKFTEA* GGE*QSICYSTRRANYPKY/HM HPIQEDPDS*SKS*VTYKET*TP TQ**WETLT/PPLSTLDRSTRQK VNKDTQELNSALHQADLID\TT ELSTPNQKNLHFFQHHTTPIPKL TTYLEVKL\PQQM*KNRNYNKL SLRPQCNQTRTQD*ETHSKLLN YMETEQPAPE*LLGT*RNESRN KDVL*NQREQRHNIPESLGHIQS SV
8449	38817	A	8506	2	376	IPYLP*ST\YMETGMIYVVQGIY GYHHYMQDRIDDNGWGCAYR SLQTICSWFKHQGYTERSIPTHR EIQQALVDAGDKPATFVGSRQ WIGSIEVQLVLNQLIGITSKILFV SNTRKNKKVGNIVS
8450	38818	A	8507	1	1008	
8451	38819	A	8508	218	343	
8452	38820	B	8509	306	1434	
8453	38821	A	8510	3	659	

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8454	38822	A	8511	3	1990	EPHRIASPRFRQAFDSDGTDRTL *FLSDIEEEELTRGDPEQRHVPL RRKSEWKWAADRAAIDSRWN WLQAHVSDLEYRIRQQTDIYK QIRANKGLIGLGEVPPP\EHTTD LFLPLSSEVKTDHGTDKLIESVS QPLENHGAPIIG\HISESLSTKSC GALRPVNGVINTLQPVLADHIP\ GDCSDAEEQLHKKQRLNLVSSS SDGTCVAARTRPVLSCKKRRLV RPNSIVPLSKKVHRNSTIRPGCD VNPSCALCGSGSINTMPPEIHYE APLLERLSQLDSCVHPVLAFPD DVPTSLHFQSMLKSQWQNKPF DKIKPPKKLSLKHRAPMPGSLP DSARKDRHKLVSSFLTTAKLSH HQTRPDRTHRQHLDDVGAVPM VERVTAPKAERLLNPPPPVHDP NHSKMRLRDHSSERSEVLKHH TDMSSSSYLAATHHPPHSPLVR QLSTSSDSPAPASSSSQVTASTS QQPVRRRRGESSFDINNIVIPMS VAATTRVEKLQYKEILTPSWRE VDLQSLKGSPDEENEEPASPDV SSSHSLSEYSHGQSPRSPISPELH SAPLTPVARDTPRHLASEDTRC STPELGLDEQSVQPWERRTFPL AHSPQAECEDQLDAQERAARC TRRTSGSKTGRETEAAPTSPPIV PLKSRHLVAAATAQRPTHR
8455	38823	A	8512	119	739	ADDRDHLHIQTWCAKAPVFLQ PGSSWLSTKGKKM/PETPASDE PPLRQPAVRFEFLQHAPPDSLQP LGSPGHS*GPSSDTGQPAAGRW PRRQP*AAVQDLGPQTRGSASP ESQTVLPAAPSAPGSARPHGSM SASAPSPTASPQMSKPPCAAAC LRGSGAGGGTVGPCLEPGGSAP PRARLPRCAAGSARPGAAAGPP PGAGTTRAVP
8456	38824	A	8513	1	343	MRMCLRLPTLMTKCTNWHVT GHLCRPT/MREPTPEP/WTGDTT TA*METRWPAEQPALAERRLFR AAPRGAFAGIAAPSPAAPPQPG SLGILPEPTPAQAWAARNQLRG RIKERGS

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8457	38825	A	8514	3	405	KKFNPAGERVCTILVDPSIPSTA YPSYGVPHS*GPSLSLPHL/SSSS RPSSISCPLNGPWKGCS*PPCRA QCAQPQQAT*ESCIHS/SSNCIPP AWEGETPSKKNKINGNPWSKIR DKTSGGEVEVWGLVAVAPVM
8458	38826	A	8515	100	1397	PPASTYLMLERLKAPWSAALQ RKYFDLGIWTAPISPMALTMLN GLLIKDSSPPMLLHQVNKTAQL DTFNYQSCFMQSVFDHFPEILFI HRTYNPRGKV/CIYLPGGWTSG AAGGSSCPSSLLCHPC/ARRDT/ CRPVPDVPSIQEV*SSMGESLYH PGGSSFPSTAYPS/SWSSPQLRSF SQPSTFVSSSRPSSISCPLNGPW KGCS*PPCRAQCAQPQQAT*ES CIHS*ATASLQPSCPSFTHTGCS TTASGWLTAGEAELRAATTSR ASRSPPTSSASSLVPPHLRNKV WLLCSVTCSRTLQTRQTSTRAC VPRTIMLPQTPSPKAPNWSSW* NPTSSTPSMPSAQGQQPNCAW ASLLWSRNPHTSLALAQKR*TY RSWKIPIRCSPSPLPAAAATLTR PSTCPAATS*PCSVPAARCSSPT CCRLSGRQAVLPV
8459	38827	A	8516	1	326	CLTQMYFLIS/FANVDTFLLAIM ALD/RLLAICSALRYCSIITPG\YS HFYCDAYLLMKIACSIHVNQH VFLGAVVLFL/APCALILVSYIRI AAA/ILRIPSPTRRRKACSIC
8460	38828	A	8517	2	669	TISYPQCLTQMYFLISFANVDTF LLPIMALDHYVAICSALQ*CSIIT P/ELCQGLPVLA*AGSSLISPVHT VIMSRLAFCSSAQISHFYRDAY LLMKIACSHT*\NQHVFLGAVV LFLAPCALILVSYIRIAAAILRIPS PTRRRKACSICSSHLSLVTLFYG TVLGICI*PPDSFSAQDAIATIMY TVVTSMLNPFIYSLMNKEVQEA VRRLFSRGSHSSWCW

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8461	38829	A	8518	1	3594	MVAAAAATEARLRRRTAATAA LAGRSGGPHCVNGGRCNPGTG QCVCPAGWVGEQCQHCGGRFR LTGSSGFVTDGPGNYKYKTKC TWLIEGQPNRIMRLRFNHFATE CSWDHLYVYDGDSIYAPLVAA FSGLIVPERDGNETVPEVVATS GYALLHFFSDAAYNLTGFNITY SFDMCPNNCSGRGECKISNSSD TVECECSENWKGEACDIPHCTD NCGFPHRGICNSSDVRGCSCFS DWQGPGCSVPVPANQSFW
8462	38830	A	8519	1	471	ALCAPQPGKCFCTTKGSSG/DE CQLCEV/ENRYQANPLRGTCYN TLLIDYQFTFSLSQEDDRYYTAI NFVATPDEQNRDLDMFINASK NFNLNITWAASFSAGTQAGEE MPVVSKTNIKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQ VQTEQ
8463	38831	A	8520	1	4289	
8464	38832	A	8521	1	3488	MDYGVLTRLTGSSGFVTDGPG NYKYKTKCTWLIEGQPNRIMR LRFNHFATECSWDHLYVYDGD SIYAPLVAAFSGLIVPERDGNET VPEVVATSGYALLHFFSDAAY NLTGFNITYSFDMCPNNCSGRG ECKISNSSDTVECECSENWKGE ACDIPHCTDNCGFPHRGICNSSD VRGCSCFSDWQGPGCSVPVPA NQSFW\TREEYSNFKA/LPRASH KAVVNGNIMWVVGGYMFNHS DYNMVLAYDLASREWLP
8465	38833	A	8522	4794	5740	YICNWYKMKDSSFPSLVQSPRS PGSCGLSGWGWGCPRVASAGS ACSCNSAVPARRTQEACRRELI GGRSTIFTDVQGQWGAPGTVN EGNSACPPTLRVTVAAWLSLLF VLCRVCAASVPSLVRLRWGPQ CSGPWGAWAPPWAARVSQPG AGPGRGAEAQLLPAASIQWPC HQAPHLLLVLALVTSQGPSRCR GFCLAGPCQGGPGGLLILFCHW NVPLQFSSLFFFF*DGVSLLLPR LECSGSISGHCNLRLPGSSDRPA LGS*VAGDYRCLPACSANFFVF LVEKGFHHVGRAGLKLL/MVIH LPRPPRVLRLQA

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8466	38834	A	8523	594	2868	CWTSRNRRPIPGSCHPMELPRPF RGKAKVQNHQLVH\HNKALIN RGSLTFWLDDGAIQAWHCPVK TYYQYTPVSSKAMY/DAFWNG/ KFRDC/AFHSWLNEDPFVCEYQ GQSSDLPQPPVNAGGGSGGGS GGGSEGGGSEGGGSEGGGSEG GGSEGGGSGGGSGSGDFDYEK MANANKGAMTENADENALQS DAKGKLDSVATDYGAAIDGFIG DVSGLANGNGATGDFAGSNSQ MAQVGDGDNSPLMNNFRQYLP SLPQSVECRPYVLSAGSEIGAA CASRSGYDNKGVRDIGYTDCK RSEDLDPLRHQILGGKKAIQFTL QGFPTLPEGAPAGNSGSLAVHK TAQSSYRHHALLILTPMSGTRF PPIPGPVVNIRVFPFAPSSECRIC YSWSWVPGSPVHCQSDGSVPIP SYAPLASQYSSSFLFFRNRQPYA PYDYLSVMTPSRTLREQIRIRYA PSAPRLPPPEVYCSNSTIVYVRN NPSGPTPGFAGGTLLEGRSGGP FRFYAKRAKGDVLKPFSLNLPL QTLIRFMVDIACGMEYLSSRNFI HRDLAARKCMYEFWRTRGWE TAAAYYGGGTTFFRKESQKLQ QSAKKRDAELANGALGIIELNN DYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGYVSNSLT GPYKPLNKTGLVLQMGLDPND
8467	38835	A	8524	302	409	
8468	38836	A	8525	199	359	ARRQQVSVKSYRWEEEDQHCG ELQGSE*VSDGLFKPP*S*HGW VEEERQKEQN
8469	38837	A	8526	1853	2032	VKQSTALLPHAVAC*PKVISSG ARGLKSILVLIRIVVMMVSMLP QLALSGWGRFRVLPG
8470	38838	A	8527	118	445	AAGGEPGDAPWVPGVWEPPES VCRGPPPSSTFPHPVLSTFGASG PENSRDCSWLSPQH*AA*VASG NNGPQAAQGSLSGIPDAATLSG I*RASILHVSVVEIISSPGFR

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8471	38839	A	8528	1	770	MRVLGIETSCDETGIAIYDDEK GLLANQLYSQVKLHADYGGVV PELASRDHVRKTVPLIQAALKE SGLTAKDIDAVAYTAGPGLVG ALLVGATVGRSLAFALGRFGDP CTPYWRASVSARCWKIPAPNFR CALLGSAAYAVNHGTGLSKKP TTLGSDHSKTPAQLAKRAGEA RRNGWQGALFPWESARSGEEE TP/VICRH*HSHRAAAKSGLGA GGTSSGGRYRLGGYSILADHGG *KFHCA*RHGATSGDGKVLD
8472	38840	A	8529	3	834	VGRVEIADQYQDLAILWNCLG SDHASSRQRRPFRGKAKVQNH QLVHLQQSSHQPWLPHFLAG* WGDSGLGGGS\EGGGSEGGGSE GGGSEGGGSGGGSGSGDFDYE KMANANKGAMTENADENALQ SDAKGKLDSVATDYGAAIDGFI GDVSGLANGNGATGDFAGSNS QMAQVGDGDNSPLMNNFRQY LPSLPQSVECRPYVFGAVRHDV RRIRVTGVTRVTPPEEVDTSVH SRGAHRIRSGFAPKRSVRVTTD TCIKRNSTCGVKSLSLWDGGGF
8473	38841	B	8530	1	811	
8474	38842	A	8531	1	1044	
8475	38843	A	8532	3	1472	GVVGERAGMARPGRPREGGGS G/GYSRPVPPAGGPGP*RGRTRI/ SGLANGAGPVVFQFLTELTRLF QKCRTSGSVYITLKKCKQREGS RAMLPGFPYTPVSSKAMYDAY WNGKFRDCAFHSGFNEDPFVC EYQGQSSDLPQPPVNAGGGSG GGSGGGSEGGGSEGGGSEGGG SEGDGSEGDGSGGGSGSGDFD YEKMANANKGAMTENADENA LQSDAKGKLDSVATDYGAAID GFIGDVSGLANGNGATGDFAG SNSQMAQVGDGDNSPLMNNFR QYLPSLPQSVECRPYVFGAGKP YEFSIDCDKIKILRGVFAFLLYV ATFMLPVIANIAIPQKRPFMQQT RCEVQCREDIEVQKLKSYDKLL ASINKKPGVNGWQKRRITVNA GEAHDQQALDYALYHLRIMTP AHDERSSIAAKGLTGEGYKGH VFWDTEVFLLPFHLFSDPTVAR SLLRYRWHNLPGRARRKRDGN GWAGGAPISVGKARAAAKK
8476	38844	A	8533	609	855	

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8477	38845	A	8534	369	1278	GHTACEWYSQGRHPGPELSPFL *GPG*NAGHVISMPAARPMEPC LGTGGLDVLLHHLRPDLPPAAL PGSAWPGEGALPLPGQVSGRG RSAACLQPGAWPGRGAAPVRR RPRPAAAGSVREAELLESPHLA AHRDC*LARKLNSGGYIPQAEY GKHAGLPLPGARALSCGCRAR APVPAALPHPLLDHQDPGPAGR IYGTGAGTQTLDGSAPRTSRAL GSTQMPEARPGLAGWGVAGV WSRG*SR*TRGSAS/SPRPRRCA LLALPGAAVSGDLRARNPRGSR PPKAPSGRGGPLLPPHRSTPRR
8478	38846	A	8535	3	2494	YQRQSSSPEDPAETASPTYALIA ACQSEIQLQTRQQPCDMAPGPL DCDPVKGSSRKRMFLMNAPPV VALQPKWEASVPPGSFRFPECF SEADKGVESMSPTMHKELPAL AACGLVADFDPVGEEETADFG PLVLDSDSDDSVDRDIEEAIQEY L/KGGGSRCKRELAHSS/APTAL CSPKLVPGSGG/GGPGSQVGSS KDQGSASPVSMSRADSFEQSIR AEIEQFLNEKRQHETQKCDGSV EKKPDTHENSAKSLSKSHQEPA TKVVHRQGLMGVQKEFAFCRP P\RLAKTNVQPRSLRSKVTTTTT QEKEGSTKPATP/TRPSEAVQN KSGIKRSASTARRGKRVTSAVQ APEASDSSSDDGIEEAIQLYQVQ KTRKEADGDPPQRVQLQEERA PAPPAHSTSSATKSALPETHRKT PSKKKPVPTKTTDPGPGDLDAD HSPKIPKETKAPPPTSPASRSKF VEWSSCQADTSAELI\AVLDIFK TILP/APMEGSDGSLSASPLFYSP NVPSRSDGDSSSVDSDDSIEQEI WTFLALKVQSRSLLARGAAGQ APERVEKQAPAGAEELPKSKRD SCEGSRKKPPSVFGSRAERTKP RPSCSSVDSDDSIELEIRKFLVE KAKESGVPGQAQPCLWKPTLA GEEGLRSPAKQEGLTSAIVAGIS AALGPEHTWVPGATTPRTPSVA PVLVPAVPTHWKKLAPACGGP

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8479	38847	A	8536	1	2463	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDSDDSVDR DIEEAIQEYL/KGGGSRCKRELA HSS/APTALCSPKLVPGSGG/GG PGSQVGSSKDQGSASPVSMSRA DSFEQSIRAEIEQFLNEKRQHET QKCDGSVEKKPDTHENSAKSLS KSHQEPATKVVHRQGLMDVQ KEFAFCRPP\RLAKTNVQPRSLR SKVTTTTTQEKEGSTKPATP/TR PSEAVQNKSGIKRNASTARRGK RVTSAIQAPEASDSSSDDGIEEA IQLYQVQKTHKEADGDPPQRV QLQEERAPAPPAHSTSSATKSA LPETHRKTPSKKKPVPTKTTDP GPGDLDADHSPKIPKETKAPPP TSPASRSKFVEWSSCQADTSAE LI\AVLDIFKTILP/APMEGSDGS LSASPLFYSPNVPSRSDGDSSSV DSDDSIEQEIWTFLALKVQSRSL LARGESCPQAAQGPLSPPGLSS QTGSPKAPLSKTLDPL/LGCKRK HRGG\SKAQPARPRDGRAPLG WDLSIQGTASEAPGGEGAARVP GDTRTSQGQGKTDEARHLDKK KSSEDKSSSLDSDKDLDTAIKD LLRESQGPAPSPGSLSDNSSSVD SDDSIELEIRKFLVEKAKESGVP GQAQPCLWKPTLAGEEGLRSP AKQEGLTSAIVAGISAALGPEH TWVPGATTPRTPSVAPVLVPAV PTHWKKLAPACGGPGQSLIDID
8480	38848	B	8537	1	3345	

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8487	38855	A	8544	1	1436	MNLPRAERLRSTPQRSLRDSDG EDGKIDVLGEEEDEDEVEDEEE EASQQFLEQSLQPGLQVARWG GVALPREHIEGGGGPSDPSEFG TEFRAPPRSAAASEDARQPAKP PYSYIALITMAILQSPHKRLTLS GICAFISGRFPYYRRKFPAWQN SIRHNLSLNDCFVKIPREPGRPG KGNYWSLDPASQDMFDNGSFL RRRKRFQRHQLTPGAHLPHPFP LPAAHAALHNPRPGPLLGAPAP PQPVPGAYPNTAPGRRPYALLH PHPPRYLLLSAPAYAGAPKKAE GADLATPA/ALPVLQPSLATVK PVGQFCSNSSGIRRRT\GNGCAP TKGAVLGGHLSAASAAAAVSG GGRGLWADIARALWAERDLTS FFSIAHAQFPGRVRRALLEPGSR QPHSPTGVQKRPLLANPAGLGQ SKSSETTENRG/CPMSCQLLAGL RSNSPLSVVRKRLRADLPSFIAN KRPGRAATAAEPRRDFL
8488	38856	A	8545	1	1287	MNLPRAERPRSTPQRSLRDSDG EDGKIDVLGEEEDEDEVEDEEE EASQKFLEQSLQPGLQVARWG GVALPREHIEGGGGPSDPSEFG TKFRAPPRSAAASEDARQPAKP PYSYIALITMAILQNPHKRLTLS GICAFISGRFPYYRRKFPAWQN SIRHNLSLNE*FVKIPREPGHPG KGNYWSLDPASQDMFDNGSFL RRRKRFKRHQLTPGAHLPHPFP LPAAHAALHNPRPGPLLGAPAL PQPVPGAYPNTAPGRRPYALLH PHPPRYLLLSAPAYAGAPKKAE GADLATPGTLPVLQPSLGPQPW E/RGQGSGVATGR\GCISFSIESI MQGVRGAGTGAAQSLSPT\AW SYCPLLQRPSSL\RTILQQQQQH QEEDCANGCAPTKGAVLGGHL SAASALLRYQPVAKGLWADIA AAPLGGEGTSPVFL

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8481	38849	A	8538	1	1339	MTKKSPGPDSFTGHWCVISIPS GYERSRLKVTLPEEGRGALPFL VSVAISSGSCSDNNAAVPTVLE GATTVISAAAVLRDPHDGAREII LEAMTISAVAIAAEISWTSQCG LCLHPGMFMPYRHGDGIRDLLP LVLSATICAEFFKGDSKKPSKK RVKRKPYSTTKVTSGSTFNENI RRYAVHTNQCRRPHGSRVKKK RYPQEDDFHHTVFSNLERLDKL QPTLEASEESLVHKDRGDGERP VNARVVQVAPLRLESSKYSGIT CQENNLDAKKA/TP/CRTPYMT SLTRTPHTTSLTRILSTA/SANEA ADKGIANEDAAQGIANEDAAH G\MPARMPPRASPTRSPPRASPT RTPPRASPTRTPPRASPRRTPPT GSPRRTPPRASPTRTPSTASPTR TPPMASPTRTLPTALLTRMPCT ASLMRTPYTTSLMRVPYMTSL MTPYKAR
8482	38850	A	8539	1	3090	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDSDDSVDR DIEEAIQEYLKVGSSKDQGSASP VSMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSVEKKPDTHE NSAKSLSKSHQEPATKVVHRQ GLMGVQKEFAFCRPP\RLAKTN VQPRSLRSKVTTTTTQEKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8483	38851	A	8540	1	2919	MHKELPALAACGLVADFDPVG EEETADFGPLVLDSDSDDSVDR DIEEAIQEYLKVGSSKDQGSASP VSMSRADSFEQSIRAEIEQFLNE KRQHETQKCDGSVEKKPDTHE NSAKSLSKSHQEPATKVVHRQ GLMGVQKEFAFCRPP\RLAKTN VQPRSLRSKVTTTTTQEKEGST KPATP/TRPSEAVQNKSGIKRSA STARRGKRVTSAVQAPEASDSS SDDGIEEAIQLYQVQKTHKEAD GDPPQRVQLQEER
8484	38852	B	8541	1	1122	
8485	38853	A	8542	1	1074	
8486	38854	B	8543	1	1017	

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8489	38857	A	8546	202	823	AQNPTAFGVKHTSSGGEETFPN IRGIKKSPPQLSSSSIRLSKNILST TGKTVHQTRDDDQPRDFFKKR NRVNESHQKSSNMNAGPSWNK VQHSKNSSGKRQSKSQVPHASS QPRSSLTAVTQPTEEKLIESISPE ARRKRNPLGFRCQGASRNKLFL DFQSMKIIKENADEDSASDLSD/ SGKNSHSSFSPHTSRSQSSS*RN RVNESHQKSSNMNAGPSWNKV QHSKNSSGKRQSKSQVPHASSQ PRSSLTAVTQPTEEKLIESISPEA RRKRNPLGFRCQGASRNKLFLD FQSMKIIKENADEDSASDLSDSE RIPIPPSPLTPPDLNLRAEEIGSSL L
8490	38858	C	8547	219	1013	
8491	38859	C	8548	252	452	
8492	38860	A	8549	25	443	
8493	38861	A	8550	20	1371	RLRGPALGAGGGSVTLRL/PRS EQAARKEAGLNTMIPLEKPGSG GSVPRRHLRLGPGSSGS*AGRA RTPPPPQARGLLTEIRAVVRTEP FQERLQPVPRAGSWAGGKFSSG EKMYKEKILGKNLLQSS*EKRR K\SQDCRMEIIHEIAVLELAQDN PWVINLHEVYETASEMILVLEY AAGGEIFDQCVADREEAFKEK DVQRLMRQILEGVHFLHTRDV VHLDLKPQNILLTSESPLGDIKI VDFGLSRILKNSEELREIMGTPE YVAPEILSYDPISMATDMWSIG VLTYVMLTGISPFLGNDKQETF LNISQMNLSYSEEEFDVLSESA VDFIRTLLVKKPEDRATAEECL KHPWLTQSSIQEPSFRMEKALE EANALQEGHSVPEINSDTDKSE TEESIVTEELIVVTSYTLGQCRQ SEKEKMEQKAISKRFKFEEPLL
8494	38862	A	8551	1	1275	
8495	38863	A	8552	1	4173	

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8496	38864	A	8553	2	5115	PDQFHNMDLRGGPHDGVTIPRS TSDTDLVTSDSRSTLMVSSSYY SIGHSQDLVIHWDIKEEVDAGD WIGMYLIDEVLSENFLDYKNRG VNGSHRGQIIWKIDASSYFVEPE TKICFKYYHGVSGALRATTPSV TVKNSAAPIFKSIGADETVQGQ GSRRLISFSLSDFQAMGLKKGM FFNPDPYLKISIQPGKHSIFPALP HHGQERRSKIIGNTVNPIWQAE QFSFVSLPTDVLEIEVKDKFAKS RPIIKRFLG
8497	38865	A	8554	202	260	ARVHQPVSLKQRFPLELGRHH QDSEAHAPPPGPAAASRGGI*V
8498	38866	A	8555	72	578	GSKGSVAGARAWVVSLLGCRS RWTAAMELQRRIPPREAAAGP WRRSMWRWRTRPSTVAPVASE SWWCRPSSRGNRCFQRHSLDPS MTIHCDMVITYGLDQLENCQT CGTNYIISVLNLLTLIVEQINTKL PSSFVEKLFIPSSKLLF\LRYHKE KEVVAVAHAVYQAML
8499	38867	A	8556	299	939	LPSPGGVGQVRGETAASETQVL YRAMRRVTAANQAFFSEAEVT AAKERGIVLPLRC\DPS\QTIHCD MG\ITYGLDQLENCQTCGTNYII SVL\NLLTLIVEQINTKLPSSFVE KLVIPSSKLLFWRYHKEKEVVA VA\HAVLSRPMLQLGRNIPCFG RTAY*V*YWGRKWTCGPLNNL PGTVCNFPEACSEIKHEAFKNH VFNVDNAKFVVKFDLN

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8500	38868	A	8557	1407	2783	SSAASHSSSPGAASRARATAGS RRRSSPIQSCHPPASACGQSGQS ETHRLAMRNRTPPS*GFSSK/H MRRSSSLASS*RG*KSVAVIL*IS ASGILPTDV\HLSPTPGSSETCHR PHPGH*EPSDCLQKLPASALG*S *QEQLSHNSPRSA*AQYA/ESSG NSFFSSKVGD*RFTTTVA\PGGP GRRTLPGKPSPEHPHRLPELPPP RSPAQVCDQTLVAPHDHNTAG/ TPGDQVCLTLVSTSRSLSVLSK GCFFLHHSTLSVQAGVRHLSLV S*AAEPTSYL*VGPKLMAPS*KS LKIRTRKPRADDSPGTSRYSSA HTRTRKPRADDSPGTSRYSIAH TRMWKPRADDSRH\SRYSTGCR SPGQMTLHAPADTALHTPG/PR KPRADDSPGTSRYSTAHTRTRK PRADDSPGTSRYSTAHTRTQKP RADDSTGTSRYSTPLASRRHRI AASASWALVVLICLTL
8501	38869	A	8558	92	1817	PLRNTGLCRGKGHPGLESSGSR RRRDGRASERRQTQRERGKTLP CSSHSPWWLKANASAPAVWSQ AHRTQKPRADDSPGTSRYSTAH TRTRKPRADDSPGT\PDTALQTP GRRSPGQMTPGTSRYSTGRGSP GQMTPGTSRYSTERRSPGQMTL QTPADTAQDAEAQGR*LQAPA DTALHTPGRRSPGQMTLQAPA DTALHTPGHRSRGKMTLQAPA DTALHTPGRGSPGQMTLQAPA DTALHTPERSEPGQMT\PRRPA DTALHTPGRGSPAQMTLQAPA DTALHTPGRRSPGKMTPGTSRY SIAHTRTRKPRADDSPGTSRYST AHTRTQKPRADDSPGTSRYSTA HTRMRKPRADDSRH\SRYSTGC RSPGQMTLQAPADTALHTPG/P RKPRADDSPGTSRYSTAHTRTR KPRADDSPGTSRYSTAHTRIRK PRADDSPGTSRYSTAHTRTQKP RADDSRHQQIQHRMQKPRADD SPGTRRYSIAHTRTRKPRADDSP GTSRYSTAHTRTRKPRADDSPG TSRYSTAHTRTQKPRADDSPGT SRYSTRAGCCPPGLASSAWAGL RLKTRKGWTW

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8502	38870	A	8559	13	299	EKGQDILQNLFWQLRHGPIMSS \PSASNTGWGSSS*SIVPSSTVSS WSTAMKLSSSLSEELAMTFHST ENIVVLGWVQWLTPVVPALWD SEAGRSP
8503	38871	A	8560	337	1879	VHVGAARRGFGVYPVLSLTVS GTQNCGPCLQTVVSTYQRV*PI SVIMVS*RLSRKETFSGRAVPILI LEPQSLSASRTVHAIMM/HNQS MYVFGGCTQSSCNAAFNDLWR LDLNSKEWIRPLASGSYPSPKA GATLVVYKDLLVLFGGWTRPS PYPLHQPERFFDEIHTYSPSKN WWNCIVTTHGPPPMAGHSSCVI DDKMIVFGGSLGSRQMSNDVW VLDLEQWAWSKPNISGPSPHPR GGQSQLFKDAWLLHMHSGPW AWQPLKVENEEHGAPELWCHP ACRVGQCVVVFSQAPSGRAPLS PSLNSRPSPISATPPALVPETREY RSQSPVRSMDEAPCVNGRWGT LRPRAQRQTPSGSREGSLSPAR GDGSPILNGGSLSPGTAAVGGS SLDSPVQAISPSTPSAPEGYDLK IGLSLAPRRGSLPDQKDLRLGSI DLNWDLKPASSSNPMDGMDN RTVGGSMRHPPEQTNGVHTPP HVASALAGAVSPGALRRSLEAI KAMSSKGPSASGRH
8504	38872	A	8561	25	313	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8505	38873	A	8562	1	1409	MIERVLEGKWALSRAEGLHRH QCLEFLIHLVFQLMKVVNEMCP NITRIYNIGKSHQGLKLYAVEIS DHPGEHEVGEPEFHYIAGAHGN EVLGRELLLLLVQFVCQEYLAR NARIVHLVEETRIHVLPSLNPDG YEKAYEGGSELGGWSLGRWTH DGIDINNNFPDLNTLLWEAEDR QNVPRKVPNHYIAIPEWFLSEN ATVAAETRAVIAWMEKIPFVLG GNLQGGELVVAYPYDLVRSPW KTQEHTPTPDDHVFRWLAYSY ASTHRLMTDARRRVCHTEDFQ KEEGTVNGASWHTVAGSLNDF SYLHTNCFELSIYVGCDKYPHE SQLPEEWENNRESLIVFMEQVH RGIKGLVRDSHGKGIPNAIISVE GINHDIRTA\TDGDYWRLLNP\G EYVVTAKAGRFHCIHPRTCMV GYDMGAHK/CLNFTLSKTN\LA RIRRDHWRSFGKAAPSALPSPG G*KLRG\RKRRQRG
8506	38874	A	8563	3	749	KTDHILGHKTCLKTFRKIEIISGI LSDHSGIKLQINNKGNFGNHTS TWKLNNMLLNDQ*VNEEIKKEI *NHPETNDNGNATYQNL*DTG KEVLRGKL/IPISTYIK*VEKLQI NNLTMHLKELEKPEQTKRKITR RKEIIKIRAEINEIEAKKTIPKFN ETNSWFLENIHKTNEHLARLRK KDPNKIREEKEDIITDTVEIQRII RSYYAKKWENLEETDKFLDTY NLPRLNNEEVQNLSRPITTTVPI
8507	38875	A	8564	1	842	

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8508	38876	A	8565	1	1203	VPELFGNCRQLLEEVEVAT*PR RFRDSPGGSVQGLWTSLRRAAE MLFPVHLVRPRM*ILERFVPHA LDYLLGSRLFKEPLPLKQVNPS RSLDHLQR\AREHFINYLTQCH CYHVAEFELPKTMNNSAENHT ANSSMAYPSLVAMASQRQAKI QRYKQKKELEHRLSAMKSAVE SGQADDERVRGYYLLHLQRW\ VDISLEEIESIDQEIKILRERDSSR EASTSN\SSRQERPPVKPFHSHF GTWLHSQSTFGAGYSKGWPTY RTVS\DWYE\QHRKLWSTYPDQ GI\AKAAPEEFRKAAQQQEDQ\ KKRRKRM\RTKQLPQSPGVGM TGSDTHP*GPMGTDRTWADLP TTPQD\SGVH\TPLPRKTMQSSP PPVSWLQLCTTEGKDAKSCFAF SKVSSDLSVYLYP
8509	38877	A	8566	1	995	GTKELLLT*LGGSPLLLT*TKPL GVDPL\LKGGVTQGFNEKAVFA ALRPSYGQPAGKPAFAGAMSL AGAQGSLWSVEGGNKLVCSGL LKLTKANVIHATVTSVTLHSTE GKALYQVAYENEVGNSSDFYD IVVIATPLHLDNSSSNLTFAGFH PPIDDVQGSFQPTVVSLVHGYL NSSYFRFPRP*AFPL\SNILTTDF PSFFCTLDNICPVNISASFRRKQP QDAAVWRVQSTKPLFRTQLKT LFRSYYSVQTAGVGRANPLYG FRPHGFPRFALHDQLFYLNALE WAASSVEVMAVAAKNVAFAW LYNRWYQDLDKIDQKDLMHK
8510	38878	A	8567	1	372	

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8511	38879	A	8568	1	1699	MHAKSIKTQALADMEKLKVVV RDKNWVARIIPQMTSKGHVGV TTTSSAKLKSQGKDSVAVKRV RSGLMIGFRFMVIPPYSFGPQVL MEIPKDADKLLCPSCAAVVLG QKKHETQTLSLKELPVQDNVV PKEDPGTWEWRTVKEGILEEV MCWLQSRVEGDWAKEERKIFH EGELAEAKAGRGGLASCTCCPL TPGKMAGPWTFTLLCGLLAAT LIQATLSPTAVLILGPK\VIKEKL TQELKDHNATSILQQLPLLIAM REKPAGGIPVLGSLVNTVLKHII WLKVITANILQLQVKPSANDQE LLVKIPLDMVAGFNTPLVKTIV EFHMTTEAQATIRMDTSASGPT RLVLSDCATSHGSLRIQLLHKL SFLVNALAKQVMNLLVPSLPNL VKNQLCPVIEASFNGMYADLL QLVKVPISLSIDRLE/F*PSVSCH QG*HHSALPGGQVVGLTGKGD QVV\HNSAASLTMPTLDNIPFSL IVSQDVVKAAVAAVLSPEEFM VLLDSVLPESAHRLKSSIGLINE KAADKLGSTQIVKILTQDTPEFF YRPRPCQGGPTDRAGSVSLQ
8512	38880	A	8569	1	1060	MGLPAQGVGGNTLAKLLASDD IAKGGKRNKSEASVVRNAADA PKVLQDLSARLMGDFELRNCN SPCTLLIGIVVLINAAAETLVFLS DHMEDQGSSQLNVAVLSYFQQ QDPEGQKEETAGIDLMDMASDI LQPKGDDVARISWYLRDIITRY QETFNVIERCPKPVIAAVHGGCI GGGGAAAPMPRPLASSLSSVM GQTVSQEAAPPPGSQGWFWWS FSIPGLYLLGVDLVTACDIRYC AQDAFFQVKEVDVGLAADVGT LQRLPKVIGNQSLVNELAFTAR KMMADEISSKSPVALQ/S/TKVN LLYSRDHSVAESLNYVASWNM SMLQTQDLVKSVQATTENKEL KTVTFSKL
8513	38881	B	8570	331	1200	
8514	38882	A	8571	3	379	TSLTFHSPEVPSS*PPSCTR*AGA ARGPRPPGAAGRPR*SC*GPPGT RRWQS*GGTSPLGPVPGGRSGA ASCGLPDCEL*PLKRSAQGRNQ CPV*SSPRSWSRSRSEPCAARG WPPSACRHGNRR

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8515	38883	A	8572	384	1718	SLQLPRGLLPESCAADPGA*PPS CTR*AGAARGPRPPGAAGRPR* SC*GPPGT/PALAKPPSCPVVTS AAPTQARPMIKPQGAAWSTQK LPIPTSASPTQKSPIPTSASSTQK LPIPTAAWSTQKLPIPTAAWST QKLPIPTAAWSTQKLPIPTAAW STQKLPIPTAASSTQKLPMPTAA SSTQKSPIPTAASSTQKLPIPTAA WST*KLPITRAAWSTQKLPIPTA ASSTQKYTIATAASYHAKATDA WST*KLPIPRAAWST*KLPIPTA AWSTQKLPIPTAASSTQKSPIPT AASSTQKLPMPTAAWSTQKLPI PTAAWSTQKLPIPTAASSTQKL PMPTAASSTQKLPMPTAAWSTI TTMGATTH\GPSTDTQNVVFLH PRCPEQASSQRSGAGAD*GLSN PKVSSAEAPSCAKDEPEVEKGR GPAPWTSQRWRRAVGRPRG
8516	38884	A	8573	302	543	KLHLGWGKTPG*HWGLY*NLP RLNGPNSLMPSLRRVRRNKAR QVTSIAGCALQMEQWMHGMT RHPTRISTPITAAREVRI
8517	38885	C	8574	253	396	
8518	38886	A	8575	1107	1751	LQDLSQYFGGSQLIKT*IG*TTSI ITNSNL*TTLEM/SVKGIAEQLG TNCQMAWENRIALDMILAERG GVCIMIKTECCAFIPNNTAPNGS ITKALQGLTALSNELASSSGVN DPFTGWLEKWFGKWKGITASIL TSLTAVMGVLILVGCCVIPCICG LVQRHRGPPLVVIETKPLGLER LAGLPVGHALKLGSGIQATPQN GENADRREAFPAAS
8519	38887	A	8576	1	1365	
8520	38888	A	8577	3	263	QLILKDKFITQSAADIKEKLQKS TLGPERNLKTLLNLAT/CCFL** RSGGAGGTGQTR*EKGHHFSH GPRASGLWRLWNAESLGKSNA
8521	38889	A	8578	365	470	
8522	38890	A	8579	1	1278	
8523	38891	A	8580	23	257	
8524	38892	A	8581	1	1812	

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8525	38893	A	8582	265	699	LLGSTVLFHDPQLLIELYHSSHG PKVPFLGIREAKNSRSENTRLAT ILGAGLLPSWKWFTTILGAL*A RTPR*HFGNH/VTDIQS/RIEAVK LQMEPKMQSKTKIYRRPLDRPA SPRSDVNDIKGTPREEISAAK\PL LRPNSAGSS
8526	38894	A	8583	2	181	
8527	38895	A	8584	1	69	
8528	38896	A	8585	1	674	MDLNYTLEQMDLTDIYRTFHPT TTEYTFYSTGHGTFSKTDDVIG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLLNECWVKNKMKMEIKKLF ELNDNNDTTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKNKNHMIISIDAEKAFDKIQH PFMIKTLSKISIRGTYLNLIKDI/S *QTHSQHNAEWGKIESIHSENW NRG
8529	38897	B	8586	1	415	
8530	38898	A	8587	1	516	
8531	38899	B	8588	110	382	
8532	38900	A	8589	140	253	QNKACQHPPKITRVHQQWIQT KKKSSIYLKKEFRRLVIKLIREA PEEGKAQCKEVQKLIQKVQGEI IDEIDTINKKQPKLQETMDTLTK MQNAQESLSNRIEQEEEHSKSL ENIFGSIMEENFPSLARDLDSQI QEAQRTPGKFITKRSSPRHIVIR LSKVKTKERILRVVRQKRK\IVL KS*PGNMTKQGLSTSPKNHTSS PTMDPNQEEILDLPEKRIQEVSY
8533	38901	A	8590	89	194	
8534	38902	A	8591	2	633	

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8535	38903	A	8592	298	2648	GSSKILLFNQNEDDKINFELFFF FVASALVLVQKAFSRSWSSMA LADKRLENLQIYKVLQCVRNK DKKQIEKLTKLGYPELINYTEPI NGLSALHLASVSNDIDMVSFLL DLGAHPDVQDRMGCTPTMRA AELGHELSMEILAKAKADMTIV DNEGKVLEGTGGLTSSPLAHIA VALHIPRRDTQGVLFYCILPTKR HYRCALIALEHGADVNNSTYE GKPIFLRACEDAHDVKDVCLTF LEKGANPNAINSILKLLFAYNG DVGLISINGNTPLHYAAMGGFA DCCKYIAQRGCDLKWKNLDHK TPRAVAKEGGFKAASKEIRR/C RENR**TSQARSQKSQIPLWAL RLHDWSVEREAFLREAFAVLD RGDGSISKNDFVMVLEE\SRIM QAQNSWLPFAHLHEKTRGGGV NIN*ILLKEPDILNKSFVLGSYGP KKKEKGMGKKGKKGKFVLPLP ICVIPEYAFPRRQDGGPPYYMIE TYKNVTDSSRFNRDHPPEHPIQ DDSVWYIDDSEKVFSNINIITKA GDLASLKKAFESGIPVDMKDN YYKTPLMTACASGNIDVVKFLL EKGYASPSGQQDIVELLVESGA LIDAASINNSTPLNRAIESCRLD TVKYLLDIGAKFQLENRKGHSA MDVAKAYADYRIIDLIKEKLDN LPKPAENQKLKGKTPPILKTEG PEIKKEEELLSSIYGVPTTSEGK
8536	38904	A	8593	3	838	MGRGWTQAVGPRWSGGSSCTL YSVGADGRGQGHQSRGCRPPG PPSASSAPCLAWGAAGRARRE GLRQNAERSSPLTAPAGRP*PC GAGPCRR*SR*R\PLVGCLRPW ASPGTGAACGRCCCPPP*P/P*P NPWHFTVSKAFSYMPSTTA/RL VRGPRLLVGPVPVAPYIPP/PGS PASRRGSRCRGRSRPSPRPRPSV LSCHGVSL*TGPSLPGWLLQIW QRSAQMS/P/PPKGPP*GSREGPP PP/GPALLPAAAPGGQGHRAPA AGSCGRRAAARRMEWVRNSPP
8537	38905	B	8594	1	2700	

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8538	38906	A	8595	1	1240	FPPYATNEIGKVTGLNRRELGH GALAEKALYPVIPRDFPFTIRVT SEVLESNGMRRIGQPPASSRPV RRVRAPLPPPLLEVRAPLPASRP SGEVLCTVTFDSLESGIKSDQVI TAINGIKDKNFMLHYEFPPYAT NEIGKVTGLNRRELGHGALAE KALYPVIPRDFPFTIRVTSEVLE SNGMRRIGQPPASSRPVRRVRA PLPPPLLEVRAPLPASRPSGEVL CTVTFDSLESGIKSDQVITAINGI KDKNFMLHYEFPPYATNEIGKV TGLNRRELGHGALAEKALYPVI PRDFPFTIRVTSEVLESNGSSSM ASAC\GGSLALMDSGVPISSAV AGRTN*DWSPKPDPEKGEIRKII VC*QIFLGIEDYNGDMDFKIAG TNKGITALQADIKLPGIPIKIVM EAIQQASVAKKEILQIMNKTISK PRASRKENGPVVETVQVPLSKR AKFVGPGGYNLKKLQAETGVT ISQVDEETVFCNLHQHPVLMLE GKRLSFTEICKDDQEQAIRNLG AVILPAHNNWKSEILGVMGKII
8539	38907	A	8596	152	305	DNQNGKLIKCS*PCNFVHRAPY AVEITVLRFHCNWTVQVAQRE RTFLILIK
8540	38908	C	8597	414	611	
8541	38909	B	8598	1	403	

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8542	38910	A	8599	1	1702	MDSDEGYNYEFDEDEECSEEDS GAEEEEDEDDDEPDDDTLDLG EVELVEPGLGVGGERDGLLCG ETGGGGGSALGPGGGGGGGGG GGGGGPGHEQEEDYRYEVLTS E\MILQHMVECIREVNEVIQNPA TITRILLSHFNWDKEKLMERYF DGNLEKLFAECHVINPSKKSRT RQM\NTRSSAQDMPCQICYLNY PNSYFTGLECGHKFCMQCWSE YLTTKIMEEGMGQTISCPAHGC DILVDDNTVMRLITDSKVKLKY QHLITNSFVECNRLLKWCPAPD CHHVVKVQYPDAKPVRCKCGR QFCFNCGENWHDPV\QCKWLK KWIKKCDDDSETSNWIAANTK ECPKCHVTIEKDGGCNHMVCR NQNCKAEFCWVCLGPWEPHG\ SAWDTVPV*NEDDAKAARDAQ ERSRAALQSYLF\YC\NRYMNH MQSLRF\EHRLYAQ\VTQTMEE MQQHNMSWIEVQFLKKAVDV LCQCRATLMYTYVF\AFY\LKK NKPSFHIFENNPKARFDENATE GLSG\YLGTRKFPKDS\LQDIKQ KVPRPSTRYCESRRKGFVTSMC HEGYEKDLWEYIED
8543	38911	C	8600	118	219	
8544	38912	C	8601	16	408	
8545	38913	B	8602	1	996	
8546	38914	B	8603	1	1302	

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8547	38915	A	8604	983	2127	DNWKSIRGSCWQDPRELLTFM APCIGVVVMQTTR*K*NTLAGH PSAGVCWCVTSAAACTGAWD ATSPLSSTFATAPGLPRCCSQAS PAPRAEPLHGQPGAPPHALKRP PGLPWP*PQEARQYRHNQAYA YSIQGDGAEDDDERIVRFHTRV INHKKRKNSPRIVQSNDLTEAA YSLSRDQKRMLYLFVDQIRKSD GTLQEHDGICEIHVAKYAEIFGL TSAEASKDIRQALKSFAGKEVV FYRPEEDAGDEKGYESFPWFIK RAHSPSRGLYSVHINPYLIPFFIG LQNRFTQFRLSETKEITNPYAM RLYESLCQYRKPDGSGIVSLKID WIIERYQLPQSYQRMPDFRRRF LQHIFVLRERPETVLIDLIQRTK DAVRELDNLQYRKMKKLLFQE AHNGPAVEAQEEEEEYGWNLD RAYDYVKERRTVTKPNPSFMR QLEEYQGILLARPKRTAYIYGS VYRRCGYADHKVEIKHPGWAS ISRGVLVCDECCSVHRSLGRHIS IVKHLRHSAWPPTLLQSGFPGP SRRAAPRAARGPTPRTEEAAW AAMALTFLLVLLTLATLCTRLH RNFRRGESIYWGPTADSQDTVA GSPDHGLLAFAYHRLVRFLLW VLCPGWAFFLVNSSRGGVFNPI LHPCPRHGQARFAGVGRAEDV TFLYHPCAHPWLKLQLALLAY ACMANPSLTPDFSLTQDRVDIE
8548	38916	A	8605	1	224	RKQEWLSKQKENIQHFQAEEE ANLLRRQRQYLELECRRFKRR MLLGRHNLEQDLVREELNKRQ TQKDLEHAMLLRQHESMQELE FRHLNTIQKMRCELIRLQHQTE LTNQLEYNKRRERELRRKHVM EVRQQPKGLKSKELPNKKSSFQ GYLQNSQTRQYKALRNHLLET TPKSEHKAVLKRLKEEQTRKLA ILAEQYDHSINEMLSTQAVSLLF LGQNKFSAPFLPPP*AVSEQLCA HSLV

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8549	38917	A	8606	1051	1875	SDQLTAHLLNCVEVAELQFLHR FMLSFIPIHHLRLFTAPAQDASL VPLKGDILGVKLSGDDGRGKP AQHLFLSGLSSSQQQLPVLPSQ CQSLCVHHPAVVVNLHDHGAC VSCLPDLGP*RQSCGSLAARSC GQSPGVWCLPSGSGRSSTLCRC H*GRSWTPGAPS**TPISSPRRSP GPCAASPGARGCPPAASPPAGS PGTEAPAAPAPGPGYSQPPGAL SSRCDSPCPRLRRAPGAHGHTP RCPSVVARCRGVRPRGSSCSMS TSLTRSCSKL
8550	38918	A	8607	714	2148	MPAVAKSKFINRSKRRMCPQV LRSASPIQEGEKISANENSLAVR STPAEDDSPGDSQVKSEVQQPV HPKPLSPDSRASSLSESSPPKAM KKFQAPARETCVECQKTVYPM ERLLANQQVFHISCFRCSYCNN K\LSLGTYASLHGRIYCKPHFNQ LFKS\KG\NYDEGFGHRPHKDLI GQAKMKTEEILER\QPQLANAR ETPHSPGVEDAPIAKVGVLAAS MEAKASSQQEKEDKPAETKKL RIAWPPPTELGSSGSALEEGIKM SKPKWPPEDEISKPEVPEDVDL DLKKLRRSSSLKERSRPFTVAA SFQSTSVKSPKTVSP\LIRKGWS MSEQSEESVGGRVAERKQVEN AKASKKNGNVGKTTWQNKES KGETGKR/R*GKVHSLEMENEN \FV\ENGARLPIEDDNQLPPKQQ SSTKNPSLLEFGPSFVDNHLLLK EFTT\QNQKSQDVELWEGEVVK ELSVEEQIKRNRYYDEDEDEE
8551	38919	A	8608	1	4479	MCFSPKKLYKHEIHKLKDLTCL KPSIESPLRQNRSRSIEEEQKQE ENGDSQLILEKIQLPQWSISLNM TDEHGNLVNLVCDIKKPMDVY KIHLNQTDPPDIDINAMVALDF EYPMTQENYENLWKLIAYYSE VPMKLHRELMLSKHPRVSYQY RQDADEEALYYTGVRAQILAEP EWIMQPSIDIQLNRPQSTAKKV LLSYYNQYSQTIATKDTRQARG RSWVMIEPSRAVQKDQTVLEG GRCQLSCNVKASESP

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8552	38920	A	8609	1	9009	MDEFAPGKHLATSGDLFGDHN YGRRTYHTLEVKCAEEHPAVS DPFQRQSLRALSPLSEDLPPSSG LRSGLTKLELLMIHGNEIPSIPD GALRDLSSLQVFKFSYNKLRVI TGQTLQGLSNLMRLHIDHNKIE FIHPQAFNGLTSLRLLHLEGNLL HQLHPSTFSTFTFLDYFRLSTIR HLYLAENMVRTLPASMLRNMP LLENLYLQGNPWTCDCEMRWF LEWDAKSRGHSCRGCAHSLSH EIQLAKGFCEMLLL
8553	38921	A	8610	1	4971	MKASGILKCKKDKAYEGGQLC AMCFSPKKLYKHEIHKLKDLTC LKPSIESPLRQNRSRSIEEEQKQ EENGDSQLILEKIQLPQWSISLN MTDEHGNLVNLVCDIKKPMDV YKIHLNQTDPPDIDINAMVALD FEYPMTQENYENLWKLIAYYS EVPMKLHRELMLSKHPRVSYQ YRQDADEEALYYTGVRAQILA EPEWIMQPSIDIQLNRPQSTAKK VLLSYYNQYSQTIATKDTRQAR GRSWVMIEPSRAVQK
8554	38922	A	8611	1	1283	LSFTTCSTFSTNYRSLGPAQAPS YG/SRPVSSVASVYAGTGNSGS RISVSCSTSFRGSMESGGLAAG MT/GGLAGMGGIQNEETMQSL ND/*LASYPDRVRHLETKNRKL ESKIWEHLEKKGPQVRDWSHY FKTIRNQRAQSLAITVDNACIVL QINNTHLAADDFRVKYETELA MCQSVESNIHGLCKVNDDTNV TRLQLETEIKALKEELLFMKKN HEEEVKGLQAQIASSGLTMEVD P\KSQHLAKIMAAIRAQYDELA WKNGEELDKYLSQQIEESTTVV TTQSAKAGAAEMTLTELRCTV QSLEINLNSMRNLKASLENSVR EVKACYTLQMEQLNGILLHLGS ELAQTQAKGQCQAQEYEALLN IKVKLEAEIATYCHLLEDGKDF NLGDALDSSNSMQTIPKTTTHQ RVDGKVVSETNDTKVLRH

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8555	38923	A	8612	2	1365	RPQSLSPVLSLSPDSMSFTTRST FSTNYRSLGSVQAPSYGARPVS SAASVYAGAGGSGSRISVSRST SFRGGMGSGGLATGIAGGLAG MGGIQNEKETMQSLNDGVASY LDRVRSLETENRRLESKIREHLE KKGPQVRDWSHYFKIIEDLRAQ IFANTVDNARIVLQIDNARLAA DDFRVKYETELAMRQS\VENDI HGLRKVIDDTNITRLQLETEIEA LKEELLFMKKNH\EEEVKGLQA QIASSG\LTVEV\DAPKSQDLAK\ I\MADIR\AQY*RAGLGKNREE\L DKYW\SQQIEVSTTVVTTQSAE V\GAA\ETTLTELRRTVQS\LEID LDSMRNLKASLENSLREVEA/R RTPLQMEQLQRGSLLHLESELA QT\RAEGQRQA\QEYEALLEHQ GSSLEAEI\ATYRRLLEDGEDFN L\GDALDSSNSMQTIQKTTTRRI VDGKVVS\ETN\DTKVLRH
8556	38924	A	8613	170	399	
8557	38925	A	8614	141	287	LPSRRAGLGTCSPPCLSLPPASR APVRPEPLR*APPPAPRRPVPST TQG
8558	38926	A	8615	356	574	
8559	38927	A	8616	552	770	
8560	38928	A	8617	158	368	
8561	38929	A	8618	1136	1410	
8562	38930	B	8619	1	631	
8563	38931	B	8620	321	2234	
8564	38932	A	8621	170	444	
8565	38933	A	8622	325	722	LIELRHLVFFVLLLFRDLQHIMA CNMRDAVRFFVCFLVIFFREGL SRSSGA/DDRFLAGP*LLSRGAG LGTCSPPCLSLLPTPWAP/AAAP ASLT\TPPPAPRRPVPSTTQGLRS ASARHGTGRQLHLQPRCGIH
8566	38934	C	8623	1	1449	
8567	38935	A	8624	326	626	LPSHGAGLGTCSPPCLSLPPPLW AP/AAAEPPRQAPPPAPWCPVPS TTQGLRNASTRRRTGRQLHMI WPFPASLKSSPATLPCEHCAPTT LTFSCSSNMQT
8568	38936	A	8625	2009	2227	
8569	38937	B	8626	182	1513	
8570	38938	A	8627	497	761	NHTSCLPLGPGTTAEELPSLVA GFGTCSPPCLSLPPTPWAPVRPE PPR*APPPAPQRPVPSTTQGLRN ASTRHRTGRQLHLQPRCGIH

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8571	38939	A	8628	218	855	GAGLGTCSPPCLSLPPTQRAPV RPEPPRRAPPPAPRRPVPSTTQG LRSASTRHRTGRQLHLQPQCGV H*VKPAGLLSLALETRTNPAA/ DKHLWQSIISLQLKSDLLKEML GSQTGNGNVQDVLRYLVKSET QKAIKVSLDCVRKRYYRSSLSL QLKLCDCWGQALFSSALTLDP KEVVVRDLEELSNYKTTLEGSG IFDSVARVREESEAEGT
8572	38940	A	8629	350	615	
8573	38941	A	8630	186	566	RLLSPAACRSGTMIFPSIHPSQC RMIGLGWKK*SSVHNATPWAP VPPEPPGRAPPPAPGRPVPLTTQ GLRSASARRRTGRQLHLQPQCG IHWVKPAGLLSHEGPRLRSSSQ SDQEPTNSGHSGMCL
8574	38942	A	8631	656	874	
8575	38943	A	8632	415	634	LPSRGAGLGNCSPPCLSLPPTPW APVQHKPPRRAPP\PTPRHPVPS TTQGLRNASAWRRSGRHLHLQ PQCGIH
8576	38944	A	8633	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDQEAVI DGRRKPEESRTTSHICRCRS

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8577	38945	A	8634	1	1743	MGQVWALVHSTLETFHTDEEE GEYNEVTEQVCLPAKAGSAAV DLCCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQIVTS TSVPWKAKPGDHIAQLLIVPKK FARFEGTASSGKTKFLPRFRISF LMAAIVKPPEPIPLKWLTDKPI WTEQWPLSKEKLEALEDLITQQ LKKGHIAPTFSPWNSPVFIIKKK SAEQDCEWFVFTILAVNNLQLK PAKRFHWKVLPQGPNQQPIWIP SRYLKPYHKPDAKEEIPEGSQG FPVAAMSRLTLRRTPTVTSNTH RTQPPTWGQIEKLPQMAEENLR KAGQPVTISNWILPRITKFKPIE GAENVFTDGSSNGKASYSGSK GPLTEGNQMADRLVAKVISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIIQRCPTCQVMLSAAE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPYHKPDA GEKIPGESR/ETPGCSHVKTDAE EDANCHEQHPSNTATHLGTDQ EAVTDGGRKPEESGTTSHNE*F NDSGDHHCLQQGL
8578	38946	A	8635	820	1344	PDGTTRDAGRGDLRSVSWETL RGCPAVRKDSIGWIRLSRTLKK NVHLCPLPRGQGLFVCPVTSSS PQHISSHRGFWNISKDAPMSWP GSYSCHNVVAPVGQGQ*SRRA RMLRGLLSKAGHHSFCTDQAID LEITKFTFTWTD*VTLGQ*FMLS ES*SSCKPNSCCPVQCLVHSGG
8579	38947	A	8636	3	760	

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8580	38948	A	8637	1	1354	MGISCPGSSKMLNSRALPVLKL TQGALRDCKERANYTNFNIYK AVESQGKFVCVLYNGQQSPEY VMIPCTSVSPTGQEVPEDRGMR MVMKNKPNKPSKMQSLKSSKH LTNSVIVIAVGIFFSVTLQARDP QLDDAIEQLRGVCIRAWEKITS GGEQYPSFSAIKQGPKEPYIDFI ARLQESLKKMIADSAAQDIVLQ LLAFDNANPDCQAALRPIRGKA HLVDCIKACDDIGDGSSNGKAS YFGSKSKVFQTSYTSAQKAELV AVIEVLTAFDMPINVISDSSYM VYSTQLIENAQLRFHTDEQLMT LFTQLQTAFRSTMHPFYITHIRA R\HTPLPGPLTEGNQMADCLVA TAVSNARHFHNLTHVNASGLK CRYSNTWKAAKAIIQRRPTCQ MVHSSSFTGGVNPQGLEPNSL WQMDVTHVPSFGRLAYVHVC VDTFSHFVWATCQSGES
8581	38949	A	8638	596	1820	
8582	38950	A	8639	275	1495	RLGSSLLEYT/LPDQQGNIIATFE PFPFKFGKAHSVDYIKACDGIG GPLTEGNQMADCLVANAISNA RHFHNLTHVNASGLKRRYSIT WKEAKAIIQQCPTCQMVHSSSF TGGVNPRGLEPNSLWQMDVTH VPSFGRLAYVHVCVDTFSHFV WATYQSGESSACVS\KHPLLQC FVVVGIPAFIKTDNAPGYTSQA LATFFSVWNIKHITGIPYNSQGQ AIVERMNLSLKQQLQKQKGGN RDYR/TTP*MQLNLALLTLNFLS LPKGQMFSAAEQHLQKPAAKT KTEQLIWWRDLITKSWEIGKIIT WGRGYAYISPGQNQQPIWIPSR HLKPYHEPDA\RKRLQEDPEDP PSCSHVKTDAEEDPNCHEQHPS NTAIHLRSDQEAVTDGRRKPEE WSGTRTWWRPWSCRT
8583	38951	A	8640	232	789	ERPWGPEGNSEGSFCPKGLE\PR TCLRGPAASAAAGAEGRQDPP GGPWCSPAAGDLGSPGVQSPG GGSPRGAQVAMSGSRRRRAEP GVWGALQ*HRR*ARRMHSFPP SL/PLL*NG*SPLFLVSKCLTGSP LRSASPCPPAARSC*KHPDSSPG RGPGARQSPALHPALPSLARRA APGRSFPLTSRK
8584	38952	A	8641	1	149	

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8585	38953	A	8642	1	2541	
8586	38954	A	8643	1	989	MQRGQQATGSSANAWGILQPK WVQTGPDNKRMARNVLKYER LLAESPNHVVAEAVIQRPNIPHL QTRDTYEGLCQTLGSQPTLYQI PSLYCSYETNSNAYLLLQPIRKE VIHLEPYIALYHDFVSDSEAQKI RELAEPWLQRSVVASGEKQLQ VEYRISKSAWLKDTVDPKLVTL NHRIAALTGLDVRPPYAEYLQV VNYGIGGHYEPHFDHATSPSSP LYRMKSGNRVATFMIYLSSVE AGGATAFIYANLSVPVVRVVQ/ WPGTS*AFDNQCQNAALFWW NLHRSGEGDSDTLHAGCPVLV GDKWVANKWIHEYGQEFRRPC
8587	38955	A	8644	2	505	AWLKDTVDPKLVTLNHRIAAL TGLDVRPPYAEYLQVVNYGIG GHYEPHFDHATSPSSPLYRMKS GNRVATFMIYLSSVEAGGATAF IYANLSVPVVRVVQ/WPGTS*A FDNQCQNAALFWWNLHRSGE GDSDTLHAGCPVLVGDKWVA NKWIHEYGQEFRRPCSSSPED
8588	38956	A	8645	298	401	KKSLLVRRSWRMKELKKKIGQ Y*RKLGRLKGKAI
8589	38957	A	8646	1	417	FRAAPAPESGGESVFGETHRAL QGAMEKLQR/RLWKEKVDLKE RVEKLELQFIHLSGQTDTIGRK YISQGAVSETQHWE/KEDIVRL AQDQEEMKVNLQELR/EQVLQ LVGDHKEGHGK/FLTIAQNPAD EPTLGAPIAQELGC
8590	38958	A	8647	2	430	AAVKPLGSAETAVPIARLGCRR FSRSRCCRRRGRGSLLSFSAAK VAFFNSAGANAQEEQRVCCQP LAHPVASSQKKPEVAAPAPESG GESVFGETHRALQGAMEKLQR/ RLWKEKVDLKERVEKLELQFIH LSGQTDTHNKISY
8591	38959	A	8648	1	2769	
8592	38960	A	8649	1	314	FVNLFEIPVRVVEFGATCRAVA EPEQQR*SPSARPRPPCPLLASV AAALAAAAAAAAGGEAAYCL SPRRR*GAVSARPAGEPREPHE WDNRRSDFKRRRRGRDG
8593	38961	B	8650	46	307	
8594	38962	C	8651	1	4584	
8595	38963	B	8652	438	532	
8596	38964	B	8653	832	927	

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8597	38965	A	8654	320	1136	RIMETIANLSSQSPVSLPLRVGL AEYLEMEED/DLDSEQEAPRPM PNIPGDLESREP\QVAFFNSAGA SAQEEQRVCCQPLAHPVASSQK KPEVAAPAPESGGESVFGETHR ALQGAMEKLQVTTLWKEKVD LKERVEKLELQFIHLSGQTDTIV SERLGHRWGELPGHPRGPSI*A MSSCRKVHQPGGSVRDAALGE EDIVRLAQDQEEMKVNLQELR/ EQVLQLVGDHKEGHGK/FLTIA QNPADEPTLGAPVAQELGCAD EQGGFYPRSPLDC
8598	38966	B	8655	97	235	
8599	38967	A	8656	1	2104	
8600	38968	A	8657	3	1107	FMTTDERKLFNHLKSPHLKYW VPFIWFGNLATKARNEGRIRDS VDLQSLMTEMNRYRSWCSLLF GYDWVGIPLVYTQVVTLAVYT FFFACLIGRQFLDPTKGYAGHD LDLYIPIFTLLQFFFYAGWLKVA EQLINPFGEDDDDFETNWCIDR NLQVSLLAVDEMHMSLPKMK KDIYWDDSAARPPYTLAAADY CIPSFLGSTVQMGLSGSDFPDEE WLWDYEKHGHRHSMIRRVKRF LSAHEHPSSPRRRSYRRQTSDSS MFLPRDDLS/HSQGPTGCALKK PPQGLTHLE/DNPASQKEAPRCT SAWESCPPSGRPARQALYRA*P HSPV*ELPPSKCH\GT*GIDHSSR STSAHIRGLPP*FRYLHLEL
8601	38969	A	8658	3	397	
8602	38970	A	8659	346	474	

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8603	38971	A	8660	1	1344	MHSTWLCFPARLLKELPFPQGL FPRLTIRSASRTPPAALERVTRD PCAATCLDRGSLKGILGHSPFQ SPPVTSHCAENPNTLKAPPPYV GATSALVLSLGGPVTPWLSVEL SIRTFASSGLIYYMAHQNQADY AVLQLHGGRLHFMFDLGKGRT KVSHPALLSDGKWHTVKTDYV KRKGFITVDGRESPMVTVVGD GTMLDVEGLFYLGGLPSQYQA RKIGNITHSIPACIGDVTVNSKQ LDKDSPVSAFTVNRCYAVAQE GTYFDGSGYAALVKEGYKVQS DVNITLE\FRTSSQNGVLLGIST AKVDAIGLELVDGKVLFHVNN GAGRITAAYEPKTATVLCDGK WHTLQANKSKHRITLIVDGNA GWR*KSHTPQSTPVDTN\NPIYV GG\YPAGVKQKCLRSQTSFRGC LRKLALF\RGPQVQSFDFSRAFE LHGVFLHSCPGTES
8604	38972	A	8661	3	92	
8605	38973	A	8662	2	158	HTFPTFSSSPHLVMMIQPSSSSP PPPLPPPPPSS\PPLPLPPSPPPLLL FFL
8606	38974	A	8663	21	471	DGPQDQPPHQPSSSSPPPPLPPPP PFPPPLPLPPSPPPLLLFFCSDEA LLCCHTGVELFFVIFAYCSG/PE TEPAISPRYASSSGLNGFPLPRT PPAYA*IPSSGIHFNPSLAIKPST TTTLVRTPTTHHHSRRPTITTQS STTAPSRLHP
8607	38975	A	8664	2	105	
8608	38976	A	8665	3	265	RKDLYANT\ALSGGTTMYPGIA DRMQKEITALAPSTMKIKIIAPP ERKYSVWIGGSILASLSTFQQM WISKQEY\DESGPSIVHRKCF
8609	38977	A	8666	3	757	NTP\AMYMAIQAVLSLYTSGRT TGIAMDSGDGVAHTVPIYEGYT LPHAILHLDLAGWDLTDYFMKI LMECSYRFTTMAEQEIVCDIKE KLCNIALDFEHKMATGASSSSL EKSYEVPDGQVITIGNEWF/*VP EALFQPS/MGMESCGIQETTFNS IMKCDVDICKELYAKMVLSSGT TMYLGIADRMQKEITALGRPST LRFRFIAPP/ERRKYSV\WIGG\SI LASLSTFQQ\MWI\SKQE\YDES GPLHPSTANCF

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8610	38978	A	8667	3	171	CPLCRGNHWKVHCPSGR/MVP* VRSPQPDDPTTGQRVPGASASS CHHPH*APGTFNH
8611	38979	A	8668	1	325	SPSRTCYQCGLQGHF*KDC/TSE KPPPRPCLLCQGNHWKVHCPR/ VTKVLWVRSPQPDDPATGLRV PDD*EHTIRRAYALGKSAVTSK PPPPYPARSRLNVRRLCSLATN
8612	38980	A	8669	3	377	
8613	38981	A	8670	1	423	
8614	38982	A	8671	1	1659	
8615	38983	A	8672	1	1449	MVNDTDRPKVQVEYKGETKIF YPEEVSSMVLTKMKEIAEAYLG KTVTNAVVTVPAYFNNSQHQA TKDAGTIAGLNVLRIINEPSAAD IAYGLDKKVGAERNVFIFDLRG GTFDVSILIIQDGIFEVKSGDTHL GEEDFDNRIVSHFIAEFKHKYK KDITIRDVKLDKSQIHDIVSIGG YTHIPKIQKLLQDIFNRKELNKS INLDEAVAYGAAVQAAILSGD KSENVQDLLLLDVNPLSFGIEL AGGVMTV/LPVLIKHSTTIPTKQ TETF*QPIYSDNQPG\YEGECAM TKDDNLLDKFELTGIPSAPHGV PQIEVTFDIDANGILNVSAVDKS VGKENTITTTNDKHRLSKEDM NIWSAEKYKAEDKRQRDKVSS KNSLESYAFHMKATVKDEKLQ GKINGEDKQKILDKFNEVIKWL DKNQAAKKEEFEHQQTELEKV CNLIISKRYQSAGGMPGGMPGG FPGGGAPPSSGASSRPITEEVD

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8616	38984	A	8673	18	1388	TRLQLLGFLWLPSLLEPGLHPS NHGPRGPAVGIDLGTTYSCVGV FQHGKV\EIIAN\DQGNRTTPSY VAFTDT\ERLIGDAAKNQVAMN PTNTSF*LPNGLIGR\RFD\DAVV \QSDMKHW\PFMVVNDAGRPK APS*NTKGETKSL\YPEEGVFLW V*PKMK\EICRSLTLGKTVTNA\ VVTVPS\YFNDS\QRQATKDAG TIAGLNVLRI\INE\PTAAAIA\YG LDKKGLEQKRNRAHLLTWGG GTF\DVSILTIED\GIFE\VKSTAG DTHLG/GEEDFDNRMVNHFIAE FKRKHKKDISENKRAVRRLRTA CERAKRTLSSSTQASIEIDSLYE GIDFYTSITRARFEELNADLFRG TLDPVEKALRDAKLDKSQIHDI VLVGGSTRIPKIQKLLQDFFNG KELNKSINPDEAVAYGAAVQA AILSGDKSENVQDLLLLDVTPL SLGIETAGGVMTVLIKRNTTI
8617	38985	A	8674	2	1559	RYLNWIGTPTKGMSLKAFVQQ PHKSYWLKTLLPDNMEALQIR K*VPNILGTCAVSWLKGPCSDV AVKKFFIFSLGNYWEGN*LI*EH GYKVW*HSNSYLEPISPAQTPK KRTTSYFSTLLCLRLRSCLSFLK RIECYEVNYQPLDEELDR*EPAP QSQGLDLSPSFDIL*DHIQSRTV YYLMNIHVTPRSIYLCRHGESE LNIRGRIGGDSGLSVRGKQVG WATHTQMGWLGCPRWAAGFP ILPSRPYPNAGVTLAAPVPTHDS VLPALPTRAGGQDETEPGLKAG PTGLPSAPPLEMGGGAPGKALS WMATPWCLPFCYVEVALTCAA PTVYQAVVWVLPIHYLKCSPQT AGQMRQCSLDMRPERGRDVSE GTRDHVRELREFNLWLIPPCQG LLPTSHMKRTIQTAEALGVPYE QWKALNEIDAVRCMG*ISCVW G*LESGIIPLRDQDKYRYRYPK GEVRFAGWPNA*DYSPVSSLQL NV\LLICHQASMRCLLAYFLIKS SGTTLISALGMFDGI
8618	38986	C	8675	16	206	
8619	38987	A	8676	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL
8620	38988	B	8677	877	2126	

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8621	38989	A	8678	1	1731	
8622	38990	A	8679	2	1675	
8623	38991	A	8680	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
8624	38992	A	8681	1	1242	

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8625	38993	A	8682	14	1785	FDQVEERVSVIEDQMNEMKRE EKFREKRVIRNEQSLQEIWDYV KRLNLHLIGVPESDWENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSSRRTTPRHIILNA HKRK*ERYKIDTLTSQLKELEK QEQTYSKASRRREITKIRAELKE IETQKTLQKINESRSCFEKINKID RLLARLIKKKREKNQTDVIKND KGDITTDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGSEIEAIINSL PTKKSTGPDRFTAEFYQRYKEE LVPFLLKLFQSIEKEGILLNSFYE ASTILIPKAGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHYNQVSFIPGIQGWFNICKSIN VIQHINRTKDKNHTIISIDAEKA FDKIQQPFMLKTLNKLGIDGTY LKIMTAIYDKPTASTILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRIKYVGIQLTRDVKDLFKEN
8626	38994	A	8683	1	5127	
8627	38995	B	8684	1	1461	
8628	38996	A	8685	2	1879	
8629	38997	A	8686	1	1299	MKLPEEGSGSIICCSAIFAVLQL PLVIHRQTGYGEDLQQTPTDLQ LRDLTDHSSSPAMEQSWMEND FDELNRSRLQKANKLENLEETD KFLDTYTLPRLNQEETESLNRPI TGSEIEAIINNVPTKKSPGPDGV TAKFYQRYKEELRTVNKNHMII SIDAEKAFDNIQQPFMLKTLNK LGIDATYLKIIRAIDDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLINNFSKVSGYKI NVQKSQEFLYNNNRQTENQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYNPLLNEIKKDTNK WKNIPCSWIGRINIMKMAILLK VIYRFNAIPIKLLMIFFTELEK\T TLKCI*NQKRAHIAKPILSQKNK
8630	38998	B	8687	1	2187	

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8631	38999	A	8688	1	1698	MMGDFNTPLSTLDRSMRQKVN KDIQELNSALHHMDLIDIYRTL HPKSTEYTFFSAPQRTYSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRIKKLTQNHSITWKLN NWLLNDYWVHNEMKAEIKMF FETNEIKDTTYQNLWDTFKATL NQEEVESLNRPITGSEIQAMINS LGTKK/SPGPDGFTAKFY/P\E*H DCISRKPHRLSPKSP*ADKQLQ QSLRIQNQCSKITSILIHQ*QTNR EPNHE*TPIHNCIKDNKIPRSPTY KGCEGPLQGELQTTAQRNKRG HKQMEEHPMLMDRKNQYHEN GHTAQGNL*IQCHPHQATNDFL HRIGKKYSKVHMEPKKSLHCQ VNPKPKEQSWRHHTT*LQTILQ GYSNQNSMVLVPKQRYRPMEH NRALRNNATYLPLSDL*ET*QK QEMGKGFPI*QMVLGKLASHM *KAETGSLPYTLYKN*FKMD*R LKC*T*NHKHPRRKPRQYHSGH RHGQGLHV*NTKSNGNKSQN* QMGSH*TKELLHSKRNYHQSE QATYRMGENFCNLLI*QRANIQ NLQRTQTNLQ/RKKQPHQQVG
8632	39000	A	8689	1	5073	
8633	39001	A	8690	128	1407	EKKASDDQTTPSYRRKFKPKA KKLNTLKKI*TN/RITRITNREKC LKELMELKAKARELREECRSLR SQCDQLEERVSVMEEIQTTIRE YYKHLYENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPITGSE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELIPFLLKLFQSIEKEGI LPNSFYEASIILIPKQGRDTTKK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSRNVIHHINRTKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDETYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLFELISNFSKVSGY KINVQISQAFLYTNYRQSAKS
8634	39002	B	8691	1	1443	
8635	39003	A	8692	1	1878	
8636	39004	A	8693	1	1479	

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8637	39005	A	8694	1	2091	MVFLEKISVGISRLSKQHPPFIR VALPLDADPTVSRIGSFQWVLG LADFRNEAVDPRDVQMCPEFIP SGGFVVFLTSGVKPQTFTVSITA LKGEPTQMRRNQKTNSGNMTK LGYLTPQKNHTSSPAMSPNQEQ IPDSPEKEFRRTEEASLTEGGTI NPIISWAVGNGSSKNLYHILGK GRKIFSSSGIKQKSIASGERQNF QRNDQTAAFAVHENPLFCSHR CWYPGKQEKCLKELMELKAK ARELREECRSLRSRCDQLEERV SVMEDEMNEMKREGKFREKRI KRNEQSLQEIWDYVKRPTLHLI DVPETLNAHKRKQERSKTDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETEKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAIKNDKGDITSDPTEIQT TIREYYKHLYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGST AEFYQRYKEELLISNFSKVSGY KINVQKSQAFLYTNNRQMESQI MSELPFTITSKRIKYLGIQLTRDI KDLFKENYKPLLNEIKEDRNKC KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLRMTFFTELEKTTL KFIWNQKRARITKSVLSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDI\DQWNRTEPSEITP
8638	39006	A	8695	1	3514	MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFFSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRIKNLTKSRSTTW KLNNLLLNDYW
8639	39007	A	8696	1	2091	

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8640	39008	A	8697	1	2781	MGKKQNRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMNEMN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRDLD
8641	39009	A	8698	1	1584	MSISGTVRMSAKSKGNPSSSCP AEGPPAASKTKVKEQIKIIVEDL ELVLGDLKDVAKELKEQHWW HPISGDTATSICTVLESEKSKIK VTAFDVWLHLWGKGTDKQKD SSNFCRLKCPCLTALKRAVVLP ARSWRCENGQTASSSGSLTPDP RAANREAPPSRGRLTPHTASDG ENGTKLENTLQDIIQENFPNLAR QANIQIQEIQRTPQRYSSRKATP RHIIVRLTKVEMKEKMLRAARE KEIQTAIREYYKHLYANKLENL EEMDKFLDAYTLPRQNQEEVE SLNRPITGPEIVAIINSLPTKKSP GPDGFTAEFYQRYKEERHINRT KDENHMIISIDAEKAFNKIQQPF MLKTLNKLGIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QECPLSPLLFNIVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFVDY MIVHLENPIISAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRIKYLGIQ LTRDVKD\LFEEND

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8642	39010	A	8699	1	1722	MAGYPSEMKLPEELSGSNICCS AVFTVLQPLLLIPRQTGSGVDL RQTPTDLQLRVLTVRRKNNKQ KRTSTPKPHLYVTIIKDQRSKKL TQNHSTTWKLNNLLLNDYWV NNEMKAEIKMFFETSENKGTIY QNLWDTFKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKASRRQEITKIRAEQKEI ETQKTLQKINESRSCFFEKINKI DRLLARRIKKKREKNQIDAIKN DKGDITADPTEIQSTIREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEDESLNRPITGSEIEAIINS LPAKKSPGPDRFTAEFYQRYKE ELHINRTKDKNHMTISVDAENA FDKIQQPFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKQEVKLSL FADDVIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYS NNRQTESQIMNELSFTIASKRIK YLGIQLTRDVKDLFKENYKPLL NEIKDDTNKWKNIPCSWVGRIN IVKMGILPKVVYRFNAIPIKLPM TFFTELEK\TTLKFIWNQKRARI AMTILS*KNKAGGITLP
8643	39011	A	8700	3	1033	
8644	39012	A	8701	1	1068	ANKLENLEETDKFLDTYTLPRL NQEETESLNRPITGSEIEAIINNV PTKKSPGPDGVTAKFYQRYKEE LRTVNKNHMIISIDAEKAFDNIQ QPFMLKTLNKLGIDATYLKIIRA IDDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI NNFSKVSGYKINVQKSQEFLYN NNRQTENQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYNPLL NEIKKDTNKWKNIPCSWIGRINI MKMAILLKVIYRFNAIPIKLLMI FFTELEK\TTLKCI*NQKRAHIA KPILSQKNKAGSITLR
8645	39013	B	8702	69	1055	
8646	39014	B	8703	1	2301	
8647	39015	A	8704	1	3189	

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8648	39016	A	8705	92	1139	ASAADTQANRVWSGPPANSNR PAA\RVLTVRRKTNKQKGHPH QNPICTSPSSKTKEIQTTIREYYQ HLYTNKLENLEEMDKFFDTYT LPRLNQEEVESLNRPITGSEIEAI INNLPT/KKSPGPDGFTAKFYQS VGSSGQGNQAGEGNKGHSIRK RGSQIVPVCR*HDCISRKPHRLS PKSP*ADSQLQQSLRIQNQCAKI TSILIHQ*QTNREPNHE*TPIHNG FKQNKIPRNPAYKGCERPLQGE L*TTAQ*NKRGYKQMEEHSML MGRKNQYHENGHTAQGNL*IQ CHPHQATKNFLHRIGKNYFKV HMEPKKGPHCQVNPKPKEQSW RHHTT*LQTILQGYSNQNSI
8649	39017	A	8706	1	2199	
8650	39018	A	8707	1	2238	
8651	39019	A	8708	3	1889	RSMRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTYTKIDHILGSKALLRKCKRT EIITNYLSDHSAIKLELRIKNLTQ NRSTTWKLNNLLLNDYWVHN KMKAEIKMFFETNENKDTTYQ NLWDAFKA/EIQTTIKEYYKHL YANKLENLEEMDKFLDT\YTLP RLNQEEVESLNRPITGAEIVAIIN SLPTKKSPGPDGFTAEFYQRYK EELVPFLLKLFQSIEKQGILPNSF YEASTILIPKPGRDTTEKENFRPI SLMNIDAKILNKILAKRIQQHIK KLIHHDQVGFIPGMQGWFNIHK SINVIQHINRAKDKNHMIISIDA EKAFDKIQQRFMLKTLNKLGID GTYFKIIRAIYDKPTANIILNGQ KLEAIPLKAGTRQGCPLSPLLFN IVLEVLARVIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVT AQNLLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSELP FTIASKRIKYLGIQLTRDVKDLF KENYKPLLKEIKEDTNKWKNIP CSWVGRINIMKMAILPKVIYRF NAIPIKLPMTFFTELEKTK\FIWN QKSAHITKGILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN

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8652	39020	A	8709	1	1779	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSNIDHIV GSKALFSKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVNNEMKAEIKMFF ETNENKDTTDQNLWDTFKAVC RGKFMALNAHKRKQERSKMG TLTSQLKELEKQEQTHSKASRR QEITKIRAELKEIET/QKTLQKIN ESR\TEIQTTIREYHKHLYANKL ENLEEMDKFLDTYILPRLNQEE VESLNRPVTGSEIEAIINSLPTKK SPGPYGFTAEFYQRYKEELHIN RTKDKNHMIISIDAEKAFDKIQ QPFMLKTLNKLGIDGTYLKILR AIYDKPTANIILNGQKLEAFHLK TGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKWSL FADDMIVYLENPIVSTQNLFKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL NEIKEDTNKWKNIPCSRAGRINI VKMAILPKVIYRFSAIPIKLPMT FFTELEKTK\FIWNQKRAHIAKS ILSQKHKAGGITLP

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8653	39021	A	8710	1	2093	MEITTNCLSEHSAITLQLRIKKL TQNCTTTWKLNYLLLNDYWV NNEMKEEIKMFFETNENKDTT YQNLWDVFKAVCRGKFIALSA HKRKQERSKTDTLTSQLKELEK QEQTHSKASRRQEITKIRAELKE IETQKTLQEINDSRSSFSEKLNKI DRPLARLIKKKREKTQIDAIKN DKGEINTNPTEIQTTIREYYKYL YANKVENLEEMDTFLDTYTLP RLNQEEVESLNRPITGSEIEAIIN SLPTKESPGPDGFTAEFY/HEGN QERERNKGYSIRKRGSHIVPVC R*HDCLFRKPHHLSSKSHEAVK QLQQSLRIQNQWAKITSMPVH Q*QTNREPNHE*TPIHNCYKEN KIPRNPTYEGCEGPLQGELQTT AQQNKRGQKEMEKHSMLMDR KNHYHENGHTAHGNL*IQCHP HQATNDFLHRIGKNYVNFHME PKKSLHCQENPKQREQSWRHH AT*LQTILQGYSNQNSMVLVPK QIHRTMEQNRGLRNNTTHLQPS DL*QI*QKQEMGKQFPI**MVL GKLASYM*KAETGSLPYTLYK N*FKMD*RLKC*T*NHKNPRRK PRQYHSGHRHGQGLHD*NTRS NGNKNQNRQMGSN*TKELLHG KRNYHQSAQTTYRMGENFCNL PI*QRANIQNLQRT*TNLQEKNK QPHQKVGKGHEQTLLKRRHLC SQQTHEKMLIITGHQRNANQN

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8654	39022	A	8711	3	1805	PLSTLDRSSRQKVNKDIQDVISA LHEAGLIDIYRTLHPKSTEYTFF SAPHHTYYKIDHIVGSKALLSK CKRTEITTNCLSDDRAIKLELRI KKLTQNYTTTWKLNNLLLSDY WVNNEMKAEIKMFFETNENKD TMYQNLWDTFKAVCRGKFIAV NAYKRKQERSKIHTLTSQLKEP EKQEQTHSKASRRQEITKIRAEL KEIDTQKTLQKISVSRSWFSERI NKIDRLIARLMKKKREKNQIDA IKNDKGDITIDPTEMQTTIREYY KNLYANKLENLEEMDKFLDTY ILPRLNQEEVELPNRPITGSENE AIINSLP/TKKSPGPDEFTAKFYQ RYKEELQG\IRQEKEREDTQLG KEEVKLLLFAEDMIVYLENPIV SAQNLLKLINNFSKVSGYKINV QKSQAFLHTNNRQTESQIMSEC PLTIASKRIKYLGIQLTRDVKDL FKENYKPLLNKIKEDT\NKWKN IPRSWLGRNNIVKMTILPKVIYR F/NTLNFIWNQERARIAKTILSK KNKAGGITLPDFKLYYKATVT KTARYWKQNIKKGSVWPISLK SEKRGHRTRPLWKLCHNDVQG ELLKTIQFLFGSPLGHSSLDPSA
8655	39023	B	8712	1	1743	
8656	39024	B	8713	1	1260	

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8657	39025	A	8714	1	1842	VPPTTCGNYGSTIQDEIWMGTQ NQTISVSEEMMFQAEEIASAQK MWNQHHITPSKVDHIVGSKAL FSKCKRTEIITNYLSDHSAIKLK LRIKKLTQNRSTTWKLNNLLLN DYWVHNEMKAEIKIFFETNEN KDTTCQNLWDTFKAMCRGKFI TLNAHKRKQQRCKIDTLTSQLK ELEKQEQTHSKASRRQEITKIRA ELKEIEAQKTLQKINESRSWIFE KINKTDRLLARIIKKKREMNQI DAIKNDKGDITTNPTEIQTTIRE YCKHLYANKLENLEEMDKFLN TYTLPRLNQEEIESLNRPITGSEI EAIINSLPTKKSPGPDGFTAEFY QRYKEEMIEKKAFDKSQQPFM LKTLNKLGIDGTFLKIRRAIYDK PTANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLAREIRQG KEIKHIQLGKEEVKFSLFADDVI AYLENPIVSAQNLLKLISNFSKV SGYKINVQKLQAFLYTNNRQTE SQIMSEFPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWIGRINIMKMAIL HKVIDRFSAIPFKL/PKD/FFTEL EKTTLKFIWNQKRPRISKTILSK KNKAGGITLR

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8658	39026	A	8715	1	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKRIKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIIQENFPNLARINKI DRPLARLIKKKREKNQIDTIKN DKGDITTNPTEIQTTIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPITGAEIVAIINS LPTKKSPGPDGSIAEFYQRYKE E/PADKQLQQSLSIQNQCTKITSI LIHQQQTNREPNHE*TPIHNCFK ENKIPRNPTYKGCEGLLPGELQ TTAQGNKRGYKQTEEHSMLM GRKNQYRENGHTAQGNF*IQC HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKPKEQSWR HHTT*LQTILQGYSNQNSMVLV PKQGYRSMEQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
8659	39027	A	8716	1	1578	MGDFNTTLSTLERSARQKVNK DIQELNSGLHQADLIDIYKTVKP KSTEYTFFSGPHRTYSKIDHIVG SKALLSKRKRTEIITNCLSDHSA IKLELRIKKLTQNRSTTWKLNN LFLNDYWVHNKMKAEIKMFFE TNENKDTTYQTLWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKVSRRQEI TKIRAELKEIETQKTLQKINESKI QTTIREYYKHLYANKLENLEE MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLPTKKSPGPD GFTAEFYQRYKEE\RPISLMNID/ AKILNKILANGIQHDIKKLIHDD QVGFIPGMQGWFNIRKSINVIQ HVNRTRDKNHMIISIDAEKAFD KIQQPFMLKTLNKLGIDGMYLK IIRAMYDKPTANIILNGQRLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIGQEKEIKGIQLGKEEVK LSLSADDMIVYLEKPIISAQNLF KLISNFSKVS/GYKINVQKSQAF LYTNNRQTESQIM
8660	39028	B	8717	1	2982	

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8663	39031	A	8720	1	1551	MEKFLDTYTLPRLNQEELESLN RPITGSEIEAIINSLPTKKSPGPD GFRAKFYQRYNEELVPFLLKIF QSIEKEGILPNSFYEASIILIPKPG RDTTKKDNFRPISLMNIAVKILN KILANQIQKHIKKFIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKSHMIISIDEEKAFDKIHLPF MLKTLSKLGIDGMYLKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQRCPLSPLLCNIVLEVLARAIR QEKEIKGIQLGKEEVKLSLFAD DMIVYLENPTVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKELFKENYKPLLNK IKEDTNKWKNIPSSWMGR\NIM KMAILPK/VTWMKLEIIVLSKLP QEQKTKHRMFSLTGVFIEGRAL QNKSETSQSRHPGATHSLPEYTI PGSSPSNFYWFTLGLKEEVTSG WKREKKKRKREGGKEGRKEG RKEGRKEGKKEGRKKGRKEVP
8664	39032	A	8721	1	1983	
8665	39033	A	8722	1	2436	
8666	39034	A	8723	1	3139	
8667	39035	B	8724	1	3558	
8668	39036	B	8725	1	2133	
8669	39037	A	8726	1	3051	MGDFNTALSTLDRSMRQKVNK DIQELNSALHQADLTDIYGTLH PKSTECTFFSAPHHTYSKIVHIV GSKALLSKWKRREIITNCLSDH SAIKLELRIKKLNQNCSTTWKL NNLLLNNYWTNK\KKREKNQI DA/IKNDKGDITTNPTEIQTTIRE YYKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGSE IEAIINSLPTKKSPGPDGFTAEFY QRMNYISFKSTWKIIKNAYSLA HSRELRDGGQ
8670	39038	A	8727	1	2706	
8671	39039	A	8728	1	2573	
8672	39040	B	8729	70	2029	
8673	39041	A	8730	81	385	
8674	39042	A	8731	301	515	SSWQAPAPVLGSSWASKK*MK KKYAAQQIEKQKSP*CKSIKCSP LRSASYAQLLSFSLSSCLCFSTC HSTLAWYCL*SSWQAPAPVLG SSWASKKRSLLWKEPSRSLPSF SITARS*ACCCLCSSTEPQLLKA QYLLSHSRTRSFRLQ

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8661	39029	A	8718	617	1155	SIAYQPKSPGPDGFTAEFYQRH KEELLISNFSK/VSGYKIDVQKS QAFLYTNNRQTESQILSEFPFTI ASKRVGYLGIQLTRDVKDLFKE NCKPLLNEIKKDTKKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEK\TTLRFIWN QKRDHIAKSILSQKNKAGSITLP
8662	39030	A	8719	1	1827	MGKKQSRKTGNFKKQRHLSFS KGIAVLHQQWNKAGQRLTFDE LREGFRPSNYSKLQKEIQTKGK EVENFEKNSDECITRITNTKKCL KELMELKAKARELREECRSLRS RCDQLEERVSGMEDEANEMKR EGKFGEKRIKRNEQSLQEIWDY VKRPNLRLIGVPESDGENGTKL KNTLQDIIQENFPNLARQANIQI QEIQRTPQRYSSRRATPRHIIVR FTKVEGKNIKGSQRERAEIQTTI REYYKHLYSNKLENLEEMDKF LDTYTLPSLNQEEVESLNRTITG SEIVAIINSLPTKKSPGPDGFTAE FYQRYKEEVVPFLLKLFQSIEKE VILPNSFYEARIILIPKPGRDTTK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIHHDQVGFIPGMAI RQEKERKGIQLGKEEVKLSLFA DDVIVYLENPIVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQRESQIMSELPFTIASKRIKWL GIQLTRDVKDLIKENYKPLLNEI KEDINKWKNIPCSWVGRISIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTFK\FLW\NQKRAR\IAKS ILSQKNK/AGGITLPDFKLYYKA

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8675	39043	A	8732	2	4207	DTHRLKIKGWRKIYQANGKQK KAGVAILVSDKTEFKPTKIKRD KEGHYIMVKGSIQQEELTILNIY APNTGAPRFTKQVLRDLQRDL DSNTIITGDFNTPLSTLDRSMRQ KVNKDIQELNSALHQADLIDIY RTLHPKSTENTFFSAPHHTYSKI DHIVGSKALLSKCKRKEIITNCL SDHSAIKLELRIKKLPQNCSTIW KLNNLLLNDYWVHNEMKAEIK MLFETNENKDTTYQNLWDTLK AVCRGKFIALNA
8676	39044	A	8733	1	2770	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VQNFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKL

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8677	39045	A	8734	3	2169	FKPTKIKREKEGHYIMVKGSIQ QEELTILKIYAPNTGAPRFTKQV LSDLQRDLDSHTLIMGDFNTPL STLDTSTRQKVKKDTQELNSAL HQADLIDIYRALHPKSTEYTFFS APHHTYSKIDHIVGSKALLSKC KRTEIITNYLSDHSAIKLELRIKN LTQNHSTTWKLNNLLLNDYWV HNEVKAEIKVFFETKENKDTTY QNLWDAFKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKASRRQEITNIRAELKEI ETQKTLQKINESR\TEIQTTIREY YKHLYANKLENLEEMDKFLDT YTLPRLNQEEVESLNRPITGSEI VAIINSLPTKKIPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIPHDQVGFIPGMQGW FNIRKSINVIQHINRAKDKNHMI ISIDAEKAFDKIQQPFMLKTLNK LGIDGTYFKIIRAIYDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIIYLEN PIVSAQNLLKLISNFSKVSGYKI NVQK\SQAFLYTNNRQTENQIM SELPFPIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIK\EDTNK WKNIPCSWVGRINIVKMAILPK LIGNCSKISGYKINVQKSQAFLY
8678	39046	A	8735	1	5166	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL

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8679	39047	A	8736	1	4553	MGRKNRKLDSRQHSYTSPQSRS HEDPAAVLQALSSSGVVIYQSL VAVQSPLAAPGCDGSRCEVRG LTVGSRYGSWRLAGCRDNEMV NACQSGWCYQNLTVLRGWKV LLEMTPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAMKR ELRIKNLTQNRSTTWKLNNLLL NDYWVHNEMKAEIKMFFETNE NKDTTYQNLWDIFKAVCRGKFI ALNAHKRKQERSKTDTLTSQL KELEKQEQTHSKASRRQEI
8680	39048	A	8737	1	2673	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTPWKLN NLLLNDYWVHNEMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDTIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEFY/PESYL*QTHSQYHTEW AKTGSIPFENWHKTGMPSLTAP IQHSVGSSGQGNQAGEGNKGY SIRKRGSQIVPVCR*HDCLSRKP HRLSPKSP*ADKQLQQSLRIQN QCTKITSILIHQKQTNREPTHE* TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQRNKRGHKQME EHSMLMGRKNQYRENGHT\SQ GNLQIQCHPHQATNDFLHRIGK NYFKVHMEPKKSPHRQVNPKP KEQSWRHHTT*LQTILQGYSNQ NS\MVLVPKQRYRSMEQNRAL RNNAAYLHYSD\L*QT*EKQA WGKGIP\IYKM\AL\GKLAS\PM*
8681	39049	B	8738	1	2792	
8682	39050	B	8739	156	391	
8683	39051	B	8740	1	2824	

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8684	39052	A	8741	3	4167	PLSTLDRSTRQKVNKDIQELNS ALHQVDLIDIYRTLHPKSTEYTF FSVPHHNYSKIDHIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTQNRSTTWKLNNPLLND YWVHKEMKAEIKMFFETNENK DTTYQNLWDAFKAVCRGKFIA LNAHKRKQERSKIDTLTSQLKE LEKQEQTHSKATRRQEITKTRA ELKKIETQKTLQKINESRSWFFE KTNKIDRLLATLIKKKREKNQI GARKNDEGAITTN
8685	39053	A	8742	1	1107	MKVEIKTFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQIQTTIGEYYKHLYT NKLENLEEMDKFLDTYTLPRLN QEEGESLKRPMAGSEIEAIINSL PTKNSPGPDRFTAEFYQRYKEE L/PDKQLQQSLRIQNQWEKITSI PIHQ*QTNREPNHE*TPIHNCFK ENKIPRNPTYKGCEGPLQGELQ TTAQRNKRGHKQMEEHSMLM DRKNQYCENGHTAQEETAFCT HSRRESSRLGLLVANFRACHQE RFRRERSVPAGVHAEAHPCWE NRGREERHWEQHPGPETVLLQ AGGHVCDQGLHHGQPQVGQV PRGSRGHSGHFQLPSVQDRSWL
8686	39054	A	8743	1971	5654	RSPTAGRNTNYPSRDYYKHLY A\NKLEN\LEEMDKFLDTYTLPK T/ITQEEVESLNRPITG\SEIVAVI NSLPTKKSPGPDGFTAKFYQRY KEELHINRTKDKNHMIISIDAEK AFDKIQPQPF\MLKTL\NELGID GT/YFFKIIRAIYDKPT\ANIRLE WGQKLEAFPFEKLAQEQGMPL LLNPLPQSNIVVGKFLA\RAI\RQ EKEIKGIQVEKQEVKLSLFADD MIICLENPI\VSAQNL\LKLISNVS

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8687	39055	A	8744	1	4901	MTGSNSHITILTLNINGLNSAIK RHRRASWIKSQDPSVCCIQETH LTCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFFLAPH HTYSKIDHIVGSKALLSKCKRT EIITNYLSDHSAIKLELRIKNLTQ SRSTTWKLNNL
8688	39056	A	8745	2	1887	SASVVPASGLRPSSTSLLTSRQP RFLGLLRSHPALLVAVPGDWD DLAVCCIVAPSHVCRMVFVMD RTLGISLPGLLKREEDACWVEA NINGRVLAQCNIDELKKEMNM NFGDWHLFRSTVLEMRNAESH VVPEDPRFLSESSSGPAPHGEPA RRASHNELPHTELSSQTPYTLN FSFEELNTLGLDEGAPRHSNLS WQSQTRRTPSLSSLNSQDSSIEI SKLTDKVQAEYRDAYREYIAQ MSQLEGGPGSTTISGRSSPHSTY YMGQSSSGGSIHSNLEQEKGKD SEPKPDDGRKSFLMKRGDVIDY SSSGVSTNDASPLDPITEEDEKS DQSGSKLLPGKKSSERSS\LFQA SLK\LKGRGLRLSKLP\SEEDEC GAEESDNTP\LLK\DDKDRKPEG KVERVPKSPEHSVEPIRTFIKAK EYLS\DALLDNKGNSSDSWSVD PRES\SPNHVSAQCKCADDLPD LKRHNLIE\LEDDSHSGKRG\IPH SLSGLQDPIIARMSICSEDKKSPS RIASLD*PSSP\EENW\P\ACQKA YNL\NRTPSTVTLNNNSAPANR ANQNFDEMEGIRETSQVILRPSS SPNPTTIQNENLKSMTHKRSQR SSYTRLSKESPELHAA\SSSESTG

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8689	39057	A	8746	1	385	EGNEAQTCSFWNTRRQLLASS DPSLSVSQRMDPSWRRSSHSWP QPMPDSGRAPVRPHLAKLEED VWPCPQFHQTKAASGPPFVTFQ PANCFPSVISFHLHCHTWSEQD RAYHPVYQMR**GSDVQLLEY EASAAGLIRSFSERFPEDGPELE EILTQLATADARFWKGPSEAPS GQ/ALRK/SVWPCPQFHQTKAA SGPPFVTFQPANCFPSVISF\ICT AIRGVSKTGLTILSTR*GNGSSE KSLV
8690	39058	A	8747	2	2015	QDFLDSQNLSAYNTRLFKEVD GEGKPYYEVRLASVLGSEPSLD SEVTSKLKSYEFRGSPF\QVTRG DYAPILQKVVEQLEKAKAY\AA N\SHQGQML\AQYIESFTQGSIE AHKRGSRFWIQDKGPIVESYIG FIESYRDPFGSRGEFEGFVAVV NKAMSAKFERLVASAEQLLKE LPWPPTFEKDKFLTPDFTSLDV LTFAGSGIPAGINIPNYDDL\RQT EGFK\NVFAGGIVLGCGLTPRK REK\LTFLEEDDKDLYILWKGPS FDVQVGLH/ESLLGHGSGKLF\V QDEKGAFNF\DQETRDPPQKRG EQIQSWNRTGETW\DSKFSTIAS SYE\ECRAESVGLYLCLHPQVL EIFGFEGADAEDVIYVNWLNM VRAGLLALEFYTPEAFNWRQA HMQARFVILRVLLEAGEGLVTI TPTTGSDGRPDARVRLDRSKIR SVGKPALERFLRRLQVLKSTG\ DVTEGRALYEGY\STVTDAPPE\ CFLTLR\DTVLLRKESRKLSVQP NTHLEGNE/VSDVQLLEYEASR AGLIRSFSERFPEDGPELEEIFTQ \LATADARFWKGPQ*GPHSGPS LRKIVVALPPKFHQTKAA\SGPS HSVCVFRGWGGGGAGAWTLV L\PQLEGW*HNPLPICQHVSSLP NCFPSVIL/SFICTA\IRGVSKTGL TILSTKMR\NGSSEKSLV
8691	39059	A	8748	1	519	
8692	39060	A	8749	786	864	
8693	39061	A	8750	1	468	

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8694	39062	A	8751	128	605	MTWGTVPLFHIFQMRCCHWSC QGIMRGWGLCSQTLNCLLLSK C*TCSRGGGQIWSRKFRLVRVE *G*GNFKTPELQQPGVPPGLPP PGSCFKCRKSGHWAKECPQPGI PPKPCPICAGPHWKLDCPTRLA ATPRSPGTLAQGSLTDSFPDIRG LAVED
8695	39063	B	8752	1	615	
8696	39064	A	8753	1533	1767	PSPTCPAIYS*KGGWSQRHSQG ACYTCRKSGHWAKECPQPGIPP KPRPICVGPH*KSDCSTHLAAN PRAPGTLAQGSL
8697	39065	C	8754	84	329	
8698	39066	A	8755	911	1497	SQRKARDQRRKRNKRASSIAK HKEPKRPILPSGKNSQEGVATH TKPLAQGKVWLDP/NETNEIPN ANFRQQIRKLIKDGLILRHRKPV TVHSRAQGWKSTLARRKGRHL GIESKKIDRHMYHSLYLKLKGN VFKHKRILTEHSHKLKADKAR KKPLADQAEARGSKTKEARKL REEHLQTKKEEIIKTLSQEEKAK
8699	39067	A	8756	34	280	EVIHAAIGEKKGSY/NA**PWVE EQLTRQPLIHHQPASLHSVY/RC RYHSLYLKVKGNVFKNKRILM EHIHKLKADKARKKLLA
8700	39068	A	8757	1	692	AFLLQELCLKSSTGELFPFAAV AAALSMLRLQKRLASSVLCCG KKNIWLDPNETNEITNANSRQQ IRKLIKDGLIIRKP\VTVHSRLRC RKNT\LAR*KGRHMGIGKRKV PANA\RMP\EKVT\WMRENEGF CRRLASEDTRES\KKIDRPHVVT ALYL\EVKGNVFKNKRIL\MEHI HKLKA\DKARKKL\LAD\QAEA RRSKTKEATKRREERLP/ARPRK REII*TLSKEEETKK
8701	39069	A	8758	46	131	
8702	39070	A	8759	5	447	PATELPGLPTRPGMLCIWRGAP DWPEGPPSSGELSSIQPTQGLHN CFQPDGARPAAPGPVPGQLGAL PWSCRPPAEPTLFMESLVQWPP GDGIRQ*CEDAAELREPGVQRH QGSPG*VRTLPPLRGPSQVPA/G SSSSASPRSIPGSRG

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8703	39071	A	8760	1	201	MPNIYTMEYYAAVKKDEFMSF VGTWMKLETIILSKLSQGQKTK HRMFSLIGTRMKLETIILSKLLQ GQKNQTPYILTHRISFEDVRNY MPLAVIHSDESPILPLHEQQDAS ENGWIKDTERDADLEIYIVSGIG SFRWVLGLADFKSEAADPCGM KLQTFAVSVTALKGGASRVVH SSWWVCVLTDFRSEAAYLSVT ALEGGASRVAHSSRFVVSLTSG VKLQTFTVNATAHKGSADPKS EQHQDLLQRAKKHTFHSMKGE PRRVVAAGWGGAIKADSNNLI LLFQTIEKYCPWFPDKGSVDLL DWDRVGTTLCQLMRDGVLLPI SVWTDWALIRVALLPFQSGDTL QLPQVNADVEPLPLPRCIGGITG PEGGDPPGPSFHYLVGVYYFLT CRSTWEQRKSPVALR**KLGPG GSPPSGPVMPPMHRGKGSGSTS ALTCGS
8704	39072	C	8761	42	179	
8705	39073	A	8762	11	1713	PKTLKMGGGTAGLVGMGFSTT G\RTPSAPGRPHPCRGAP/GSPG KAGLFLQRPRLGTGL*GSAPRG PG*MGCP\GTGRGSNSRH*RGPP RRPQAS*AAPFQPGPLETWTPG *SQVPGAPSPCNFSYPHREVPP WGPVPPPAPHGSCGWALALPR RKRAAVFSSWAPGQAGQLLDA ASVGAAP*QDIPPCRGSSAPSPC SPHPPPGLESGPK\PGAASWAGP QTPFSGRAQQLCQEGPAGAGN TSGRSA*AASAGTCDGPRSGGR VRTYPGLP*CRWTPGSRSSAAS SHHCRMPSPGGHCTRLSMKRV GSAGGRQLQGRAPS*PARGT*Q RPRGGQSGLAAPLESRH*DGEC *AFWRAETVRSSVQRRREFATG LSGPSS*PRWSTCSVP/ASSPGG GDVAGPQEGPRSFHCLPSCL*V RPSHPEGDAA\P*GALHK*RMH EEGRPGPCGGWGLV/GSWEPV QGCRRNLARWGRAWNCLQFPE *PPGGPGLADSGFIIQTARLNFQ GWASVSFSIKRPGRAILRPCPTS EFLLPESFVSGNCSSTERAMWP FWAPPRSAPGAENFPCASVPCK

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8706	39074	A	8763	1	409	LTHLTAQNVPNLFARNERVICL FDTEFGPMAQILVGATIVGSIET VWAGTITPPREGIIKRWTWPAG ENDGSVALLKGQEMGRFKLGS TVINLFAPGKVNLVEQLESLSV TKIGQPLAVSM*SKATQLGNPR
8707	39075	A	8764	1	1528	MTFVNAQAEDSQIFLYKRRYVP VEGYAPWLVSGNASELERIHYE GMDDVILLDFLPKELGFDMNM HILSFAPGANHGYIEHTFKEHG GATQAFAKENNHKAYKDTYG VSHITRHDMLQIPKQQQYEKYQ DTHDTPYCEPLPGETRLWGDT DVIGLFDAETDMNDVVAILENH PLLGAGFAHKIEQLEDKDWERE WMDNFHPMRFGERLWICPSWR DVPDENAVNVMLDPGLAFGTG TIQTLSVPAMLDSSTHTRRMRS TLNLYEITRMSTVSTSEHSMTY TLVQVDMKEAQKPDTASYRTF NEFFVRPLRDEVRPIDTDPNVL VMPADGVISQLGKIEEDKILQA KGHNYSLEALLAGNYLMADLF RNGTFVTTYLSPRDYHRVHMP CNGILREMIYVPGDLFSVNHLT AQNVPNLFARNERVICLSDTEF GPMAQILVGATNGGSIETPESE GATVDESFVVGGPVGDFELLLC \QERSALSGRCVI*SFNSAKVRFI QQSRRPVKSA
8708	39076	A	8765	2	420	QNFKEIFVRPLRDE/VRPIDNDP NVLVMPADGVISQLGKIEEDKI VSNLFARDERVICLFDTEFWPN AQ/ILVGATIVCSIETVWAGT/IT PPREGIIKRW\TW\QAIEEDSWQ NLGRVAG*NKLPTELCNNFDW AQTLSSRNRG

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8709	39077	A	8766	1	1130	MHFAKKEDVSEIETGSDGEKPK ARAGCLIGNSERLFSVTFCVQF QATLPLSYTIMKHKDTGTSSVP ESIDASLEASQQNPAFLKTLTRS CSPSWPCSRNWPHLLIPLTCPA QAGATPQLPGLGPPGHLPMNQ PASSFPP\RPNAASQILTSTFHKP PPGSSLACCCCPGPCDWQEDSQ *PTPACPSWPPWPTQLSPSAAGS PI\IHSPIQGFHSQLLS*RSPGTEE P*EANKLPPWTGHREPEPHPGL PGHPCAAG/MHRPLAPTTA\RPL ATLHGERQRHLHPGQRRRVPR APAESTEAPALWLHRPPECPEC SGHGPAALEQGAGMA*CRSCR HLPCFPGEEADAGSREGPHQEV PRSKICQQPQAASFRICLHSIF
8710	39078	A	8768	179	1908	KKQNKSRGCNVNWAMRRALK MCIPYRNGHSIFLVMVKVERSK RFALKLSVAEKNQMPRNATVIE NSAGYSYGKMAFS*PRICTQIV GPRIISTTAVIS/SQPATHHRATR GAIIRTAFCGPCFGAGDTPINNG LSIRHTTRNFPNREGSKPANGQ MSAVALMDARSIAATAANGGY LTSASELDCWDNVPEYAFDVTP YKNRVYQGFVKGATQQPLIYG PNIKDWPELGALTDNIVLKVCS KILDEVTTTDELIPSGETSSYRS NPIGLAEFTLSRRDPGYVSRSK ATAELENQRLAGNVSELTEVFA RIKQIAGQEHIDPLHRVYRHCS RSGNCPSDVFDSKKDPVQDHRP QKRVTLIWGYDIHPQIEIIQTGD NFFQFRAIANNFGFLRFYQIRHF GLSGQHGVQIFTADVERGVGL RLQRFPVVKHAIVQRQVEVIAV AHIEVQADIFTRSFRAIEANGHK VEQHFDRHPANGVRGTGGAVA ELMHPFAQLFRAGQVETAPCG GLGLIAQLFKVIRLQILRGESKK FSANLTALKLPLPMVYEGDKV LKHLLRPKFNLPPLVQPPKKML
8711	39079	B	8769	1	1881	
8712	39080	A	8770	2093	2287	

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8713	39081	A	8771	1	1358	MKINLKLTNDSKVADGQFANI VVFLINWFYIHATTCEIDNGGVI VADGFQASKAYSADSIVDYND AHYKTSVDQDAWGFVPGGDN PWKKYEPAKAWSASTVYVKG DRVVVDGQAYEALFWTQSDNP ALVANQNATGSNSRPWKPLGK AQSYSNEELNNAPQFNPETLYA SDTLIRFNGVNYISQSKVQKVSP SDSNPWRVFVDWTGTKERVGT PKKAWPKHVYAPYVDFTLNNH HRRTDSFRSKATAELENQRLAG NVSELTEVFARIKQIAGQEHIDP LQTEIGSMVYAVKPGDGSARE QAASCQRVIGGLANIAEEYATK RYRSNVINWGMLPLQMAEVPT FEVGDYIYIP\GIKAALDNPGTT FKGYVIHEDAPVTEITLYMESL TAEEREIIKAGRIRHLLSDAMLA HLIRPTNRIESVGQIRHFRSIRHL LSDAMLAHLIRPTNRIEP
8714	39082	B	8772	21	1623	
8715	39083	B	8773	32	1850	
8716	39084	A	8774	1	1193	MSEVEAAAGATAVPAATVPAT AAGVVAVVVPVPAGEPQKGGG AGGGGGAASGPAAGTPSAPGS RTPGNPATAVSGTPAPPARSQA DKPVLATRVLPG\TAKRFNVRS GYGFTNRNDAKEDVFVHWTA VKRNNPRKFLRSVRDGETVEFD VVEGEKGAQATNVTGPRAAGV PMKGSRYAPNRRRFR*FIPRPPS VAPPPMVAEIPSAGTGPGSKGE RAEDSGQRPRRWCPPPFFYRRR FVRGPRPPNQQQPIELTGAFACS QGTDRVEPKETAPLEGHQQQG DERVPPPRFRPRYRRPFRPRPRQ QPTTEGGDGETKPSQGPADGSR PEPQRPRNRPYFQRRRQQAPGP QQAPGPRQPAAPEEAPTEAIKP MIAHDGHAPPNPSPTCCLEPSY QLVDVN

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8717	39085	A	8775	3	933	RHQESLCAPLEILQKKGCPCLE EPLQRQPCPCQSSEVTA**NISF RFASPGGN/SPWASH*APSVRG AAPAGPVGLEAAAGSEPHPGP/ PDAGGARPVPGGAGSRPRMVL/ SPRSAPHLGGGRSA/PAMRTGN PCTHTQVVTTSPNLPNIP*GAKS HPI/VERPLS*KGTGPSAPQIATE NIYP*QLHGKGPLIRD*KIVPHD GAAGQSPLLPVRSCQRGYLPSA K*FFDALKIKFTLKFLHLRRFSC TLSLRGLLVSPLLLPVRLLLAG WAHAWMHGCGGWEPRITQQR ASCQLPDRTKSKMRVKIPAANS SWLCH
8718	39086	A	8776	3	925	RGSEQIPPSSIPGAP*KMLFPSG/ SSEPEHL*TVPASSLGCRPGGPV ASRSRPPRPPARAALRGPPASSP IRFP\GASPRAPPTS*MRSGAGS KT/TPRPGPSASGDRPRAPCVRG PGCGSEPAAASSPTGPAG\VPRA R*GPGHGQTSPHGW*PSSMQQ RTRRCSPPSSVPGQFPLLP/LSCS QVSPWTW*GLPYSLLIPVSSLLP WPEDRVPSSFVA/GPLPSFDNTS LPVEGGS*L/HPVCLLYVYQENS SKHIPYSCRGSRIFPFSQRQRVM AGQRKLCDHPGGLISKPLAWT RIPEAPVVAAMVEGGGGL
8719	39087	A	8777	144	503	
8720	39088	A	8778	15	427	
8721	39089	A	8779	1	1055	
8722	39090	A	8780	280	1480	FQTRMGISVATIPGTSCSWSMR ASEKEKDTFESTVQVSKLQDLI HRSKMARCRGRFVCPVILFKGK HICRSATLAGWGELYGR\QATT YFFSGGADDAWADVEDVTEED CALRSGDTHLFDKVRGYDIKLL RYLSVKYICDLMVENKKVKFG MNVTSSEKVDKAQRYADFTLL SIPYPGCEFFKEYKDRDYMAEG LIFNWKQDYVDAPLSIPDFLTH SLNIDWSQYQCWDLVQQTQNY LKLLLSLVNSDGQTDSKSLVAI RTSVGVALAQTSGNALAYGTK KAQEQSQDGLIHTSLKPTEILYL TVAYDWFLFGHMLVDRLSKGE EIFFFCFNFLKHITSEEFSALKTQ RRKSLPARDGGFTLEDIC\C*DE RTVAVPPDLVCDCLPGHGEFPR

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8723	39091	A	8781	2	588	HSFFFPNREKCSTKR*RLSASRF PP*PWSRLPSG/QPAGGASAGSP SAPRGTGRGAGSRPAHG/VQPP RAHPEAPCPACPRSVGGAR/RA PEPSSNLSGEAPASGDRDVPPPS PLAR*VPLGGREFGWPWANAA LRPGKTP/RSDRVS\RSPWS/PAG FSVPASWPRRSTSGNRGPPSRPS RLSRTSGPLNRLGEPFDVQGPL
8724	39092	A	8782	1	198	
8725	39093	A	8783	1	275	MAGAPAPASLPPCSLISDCCAS NQRDSMGVGPSEPGAGYNLVP V\EKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLALL QLAH
8726	39094	A	8784	349	478	KLSKFPYTEELSSGLYGIGSLCP HKYNCLVSSHSRCKN*VTGY
8727	39095	A	8785	1	325	FSEGNSYLVGIMHPLKAMLPGL QYQTETFPPPGYLM/PCRLQQQ SHLLTLRDCCASNQRDSVGVGP SEPGAGYNLVVRRFLSLLEKRSI WVRVTRFSSALNHELKVNDH
8728	39096	A	8786	113	313	
8729	39097	A	8787	2	1991	
8730	39098	A	8788	512	1178	
8731	39099	A	8789	135	1562	DTLVPTSQGDISRGLEGNLNSC PT*Q**RAPFLWCQ/PKAEWGT WIFNPEAEESLEPRSLISDCCAN NQRDSVGVGPSEPGAGYNLVV RSFLSPSEKRSVRVGVTRLSRCR PSPLSLTQKGNPLTPCASQVRQ CLALLRLRHVYFYNFGWKDYG VASLTTILDMVKVMTFALQEG KVAIHCHAGLGRTGVLIACYLV FATRMTADQAIIFVRAKRPNSIQ TRGQLLCEAQQSGAFSADVSGS HSPGEPVSPSFANVHKDPNPAH QQVSHCQCKTHGVGSPGSVRQ NSRTPRSPLDCGSSPKAQFLVE HETQDSKDLSEAASHSALQSEL SAEARRILAAKALANLNESVEK EELKRKVEMWQKELNSRDGA WERICGERDPFILCSLMWSWVE QLKEPVITKEDVDMLVDRRAD AAEALFLLEKGQHQTILCVLHC IVNLQTIPVDVEEAFLAHAIKAF TKISIIFVNQNPEVTVLL
8732	39100	B	8790	563	2017	
8733	39101	A	8791	108	194	
8734	39102	A	8792	1	164	

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8735	39103	A	8793	1	1068	MEESRYWGTGRNRREGLKLQ WAQPAPLFNIRQGPNEGDNQQ GSYWEALASIMQIIHLVPSGLG MVTAFHCSWYLSTTATFPGVL NPALTEIKSGNYYVHGSFILQV ADYKEFQTLLMITKATFHQKTQ CWACEEGVQQSFHCPCRMQAA ASVERYTELLKEFLFKEHTCDN QEPTSTLHYHSKLTVHIHVYSS RCTLPCQPSQAAQAEGISQPAP ACEDFVFAALAPP/ESG/RCPTL RLLGGLCTPTNARRTRTHSTTA CWARAQWDSLGPLKLSHR\PR VCGGTRAPGRQGCMGNQRLGT SNSEARDPGGLRVKHR/CEAIQ EPPNRSRRQGAPLHSPPAY*MS SWRP*SFSKRHNLS
8736	39104	C	8794	78	331	
8737	39105	A	8795	129	1734	QWMHRMLDIFKGSSQHPSVPR VSSRPPLGPQGYSLHHFGTQGI HSATPINTQGLQPAPMGTQQPQ PEGKTSAVVLADGATIVANPIS NPFSAAPAATTVVQTHSQSAST NAPAQGSSPRPSILRKKPATDG MAVRKTLIPPQPHDVASPRVES SMRSTSGSPRPAGAKPKSE\STC LWPLRSLCPWRLYPIKIMISLPL PSLKLPSSPHRPFQL*LQQPVPR HNQPLPFQPFLERSPSLHPSPPL\ HCTTSISHCGWQSFLRLGPSRS* N*SERRSRTNGYHEASF\SVPPL ATNTVSPSLALLANNLSMPTSD LPPGASPRKKPR\NNSMWISTEE GDMMETNSTDDEKSTAKSLLV KAEKRKSPPKEYIDEEGVRYVP VRPRPPITLLRHYRNPWKAAYH HFQRYSDVRVKEEKKAMLQEI ANQKGVSCRAQGWKVHLCAA QLLQLTNLEHDVYERLTNLQE GIIPKKKAATDDDLHRINELIQG NMQRCKLVMDQISEARDSMLK VLDHKDRVLKLLNKNGTVKKV SKLKRKEKV
8738	39106	A	8796	1	169	RPTRPPKSNKRQCLVFVTP\KEE EPVRNILEKFNTISGSKVRSLYL HAPPLLPLER
8739	39107	B	8797	156	398	

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8740	39108	A	8798	20	723	VWGGEFLPRIWFMLPTSHQWM LFSVFLGWGSCQWSCSHLLSCL WRAAFSEFPLGPEPGEGIGPELC LCFQMEAIELSVDPKSNKRQCL VFVTP\KEEEPVRNILEKFNTISG SK/CTEVQRGVIYPGHIR*R**SI PRGF*FYSK*GRPDSAGGHGPG GVLQGEKGHSACARQGGRFQE GAAFAQRETAGRRVGQRWCG DCFRTPVHRKSLSSPNFGGFGA GSEAVPCHLVLYLVW
8741	39109	A	8799	79	256	LRLTLLFFQNLLGGKSSMLWTA HPCPEGACSSSCTSLGSHLLLSS FPVLGR*PGPSGDH
8742	39110	A	8800	402	996	TFFKFPPDSGAQLASPRGSRIGA AGGAA\SSPEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPQ\GRQ SGSPGRGGAESERGL*GLPSCC HLSPGSGAAAVPRSVGSRWPC GA\PTLATPPTSASFFSAATPEGP PLAS
8743	39111	A	8801	7	602	TFFKFPPDSGAQLASPRGSRIGA AGGAA\SSPEPSAALLSPWVVD GTGRPGAGGGARRGGSGCTGA HGGGGSSGM/VG/PAGPEPCPA GRQLRPGEKSSAAPLREPASAL AGPERGSHSAAAG*RAPQ\GRQ SGSPGRGGAESERGL*GLPSCC HLSPGSGAAAVPRSVGSRWPC GA\PTLATPPTSASFFSAATPEGP PLAS
8744	39112	A	8802	262	349	KEGEGGK\PD*PVRMCPPKPSG HWKHPGE
8745	39113	A	8803	2271	2863	GGASGVVRSSWWARGLAGFRS EAADLRGLPVELRASPAPCVRT PQPLGGR\GIGRPGAEGGPCWG GSGRTGAHGGAEGAGSSLGQP RKGLPQCSGG/PEGLLKCGQSG SPGRGRAQSERGL*GLPACCHL SH*PQGRQI*PRTCPTPFQSKTS DQGGPSGPAVSGSERQV*LHHQ *PGCRDYLCGPFCSWEINPVWG

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8746	39114	A	8804	3	561	NCPSLLVESCFQECGSSIPFALPS TQVEHALYASER*QRAGSPHSP HSLSVPPLPGLPLWRHLRSPS/G PPLH*PP*ASTLTGGPQ*RLGSA GINVSSEPVSSSRPNV*SFPFPQY TVTLVKGWRSREPSPKSSVLGS/ MVP*STKSEP*REPPI*SLTGKA GERGEKGREKAIGSGR*GVAKC SDHVR
8747	39115	B	8805	298	380	
8748	39116	B	8806	1	1292	
8749	39117	A	8807	1	1224	MKPRTLAVSVTALKVARLEFV PSDVRMCSEFLPSGGLVVSLAS GVKLQTFAVSVTARNSVDPKN SGAQLASPSGSSTRAASGAAC* SPSPPPCARTPQPLGGR\GTGCP GAGGGTRRGGSGRTGAHGAAE GVGSGLGQPRKGPPTVQWWAE GLLKCRQSGSPGRGGAESKRGL *GLPASTLSP\PPG\ECAGKSENS HMNLNCSGGSLGPGTGAHLPL GPDSGQPAETLLWGPCCGPGG TGLTGSGQTISLGCQGGQPRRE VKPPVPQRVSVLLVAVNPPPDS RCRVETDRPWRLCIQSCLCGTL KRDVLHSPSVVFNTTRGGTAE WSREDKDALLPEYALHMPFAV GFKLEYKEGVLGSNLAAGPEK ELCEAKRNQCPKSGVSHTSRPL KPEWSDFVAEIDESKLPDRS
8750	39118	A	8808	1	1298	ESLRAGSFQQEIQPELAPLIILRG FGTWPGWSFQATGFCVGVRGS PGSGFRGCGAYRAP*SFRTQLW PWQPLQGLDPKPLKDALRPSPL GRRACAEHHLCSADERPDLGFE GLQRWGGCRGSQGKPAVHQA WGRCGEGTGGGHTGSPPPRLTP P/PGPGSFRAQPGERRPAACGQ QRALGPMRPPPAC/GPSPT*GCA LNPTSPPAPLV*GFIHIVAAFCSF VTPVSKSHSFQLGGELRVAGSD \GGRWGERENTQGSTLPPSSPAS SPGSPSPDPATPPGPATPGLIDIL LLLPMVASSRKHDF\SGFSGRLP PQGEFFQ*GPTGWQSWVWPLD PSYLGGCQGGCGQGPRTGRRG ASSHCCVPAAP/GLSMDCSRGS GGSPPRSPPWALLGDLPSSLET VCLVMMFPCPIWMASEFAMEI QLLGPFWQIMLIGLCW

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8751	39119	A	8809	2	662	RIPLLVTRLKINEKVLQVLTNIF LFHDFSVQNFIKGLQLSLLEHFY SQPLSVLCCNLPEAKRRINFLSN NQCENIRRLPSFRRYVEKQASE KQVALLTNERYLKEETQLLLEN \LHVYHMNYFLVLRCLHKFTSS LPKYPLGRQIRELYCTCLEKNI WDSEEYASVLQLLRMLAKDEL MTILEKCFKGFKSYCENHLGST A*RIEEFLGQFQSLDEPRGRR
8752	39120	A	8810	326	1215	NPILHGNFIFMLDHSLKNVQDQ E*TLM*/HYGPQVVTMCQCSFIE RNKRIPVVQGIRRGRGHVQWG RYVEKQASEKQVALLTSERCL KKETQLLLENLHVYHMNYFLV LRCVHKFTSSLPKYPLGRQIREL YRTCLEKNIRNSEEYASVLQLL KMLAKDELMTILEKCFEVFKSS CEKHLGSTAKRIQEFLAQFQSF DETKENEALKREEGCIPNITPDI CIAYKLYLECRRLINLVDYSQA FATILTAAEKMDANSTSSEEMN EIIYAWCIRTVFELELLGFIKPTK QKTDHVARLT
8753	39121	A	8811	70	613	SLLEMKELRRSKKQTKFEVLRE NVVNFIDCLVREYLLPPETQPL HEVVYFSAAHALREHLNAAPRI ALHTALNNPYYYLKNEALKSE EGCIPNIA\PDICIAYKLHLECSR LINLVDWSEAFATVVTAAEKM DANSASSEEMNEIIHARDIRAVS ELELLGFIKPTKQKTDHVARLT WGGC
8754	39122	C	8812	598	762	
8755	39123	C	8813	138	296	
8756	39124	A	8814	1	395	

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8757	39125	A	8815	2	1289	DDLCALAFKVLHDKQRGPTGF YAPFNSRPL*KPQLAHSIILMET ATERISRLLLPFADQHVEIPSLT AGNIALTVGLKHTATGDTIVSS KSSAL\LQLVEPNGREKRSTDK TMKAERLLLAGSGRFQEPVFFC TIGTPITV*GSQIWEHAFEMSFS VRIPVLKVRLDPDSGQTV\LCG MGELHIEIIHDRIKREYGLETYL GPLQVAYRETILNSVRATDTLG *EL*GDKRHLVDLLGSGKARPI ETSSVMPVIEFEYAESINEGLLK VSQEAIENGIHSACLQGPLLGSP IQDVGNYLYIP*QIHPWAPSTTY DFCLCLKMPCKKALERKADKQ VLEPLMNLEVTVARDYLSPVL ADLAQRRGNIQEIQTRQDNKV VIGFVPLAEIMGYSTVLRTLTSG SATFALELSTYQAMNPQDQNT
8758	39126	A	8816	545	849	LAIHLSSLI\SRHDDEATRTST\SE GLEEGEVE\GETLLIVES\EDQAF S/VDLSHDQSGGISLNSDEGDVS WMEEQLSYFCDKCQKWIPASK ELLNSFDLSIPV

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8759	39127	A	8817	1	2395	MDSSIHLSSLISRHDDEATRTST SEGLEEGEVEGETLLIVESEDQA SVDLSHDQSGDSLNSDEGDVS WMEEQLSYFCDKCQKWIPASQ LREQLSYLKGDNFFRFTCSDCS ADGKEQYERLKLTWHQVVML ALYNLSLKGSGRQGYFRWKED ICAFIEKH*TFLLRNRKKTSTCR STGAGCLSVGSPMYFR*GA*EF GEPRWWKLVHNLPLTMKPERE KTAASTLNIFAASKPTLDPIITVE GLRKRASRNPVESAMELKEKR SRTQEAKDIRRAQKEAAGFLDR STSSTPVKFISRGRRPDVILEKG EVIDFSSLSSSDRTPLTSPSPSPS LDFSAPGTPASHSATPSLLSEAD LIPDVMPPQALFHDDDEMEGD GVIDPGMEYVPPPAGSVASGPV VGGRKKVRGPEQIKQEVESEEE KPDRMDIDSEDTDSNTSLQTRA REKRKPQLEKDTKPKEPRYTPV SIYEEKLLLKRLEACPGAVAMT PEARRLKR\KLIVRQA\KRDRGL PLFDLDQ\VVNAALLLVDGIYG AKEGGISRLPAGQATYRTTCQD FRILDRYQTS\LPSRKGFR\HQ\T TKFLYRLVGSEDMAVDQSIVSP YTSRILKPYIRSDPHWTPEPDAP LDYCYVRPNHIPTINSMCQEFF WPGIDL\SECLQYPDFSVVVLY KKVIIAFGFMVP\DV\KYNEAYI SFLFVHPNW\RRAGIATFMIYHL
8760	39128	A	8818	3	364	GDSVPTAEGGDQVCVILSSVPQ TVWEPMFNKRACG/P*SP*SLSA TSIYPRELKAGTQKDTCPPVFR AVLFTTATQCPSTDAWMNKM WYSRTMECYSALKRKEIPPHAT ARHPMCLQFCRW
8761	39129	A	8819	292	508	ARPGDQATSGGQGTTFQHPLFC FELGGSQNPALQ*PFAAACPVG AD*TKFTFAFCCRLK*KRTCCL SLGSRC
8762	39130	C	8820	253	369	
8763	39131	A	8821	295	393	IYFGCLLGEPVVAAEAGI\WDN DCVKKQLLHSW
8764	39132	B	8822	91	479	

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8765	39133	A	8823	1	544	ARHPDMKKRVEDASILPCNVSL EYEKTEVNSGFFSKSAEEREKL VKAERKFIEDRVKKIIELKRKV CGDSDKGFVVINQKGIDPFSLD ALSKEGIVALRRAKRRNMERLT LACGGVALNSFDDLSPDCLGH AGLVYEYTSPACPKQSGLCILSS TLGEEKFTFIEKCNNPRS\VTLLI KGPNKHTLTQIKDAVRDGLRA VKNAIDDGCVVPGCWCRGKW AMAEA\LI*P*APVLKGRAQLGS PKHLLDAFAHYFPKVLCFRNSG FLTFQGNIKLKFKAEHSRIQVQL VGVDL\NTGEP\MVASRSKAVW GHT*LW*KKTSLPSTPCTW*IA\ TNILLGLNEIMRAGMSFS*KGF VVINQKGIDPFSLDALSKEGIVA LRRAKRRNMERLTLACGGVAL NSFDDLSPDCLGHAGLVYEYTS PACPKQSGLCILSSTLGEEKFTFI EKCNNPRSCHIIDQRTK
8766	39134	C	8824	636	1025	
8767	39135	A	8825	33	1505	KCISASVKVDFSDLLLSNNTS*S AFTPTRTQKSSSKLLRKESHYS GMMSIQEKSKENSSKVTKKSD DKNSETEIQDSQKNLAKKSGPK ETIKSQAKSSSESKINQPELETR MSTRSSKAASNDKATKSINKNT VTVRGYSQESTKKKLSQKKLV HENPKANEQLNRRSQRLQQLT EVSRRSLRSREIQGQVQAVKQS LPPTKKEQCSSTQSKSNKTSQK HVKRKVLEVKSDSKED/GKSSN **SNKFS/SKGKNAR*NIR/SACA CSSQCTQGSEKCPQKTTRRDET KPVPVTSEVKRSKMATSVVPK KNEMKKSVHTQVNT/KHNTPK KSTAISA*TK***AGASRKEQTR *YSPA\REEIAGEIESDNVEVKK ESSQMESVKEEKPSEIKLEETSV ERQILHQKGTNQDVQCNRFFPS RKTKPVKCILNGINSSAKKNSN WTKIKLSKFNSVQHNKLDSQVS PKLGLFTNQFFTTSFRNASSSDS KYIFRDKAT
8768	39136	A	8826	1	394	AISRALGRYVLFPCLIQDGIFVA HTAHAILTSLED\SL*MFQPKTC WCL\AN*HDTLSVNMETPHPSF QEELSGLLLLKMLRSPIEASKD KDKVKSNAVRALGNLLHFLQP SHIE*PTFAQINEEAIQALIS

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8769	39137	A	8827	52	730	KSACDALSSILPEAFRNLPNDR QMLCITVLLGLNDSKNRLVKA ATSR\ALGVYVLFPCLRQDVIFV ADAANAMVMSLEDKSLNVRA KAAWSLGNLTDTLIVNMETPD PSFQGRVLWSPALENGYDQAL EASKDKDKVKRH\AV\RALGNL LHFLQPSHI/GKTPHLQKFI*GSL SRALNFLLF*QKLAMKVRWNA CYAMGNVFKNPALPLGTAPWT SQAYNALTSVVTS
8770	39138	B	8828	47	1576	
8771	39139	A	8829	2	2753	
8772	39140	A	8830	1	273	
8773	39141	B	8831	104	206	
8774	39142	A	8832	1	987	
8775	39143	A	8833	111	2187	DERRVGAADMFGRSRSWVGG GHGKTSRNIHSLDHLKYLYHVL TKNTTVTEQNRNLLVETIRSITE ILIWGDQNDSSVFDFFLEKNMF VFFLNILRQKSGRYVCVQLLQT LNILFENISHETSLYYLLSNNYV NSIIVHKFDFSDEEIMAYYISFL KTLSLKLNNHTVHFFYNEHTN DFALYTEAIKFFNHPESMVRIA VRTITLNVYKVDNQAMLHYIR DKTAVPYFSNLVWFIGSHVIEL DDCVQTDEEHRNRGKLSDLVA EHLDHLHYLNDILIINCEFLNDV LTDHLLNRLFLPLYVYSLENQD KVFLIIHHAPLVNSLAEVILNGD LSEMYAKTEQDIQRSSVLPTLSS LWQGSHLSLNQLQSGLHKCSS HLCGAQAAADSVTGEIPAIRSL EWLISAGSKARTFFFLKMLIGF WEKVDCEYQRRQVLSTRLQEA LPSNRLTDVAAVHSSCMLGFGS TAPRGSWIGDPAAVHLPLPGEL AEHLGSKGTTTVTKHQPQAKPS IRCFIKPTETLERSLEMNKHKGK RRVQKRPNYKNVGEEEDEEKG PTEDAQEDAEKAKGTEGGSKGI KTSGESEEIEMVIMERSKLSELA ASTSVQEQNTTDEEKSAAATCS ESTQWSRPFLDMVYHALDSPD DDYHALFVLCLLYAMSHNK/G KSPEKEEGLSGTQSHPGKAGTF GKEGAEERKRAQV

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8776	39144	A	8834	1	3050	RNLLVETIRSITEILIWGDQNDS SVFDFFLEKNMFVFFLNILRQKS GRYVCVQLLQTLNILFENISHET SLYYLLSNNYVNSIIVHKFDFSD EEIMAYYISFLKTLSLKLNNHT VHFFYNEHTNDFALYTEAIKFF NHPESMVRIAVRTITLNVYKVS LDNQAMLHYIRDKTAVPYFSN LVWFIGSHVIELDDCVQTDEEH RNRGKLSDLVAEHLDHLHYLN DILIINCEFLNDVLTDHLLNRLF LPLYVYSLEN
8777	39145	A	8835	111	270	
8778	39146	A	8836	240	406	
8779	39147	C	8837	86	286	
8780	39148	A	8839	172	243	DPS*EARSMLLLLFLPPDHSGLP H
8781	39149	A	8840	280	526	GRNAVVQS*AHCRSQTPGPK*S SL/LVFPSS\WTYRHMPPHLAN* KKFFLHRDGGLDMLPRLVWNS WPQVILPPQPPKALGLLL
8782	39150	A	8841	3	1785	VLDARNAGAGGLAGPAGVLRG RASRCDPGAAVGAGQGGARVR PGRAAAPSPGPPGGA*CVPTDA GAGPGSAGARQPLPFAAGALS HSGHC*RGLRGPGSLASPAQAK AAWSGLLLSPAAAGRDGGRGH NPRDPPPLREHGPGIPGFHGDR G*ELYQCHLGGEGG\GPDKPGS PCASCGLDGHWYRALLLETFRP QRCAQVLHVDYGRKELVSCSS LRYLLPEYFRMPVVTYPCALYG LWDGGRGWSRSQVGDLKTLIL GKAVNAKIEFYCSFEHVYYVSL YGEDGINLNRVFGVQSCCLAD RVLQSQATEEEEPETSQSQSPAE EVDEEISLPALRSIRLKMNAFYD AQWKENGYYRAIVTKLDDKSV DVFLVDRGNSENVDWIINMLL RFLTNQEQGEETISKVIAQAGY AKYQEFETKENILVNAHSPGHV SNHFTTESNKIPFAKTGEGEQK AKRENKTTSVSKALSDTTVVTN GSTELVVQEKVKRASVYFPLM QNCLEIKPGSSSKGELEVGSTVE VRVSYVENPGYFWCQLTRNIQ GLKTLMSDIQYYCKNTAAPHQ RNTLACLAKRTVNRQWSRALIS

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8783	39151	A	8842	2090	2901	THLLVPGMQPLTWQMPFSPFLS ISPTRSNLPSAATPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLATVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGIPHSIA SDQARIHRSRNQEVEVEVAPLT ITPSDPLAKFLLSVPVTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPPGHFGLLLTLSQEAKNG VTVLAGVIDLDYQDEISLLLHN GGKKEYARNTGDPLGRLLVLP CPVIKINGKLQQPNPGGTTNGS DPSGMKV
8784	39152	A	8843	1	585	
8785	39153	A	8844	1	1697	MDKYFMIKTPKAMATNTTIDK WDLIKLKNFCTAKETMIRVNR QPIECKKMFAIYPSDKVILLFKM APKRNAEGLSTVSTCKKAAMC LIEKGCELVGPVGPQTHPVVTS PVSECIIGIDILSGWQNPHIGSLT GRVKAIMVAKDKLKPLELPLPG KIVNQKQHCIPGWIVEISATIKD LKDAVIGIPTLPPFNSPIWPVQK TNGSWRMTVDYHKLNQVVTPI AAAVPDVVSWLEQINTSPGTCL HWWPHGEFPRLVDREERTRTW FTDGSAQYAGTTQKWTPAALQ PLSRTSLKESECFIHHHGIPHSIA SDQGTHFMAKKVRQWAHAHEI HWSYHVPHYPEAAGLIEKWNG ILKPQLQCQLGDNTLQGWDKV LQKALYA\LNQHSVYGTISPIAR IHRSRNNQEVEVEVTPLIITPTD PLAKFLLPVPSTLHSLDLEVLVP EGGMLPPGHTAMIPLNWKLRL PPGHFGLLLPLSQQAKKGVIVL AGVIDLDYQNEISLLLHNGGKE EYALNIGDPLGHLLVLPCPVIN VNGKLQQPNPGRITNGEDPSG MKVCVTPPGTTTTTKKP
8786	39154	C	8845	1	720	
8787	39155	A	8846	57	261	WNF/CDPGGPMMKL\FISFKLKT ISSTFLSPTCLVL*RRPSRSASSL TVLCTTTRSSSPLLGALV*TWP
8788	39156	B	8847	1	1158	
8789	39157	B	8848	1	2523	
8790	39158	A	8849	3	375	
8791	39159	A	8850	3	169	DFQPFTRVTVHWGKGNDQTFR GLLDTGSELTLIPGDPKHHYGP PVKVG\AYGAQLL
8792	39160	A	8851	3	376	

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8793	39161	B	8852	1	592	
8794	39162	A	8853	1	319	
8795	39163	A	8854	1	1071	
8796	39164	C	8855	1	862	
8797	39165	A	8856	1	1488	MGRARRLTPVIPALWETEADGS RALTVETTVTQLQHLNTVGIIG FRGGRGQVAAVNCQKRDIQPF TRVTVHWGKRNDQTFQALVDT GLELTLIPGDPKHHCDPPVKVG AYGHQVINGVLAQIQITVGPVG PWTHPVVIFTVPKCIIDIDILRW QNSHTGSLTGRMKAIMVGRAK WKPLELPLPRKTVNQKPYHTPV GTAEISATMKDLKDAGVVIPTT TLFNSPIWSVQKTGGSWRMTV DYCMLNQVVSAVEAIVLDVVS LLEQINTS/P/WP*SGSCTAAFHH QMEVVHT*SGSSRS*RHN\CTN GLMGSFL*SVDRGREDYGLVH RRFFTIC*HHPKLDSCSTTVPF* DIPEGQL*REIFPPPVSWRQGWR LCMGSATWTFTHQG*PGYGHC *VPNLPAAETNTEPSIWHHSSG* SASYLVAG*LYGTSSIMERAEV CPHWNRHLF*IWVVCLSCTLCF C*DYHPWTLEMPYPPSPYSTKL CCCPRHLLYG*RSAAV
8798	39166	A	8857	1	1056	MSSVLLRLIYQLTQKTASFEGG PEQKALQQIQAAVQAALPLGPY DPANPMVLEVSVADRDTVWSL WQVPIGESQQRSLGFWSKVLPY SADNYFPFERQLLACYWALLET DRLTVGHQVTLQPELPIMNWV LSDPSSHKVGHVHQHSIIKWK WYIRDQTRAGPEGTTTPVITQ/ WDAHEQSGLSGRDG\KGQRFV LTGVDTYSGYWFAYPAHNASA KTSIYGFTECLIHCHGIPHSIASD QGTLFTAKEVWQWAHAHGIH WSYHIPHHPIAAGLIEWWNGLL KSQLQCQLGDNTLQGWGKDL QKAMYSLNQRLIYSTVSPISRIH GSRNQRVEVEVAPLTITLSDPL AKFFFLLP
8799	39167	B	8858	603	1785	

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8800	39168	A	8859	3	467	RIHVRPEITLTA/ANTARPY*IDP HDTLLSHSNFGSSDCPSSSKMR QALELVRERAPELMIDGEMHG DAALVEAIRNDRMPDSSLKGSA NILVMPNMEAARISYNLLRVSS SEGVTVGPVLMGVAKPVHVLT PIASVRRIVNMVALAVVEAQTQ PL
8801	39169	A	8860	1	1878	
8802	39170	A	8861	3	684	MPNYLRFVRGLIDSSDLPLNVS REILQDSTVT\RYLRNALTKRVL QLLEKLAKDDAEKYQTFWQQF GLVLKEGPAEDFANQEAIAKLL RFASTHTDSSAQTVSLEDYVSR MKEGQEKIYYITADSYAAAKSS PHLELLRKKGIEVLLLSDRIDE WMMNYLTEFDGPPFQSVSKVD ESLENLADEVDESAKDAEKALT PFIDRVKALLGERVKDVRLTHA GSGLVGENV
8803	39171	A	8862	2	393	LEFGKKLGNAAADYFIANKIDQ PKIAVINCEAFEVCVQRRKGFE EVLKSRVPGAQIVANQEGTVLD KAISVGEKLIISTPDLNAIMGES GGATLGAVKAVRNQN\RPEKL LFSVRI*QPKLLRSWKTIRC
8804	39172	A	8863	414	805	TPSRVEGNQEYPSLVYIP\SQAP\ WNM*TRDHKHGLNLYVQRVFI MTDAEQFMPNYLRFVGGLIDSS DLPLNVSREILQDSTVTRNLRN ALTKRVLQMLEKLAKDDAEKY QTFWHQFGRGIIIFTDSQFNR
8805	39173	A	8864	3	684	MPNYLRFVRGLIDSSDLPLNVS REILQDSTVT\RYLRNALTKRVL QLLEKLAKDDAEKYQTFWQQF GLVLKEGPAEDFANQEAIAKLL RFASTHTDSSAQTVSLEDYVSR MKEGQEKIYYITADSYAAAKSS PHLELLRKKGIEVLLLSDRIDE WMMNYLTEFDGPPFQSVSKVD ESLENLADEVDESAKDAEKALT PFIDRVKALLGERVKDVRLTHA GSGLVGENV

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8806	39174	A	8865	1	624	AKLLRFASTHTDSSAQTVSLED YVSRMKEGQEKIYYITADSYAA AKS\SPHLELLRKKGIEVLLLSD RIDEWMMNYLTEFDGKPFQPG AKVDESLEKLADEVDESAKEA EKALTPFIDRVKALLGERVKDV RLTHRLTDTPAIVSTDAD*M\TP RMA\KCFGGAGQKVPEVKYIFE LNPDHVLVKRA\ADT\EEEAKF CVWGKNCVLGPF
8807	39175	A	8866	471	659	
8808	39176	A	8867	638	834	SSNTMMHFQIHMKQESTEQQT MTARR*Q*SEVDE*REDTTLAA RGRTEA*SARYQLT*QSVPSPH
8809	39177	B	8868	1	1383	
8810	39178	A	8869	4452	4896	SQHSEVFVCHMLSQPRAPGAG RYL/LQRKA/SEALEVEV/VDTW QADAVRDTRTLS\GGESFLVSL ALALALSDLVSHKTRIDSLFLD EGFGTLDSETLDTALDALDALN ASGKTIGVISHVEAMKERIPVQI KVKKINGLGYSKLESTFAVK
8811	39179	A	8870	31	185	GHRRRPFKRGRKSR*RGGSQRR VNEDARRSAWMRKKQRRLISK ISDRTARK
8812	39180	A	8871	1744	2670	

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8813	39181	A	8872	1	1680	MGFWVENGEIQYPVSEITIAVSS LVFSSASFAADLEDNMETLNDN LKVVEKADNAAQVKDALTKM RAAALDAQKATPPKLEDKSPDS PEMKDFRHGFDILVGQIDDALK LANEDVFTRTLGADALYQFQNI RHVLRMQRIAAGEGNTLAFDT SVIQIVNDLVFHCFGKWLTGIY PPCAFVIATGAFMNTPGDKQGA TSAGAVDDVDRISNEITIGIPML TGYILLHVKGVRAKSSADHRR RPLASLATPPHKSWTCTLLFFR LPNVVCYANRIQQLTPILETLPQ SDELPHCEETVVLENWRQVHE QCLALHSQQQTLQQQDVLAAQ SLQKAQAQFDTALQASVFDDQ QAFLAALMDEQTLTQLEQLKQ NLENQRRQAQTLVTQTAETLA QHQQHRPDDGLALTVTVEQIQ QELAQTHQKLRENTTSQGEIRQ QLKQDADNRQQQQTLMQQIAQ MTQQVEDWGYLNSLIGSKEGD KFRKFAQGLTLDNLVHLANQQ LTRLHGRYLLQRKASEALEVD VVDTWQADAVRD/TRTLSGGE/ SFLLRLR*VTRRHQLWLHPLRH
8814	39182	A	8873	3	823	
8815	39183	A	8874	287	426	YSGLSAVNPVNDAYGVRFQLP SVNRIPVS***VKLAPPAHQIKRI SGKCRFIPLC*YAPPGFSSASTM RATGILSTASQPPGKLPCMEEST AERRVGLPPLAKW
8816	39184	C	8875	1	2058	
8817	39185	A	8876	1	1989	
8818	39186	B	8877	1	3132	
8819	39187	A	8878	194	789	LTKLPSLFTFTRLSSSDNDLRGG DKRGGANGARLAL*PQTRTGD VTRRQPIRVCTVIEMFELLE/PIA DGFRNYRARLDVST/TESLLIDK AQQLTLTAP/EMTALVGGMRV LGANFD/GSKNGVFTDRVGVLS N/DFFVNLLDMRYEWKATD/ES KELFEGRDRETGEVK/FTASRA DLVFGSNSVLFVRILGGFFCEYS LTIRILH
8820	39188	A	8879	1120	1395	

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8821	39189	A	8880	1	629	THRPPKSGPPCAKITRTTHVTA KPLFPQTNPKQTVRRMQGELY LVDESGQEFVSALNYRRRKTR NNATAYPIRLFYLSVRPRAGSK SSRTIWILLAD/AKITPYERRQL VARIEA/LSTEIPAQVRPLYQLW RDGQALQLQLAEERQR/YTGG ADTKQDGATTTKDKQQR*TKG TRSQPSTREVQQQSTQKHSTSR PPNHSAQPSNSALVTRQ
8822	39190	A	8881	3	307	
8823	39191	C	8882	161	337	
8824	39192	C	8883	34	168	
8825	39193	C	8884	172	456	
8826	39194	A	8885	174	516	VSGVRCWIHSSAFPPVFPGFFLP VAFFDRPPARLYRMHTWSHME SQEPARLPSHYAD*GQGSQKR\ DSCSSGWAGLLFISPQFVLWSA EIEGSLNHITLGFRLSHGTTSAD GMTF
8827	39195	A	8886	1	2964	
8828	39196	A	8887	1	2724	
8829	39197	A	8888	3708	7098	
8830	39198	A	8889	115	339	
8831	39199	A	8890	445	634	VINTFSLHTMGSTS*HQGNGWR HLTLHPRNSKHPLEQPTPGVLQ LRPPTASLRQLLSNAGCSG
8832	39200	A	8891	1663	2234	GEGLRRGLFPGAEAQGRAETA GCLRRGRGALALALPGSPGLSP WVEDAGGHRVLHGRAVLRCA RAPPVPQPAGLAKVEPYSGVSS LTAFPQAPILLSSGGQSRAGERT TM*G*PEMEKL*SCIGEGHQPC HR\KSRPAAPCPPPSAMLFLTPR SSATLLSSSSKGASGGWEPSAA PLGGSGQPFREMVSQH
8833	39201	A	8892	202	542	
8834	39202	A	8893	564	1179	QHRLTYRTALWIHYRPDPKPL MSFRPGHQRLSVTSLLVCHGLL MVGTSLGVLVALPVPRLSSPSL PPVELL*HSVCVSVCRGISCL*W RLWDQISDW\SRTLIQPPRPPSC CPVVASPGPGKGPQCNGDPKW KSCEAASVKGTSPATGKSRPAA PCPPPSAMLFLTPRYSATLLSSS SKAASGAREPSAAPLGGSGQPF REMVSQH
8835	39203	C	8894	321	539	

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8836	39204	A	8895	630	983	NLETNGKIPFENPWSKVPIRFGR QNLRRVCLTTGGQIPTGRWVT ATDSRGAGDYRLCLHHLR*PD GARLSAGSADCAANRRDVDGS GRGLPGRLSVQQPRRVRRGQP DVQPVSWPGC
8837	39205	A	8896	31	144	
8838	39206	A	8897	1	1775	MEISFTRVALLAAALFFVGCDQ KPQPAKTHATEVTVLEGKTMG TFWRASIPGIDAKRSAELKEKIQ TQLDADDQLLSTYKKDSALMR FNDSQSLSPWPVSEAMADIVTT SLRIGAKTDGAMDITVGPLVNL WGFGPEQQPVQIPSQEQIDAMK AKTGLQHLTVINQSHQQYLQK DLPDLYVDLSTVGEGYAADHL ARLMEQEGISRYLVSVGGALNS RGMNGEGLPWRVAIQKPTDKE NAVQAVVDINGHGISTSG\SSRG D*DGYGQGLSRVIDPQTGRSIE HNLVSVTVIAPTALEADAWDT GLMVLGPEKAKTCSPGGLRGT ESLNTLRDRITQINGIDEVRMD DSWFARLAALTGLVGRVSAMI GVLMVAAVFLVIGNSVRLSIFA RRDSINVQKLIGATDGFILRPFL YGGALLGFSGALLSLILSEILVL RLSSAVAEVAQVFGTKFDINGL SFDECLLLLLSSMVTFWCRNLF TSLLELWINHADKQDDNSCLSS ASVYLKAKMMKVMLPMQLLS SGTGFYRDRLENSGGRYESRRS LTRQFREEPTAPIPRECSQRIDFL LFETPSVSASSSAGFWLRFGSTA
8839	39207	A	8898	10	300	PTSIPRESSSGTWFQVASTTVLF SAILAGLGSASAFCLGPGIPQAR PNNSAVNSKNSRFGIPRPQAE*P EQGGVYHHTAGVLKKLIPPSAR QHPDRC
8840	39208	A	8899	1657	2061	QMPGNNPAFSALLVAFKHQFAI AGGIFIKEVTFAIKTSQLLWFGQ PIFNNETTHQTACFLSVEADDL KFAVLLIEEHRLDNLGIQFLRLH RFKILI*RQINHHIIALCCERLVQ LVGDDISPEFDELELRFSEVH
8841	39209	B	8900	26	1540	
8842	39210	A	8901	1	3396	
8843	39211	A	8902	1	3522	

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8844	39212	A	8903	1	105	SPQPDRHYRHHRQGPLVCIVIIF YFCAKRWMAAIL*TQHRHRFL TTDDGKFAVANGSFS*RGLHH/ ATGLLRRFPPIC*GPLVCIVIIFY FCAKRWMAAIL
8845	39213	B	8904	1	960	
8846	39214	B	8905	1	2618	
8847	39215	B	8906	1	490	
8848	39216	A	8907	2820	3332	ATEGYRQQCRQFHPAAYDESP HRNRRRKWRPTYRCHPAPDHR TACLRSAFYGNAPGCVQTGPV RRSGAASASSPAVFLSGTSPWS FARTIALVRGRS/LKIDTNSPWA YFSALLM/F/DLLSHVHEWCGR YISPPRFAQTGETLPCRRHQGSR YSAYLSASRYPARRKWYFSPR
8849	39217	A	8908	3	716	EVDDTAKHRRRDSFPQ*DP/LM NIRYAPSP/HLPATVALTGAVIIT VLYALAGKRLFCSWVCPLNPIT DLANWLRRRFDLNQSATIPRHI RYVLLVVILVGSALTGTLIWEW INPVSLMGRSLVMGFGSGALLI LALFLFDLLVVEHGWCGHICPV GALYGVLGSKGVITVAATDRQ KCNRCMDCFHVCPEPHVLRAP VLDEQSPVQVTSRDCMTCGRC VDVCSEDVFPITTRWSSGAKS
8850	39218	A	8909	3	323	
8851	39219	B	8910	94	2205	
8852	39220	A	8911	504	694	FNQLGRDWRTYYRKSDPPR/Q WLRHSPVR*VLKMVPMAIRGL LWMLSAQPAPAICSSRQTKMV
8853	39221	B	8912	1	2031	
8854	39222	A	8913	3	190	FIATPGYTGEAGYEIALPNEKA ADFWRALVEAGVNPCGLGARD TLRLDGDESYG/QEM/DETVSP* AMKLRCPMKKRPISGVRWWK RVLTHVAWARVTRCVWTGMN LMARDGETVSP
8855	39223	A	8914	1	621	MWPSVSHLTQMNIPSRFSEPSG AIEVPPDKVHELRLRLAQQGLP KGGAVGFELLDQEKFGISQFSE QVNYQRALEGELSRTIETIGPV KGARVHLAMPKPSLFVREQKS PSASVTVNLLPGRALDEGQISAI VHLVSSAVAGLPPGNVTLVDQ GGHLLTQSNTSGRDLNDAQLK YASDVEGRIQRRIEAILSPIVGN G\TAQLDFAS
8856	39224	A	8915	1	2274	
8857	39225	A	8916	957	1067	

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8858	39226	A	8917	1	1242	MDGLNTDKGSSVFHTPTDRLVI CCPVDADERMTTPPRLWDHEP SKPLFFTNYPVSAPFVGL/PPGK RPQGGFRAGNL*TSSKTIGRDL NDAQLKYASDVE\GRIHRRIEAF LSPIVGSGNIPAQVRAQLDFASK DQPEEQYRPNGDESHAALRSR QLNESEQSGSGYPGGVPGALSN QPAPANNAPISTPPANQNNRQQ QASTPSNSGPRSTQRNETSNYE VDRTIRHTKMNVGDVQRKLGII GQGKNEKPLKQLERVEEKPNG EGWEKKWQGKEVWKKEDGTI YLQKNKLRAPTDSTLWFAKNG RVAKIAKALVEPANNFNPGVD EDDTEKLLEVVPEELTNEKLDL EQKCIHIYDDKRKQTKQTPQDV FLKRVTSPQEPQPGPSGGIPEEG IVIIGEDSSVQVLAPEDLPVEKL
8859	39227	A	8918	256	1510	RRFVGFRTGVTKEDAIGKRGV DQFFRQSQYRLVGVTVAGMPE LTRLFVQRFTQFRMRMAQRVH RNATREVDILFPLLIPQARTFAT YRYKGCRSVNRYHPFIKVFTRN WREADLSLKRV*TLLNDTGYQ EVITYSFVDPKVQQMIHPGVEA LLLPSPISVEMSAMRLSLWTGL LATVVYNQNRQQNRVRIFESGL RFVPDTQAPLGIRQDLMLAGVI CGNRYEEHWNLAKETVDFYDL KGDLESVLDLTGKLNEVEFRAE ANPALHPGQSAAIYLKGERIGF VGVVHPELERKLDLNGRTLVFE LEWNKLADRVVPQAREISRFPA NRRDIAVVVAENVPAADILSEC KKVGVNQVVG\VNLFDMYRGK GVAEGYKSLAISLILQ\DTSRT\L EEEEIA\AT\VAKCVEALKERSQ
8860	39228	B	8919	47	156	
8861	39229	B	8920	139	993	
8862	39230	A	8921	1	284	MRRKRLIRPTVQAQVCRPDKTR KRRIRQWC/YGCRMRRKRLIRPI KYANRQAETA*GLDALHLSCSS HG*KGPT*SSGHGFRGCKPQAL EASMWC
8863	39231	A	8922	1	813	
8864	39232	A	8923	1	1176	

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8865	39233	A	8924	3	618	AGGPPLNPIEMA*KS\WDEIIVK LEKDPQLKTQFLEVYPQGFSGE NITDAIAEFEKTLITPDSPFDKW LRGDENALTAQQKKGYQLFKD NKCATCHGGIILGGRSFEPLGL KKDFNFGEITAADIGRMNVTKE ERDKLRQKVPGLRNVALTAPY FHRGDVPTLDGAVELMLRYQV GKELPQEDVDDIVAFLHSLNGV YTPYMRDKQ
8866	39234	A	8925	2	212	QYPGLDLHGAKGLGDGLAGKR YRQLLVSC\RHVLYRHPAGPGT RK*RRSGIRWLHRLCGNEPRGK LLVDQ
8867	39235	A	8926	1	640	
8868	39236	A	8927	1	704	MSSFQFEQIGVIRSPYKEKFAVP RQPGLVKSANGELHLIAPYNQA DAVRGLEAFSHLWILFVFHQT MEGGWRPTVRPPRLGGNARM GVFATRSTFRPNPIGMSLVELK EVVCHKDSVILKLGSLDLVDGT PVVDIKPYLPFAESLPDASASYA QSAPAAEMAVSFTAEVEKQLL TLEKRYPQLTLFIREVLAQDPRP AYRKGEETGKTYAVWLHDFN VRWR/VSP*ACSTFQLEP
8869	39237	A	8928	3	313	AQRGGI*RGSLATAGLRSFGGL HPIRTSQQFCL\PVRGKPPTQAS VMVDAPHSTKLKHLRSISDCCT GSKNFKPVDLSLLGSMGVGSTE LDHLAPWLQAPFPGE
8870	39238	A	8929	13	453	
8871	39239	A	8930	380	966	LRHAVLLTEGF/SYKPHAFALG FVEAPRGEDVHWSMLGDNQKL FRWRCRAATYANWPVLRYML RGNTVSDAPLIIGSLDPCYSCTD RVTLVDVRKRQSKTVPYKEIER YGIDRNRSPLNRSLYPREVPSTT LQPLRTPRCPGKNLALAVNVST GTNGQKPESCGPGRCRMKKGE YKRTISGGRTIIRVHIARLLRTF

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8872	39240	A	8931	1415	2085	SQVPICQRSTSCRVKRLFSWKM AYRSALVTPWRVFRRNPAVPR TSPVVFTGGDVFSRVMVRVKE T/FDSLAMLEFALDNMPDTPLL TEGFSYKPHAFALGFVEAPRGE DVHWSMLGDNQKLFRWRCRA ATYANWPVLRYMLRGNTVSD APLIIGSLDPCYSCTDRVTLMPS QCIACGACACACPANALTIQTD DQQNSRTWQLYLGRCIYCPSST NNNGPVISFN
8873	39241	A	8932	1	1127	MKKRKTVKKRYVTALVIVIAG LMTLWRIRNAPVPTYQTLIVRP GDLQHSVLAPGKLARTSKNFA Q\FIRVRYSAFSLAGEKKKR**P RVHGVQNASSGRYRGTGCRLG SDSRKKLVEIL\LAT\PNMEQRT QGIGILDPQIARDLRFDHPYAEY DNIPK\TLFTFTAADVFSRVMVR VKETFDSLAMLEFALDNMPDT PLLTEGFSYKPHAFALGFVEAP RGEDVHWSMLGDNQKLFRWR CRAATYANWPVLRYMLRGNT VSDAPLIIGSLDPCYSCTDRVTL VDVRKRQSKTVPYKEIERYGID RNRSPLNRRCTGEGWTRAWITL PLLIKPLTPLMIASFAFNFNNFV LIQLLTNGGPDRLGTTTPAGYT

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8874	39242	A	8933	1	2466	MLRGVNVLADAVKVTLGPKG RNVVLDKSFGAPTITKDGVSVA REIELEDKFENMGAQMVKEVA SKANDAAGDGTTTATVLAQAII TEGLKAVAAGMNPMDLKRAS RSRKGYGPARIRQELNQKGISR EATEKAMRECDIDWCALARDQ ATRKYGEPLPTVFSEKSRKLIA GVKRAFTHQAVNAGFCTQPAV SVIAGDFDRHGFNTRHFTFRLF DDFSFETTRFCPAQIHTLKHARP VLCFRTARPRLNIEVAVGAVIF AREHTAELKLRQFFQGAPQKA VISIPVVPQVTGVVIEVTDKKNT LIKKGEVLFRLDPTRYQARVDR LMADIVTAEHKQRALGAELDE MAANTQQAKATRDKFAKEYQ RYARGSQAKVNPFSERDIDVAR QNYLAQEASVKSSAAEQKQIQS QLDSLVLGEHSQIASLKAQLAE AKYNLEQTIVRAPSDGYVTQVL IRPGTYAASLPLRPVMVFIRSET SLRTHCPGHADYVKNMITGAA QMDGAILVVAATDGPMPQTRE HILLGRQVGVPYIIVFLNKCDM VDDEELLELVEMEVRELLSQY DFPGDDTPIVRGSALKALEGDA EWEAKILEL/RWLPGFLYSGTR ACD*QAVPAADRRR/SSPSPVV VPLLPVV*NAVSSKLVKKLK\R WYPRDSEVYLYWR*NVPPTAG RRPCW*ERRCSAAWYQT*RNR

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8875	39243	A	8934	1475	2904	FWRAAAPIPDCWRSGAVKKQH VEVTQLDWTPPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGFTGTV MQTAGSSVFNLYTDPQESDSIG VRHIPMGVPLQTEMHAPGLPLA SSMKRWIRRATGFIFGKEQFED VVPVLGSKVNGVQFNAELVAD SLGISQIRCRCAIFLTVVFFPVLH KQAFDLISLLLQQPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFTT LVQGSLPELHQAWQAVDERPH ANRFLPPDEIEQSLNGVHYQHH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRILTRSQLQRLQ LAWPQQQGRYPLTYHLFLGVI
8876	39244	A	8935	1	920	MARADTVSVPMFMGLAAKPC WRDTEPNTGYRGPHVRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDAC\LSNAILVHNKKGGP LADGIVITPSHNPPEDGGIKYNP PNGGPADTNVTKVVEDRANAL LADGLKGVKRISLDESDGIRSK NDVIDTSDDDM**QCLSRRSN\ GHPGAKVANLVPKTTFIDGVD QTSFFLGTNGQSNRKAEHYFLN GKLAAVRMDEFKYHVLIQQPY AYTQSGYQGGFTGTVMQTAGS SVFNLYTDPQESDSIGVRHIPM GVPLQTEMHAYMEILKKYPPR
8877	39245	A	8936	471	668	
8878	39246	A	8937	1	1233	
8879	39247	C	8938	1	1548	
8880	39248	A	8939	1	1260	
8881	39249	A	8940	1	1468	
8882	39250	A	8941	261	596	RSESCCCGHEPDGPETRQP*PQR LWTCAYSPGTESERYFPRSDRK SDA*M*HRLVRTGARSGDAKI WRTFANCLFRKIKKTYRRSQTG FYAPGGERRFLYAASRKRNRRR F

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8883	39251	A	8942	2	1356	CLPGLKLVRLLYRLEERNARRT SAAVDAT*RAGAWLAQCGLTV EQLAR\QVD\PDMTTRAHLYHC DHRGLPLALISEDGNTAWSAEY DEWGNQLNEENPHHVYQPYRL PGQQHDEESGLYYNRHRYYDP LQGRYITQDPMGLKGGWNLYQ YPLNPLQQIDPMGLLQTWDDA RSGALTWYGWDGDRLTTIQND RSRIQTIYQPGSFTPLIRVETATG ELAKTQRRSLADALQQSGGED GGSVVFPPVLVQMLDRLESEIL ADRKRAATTWSHNHYANKKE GIKATGYRLAQTLGFKCEESSV FRVTRKSHSSFVWLDKAVTPHP TSNVRAGCLMRRWRVLSGLHR CEVLHPHTPHPAYHAGCGVSL QRNIRHFFLNGLRFQLRFRRTIC CLRLVVVQPQHFAGVLQLAFC CRYITVQLASIRRNDRFQRSLPL RAGNTIAKYFFQQIQHNRRGG
8884	39252	B	8943	1	1159	
8885	39253	A	8944	1	1304	MAETQQQFKKRMAASGLETRF DEVGNLYGRLNGTEYPQEVVL SGSHIDTVVNGGNLDGQFGAL AAWLAIDWLKTQYGAPLRTVE VVAMAEEEGSRFPYVFWGSKN IFGLANPDDVRNICDAKGNS/IC RCDEGLRIYSSERPTNS/VVRIL KPLLNCILNRA/DVLERITAWD KPDCH\TLHHHADLSGHFPEEIG PLLFAGFSSAWQNGPSAFSWQK HGSAQTSSIAVLHRTPRHAGCL AQCDFTRAFFQIMLKNYLRKK RWKKKIHFPNASGKSS/RAIPEG YVTTYGDVAKLGGIAPGRAPG GR/VQRQALLAEGAGTAEDGFT *VGEVEDAARDGP*TDAERTG* TYADAGRQDPQSAEDRQRANL HGNADR***RFASGGFHRGYHP RAAAGFCDHRKPACGNARRAG WPDRA*SKSSAYAFRYRYEHRL HAGRSG

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8886	39254	A	8945	1	1695	MRSDPDTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRFV TLEMKYGRIMLDTAKIIDEQDV PTHILSKLTFTLRNHPEGVVMK NFEVLQPLQNSLSGLPLWVSER ILQQINQLTHYEPVIGIMGKTGA GKSSLCNALFAGEVSPVSDVAA CTRDPLRFRLQIGEHFMTIVDLP GVGESGVRDTEYAALYREQLP RLDLILWLIKADDRALATDEHF YRQVIGEAYRHKMLFVISQSDK AEPTSGGNILSTEQKQNISRKIC LLHELFQPVHPVCAVSVRLHPV VALLQQFRTDDERTHRYHYDS QHRLVDYTRTQYEEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPQVTWYGWDGDRL TTIQNDRSRIQTIYQPGSFTPLIR VETATGELAKTQRRSLADALQ QSGGEDGGSVVFPPVLVQMLD RLESEILADRVSEESRRWLASC GLTVEQMQNQMDP\TEGTTAW Y/AEYDEWGNLLNEENPHQLQ QLIRLPGQQYDEESGLYYNRHR YYDPLQGRYITQDPIGLKGGW NFYQYPLNPISDIDPLGLSMWE
8887	39255	A	8946	605	1395	SMSLLKNIRLSSASKQCAACSG WPAAAGIRGVSGGQG*ARVSSS ANTATALSSRLLPGQNSVTVPH A*RMNCVLRVTPL\SKNRGGKP APSGTEGKGLPEVQPGQL\RAH GLPVSENLLEQDFYASGPNQK WAGDITYLRTDEGWLYLAVVI DLWSRAVIGWSMSPRMTAQLA AGCPKPLWGTPSFPGPACGLAP SSAGVLPRGFVPAVWLDSEDPE EYVGSSDFLTKMQSMKKVDLK KNRAATDADGQFSPRCCMPEK YAGSHN
8888	39256	A	8947	1	1914	
8889	39257	A	8948	1	4767	
8890	39258	B	8949	1	2294	

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8891	39259	A	8950	115	3551	NPALTRIVPAQQNLYTNTLLAA RIKQRLTEQFELMLRQAQIDFA GKAHSLTEAQANTTQVSAERD RLFKNYQRYLKGSQAAVNPFS ERDIDDARQNFLAQDALAQIQS QLDSLVNGEQSQIVSLKAQLAE AKYNLEQTIVRAPSNGYVTQVL IRPGTYAASLPLRPVMVFIPDQK RQIVAQFRQNSLLRLAPGDDAE VVFNALPGKVFSGKLAAISPAV PGGAYQSTGTLQTLNTAPGSDG VIATIELDEHTDLS
8892	39260	A	8951	845	1213	DKGEIGGWAAQTHRGSHEQGA RRVPEDRDARARRKNEEP\AAR PRTTNTRNGSRKGPERK/WADG RGHKAEAGRRKRRKRQ*KEEM RKIRQQESGGEKKRGLCGRPPG GGNNCMEGRERRGRKR
8893	39261	A	8952	843	1061	NRPPPVCACHRQVVLPVPVNR APAEKWQVPRVTLPGRQSTSW FAAVVYRN*YQYCALTAQRGR RSPRQLPHR
8894	39262	A	8953	1	682	MIRIPGCEDKLGADQQPAFVLY LEIDPHQVDVNVHPAKHEVRF HQSRLVHDFIYQGVLSVLQQQL ETPLPLDDEPQPAPRSIPENRVA AGRNHFAEPAAREPVAPRYTPA PASGSRPAAPWPNAQPGYQKQ QGEVYRQLLQTPAPMQKLKAP EPQEPALAANSQSFGRVLTIVH SDCALLERDGNISLLSLP\ITGIW CSD*H**PMIPRLLIPASVRSSSM VESAK
8895	39263	A	8954	1	1887	
8896	39264	A	8955	189	552	LFRGEKGARNEVLATRYYRQT VSGDFRHLHCLADQYALGGAY QF*AGLY*LHQAWEMNRGLQL LSDALGEQYAQHGNWRFLRNN DRFVFQILRSFEHDNSEDKPGP GMPPHGWRTQFWGG

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8897	39265	A	8956	263	3549	TGGPSSPSSHWKTPVVIYWDGT ALRCVFVPVLGETGAQRKRISA RKGSLTTSCPQGALSEHCPTTP APLPSQRRNHWMENISPFRSVG VSASRCSES*MRPWNSRMPRLG RSQGDSSSAL/MSTGVAFRGRF LKGGLPQAPAVAAATPWLCTQ GVAGETTPAVNVKYNVRVRVS EYISMHVHREVTARNVYVTQT RRPMTTFPTLAWETPHYHRRY GVSLLSSAWVQVGPPRYCRQT NALSNLPNFNLKSGADTQ
8898	39266	A	8957	1	1799	MMRDRLINH\AIRPACE*QLGA DQQPAFVLYLEIDPHQVDVNV HPAKHEVRFHQSRLVHDFIYQG VLSVLQQQLETPLPLDDEPQPA PRSIPENRVAAGRNHFAEPAAR EPVAPRYTPAPASGSRPAAPWP NAQPGYQKQQGEVYRQLLQTP APMQKLKAPEPQEPALAANSQ SFGRVLTIVHSDCALLERDGNIS LLSLPVAERWLRQAQLTPGEAP VCAQPLLIPLRLKVSAEEKSALE KAQSALAELGMVNSTRFSLHE HPDAERSPGQSGEQRQQPAVD DYAIVDEYGRHYRRAVAGTLL HVSVDSGTTQTVFMYTWLSMA LIIALPAFIFARVPNDTHQNVAIS RRKTESRNEVLATRYHRQTVS GDFRHLHCLADQYALGAPIPPD GTRRPILVNGAEVGAVIASPVE RLTRNTDINFDKQQRQTSWLIV ALATLLAALATFLLARGLLAPV KRLVDGTHKLAAGDFTTRVTP TSEDELGKLAQDFNQRASTLEK NQTPITSRGHPRIFLARHPAPAP TTLTSLALKIIRSPAFLPDTASEC AMAIDCYILAASTQAYKAASSL SLSVVLATSARFKTSSTSIWVKS SSTNSCE
8899	39267	A	8958	1348	2190	
8900	39268	B	8959	1	105	
8901	39269	A	8960	1	781	
8902	39270	B	8961	1	1716	
8903	39271	A	8962	754	807	
8904	39272	A	8963	821	875	FFSLFFFISLASGLSIL*W*FVFL WDRW*YPLYHFLLHLFDSSLFS SLLVLLVVYQFC

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8905	39273	A	8964	1	315	SGSVMPPALFFWLRIDLAMQAL FWFHMNFKVVFSNSVKKVIGS LMGTALNL*ITLGSMAIFTILILP YP*AWNVLPFVCVLFYFLEQW FVVLLEEVLHIPCKLDS
8906	39274	A	8965	42	403	GLCSVPLVYISVLVAVPKLFW* L*PCSIV*SQVA/SIPPALFFWLRI DLAMWALFWFHANFKEVFSNS VEKVIGSLMGMALNL*MTLGN MAVFTILILPTHEHGMFFHLFVS SFISLSSGL
8907	39275	B	8966	179	1225	
8908	39276	A	8967	342	407	
8909	39277	B	8968	143	3122	
8910	39278	A	8969	692	1360	MCGIISEGSILFHCSITLFWYQS HAVLVTVAL*YFLKSGGLMPP ALFFWLRIDLGMLALLWFHMN LKVVFSNSLNKVIGSLMVMAL NL*ITLGSMAIFTILILPIHEHGM FFHSFVSSFISLSSGL*FSLKRTF TSLVSWIPGYFIFFVAIVNGSSL MIWLSVCLLLVYKNACDFCTLI LYPETLLKLLICIRRFWAETMGF SRDTIMSSANRDNLTSSFPN
8911	39279	A	8970	2116	2418	FFSLFFFISLASGLSIL*W*FVFL WDQW*YPLYHFLLHLFDSSLFS SLLVLLVVY/PILLIFSKIKNKKP APGFIDFFEGFFVSLSPSVLL*S* LFLAFC*LLNVFALASLVLLIVM LGCQF*IFPAFSCGHLVL*ISLYT
8912	39280	A	8971	1	558	LYKNSVKYFHN*PVGNIMSNIPI VGALFSGPAFGIGILAAGVILAI MIIPYIAAVMRDVFEQTPVMM KESAYGIGCTTWEVIWRIVLPF TKNGVIGGIMLGLGRALGETM AVTFIIGNTYQLDSASLYMPGN SITSALANEFAEAESGLHVAAL MELGLILFVITFIVLAASKFMIM RLAKNEGAR
8913	39281	A	8972	1879	3735	
8914	39282	A	8973	16	452	VGQLFWKGYPLAGFPDPCAQS WKVAHVLLLRLGHIKSVSANG KEVTSKFHRKENLARGLHSRPR RGQRVRGGVAQHCEPR*TPPPA CRVRLPGCPVDPASPGRGRRTS AGTPEPALRHPHTPRGPVAART LPAEPGPARPSGLPP

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8915	39283	A	8974	158	531	CSLRRGPPDP/PGAYCKRRATG AASTRSLSGAVAGSPAHRCESR PLQAMGA\GGLPHPEGGRGGSG GRKRTDGPVCGCGERAPREYP DPSRSWRGPQRKPAPSQHPCLP RLSRGPGRHPEGPHQVR
8916	39284	B	8975	22	387	
8917	39285	A	8976	241	389	VASQAPGVRALQVGPAHSC*G RGHVSWPPPWPWGPPCCPLCL LNGLPNI
8918	39286	A	8977	1620	1936	TLFFFESESHSVTQDRVQWYDL \NSLQPPPPGLK*FSCLSLPSSWD YRRPPPCPANFF\FLVELEFHHV GQDGLELLTSGDPPALASQSAR ITGMSHCAQQNKHIL
8919	39287	A	8978	3	105	
8920	39288	A	8979	1	1821	MLKNFKKGFNGDYGVTMTPG KLRTLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIQMPLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWKNNTPSCTEKPQALIDLL QTIIQTHNPTWADCHQLLMFLF NTDERRRVLQAATKWLGEHAP ADYQNPQEYGKEESPAQFYER LCEAYHMYTPFDPDSPENQRMI NMALVSQSAEDIRRKLQKQAG FAGMNTSQLLEIANQVFVNRD AVSHTGAEHSVVTGPVAPLSK KTIDIIGAMGVSAKQAFCLPRT CTPGTKDYRLVQDLRLVNQAT VTLHPTVPNPYILLGLLPAEDS WFTCLDLKDAFFSIRLAPERQK LFAFQWEDPESGVTTQYTWTW LPQGFKNSPTIFGEALARDLQK FPTRDLGCVLLQYVDDLLLGHP TAVGCAKRTDALLRHLEDCGY KVSKKK\AQICQQQVRYLGFTI RRGV\RLGSERKQVICNLPEPKT
8921	39289	B	8980	209	2272	
8922	39290	B	8981	1	228	
8923	39291	C	8982	375	472	
8924	39292	C	8983	266	408	
8925	39293	A	8984	1	1105	

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8926	39294	A	8985	108	708	LTNQKKSRTRRIHSRILPEVQGG AAADRHCPIDRLGSLQDHHRRS RLLSQWSP*KSTHD*HGFS\YQS AEDIRRKLQQQAEFAGMNTSEL LQIANQAFVNRDAVSRKENHR DNERQAQRNTDLLAAAIRGVPP KRQGKGGPGKETQPGCQSLQR NQCAYCKEIGHWKNKCPQLKR KPGDSEQEAPDKDEGALLNLA EGLLD
8927	39295	A	8986	125	444	DCLAVKRASWVQPTGYSCKPL L/QGVLTYQRRQAAFPPLRRER LASSSRDKPKCAGKHTSSLVRA GDMQGTIVTGTEVLRLDMEPK FEDDQLRPVLLEHKVPRREMA
8928	39296	C	8987	80	325	
8929	39297	A	8988	566	1857	
8930	39298	A	8989	1	1037	MEEGWIRLPDGRVAAPQLLGA AVVLAVQETTHRGQESLEKLL GRYFYISPLSALAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWWVLGLTDFKN EAKELRLYKQEKREKAKRWKE TEKGFNGDYGVTMTPGKWRT YFEIDWSKLEVGWPSEGNLERS LVSKVWHKVTGKSGHSDQFPY IATWLQLVLDPPQWLRGQAAA VLVAKGQI\PRKDPTPPAEGNQ LLK/SLFDPTSEDPLQEME/PSDP SGALPLPGKDAPHS*AHSPCAS TRQTYP*ATRSRQERR*SLERNP YIGSSFKTQNWDTNAPERAVV
8931	39299	B	8990	1	2082	
8932	39300	A	8991	6	367	ENLNIKAPHAVVTLMTTTGPD WISNAILTKDFCLLCENTHISRW GCNTLNATTLLLVSESPVKHNC LEVLDSVYSSRPNLRDHP*TSV DWELYVDGSGFANPCKVTLKK ETSPAPVTPRS

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8933	39301	A	8992	1	2991	MLKNFKKGFNGDYGVTMTPG KLRTLCEIDWPTLEVGWPSEGS LDRSLVSKVWHKVTGKSGHSD QFPYIDTWLPQWVRGQAAAVL VAKGQIVKEGSRSTHRGKSTPE VLFDPTSDDPLQEMAKVIPVVP SPYQGERLPTFESTVLVPPQDK HIPRPPRVDKRGGEASGETPPL AARLRPKTGIQMSLREQRYTGI DEDGHMAERRVFVCQPFTSAD LLNWKNNTPSCTEKPQALIDLL QTIIQTHNPTWADCHQLL
8934	39302	A	8993	1	444	SSASTPETRAKFT*DNLCCASW QRLASANFRVLVDCILSDTFED LRLQCDAVNLAFGRRCEELED ARYKLHHHLHKAVE*GGGAEH VPH\RLREKLLEAEQSLRNLEDI HMSLEKDIAAMTNSLFIDRQKC MAHRTRYPTILQLAGYQ
8935	39303	A	8994	1	1576	MVQTDVLLPEPAPQTVSPCELP CKEYDVARNMGPGHRQLEVW FQNCYARYHQAFADCNQSERE LQGRESQQLAAETQALAQPTQ QDSTCRVGERLQDTHSWKSEL QHEVEVLAAETDLLLAQKQRL ERALDAMEVPFSIATDNMQCS QRHQHANLVRDYVETELLKAY PPAPSQCLKNCCSSRKPSACNK GACEVMETLTVQEEANPGTEG CRTRALAHKEEAEPIRNIQELLK RAIVQAVSQIQLNREHTEICEM DWLDKVEAYNLDETCGRHHSQ STERP/WTKFTQDNLCRAQRKR L\SSANLWVLVDCILRDTSEDL GLQCDAVNLAFGRRCEELEDA RHKLQHHLHKMLREITDQEHN VVALKEAIKDKKEPLHIAQTRL YLPSH\RPNMQLCREAAQFRAA FPG*ESFQWRLPRTSLPAPNWE FWVPFHPSRCILLPSPAPAHTPP TPPSW*VRWRSLYKSITALREK LLQAEQSLRNLKDIHMSLEKDV TAMTNSVFIDRQKCMAHRTCY PTILQLAGYQ
8936	39304	C	8995	99	442	

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8937	39305	A	8996	177	622	TESSASEKTTGEDGTRVFVSLL RSLLSLLPSAPLRHHPPSA*LSL CSCVSD*AVALIPQSAHHFPNIS *PFPLHCFAHAKPPVWIFHSH/S LWLP*AFLAPMTSFTDQVAVD DFLSIVYLFTFTPFLAFCGEPST ALATREQVWVESAS
8938	39306	A	8997	1	329	AAARPGRGSETGDWVLLCYPG WSAVV*S*LTTA/SELLGSRG*G SLLSLPSSWDYRLSAPCLANSK KPSER*GLSMLP*LVSNSWPQVI LLLGPPKALGLQAPGTMGLRP
8939	39307	A	8998	1	814	
8940	39308	A	8999	57	274	TASSSLTLVYGHRLCWLGPSHP *PSLWLP
8941	39309	A	9000	1	1236	
8942	39310	A	9001	1	1095	
8943	39311	A	9002	1	2313	
8944	39312	A	9003	166	494	FSQQLCGENHPHLRTENTQAQR AGVPLGVRILSRPGFP*LSTHSC FSCPLV*PPSQGQPGPLSLWTLC SAIQAPAELESCRSSCDRDGRSH WPRVSGGLWLSQVPRPRR
8945	39313	A	9004	3	974	MGESPAV*GYFVLAGMNSAGL SFGGGAGKYLAEWMVHGYPSE NVWELDLKRFGALQSSRTFLR HRVMEVMPLMYDLKVPRWAF KTVSQLRTSLLYDRLDAQEAR WMEKHGFERPKYFVPPDKDLL\ ALEQSKTFYKPDWFDIV\ESEV KCCK\EAVCVIDMSSF\TKFEITS TGD\QALEVLQYLFS\NDLDVPV GHIV\HTGMLNEGGGYENDCSI ARLNKRSFFMISPTDQQVH\CW AWLKKH\MPKDSNLLLEDVTW KYTGTGVRALYGDVEHESWLS CVRHAHHPDPICIAHTYLHLRS FSQADGREWRKVLDKHKIFLF ARSLC
8946	39314	A	9005	1	1872	
8947	39315	A	9006	1	2250	
8948	39316	A	9007	1	1257	
8949	39317	A	9008	1	1596	
8950	39318	A	9009	1	1584	
8951	39319	A	9010	1	1461	

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8952	39320	A	9011	110	993	TSTELSTPSQQNIHSSQHHIALV PKLTT*LERIKYLGIQLTRDVKD LFKQNYKPLL/NKIKEDTNKWK NIPCSWTGRINIVKMAILPKVIY RSSAIPIKLPMTVFTELEKSTLK FIWNQKRAHIAKTILSQKNKTG GIMLLDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIIPHIC NHLIFDKPDKNRKWGKDSLFN KWCRENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRSKTIKTIE ENLGNTIQDIVMGKDFMAKTP KTMATEAKIDKWDLIKLRASA QQKKLPSE
8953	39321	A	9012	1	1185	
8954	39322	A	9013	1	185	
8955	39323	A	9014	2	1321	
8956	39324	A	9015	2	1757	
8957	39325	A	9016	1	1008	
8958	39326	A	9017	1	1311	
8959	39327	A	9018	1	1152	
8960	39328	A	9019	1	526	MPSLTTPIQHSVGSSGRAIRQEK EIKGIQLGREEVKLSLFADDMIV YLENPIISAQNLLKLISNFSKVSR YKINVQKSQAFLYTNNRQTESQ IMSELPFTIA\KRIKYLGIQLTRD VKDLFKENYKPLLNKIKEDTNK WKNIPCSWVGRINIVKMATLPK MTWIANWLRNSLQAQ
8961	39329	B	9020	1	1626	
8962	39330	A	9021	1	2361	
8963	39331	A	9022	1	1140	
8964	39332	A	9023	1	2112	
8965	39333	B	9024	1	1065	
8966	39334	A	9025	1	1416	

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8967	39335	A	9026	1	1690	MPMVEELYGNYGIMADTTERV GQHKDAYQVILDGVKGGTKEK RLAAQFILKFFKHFTELADSAIN AHLQTVSGRQQLVKLVAEQAD LEQTFNPSDPECVGRLLQCTQQ AVPFFSKTVHSTRSVTYFCEQV LPNLGILTTAVEGLDIQLEVLKL LVEMSSFCGDMEKLETNLGKL FDKLLEYMPLPPEEAENGGNA GDEEPKLQFSYVECLLYSFHQL GQKLPDFLTAKLNAEKLKDFKI RLQYFARGLQVYIRQLHLALQ VKQCFAQYMEKENGIDAKILN KILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLGIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMGKLPFTIA/S/KRIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIV KMAILPKNWKKLL
8968	39336	A	9027	1	1575	
8969	39337	A	9028	1	2682	
8970	39338	B	9029	1	2088	
8971	39339	A	9030	1	2406	
8972	39340	A	9031	1049	1500	
8973	39341	A	9032	1	4341	
8974	39342	A	9033	103	366	NHPQLKVAGLKNGCCVCMCV CVC\CVCVRVWIWVCVCVCVC VCVCVC\CVCVC\CVCICVCI*V WVCVCVCLCLSLPKCWDYRHE PQRPA
8975	39343	A	9034	232	735	YLSGNGGEKGFCHALPDHRLR VLHQHPPHACVETDTVDLGITS ISLADVRVCVCMCVCVC\CVCV RVWIWVCVCVCVCVCVC\C VCVC\CVCICVCI*VWVCVCVC\ CVCVCVCIC\CVCVCVCVC\ CICVCI*VCVCVYVCVCVCLCT VLGIHSFLTARNAHQPIGH
8976	39344	A	9035	163	795	

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8977	39345	A	9036	34	758	RVPHRHGMKRVRQRHGMKRV PHRHEMKRVPHRHGMKRVPHR HGRKRVPHRHGRKRVPHRHGR KRVPAQVQDEEGHCQKPGRCV CMCVCVC\CVCVRVWIWVCVC VCVCVCVCVC\CVCVC\CVCIC VCI*VWVCVCVC\CVCVCVCIC\ CVCVCVCVCVC\CICVCI*VCVC VYVCVCVCLCLFYLVLQCFICS/ CIISGGQRWC*RKTMCSLPFAH SHHSFPGHFFLIFQSRSFQVSFHP
8978	39346	B	9037	34	156	
8979	39347	A	9038	3	419	GGENVKAINQQTGAFVEISRQL/ PPN/GDPNFKLFIIRG\SPE\QIDH AKQLIEEKIEVGWGGLWGFGL TARIPAHLPWLLSFLLG\PLCTV G\PGPGGPGPAGPMGPFNPGPF NQGPPGAPPQ*VSSASWVLRP/E GLLSWQEE*QTPFPFP*KCRAG ALIQAHFCGYHQQALSCL/PGR ACAFQHPSVHVQVSRLLSCPQA DAARPSSCFLSRPFPGAPLSLVV WVSGASPLKNIPTPGGPAA\PPP HHCSSIPFFSPAVPGGPLLTSTH PRAGAIPTPSGS/QPAPHDPSK* WALQPGATRGSPTVSILCLLGF EAGGLLSWQEE
8980	39348	A	9039	1	445	ATADPNAAWADDY\SHYYQQP PG\PVPCPAPAPAAPPAQGEPPQ PPPTGQSDYTEWAWEEYYKKI GQQPQQPGAPPQQDYTKAWE\ EYYKKQAQVA\TGGG\PGAPPG SQPDYS\AAWAEYYRQQAAYY GQTPGP\GGPQPPPTQQ\GQQQA

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8981	39349	A	9040	38	1297	TCVSALSVLASDDGTGPEKIAHI MGPPDRCEHAARIINDLLQSLR VGGPGC*RGWQGLQGSARPDR LPGFIILLLLLSCRVVPQGPP\GG PGMPPGGRRPKEEGQGN\WGSP WAGKMTFSIPTHKCGLVIGRGG ENVKAINQ\QRGAFVEICRQLPP N\GTANFKLFII\RGSP\QQIDHA KQLNE\EKMKGPLCPVGPGPGG PGP\AGPMGPFNPG\PF\NQGPPG APPHAKK\PPPHQYPPQGCGNT YPQWQQHAPHDPSISAGKAAA AAADPNAAW/AAYYSHYYQQP PGPVP/GPAPAPAAPPAQGQQP Q/QPGAPPQQDYTKAWEEY/YK KQAQV/ATG/GGPGAPPGSQPD YS/AAWAEYYRQQAAYYGQ/T PGPGGPQPPPTQQGQQQQWVA PETPSPRGVPLMPAAGAVWPE VPGVPTHRQGSIRWVQR
8982	39350	A	9041	1	1777	MPVLPVTATEIRQYLRGHGIPF QDGHSCLRALSPFAESSQLKGQ TGVTTSFSLFIDKTTGHFLCMTS LAEGSWEDFQASVEGRGDGAR EGFLLSKAPEFEDSEEVRRIWN RAIPLWELPDQEEVQLADTMFG LTKVTDDTLKRFSVRYLRPARS LVFPWFSPGGSGLRGLKLLEAK CQGDGVSYEETTIPRPSAYHNL FGLPLISRRDAEVVLTSRELDSL ALNQSTGLPTLTLPRGTTCLPPA LLPYLEQFRRIVFWLGDDLRSW EAAKLFARKLNPKRCFLVRPGD QQPRPLEALNGGFNLSRILRTA LPAWHKSIVSFRQLREEVLGEL SNVEQAAGLRWSRFPDLNRILK GHRKGELTVFTGPTGSGKTTFIS EYALDLCSQGVNTLWGSFEISN VRLARVMLTQFAEGRLEDQLD KYDHWADRFEDLPLYFMTFHG QQ\NIRTVIGTM\NHAVYVYDIC HVIIDNLQFMMGHEQLSTDRIA AQDYIIGVFRKFATDNNCHVTL VIHPRKEDDDKELQTASIFGSA KGGEWSAPHSTSSRPSAQPKSD STVAEAAPLASDFTAYWIWFLT WGRGRASRDREFGYLAALN

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8983	39351	A	9042	3	679	SPLIVSSARMHAGRDLPLYFMT FHGQQSIRTVIDTMQHA\VYG\Y DICHVIIDNLQFMMGHEQLSTD RIAAQDYIIGVFRKFATDNNCH VTLVIHPRKEDDDKELQTASIF GLSQRQAR\EADNVLDPAGTGK LGNRGQGKRYFAGVPKEPF*W EM*GVFPLEFNKNSLTFSIPPKN KARLKKIKDDTGPVAKKPSSGK KGATTQNSEICSGQAPTPDQPD TSKRSK
8984	39352	A	9043	90	317	GTLRKRYRAFHCRITIFKALTEV CKNFSALHCEFSWGFFFFCSFFF LASS*G*NCLPSQPQPCWFLQPP CPWQIL
8985	39353	A	9044	2	2136	PRLSSVLSEFITTHIYFLLSETTY NYEWNLISLYVVDPSRLAC*TV QLFFMLQLSVGLYVFNVGNDIC LHKMGSVTVLFFVTARRVNLPP VAVIKLMSSSSCISFLSLFLNLV ESTDDTEIVSYHWEEINGPFIEE KTYLCFFTFLFCFVFIFVFAIT*G VQTPYLHLSAMQEGDYTFQLT GLQT*CKEIILFHTVSVIPENNRP PVAVAGPDKELIFPVESATCLS YSKPHAPSLMLTTSMFYRGPSA VEMENIDKAIATVTGLQVGTY HFRFYSITGVLNQSLCFHFAIFD LENNSPPRARAGGRHVLVLPN NSITLDGSRSKKPRNWDPRIDSC PVIRVLSQDVIDGSDHSVALQL TNLVEGVYTFHFLML*SLCKCP SANPVSSLSPDPRKSGLVELTLQ VGVGQLTEQRKDTLVRQLAVG VSW*SPSDHVAVLSHCLLHSTV IVFYVQSRPPFKVLKAAEVARN LHIS*\SRDSLFCMLPSALHTS/S AGCLLKCSGHGHCDPLTKRCI* K*SWSTNSL*LCPLWFSCVSEW SIFYVTVLKS*LSVTFLKI*VELF IVPFRQKRTKIRKKTLNMY*VH LKYFTH*ILILPIAVRGMCNDYP HD*QLEVNHGVPPQMLLCFSLG IKHRSTEHNSSLMVSESVRSFD RDCLQSLNYLLSGLLQKEKNLQ KAGLTSPAPSLWEDKCSGRTEH AQSARLPLKEDTEKTLMQF
8986	39354	A	9045	47	157	FDKICIFKRQVTKSEVILNLTN* VL*YLEYHIRNIN
8987	39355	A	9046	1	393	
8988	39356	C	9047	274	357	

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8989	39357	A	9048	727	1089	
8990	39358	A	9049	175	608	CGWEYGN*A\DTMDEQYCKVC QAYKAPRSHHCTKCNTCVMK MDHHCPWINNCCGYQNHASFT LILLLAPLGCIHAAFIFVMTMYT QLYSFGMENNFFRKQNFYLSS WDWKEEGLKDPDFSIIQLGWK SFVFFHMDMGEVDGEGTF
8991	39359	B	9050	780	1166	
8992	39360	A	9051	3	681	HIRGPRYSGHHSAFGCPYSDMN LKKEATLHDRLREQTQAN\LES DSSHSKSKSLCSLNFNGKHEKV NSQPRLVQQAKCLKIKGKEDID LDNLFREYSVEQAQQVLHQSV SMSTVSAHPFRDLPLGREQHCK LLPGVADIRASQVARWTVDEV AEFVQSLLGCEEHAKCFKKEQI DGKAFLLLTQTDIVKVMKIKLG PALKIYNSILMFRHSQELPEEDI ASGQEVRG
8993	39361	A	9052	30	981	TQDPWPSLPVLWSRASSDPAAG HRAEHI*TYWPWKLEGT\DIWL VLYMPLVQPDNFIKKHSHLPTY CLFKEDVKFPFRTCRLTYCWLN YTEEITYLHTKKVSVGQSAVRE EFAAACTWSIRIGEKLAILLSLY LCRQQALLNMRMSVPIHESGV AQRSPVMDKLAQYSVEQAQQV LHQSVSMSTVSAHPFRDLPLGR EQHCKLLPGVADIRARQVARW TVDENLHGLIQTKQTPHLDESIS KGESPALVVTELRMCMTATEP LVPTKNPYQERGHIGDSFLHYT DQEPQPWDQSSVHPTPAPIYSV SSGFRVTRGSDI
8994	39362	A	9053	1	864	MVSALPEVGRAQILRLIAYIRSP APPVVGVERAARRPAQAFGLV ALPSTDATVFANQPLARACIGA ARHREPDAPGQSAWVGEECLK DALRSPETPKLGSLSPPCQDTRP GRASNDFSLEMGYSSLSAARLK IHGQVFQCCGPGPLRTL\HWTQ S*TYLNILALET*GAQNQP*EW QAVD*GAPGLFSHTLGVFPR/RL PQHPKQIICFQNYEYSVEQAQQ VLHQSVSMSTVSAHPFRDLPLG REQHCKLLPGVADIRASQVAR WTVDEPYSSAPRGPELSAGANS SRGA

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8995	39363	A	9054	1	1737	MKEKPAVEVRLDKWLWAARF YKTRALAREMIEGGKVHYNGQ RSKPSKIVELNATLTLRQGNDE RTVIVKAITEQRRPASEAALLYE ETAESVEKREKMALAQMIMPQ HDQLHRYLFENFAVRGELVTV SETLQQILENHDYPQPVKNVLA ELLVATSLLTATLKFDGDITVQ LQGDGPMNLAVINEINERAQNP LLCAFRCVNTYGSYECKCPVG YVLREDRRMCKAVFPYCQNES SDVLWQFDSTSQIFLKGTPKTT VRRGGEHNLKNPDECEDNPNIC DGGQCAGIPGRNRCLCYDGFM ASEDMKTCVDIDECSLPNICVF GTCHNLPGLFRCECEIGYELDR SGGNCTEDPDHSKSRSGRSQND WGRRRKT/S*KRSAVYR*RQLY IRRQPYAERPSLR*RQRP*IPCIR SQHGNRKRMRRRRIFI/STKRTT AAARTSSVKKARSFSRALKNA MLS*RTAPSVS*S*IMITH*KK** SR*SLQTR*LMKSSARVFSK*TA NGTWSL/HSRGSKVTIDGINSND IYMLGYVSNSLTGPYRPVDKTG LGLEMGLDPNDVTLTYSHFRVP EAEAAMWVSHAT

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8996	39364	A	9055	1	1743	MTTSTMTHMMTMHFPIIVCAD SRDDVDVTNDVNDHDDSAKR KSHRERPIAAKRTETK/KRRRRA RPKR/RTKARS*SAK*QTAQHT RTTAAIIMRDTQARRV*RPTKH AAEQRQNTTGKQRR*TKRVKA AKKEGE*RRRKMARRTTPQTR R*TRAKRRINRPRHGAKKRA*N /RRLKSAPKRHRVNRRDENART TTRHKKRRNRRVKRAERSGAE RTPYKQRHQQTREKRTCKRRQ TK/RRTKAK*T*RDHENDGTRA YNKTPKKAAKRTRNNLRIHNA TKGGDNRGQTRRA*TKPRKYR PDENRYNTSSPERTPRKRRGKS E/RRDKTAQRAQ*ADRYNSRKT QQRL*KGHTHTER*RQARMHT RHAQNLDTQHSTRLCNA*ST/C HDRRSSSTMCHRYDQLYSRSH ALTMIIVNKPLRQCIRMLSFHD RHRSLAIDGDSASTGSPAFRCV NTYGSYECKCPVGYVLREDRR MCKDTCTEKAFPAGGCEVDKT HTVPQERAYIHRTRLGRARTKK RDLYRRAHNDRRRQKSAAYYE STSVRRAHKYNSGKSDTQNGS HHRQKLRQYGDAGKSHYLQY NIHFMYPLFNT
8997	39365	A	9056	3	451	FFEMKSHSVAQAGVQCSGVILA HCNLHLLESSDSPASAFRVAGII DARPHAWLIFVFLVETGFHHVG QAGLELLS*VIHPPWPPKVLRL QHETPCPAVSLYLNQSPENNLE EDSLAMSNNRRSKGPGIWQNP GFEILALSTFLVESDLK
8998	39366	A	9057	53	343	
8999	39367	A	9058	14	234	CLFIRIFNVICYSKTCKNSIC\IGV IEIVIDGCMCGGEDGGGGGSV TAGGAPSPIETGSHGPPQPAVYF WRF

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9000	39368	A	9059	3	865	INFSVCVLARFFLGVVVLCVSC CWFRCVCACVCALAFPFCSCC VVVLCPVGCR\CTLFAV/CCCL/ CVCALFCGFLLRFLFCLCV/CPC S/CSARCRC/VCLALGAVVCFPP CSVVASCGCCDWVWLCCGAV VALVGLLCCVLVCAWSFRCG/C V/CLC/VCVVVVLVVRCC/VCW CGSCVVDCAGVVLVCC\LLVVL MMSL/CGCRVYSWYGVCWVCS VVCRVIDL/CPCCLCW/CVT*RG CWSVWCM/CTCCG/CVCGLAV M\CWCRCVVRLVCLCAV*FI\C ACVCFECAVGGFVGGCFLGSCL
9001	39369	A	9060	1606	1849	QGVSASLCREAGLTKISPGAPL WLPCSPGVTAECSGERTVRHN VTDRVCGVLGAVTSPGRN*RG HVTHKFCILCTDTVRDC
9002	39370	A	9061	2	682	ALEAVFGKYGQIVEVHLMKDC ETNKSRGFAFITFERPADAKDA ARDMNGKSLDGKAIKVEQATK PSFESGRRGPPPPRSRGPPRVL RGGRGGSGGTREPPSRGGHMD D/SGRDSYRGPPRRESLPSCR/D APPTRG/PPPSYGGSSRYDDYSS SRDGYGGSRDSYSSSRSDLYSS GRDQVGRQERGLPPSMERGYP PPRDSYSSSSRGTPRGGGRGGS RSDRGGGRSRY
9003	39371	A	9062	90	443	NVVYIQFIVLPYYLTIDPAGNSR SAPPTRGPPPSYGGSSRYDDYSS SRDGYG*SRDSYSSSRSDLYSSY DRIVSTLFFVSLNWDFGPKFCLF LVSASASPSIRSASSRASTSWCS AA
9004	39372	B	9063	12	1373	
9005	39373	A	9064	2	206	

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9006	39374	A	9065	2	1423	IHFREMASKSWLNFLTFLCGSAI GFLLCSQLFSILLGEKVDTQPNV LHNDPHARHSDDNGQNHLEGQ MNFNADSSQHKDENTDIAEK\L EEKVRILCWVMTGPQ\NLEKKA KHVKATWAQRCNKVLFMSSEE NKDFPAVGLKTKEGRDQLYWK TIKAFQYVHEHYL*DADWFLK ADDDTYVILDNLRWLLSKYDP EEPIYFGRRFKPYVKQGYMSGG AGYVLSKEALKRFVDAFKTDK CTHSSSIEDLALGRCMEIMNVE AGDSRDTIGKGNFFHPFV\PE\H HFNLKGYLPRTFWYWNYNYYP PVEGGELRFLFSTVTIRHSKALS LGVAQCSWLLKQQVISDDKTK RPDFPDRSRIMKERVQIVLYES GQAPVESSPPLPGYCSALFATCF QVTKGNFSQDPTQAILYTQADK IEGWMRASGERVAEQQSGQTA MDGGKKEAEWKRTRKAKYRD DVCSKHHPPYPTPVPPSLED
9007	39375	A	9066	1	311	
9008	39376	A	9067	1	493	ITRQHMRKAVPFQVPRKEILKL LKGKVVVGHALHNDFQALK*S TLGARPGDTTYVPNFLSEPGLH TRARVSLKDLALQLLHKKIQVG QHGHSSVEDATTAMELYRLVE VQWEQQEARSLWTCPEDREPD SSTDMEQYMEDQYWPDDLAH GSRGGAREAQDRRN
9009	39377	A	9068	45	365	NQAAASRPHCAARTMAGEEQA ACVHEDRTQCRGDKAAPQAAH LCGPPRGSGSVSTAPRAR*CPV CSSCPGPGAPEDTPEEVDVGAA SAHRSPRLCCSHLTHRWPKH

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9010	39378	A	9069	3	1687	ICVPKSVPSFLWAGRGPHCLLP CGSSSP*SGGLARA*GVFQGRA GVARAPSHLSFHNSPCVWSLST CCRAGSQDGPCPHAAGQGPGK QTSSGTGASSSPWTSCL*KSLPK \VCS*GLETTIGRGRVKPIKVTD TAQ*CAASVTAPLLSS*LQDGG STAKVTRCT/TAGGRAVYGTAE GKAFPEAPELTCRS/ALAALGT WPLPPLQVSCGLRNPSPDLPSV VGSRASV*TKSGSSPAKVWPLA EWFKSGSA\PVTGQEAWLLWA SDSSSELSLCPRKHAAPPHSAEH RQISQGLASSCWGAGGDKVVS ASMVGSAPGQCPMSALMTGSA SGQCPGHPCWSGTNADS*GRDP HRASRLLALPTASYEQ*PQPHW GSWTAHGQNGLGIFFQRVSWF V*GQTMVSRPRISGLGQPVCLS AASPQAAPLGSHDPTPAGR*GL EPGGRQPSSS*IYVWEAPPGLW VPPGPFLSH*SWRFGRTKAAPL KEPRPGGRCPGDRPSPRAEAGL PQTRKPALPAIGR/PKKACSLRR PRVILEQSSQHLAAALSSWMQP ALLETGGKAVFFTPGGL

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9011	39379	A	9070	66	1956	PLLAIPAHSTFPARKPEEPPRPD* LCPHIHCAAV*GEIRTVP/SKTV RGVATRTRPRSASSLGTTTGLR VSSVRRVQLSIKPGCSRVNENSS NSPCSSSQPGT\SVLPCPTVCRE AGP/AGP*PPG*ALSLPAAGFTT ATEWKQSQLSSGG*THSGEDM GRATAAATEKAQEQCMLREKL GTRQKAESGSRGA\AGLQHFCS APRTAWQPRASRA/RAGVRAW PCADPM*PPSHSPSFPKPFIPAA/ PGAQTLGAAGVEHVAGSARIPC CRTGLE/PHPHSPRRTLERQARI SGAGRRSSPNAATGARPRPAAG SPVSARRAPRRRPA*SSPCSGPW TAVSAPRSPGPRGGGRPPSPGR RRPCCSVFSGGASPSSARVSSPS GSCSASPPAAPA\PGASGAVVA GPVVGSPREHGG*LRPPLPRLG VPGLLAARTSGAEVIHEQAAAQ GTAADTPGAPGLLLAPAAAGA V/TRPGPPGASGCPRPAPRPPTP ASRSGRP\VPGGGRGRRGGRGA GGEALQGAVVGGQVGGSGAL A/ATARGSPAAGVSRWTAPRCR HRRSDASASGTPARFPGAGRKG RTLWQ*SWRSAPPPGLSELL*G LPRPLPESGRSKAPLPSGSTPLPS GRTPLPSGRSPSTRRSPS
9012	39380	A	9071	95	1423	GLENKRAKGTEAHTRACP*GK STEQDTTWTNTGRNEQQGPRP KGEQTQRKTERKPGRERQVQV LSSPPGRWC*DVGPLGGLPSRA KAEAALTAAQKAQGRRGSPGS LPKSSPLPSAPGKR/TPPRGHLL VPLPSPYYPALLSQHPPQGPPCG ASAPPSALLQRAPPPGTRTL\QR PPGPRVTCGTTP/MAAKAKSQS NAPRGSLLKKSNSFYNIPLKQV SCLITISKHSRNEVSVYQTSRPR AAATDVPRT\PSLSVGCSWSCT RGHWPSSCCPTAPRGQGL*EHS QGPGSRSKLPWPTGPCGGLTPS CWSLAGSAGERVDLNQAAASR PHCAARTMAGKTLSGGCGCVD VGAASAHRSPRLRCTTSPTDGP NTERGSRKTGWTPGPPGFWPCP RPPTSNTTTPLGLMDSARPGKA PAPFTDFRTPSGLLLPGWAVRA RREEDGCG

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9013	39381	A	9072	42	380	LGAPCTPPRSAPRTGRPEYA*A RG*PVGDLCRGPEAVVSTQVLL PRGLQ*NFAVLLLQMSCATPPP NCALKGCV*VPLEQSPFFHQAV ACREWKRGKGMVCGGNASPQ RTEA
9014	39382	B	9073	116	341	
9015	39383	B	9074	52	190	
9016	39384	B	9075	70	310	
9017	39385	A	9076	1349	2456	HCSVPGAEWPRKPPAQICPQLT SRPHLSSPRSLSPGCGHSPGPG* SPQPPVMSLHEGPPRGPQV/PSP VANPQPKPWLLRSVDLPVPWH LPTVDRTTSL/APSLQSDV/PAPS GAL*PSGRACSGV/PPID*APEA ALSAAAPRPSLGSGQNASGLPA ASLPPQDSSQPHKTVPSPARSVP PLGAQARAAPPRLWCPHALVS G*EASPEAVSVAAGPPVPGPTPS TSGSTASHSRRGC*SPR*TPAPP RRDHGRSAAFEVLAAAASAQP CASQGGPRPTGAGRTPSPLGLP FSRGPPAASARPFCRHPSL*FSW *SSPSGLSLSDTPHSPRRPLGPV CGLRAPCPPQIPACRVPAAHSQ RWPGSSSRSCRCQCC
9018	39386	A	9077	462	739	ACEPMVLFCLLALLLQDLFLGS YPRVLAAFDIQVFFLGTSDRM* NTG\LEYFMLNSWLWLLNRL*S WGELCHFIPLHSPVKRGLNFYL QEFFI
9019	39387	A	9078	1	678	GTRVNMILMKMGFSGIVVHQE SVCATYGSGLSSTCIVDVGDQK TSVCCVEDGVSHRNTRLCLAY GGSDVSRCFYWLMQRAGFPYR ECQLTNKMDWLLLQHL/KRNF LSFRSRTSLGFRTMSFRFRHPDS PALLYQFRLGDEKLQAPMALF YPATFWICWTGK*RPLHTDLRA ILKILTMNITCWPHKAHENSLQ KLLLTESLHPNLLDLKGIFVASP LIFQKDSIPR

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9020	39388	A	9079	227	1980	GERLRYGVTENGKEKGGEKEK EQRGVKRPIVPALVPESLQEQIQ SNFIIVIHPGSTTLRIGRATDTLP ASIPHVIARRHKQQGQPLYKDR WLLREGLNKPESNEQRLNGLIM VDQAIWSNKMSNGTRRNPVSP EQARSYNKQMRPAILDHCSGN KWTNTSHHPEYLVGEEALYVN PLDCYNIHWPIRRGQLNIHPGP GGSLTAVLADIEVIWSHAIQKY LEIPLKDLKYYRWILVIPDIYNK QHVKELVNMILMKMGFSGIVV HQESVCATYGSGLSSTCIVDVG DQKTSVCCVEDGVSHRNTRIFS WRSGHLW\VQDHEFQIRHPDSP ALLYQFRLEDEKLQAPMALFYP ATFGIVGQKMTTLQHR\LRAILR ILTMNITCWPHRANKNSLQKLL LTESLHPNLFEFERGFLWASPLI FQKDSIPRR*IWGLHREMA*WP ATIPRRPLTALMSRKTAISLFEG KALGLG*SPSSIAIDCCSSDDTK KKMYSSILVVGGGFDVFIKASR IFCSTEFSTKCPPSLQADYLKM WM*SQGLKDMDPRLIAWKGG AVLACLDTTQELWIYQREWQR FGVRMLRERAAFVW
9021	39389	A	9080	1	756	MRRIVALVETGEQPFGAATVGS RFGCLEDLGTDQRERHDHEMA AAHTYFIGDGDTLTEDEDEDT WGMAKGHHAINIEGFKLARVE DEMQFQEREPEKVKIRGRTRGY TFIMLAALAAAEAEDMQVGEE L\C*KVSLKASQLGQMALMLQS VTVQIGMVYGLPACGAQVNLQ DDKGSMVL/MCASKHGHMEIIK LLLAQLGCNVHLQDNDGSTML SIALEVGHKGITVLLYAHISFAK AQSPGTPRLGMKPQSFI
9022	39390	B	9081	5	5440	

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9023	39391	A	9082	1	4294	WAVFDGNYYYYLPWAHTKPV VTLTSYWEDISHRLDAVNALLA MAERLQTNIEALKSGIQGKIPA NQLAELWLKLIDEVIEDTRYTL PLTEGKANVTVLDTQIRKLRSR SLSQIHEAAVRMRSEATDVKST LAEIEDWLDKLMQLTEEPQNS MPDIIIWMIRGEKRLAYARIPAH QVLYSTSGENASGKYCGKTQTI FLKYPQEKNNGPKVPVELRVNI WLGLSAVEKKFNSFAEGTFTVF AEMYENQALMFGKWG
9024	39392	B	9083	1	339	
9025	39393	A	9084	2	1767	KLYRGKSDENEDPSVVGEFKGS FRIYPLPDDPSVPAPPRQFRELP DSVPQECTVRIYIVRGLELQPQ DNNGLCDPYIKITLGKKVIE\DR DHYIPNTLNPVFGRMYELSCYL PQEKDLKISVYDYDTFTRDEKV GETIIDLENRFLSRFGSHCGIPEE YCVSGVNTWRDSLR\PTQ\LLQ NVARFKGFPQPILSEDGSRIRYG GRDYSLDEFEANKILHQHLGAP EERLALHILRTQGLVPE\HV\ET RTLHSTFQPNISQGKT/LQMWG GMFFPKSLG\PPGPPF\NITPRKA KKYYLRVIIWNTKDVILDEKSIT GEEMSDIYVKG\WIPGNEENKQ KTDVHYRSLDGEGNFNWRFVF PFDYLPAEQLCIVAKKEHFWSI DQTEFRIPPR\LIIQIW\DNDKFS\ LDDYLGFPRTLTCRHTIHFLQK SPGGNCRVWT*FPGPSKAMNPL KAKTASLFEQKSMKGWWPCY AEKDGARVMAGKVEMTLEILN EKEADERPAGKGRDEPNMNPK LDLPNRPETSFLWFTNP\CKTM K\FIVWRRFKWVIIG\LLFLLILL LFVGRAPLTLLPNYFVQWKIVK PNVLTKGKGFISRVIQQ
9026	39394	A	9085	2	407	

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9027	39395	A	9086	15	759	SARPSHDYSHYYGTIEYLCYKI LGDIIENSRIVLQINNACLAADD F*TKYEREQT/LA/RTDLEMQTE GLKEELAYLKKNHEGEINALRG QVGGQISVEVDSALGADATNIL SDMQSQYENRKDAERWFTSCT EELNWEVVGHMEQLQMNRSQ VTDLRCNLQGLEIELQWQLSM KAALEARFGPQLAQIQALISSIE AQLGDVRADSERQNQEYQLLM DIKLWLEQELATYLSLLEGQEE HYNSLSTSKIL
9028	39396	A	9087	3	2026	AGPWDRMGAMGSLVGGDLGL VWGCAGEGFAGIPFSPCALTQC EGNQGTRAKWVQTSTRILKGQ VKQARGAQVTPYSPLWHGKLG RAAPTFNAPGRWLLPLLLPPPL L*ITTCLLGKRTLQEALSLKLQE LRKVCLQEAVRAWP*GYQAGR LGGGEELGPLGRPPTARAYPPP HPNQAHHSLCPAEV/MQMGVE SKRVGRGDRYRGVARR\MALA PDLSTEQRRRRRQVQADALRRL HELEEQLRDVRARLGLPVLPLP QPLPLSTGSVITTQGVCLGMRL AQLSQGEHPLVRVGEWTLANG RGRAGMGDSYPPNLPPTPTSL* PIPFIHPVSGGSPERRTPWKPPPS DLYGDLKSRRNSVASPTR*E*A PPPLRRSWEWDSKPGLAEGPAS DRASLFVARTRRSNSSEALLVD RAAGGGAGSPPAPLAPSASGPP VCKSSEVLYERPQPTPAFSSRTA GPPDPPRAARPSSAAPASRGAP RLPPVCGDFLLDYSLDRGLPRS GGGTGWGELPPAAEVPGPLSR RDGLLTMLPGPPPVYAADSNSP LLRTKDPHTRATRTKPCGLPPE AAEGPEVHPNPLLWMPPPTRIP SAGERSGHKNLALEGLRDWYI RNSGLAAGPQRRPVLPSVGPPH PPFLHARCYEVGQALYGAPSQ APLPHSRSFTAPPVSGRYGGCF
9029	39397	A	9088	1	136	
9030	39398	A	9089	14	310	TFLFIYFFFTETESHS\VPRLECS GVISAHCNLHLLGSNNSATSAS *VAVITGACHHAWLIFVFLVEA GFCHVG/RRLVSNS*PQVIRLPW PPKVLGLQA
9031	39399	A	9090	1	436	
9032	39400	C	9091	75	410	

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9033	39401	A	9092	1	6691	MVNTYREVKEGPVILEDVLIEV FRTLYSQCKAELDLQTEPPFSK DHAQLSSKLRENKKTAELIKTA NLLFNSFEPYYMWDYVARWFE ECCRRTLHVRLQIGPGDSNDSS ELQLTNFCLLVDFLLDIVSLETY IEIQTEHLPQLLLRMISALTSHL QTLHLSELTDSLRLCSKILSKVQ PPLLSASTGGVLQFPSGQNNSV KEWEDKKVSSVSHENPTEVFE DGENPPSSRSSESGFTEFIQYQA DRTDDIDRELS
9034	39402	A	9093	293	687	PTAKVYIFSIFLTYHIVCCINTSS LFGFLQKNPEEDNSGRTLG\WE PGHLL\LTICTVRSMEQLLPFFN VLSQVFNSKVTSRCGGHSGSPI LYSNAFPNKDMKLENHKPCSS KARQKIEEMVEKDFLEGMIKT
9035	39403	A	9094	3	4173	IPMVVSDFDLPDQQIEILQSSDS GCSQSSAGDNLSYEVDPETVNA QEDSQMPKESSPDDDVQQVVF DLICKVVSGLEVESASVTSQLEI EAMPPKCSDIDPDEETIKIEDDSI QQSQNALLSNESSQFLSVSAEG GHECVANGISRNSSSPCISGTTH TLHDSSVASIETKSRQRSHSSIQ FSFKEKLSEKVSEKETIVKESGK QPGAKPKVKLARKKDDDKKKS SNEKLKQTSVFFSDGLDLENW YSCGEGDIS
9036	39404	A	9095	5	1055	FDLERVRNLTYMVTRREKIKRS VCKVQEQIFNLYTKLLEQERVS GVPSSCSSSSLENMLLFNSPSVG PDAPKIEDLKW/PFCISSENKWV LPWVSFG*KRPIKSRILLQN*PW K*RQNPAEAARPVW*KGGDGG PRELFGFRKDLCRSTSHISTTEK WCGDARPWEKKRQSFSL*SH*R RLKGRIF*TESQAS/PGPQMCPR GIWTTQELPPPLEWGSQHLGTR KEIVPKCNGSLIKVNYNQTAVK VPTTPASPVKNWGGFRIPKKGE RQQ/PGRGPRWGLPPALRLPIFG LRPSS\TKERAKSKLKSDNEND GYVPDVEMSDSESEASEKKCIH TSSTISRRTDIIRRSILAS

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9037	39405	A	9096	3	1136	FDIPFPKIGKLIKSNVPELRGHFP LSITLVLRLMLLASKGDDPEDA KAKVLSVLKHSLLSFKQPRVM DMLKLYFLFSLQFLGGKRAI*IQ EG*SYGVCWDLVFTFGIYPWNL SNLVFVSFLVNGLFHDLCQPTR KGSKHFSQDVMEKLVLVLAHL FGRRYFPPKFQDAHFEFYQSKV FLDDLPEDFSDALDEYNMKIME DFTTFLRIVSKLADMNQEYQLP LSKIKFTGKECEDSQLVSHLMS CKEGRVAISPFVCLSGNFDDDL LRLETPNHVTLGTIGVNRSQAP VLLSQKFDNRGRKMSLNAYAL DFYKHGSLIGLVQDNRMNEGD AYYLLKDFALTIKSISVSL/HVT YCENEDDNVVLAFEQLSTTFW
9038	39406	A	9097	2	522	
9039	39407	A	9098	3	1080	FLLPFSHQSKKENSDQLMTLFT SFNSLHSAMESFFQATGNSTNL ADDGKRRTVVTPVILTKIDGVN VDTHHIPVNVTLRRIAHGADAV AARWDFDLLNGQGGWKSDGC HILYSDENITTIQCYSLSNYAVL MDLTGSELYTQAASLLHPVVY TTAIILVLCLLAVIVSYIYHHSLI RISLKSWHMLVNLCFHIFLTCV VFVGGITQTRNASICQAVGIILH YSTLATVLWVGVTARNIYKQG H*KS*KMPRIPDEP/RTFNQDQW LRFYPDLVGGYPPSLVLRA*LA AANIKELRQSAKPHPY/WLGW HGNPPWEAFYGPASFSTFVNC MYFLSIFIQLKRHPERKYELKEP TGQQQRLACQ
9040	39408	A	9099	1	307	
9041	39409	A	9100	2	286	

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9042	39410	A	9101	35	1211	EKDLLWEEKFPDRTTVTELPQT SHVSFSEPDIPSSKSTELPVDWSI KTRLLFTSSQPFTWADHLKAQE EAQGLVQHCRATEVTLPKSIQD PKLSSELRCTFQQSLIYWLHPAL SWLPLFPRIGADRKMAGKTSP WSNDATLQHVLMSDWAVSFTS LYNLLK\KNFSPYFYVCTYQFT VLFRAAGLAGSDLITALISPTTR GLREAMRNEGIEFSLPLIKESGH KKETASGTSLGYGEYVIKITL/S SSTDLWTHEIDLHRNSL*NRDS NCSNF/LREQAISDEDEEESFSW LEEMGVQDKIKKPDILSIKLRKE KHEVQMDHRPESVVLVKGINT FTLLNFLINSKSLVATSGPQAGL PPTLLSPVAFRGATMQMLKARS VNVKTQALSGIQRPI
9043	39411	C	9102	48	464	
9044	39412	A	9103	1	140	MNRLKKEWMLEHIVENNSGM ESQDIKGHFHAADKDLLEMGY LQKRGLIGLTVLHGWGGLTIM AEG*KRSGCLSTLWKITPAWNL KTLKAIFMLLIKTYLKWAIYKR
9045	39413	B	9104	1289	2767	
9046	39414	A	9105	3	1278	INNTNTFRVLPHPSFVYTAKFHP AVRELVVTGCYDSMIRIWKVE MREDSAILVRQFDVHKSFINSL CFDTEGHHMYSGDCTGVIVVW NTYVKINDLEHSVHHWTINKEI KETEFKGIPISYLEIHPNGKRLLI HTKDSTLRIMDLRILVARKFVG AANYPGEDS*YFD/VH/GGTFLF AGSEDGIVYVWNPETGEQVAM YSDLPFKSPIRDISYHPFENMVA FCAFGQNEPILLYIYDFHVAQQ EAEMFKRYNGTFPLPGIHQSQD ALCTCPKLPHQGSFQIDEFVHT ESSSTKMQLVNQRLETVTEVIR SCAAKVNKNLSFTWPPAVSSQ QSKLKQSNMLTAQEILHQFGFT QTGIISIERKPCNHQVDTAPTVV ALYDYTANRSDELTIHRGDIIRV FFKDNEDWWYGQHRERGQEG

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9047	39415	A	9106	1	1249	MAVLIFLGCLLGGIAIGLPIAWA LLLCGAALMFWLDMFDVQIMA QTLVNGADSFSLLAIPFFVLAGE IMNAGGLSKRIVDLPMKLVGH KPGGLGYVGVLAAMIMASLSG SAVADTAAVAALLVPMMRSA NYPVNRAAGLIASGGIIAPIIPPSI PFIIFGVSSGLSISKLFMAGIAPG MMMGATLTLGKRARFTEDDTR ERDAISVINHQRNAVLIRQRVK LQQLFVIRVLAMRIFVYGSLRH KQGNSHWMTNAQLLGDFSIDN YQLYSLGHYPGAVPGNGTVHG EVYRIDNATLAELDALRTRGGE YARQLIQTPYGSAWMYVYQRP VDGLKLIESGDWRVLRWLRVH SIDVPDPIFGLTVTGDRTDRAG KTSPAQAGCKLFLTNPLGIGVL TTAEKKSLLKPEHQGLATEVM CRMNIAGASFANIEGVKAMTD VTGFGLLGHLSEMCQGAGVQA RVDYEAIPKLPGVEEYIKLGAV PGGTERNFASYGHLWLR*LAL AP/LEVVEANGSL*CSGERGCL YGQTTTIQLNFRPAFCPEHAIAG QKVAILRLNMQIDIKRVSSRTH GNHFTNFKFTVQHYRSCLT

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9048	39416	A	9107	162	2106	KMSKLKIAVSDSCPDCFTTQRE CIYINESRNIDVAAIVLSLNDVT CGKLDEIDATGYGIPVFIATENQ ERVPAEYLPRISGVFENCESRRE FYGRQLETAASHYETQLRPPFF RALVDYVNQGNSAFDCPGHQG GEFFRRHPAGNQFVEYFGAVPC RLVIPALKKQRKLSDLETAIVV VDRFSGEVRAMVGGSEPQFAG YNRAMQARRSIGSLAKPATYLT ALSQPKIYRLNTWIADAPIALR QPNGQ\ESVRVMLVDALTRSM NVPTVNLGMALGLPAVTETWI KLGVP\KDQLHPVPAMLLGALN LTPIEVAQAFQTIASGGNRA\PL SALR*TIAEHGKELYQSFPQAER AVPAQAAYLTLWTMQ\QVVQR GTGRKLGAKYPNLHLAGKTGT TNNNVDTWFAGIDGSTVTITW VGRDNNQPTKLYGASGAMSIY QRYLANQTPTPLNLVPPEDIAD MGVDYDGNFVCSGGMRILPV WTSDPQSLCQQSEMQQQPSGN PFDQSSQPQQQPQQQPAQQEQ KDSDGVAGWITDMFGSNEHLS GYELDSYPLSSARRRARFTEDD TRERDAISVINHQRNAVLIRQR VKLQQLFVSNHIACWIRRPGDA NHPGFFANMQMLKIDVVFKLA FRQQFNIRTRRDKQIFFQSGVT
9049	39417	A	9108	1	66	
9050	39418	C	9109	79	150	
9051	39419	A	9110	2	475	GRGRWGAPRLRGAL*DP*GHF LGQQPRPQLHSPAPDR\PAPTPT DAEGL/PPAAAAAAAGATARVP GSRGG*GQAAEELHEAGEAQA CRGGTEDEEHG**HLCHGRAS* CPGVSGSTGSPHPSPSMAPDDT SGLLEFVGVPLQTLFAWVSPAE AAEQQRL
9052	39420	A	9111	171	462	PTSMGHLYSFPGN*SHAHYHPI KT*SPLPHSTPISNPSA\PLKGLK PVITRLLQHGLLKPINSPYHSPIL PVLKPDKAYKLVQNLRLINQIV LPIHSM
9053	39421	A	9112	1	573	
9054	39422	C	9113	100	297	
9055	39423	A	9114	1	1401	

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9056	39424	A	9115	24	482	VGSGDLPWEGNPLSSCSLLHEK DPPTTSGPQT/GP/GPRNISPILNR AAPRQAQLGPNSSSASAPPPYN PFITSPPHTWSALQFRFVTSPPPP AQQLTLKKVAGAKGTVKEHFC HDLPASSMQSNYPVHDSGHLT TGPSLFKPTLNIEYSTGHAP
9057	39425	A	9116	1	489	
9058	39426	A	9117	1	642	
9059	39427	A	9118	237	748	ETNPLSSCSLLRDKDPPTTSSPQ THQPKKH\PPISNPAAPHQAELG PNPSSASAPPPYNLFITSPPHTW SGLPFRSVTSPPPPAQQFTLKKV AGAKGTVKTITDIELQVTLTVE ARLRPGEINSHVAHTKPVWWS LHTDTCDIWCRRPGTGGLLQET SPLSSPSLCEEIHL
9060	39428	A	9119	63	255	WVSGSVQVKVERGWDEGCKGI VKKACLTYTNRIMHCVGRY*A *ESIWVWHHGVNRQNNLVDKA
9061	39429	A	9120	24	389	SDVKANLSTGGPVGCGGDTL/P VAEKPSDAVEAPGV*APSAGG AGPA\PSPGLEPSGAPPPP/ALPP RAVLDSGLAPGRPLPLASSNP/P PAGRRLLLCTSPGRRGGAAGSG PRCPESKSIPLRCL
9062	39430	A	9121	704	867	CVKECLDVRHLRPFAYFTTRII* ILQDGKIQSAIF/CVIWNYCRVCI GVKRHSRRK
9063	39431	A	9122	1	7068	
9064	39432	A	9123	2	165	LLKRELNFDFYKISTTKERHLQ QS*PKDS\VPSLLASQTPNAPFL APQRRLCLA
9065	39433	A	9124	1	148	IRHSVNLLRAG/RIFVFEPPPGLK ANTQRTFESGMKHVRIIYMMEF HVFM

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9066	39434	A	9125	1	2340	QFGIWLDSSSPEQTVPYLWSEE TPATPIGQAIHRLLLIQAFRPDR LLAMAHMFVSTNLGES\FMSIM EQPLDLTHIVGTEVKPNTPVLM CSVPGYDASGHVEDLAAEQNT QITSIAIGSAEGFNQADKAINTA VKSGRWVMLKNVHLAPGWLM QLEKKLHSLQPHACFRLFLTME INPK\VPV\NLLRAGRIFVFEP\PP G\VKANMLRTFSSIPVSRICKSP NERARLYFLLAWFHAIIQERLR YAPLGWSKKYEFGESDLRSAC DTVDTWLDDTAKASGRQNISP DKIPWSALKTLMAQSIYGGRV DNEFDQRLLNTFLERLFTTRSF DSEFKLACKVDGHKDIQMPDGI RREEFVQWVELLPDTQTPSWL GLPNNAERVLLTTQGVDMISK MLKMQMLEDEDDLAYAETEK KTRTDSTSDGRPAWMRTLHTT ASNWLHLIPQTLSHLKRTVENI KDPLFRFFEREVKMGAKLLQD VRQDLADVVQVCEGKKKQTN YLRTLI\NELVKGILP\RSWSHYT VPAG\MTVIQWGVPISARRI\KQ LQNISLAAASGGAKELKNIHVC LGGLFVPEAYITATRQYVAQAN SWSLEELCLEVNVTTSQGATLD ACSFGVTGLKLQGATCNNNKL SLSNAISTALSLTQLRWVKQTN TEKKASVVTLPVYLNFTRADLI FTVDFEIATKEDPRSFYERGGG
9067	39435	A	9126	3	6375	HKVAAPDVVVPTLDTVRHEAL LYTWLAEHKPLVLCGPPGSGK TMTLFSALRALPDMEVVGLNFS SATTPELLLKTFDHYCEYRRTP NGVVLAPVQLGKWLVLFCDEI NLPDMDKYGTQRVISFIRQMVE HGGFYRTSDQTWVKLERIQFV GACNPPTDPGRKPLSHRFLRHV PVVYVDYPGPASLTQIYGTFNR AMLRLIPSLRTYAEPLTAAMVE FYTMSQERFTQDTQPHYIYSPR EMTRWVRGIFEALRPLE

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9068	39436	A	9127	3	617	SWFQPPSGPPWPGA\PPPPPLAR VNPGV\PSLTTSLMDVEP*AQV ELPSHPRVPSPAPGPAP*VLEPP RSLLTSVVGPQGPSWAGGGMA VRQALEEAACRDPCIAISSWAG GDRPLWWLDGLLLRRVYPDSC PPCPSRIPAIFGASLQGSINPILQ MRKLFPHDMDLL*GQDPFSCR RPESWNRDVGWLALGVFCLVP FSLVGSLN
9069	39437	A	9128	1	702	
9070	39438	A	9129	1	1317	
9071	39439	A	9130	1	2641	MGLKARRAAGAAGGGGDGGG GGGGAANPAGGDAAAAGDEE RKVGLAPGDVEQVTLALGAGA DKDGTLLLEGGGRDEGQRRTP QGIGLLAKTPLSRPVKRNNAKY RRIQTLIYDALERPRGWALLYH\ ALVFLIVLG\CLILAVL\TTFKEY ETVSGDWLLLLETFAIFIFGAEF ALRIWAAGCCCRYKGWRGRLK FARKPLCMLDIFVLIASVPVVA VGNQGNVLATSLRSLRFLQILR MLRDGPGEGGTWKLLG\SAICA HSKELITAWYIGFLTLILSSFLV YLVEKDVPEVDAQGEEMKEEF ETYADALWWGLITLATIGYGD KTPKTWEGRLIAATFSLIGVSFF ALPAGILGSGLALKVQEQHRQK HFEKRRKPAAELIQAAWRYYA TNPNRIDLVATWRFYESVVSFP FFRKEQLEAASSQKLGLLDRVR LSNPRGSNTKGKLFTPLNVDAI EESPSKEPKPVGLNNKERFRTA FRMKAYAFWQSSEDAGTGDP MAEDRGYGNDFPIEDMIPTLKA AIRAVRILQFRLYKKKFKETLRP YDVKDVIEQYSAGHLDMLSRIK YLQTRIDMIFTPG\PPSTPKHKE VFRKGQHFTFPSQQSSRGLNHM *ARPST\SEI\EDQRH*WGKFVKS LKGQV\QGLGRKLDFLVDMHM QHMERLQVQVTEYYPTKGTSS PAEAEKKEDNRYSDLKTIICNY
9072	39440	A	9131	353	477	QNEILPQISKSNNEI*SRSPH*ITR NLNNSNKMAHKMKFAN
9073	39441	C	9132	170	310	

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9074	39442	A	9133	1	859	MSCGRPPPDVDGMITLKV\DNL TYRTSPDSLRRVFEKYGRVGDV YIPREPHTKAPRGFAFVRFHDR RDAQDAEA\AMDGAE*EGRAL RI\QVARYGRRDLPRSRQG/PTP RGRSRGGGYGRRSRSYGRRSRS PRRR\HRNRFFCPSCSRSRRRGR YRGSRYSRSPYSRSPYSRSRYSR SPYSRSRYRESRYGGSHYSSSG YSNSRYSRYHSSRSHSKPGSSTS SRSASTSKSSSARRSKSFSVS\RS RSR\SRSSSMTRSPP\GVSKRKSK SR\SRSKRPPKSPEEEGQMSS
9075	39443	A	9134	161	332	SCLNQLN/YLEMWKLFRKAQE DHTLGRDISYVAEVRPGEAGGR AHTGDSLLTMNPSFL
9076	39444	A	9135	1123	1489	LQTILQGHSNQNSMVLVPKQR YRSMEQNRALRNNVTYLQLSD L*QA*EKQAMGKGFPIS*MVLG KLASHM*KAESGSLPYTLYKN* FKMD*RLKH*T*NHKNPRRKPR HYHSGHRHGQGLHV
9077	39445	A	9136	277	367	
9078	39446	B	9137	1	1136	
9079	39447	A	9138	3	1168	
9080	39448	A	9139	1	1460	ERGLETNSCSEEELSSPGRGGG GGGRLLLQPPGPELPPVPFPLQD LVPLGRLSRGEQQQQQQQQPPP PPPPPGPLRPLAGPSRKGSFKIRL SRLFRTKSCNGGSGGGDGTGK RPSGELAASAASLTDMGGSAG RELDAGRKPKLTRTQSAFSPVS FSPLFTGETVSLVDVDISQRGLT SPHPPTPPPPPRRSLSLLDDISGT LPTSVLVAPMGSSLQSFPLPPPP PPHAPDAFPRIAPIRAAESLHSQ PPQHLQCPLYRPDSSSFAASLRE LEKCGWYWGPMNWEDAEMK LKGKPDGSFLVRDSSDPRYILSL SFRSQGITHHTRMEHYRGTFSL WCHPKFEDRCQSVVEFIKRAIM HSKNGKFLYFLRSRVPELPPNS CQ\LIYPMSRFSIYESFQHLAKF RIRQLVRIDHIPDLPL\PKPLISYI RKFYYYDPQEEVYLSLKEA\QS VSKQKQEVEPST*RGAPCWSPP RAFGCQAPALKNQIKLP

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9081	39449	A	9140	2	418	KSPSKYLCYTFIISTAALVLLIM LPHESMPVYLGMACTLGFGAIV FTQRAV\FFAPIGEAKIAENKTG AAMALGSFIGYAPAMFCFSLYG YILDLNPGIIGYKIVFGIMACFA FSGAVVSVMLVKRISQRKKEM LAAEA
9082	39450	A	9141	26	180	KPAHQCQVFFCPVVSAHQGEV LPYKSGVTSIESFVTIICKVIRR* LLSFLA
9083	39451	A	9142	299	921	FGTAALVL*IVLPPEISPSH*GM ACTLGLGAIVLTQRAV/FFAPIG EAKIAENKTGAAMALGSFIGYA PAMFCFSLYGYILDLNPGIIGYK IVFGIMACFAFSGAVVSVMLVK RISQRRIRRLRRIRQFHIRRNTSS RYGSGFARGGRKATRGISSQEL GQGLSGEEQDGASGGVTAGDI ATGDYFLLTPHLQICTGAKGGL GCVVEGR
9084	39452	A	9143	1	752	MSELPFAIASKRKEYVGIQLPR YTIQKLEENLNVVLFDRSGHRT KFTNVGRMLLERGRVLLQAAD KLTTDAEALARGWETHLTIVTE ALVPTPAFFPLIDKLAAKANTQ LAIIT*VLAGAWERLEQGRADI VIAPDMHFRSSSEINSRKLYTL MNVYVAAPDHPIHQEPEPLSEV TRVKYRGIAVADTARERPVLTV QLLDKQPRLTVSTIEDKRQALL AGLGVATMPYPMVEKDIAEGR LRVVSPESTS
9085	39453	A	9144	389	760	SWRIDVHPV*YTTRLFPFVLPY MQKGTSIRTSSRQLLDKQPRLT V/STIEDKRQALLAGLGVA/TMP YPMVEKDIAEGRLR/VVSPESTS EIDIIMAWRVTKRTPKN*WTM MPENIGEYTKTTHILG

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9086	39454	A	9145	1	941	MTAMERSRILRRAVDILRERND ELAKLETLDTGKAYSETSTVDI VTGADVLEYYAGLIPALEGSQI PLRETSFVYTRREPLGVVAGIG AWNYPIQIALWKSAPALAAGN AMIFKPSEVTPLTALKLAEIYSE AGLPDGVFNVLPGVGAETGQY LTEHPGIAKVSFTGGVASGKKV MANSAASSLKEVTMELGGKSP LIVFDDADLDLAADIAMMANF FSSGQAKR/NGARVLCGGDGVR ARDRPNLRRENLRGKYHS*QR HRRPDAC*YRPRL*RCGGRYAD D*VQAGAGSDGL*ATGHGGRR EC*PYVTGEAG
9087	39455	A	9146	3	504	DQQQNRQR\LIDCFPHAQWAKE VDVSDKEARCGVRCATRDHLP MVCNVPDYEATLVEYASSAEH KDDAVSAPVFDDLFIL\GSRGLC SGPLCAEILAT*IS\DEPMPMDA SML\AALIPNRLWVRKLLKGKA VKAGAVHFRRSIIYFHPQQANA LDFPSTHIIKYCTMLL
9088	39456	A	9147	197	353	YGFRWPD*AHPAIN*ASAASISF LRWLIRLTSITETTAPLNAKQAI MPNTIL
9089	39457	C	9148	1	1263	
9090	39458	A	9149	3	726	GAKNAREAIYHIEGDPDHP\EN RLRYPEYRAPGSDKWQRISWEE AFSRIAKLMKADRDANFIEKNE QGVTVNRWLSTVNKKKISLRT VGAALVLQVVIGGIMLWLPPG RWVAEKVAFGVHKVMAYSDA GSAFIFGSLVGPKMDTLFDGAG FIFGFRVLPAIIFVTALVSILYYI GVMGILIRILGGIFQKALNISKIE SFVAVTTIFLGQNEIPAIVKPFID RLNRNELFTAICSGMASIDG
9091	39459	B	9150	1	1662	
9092	39460	B	9151	1	2658	
9093	39461	C	9152	1	2526	
9094	39462	A	9153	422	585	PYRLKQNIAGA*PIKLPNAIAAP VLFSAIFASTIGAKILLAVLRLSR PHPSVHA
9095	39463	A	9154	1275	1485	
9096	39464	A	9155	1	439	

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9097	39465	A	9156	1049	2195	NMPKASSCRFSTATTYLRDRSC K*PWAGS*KKNSWR*CRRRTTS SHRTRLNATWGVSVKRRTKAR CSMVCASRGS/SNARGLELVKE GRAQACVSAGNTGALMGLAK LLLKPLEGQNHRMLLRWEAKL AALVRLQENTAQPVPFAPNNA RPLTLEDDRLSCTVRGYNFAITF SKMSGKPTSWQLVASALATKI AHEVNPQNQVGCMLAGGNFYP YSCKPEDVWAALEKDRENLFFI DVQARGTYPAYSARVFREKGV TINKAPGDDEILKNTVDFVSFSY YASRCASAEMNANNSSAANVV KSLRNPYLQVSDWGWGIDPLG LRITMNMMYDRYQKPLFLVEN GLGAKDEFAANGEINDDYRISY LREHIRCNGRSDCRQAFR
9098	39466	B	9157	482	542	
9099	39467	A	9158	115	1662	TPYPDAITTHDIVDTYPVQGGA VRVLVFSAWSLRVVSSVLFSLV WGFVSFCRRFVPCRVCVLLCCL FWCFVFGVWLPRRHMSNHAAI GVGEQQCQRGNINGAPETFAS MANTGT*QW/QRISWEEAFSRI AKLMKADRDANFIEKNEQGVT VNRWLSTASLAPTFGRGAMTN HWVDIKNANVVMVMGGNAAE AHPVGFRWAMEAKNNNDATLI VVDPRFTRTASVADIYAPIRSGT DITFLSGVLRYLIENNKINAEYV KHYTNASLLVRDDFAFEDGLFS GYDAEKRQYDKSSWNYQLDE NGYAKRDETLTHPRCVWNLLK EHVSRYTPDVV\ENICGTPKADF LK\APDRT\TTFLYALGWTQHT VGAQNIRTMAMIQLLLGNMGM AGGGVNALRGHSNIQGLTDLG LLSTSLPGYLTLPSEKQVDLQS YLEANTPKATLADQVNYWSNY PKFFVSLMKSFYGDAAQKENN WGYDWLPKWDQTYDVIKYFN MMDEGKVTGYFCQGFNPVASF PDKNKVVSCLSKLKYMVVIDP LVTETSTFWQNHEAAVSGGKR PGRKRLNLLPMARLTTTIASAT YANISAQWAKRLQTAFR
9100	39468	A	9159	1	2235	
9101	39469	A	9160	1	1821	

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9102	39470	A	9161	14	1785	FDQVEERVSVIEDQMNEMKRE EKFREKRVIRNEQSLQEIWDYV KRLNLHLIGVPESDWENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSSRRTTPRHIILNA HKRK*ERYKIDTLTSQLKELEK QEQTYSKASRRREITKIRAELKE IETQKTLQKINESRSCFEKINKID RLLARLIKKKREKNQTDVIKND KGDITTDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGSEIEAIINSL PTKKSTGPDRFTAEFYQRYKEE LVPFLLKLFQSIEKEGILLNSFYE ASTILIPKAGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHYNQVSFIPGIQGWFNICKSIN VIQHINRTKDKNHTIISIDAEKA FDKIQQPFMLKTLNKLGIDGTY LKIMTAIYDKPTASTILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQT LLKLISNFSKISGYKINVQKSQV FPYTNNRQTESQIMSELLFTIAS KRIKYVGIQLTRDVKDLFKEN
9103	39471	B	9162	1	2025	
9104	39472	B	9163	67	3156	

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9105	39473	A	9164	1	2019	MDTIKNDKGDITTDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRK\AFDKIQQAFTLKTLNK LVIDGTYRKIIRAICDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVLDRAIRQEKEITCIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGRINIMKMAILPKVIYR FNAIPIKLPVAFFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSLFN KWCWENWLDIWRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTL EENLGNTILDIGMGKDFMSKTP KAMATKAKIDNWDLIKLKSFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELKQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLTPVRMVIIKKSGNNR PPLSKEQPPIFRLSIILATTRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
9106	39474	A	9165	1	3477	

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9107	39475	A	9166	1	2460	MGDFNIPLSTSDRSTRQKVNKD TQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNNL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TEIRAELKEIETQKTLQKMNES RSWFFEKINNIDRLLARLIKKKR EKNQIDAIKNHKGDITTNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEQVESLNRPI TGAEIEAIINSLRTKKSPG\PGGF TAEFYQRYKEE/HVLEVLARAI RQEKEIKGIQLGKEEVKLSLFA DDMTVYLENPTVSAQNLLKLIS NFSKVSGYKINVQNPQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDMKELFKENYKPLLS EIKEDINKWKNIPCSWVGRINIV KMAILPKVIYRFNAIPIKLPMTF FTELEKTTFKFIWNQKRARIAK SILSQKNKAGGITLADFKLYYK ATVTKTAWYWYQDRHIDQWN RTESSEIMPHIYNYLIFDKPDKN KKWGKDSLFNKWCWENWLAI CRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQDT GMGKDFMSETPKAMATKDKID KWDLIKLKSFCTAKETTIRVNR
9108	39476	A	9167	1	1389	

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9109	39477	A	9168	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRSLH AKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWIHDEMKAEIKMFF ETNENKDTTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGDI TTDPTEIQTTIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESLNRPITGAEIVAIINSLPTK KSPGPDGFTAEFYQRYKEELHI NRAKDKNHMIISIDAEKAFDKI QQPFMLKTLNKLGIDGTYFKIIR AIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMTVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIPCSWVGRIN IMKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQK\RARI AKAILSQKNEAGGITLP
9110	39478	B	9169	1	1716	
9111	39479	B	9170	1	3171	
9112	39480	A	9171	1	2952	MLLNQGRKLPRVFAEETLKFK GTSNKPQTLEQISTSIIAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLFEQTLNYLQEFLFTP QWHLECQQERTVHSPGKAAEA REPSVIDRHLIQESSNWHLVGA ALGQSFQRKEQAAIFAVLQPLL VIPRQTGSGVDLQKTPTDLQQR GLIVRRKTNKQKGIVHNSTTRE QNWTENEFDKLTEGGFKRWVI TNSSELKEHVLTQCKEDKNLEK SAIKLELRIKNLIQN
9113	39481	B	9172	1	2406	
9114	39482	A	9173	1	2307	

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9115	39483	A	9174	3	2776	QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHILGSKALLSKCKRTEII TNCLSDHSAIKLELRIKTLTQSH STTWKLNNLLLNDYWVHNEM KAEIKMFFETNENKDTTYQNL WDAFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITKIRAELKEIETQ KTLQKINESRSWFFERINKIDRP LARLIKKKREK
9116	39484	B	9175	133	3213	
9117	39485	A	9176	284	1689	QNFGNFKDLL*RSLW*REKSWI CML*ARNTASRQQRNKAGQR MTLMS*EKKASDDQTSPS*R/Q EVRTHRKEAKNLVKRLDKWLN RITSVEKSLNDLMELKTM/RTR TTT**MHKLQ*PI*SFGRKEIQTT IRE\KHLYANKLENLEEMDKFL ETYTLPRLNQEEVESLNRPITGS EIEAIINSLPTKNSPGPDRFTAKF YQMYKEELVPFFLKLFQSIEQE GILPNSFYEASIILIPKPGRDPTK KENFRPISLMNIDAKIFNKILAN QIQQHIKKLIHHDQMGFIPGMQ DWFNIRKSINVIQHINRTKDKN HTIISIDAEKAFDKIQQCFMLKT LNKLGIDGTYVKIIRAIYDKPTA NIILDGQKLEAFPLKTSTIQGCP LSPLLFNIVLEVLARAVRQEKEI KGIQSGKEEVKLSLFADDMTV YLENPIISAQNLLKLKSNFSKVS GYKINVQKSQAFLYTNNREPN
9118	39486	A	9177	1	1515	

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9119	39487	A	9178	3	1601	ESRS*FFEKINKI/D/RLLARLIKK KREKNQIDAIKNDKGDITTDPT EIQTTIREYYKHLYTNKLENLEE MDKFLNTYTLPRLNQEEVESLN RLITGSEIEAIINSLPTKKSPGLD TFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEAIIILIQKPG RDTTKKENFRPISLMSINAKILN KILANRIQQHIKKLIHHDQVGSI PGMKGWFNICKSINVMQHINRT KYKNHMIISIDEEKAFQKIQKRF MLKTLNKLSIDGTYLKIIRAIYD KPTANIILNGQKLEAFPLK\NGT RQGCPLSPVLFNIVLEVLARAI/ RLISCFSKVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLGIQLTRDVKDLFKENYKP LFNEIKEDTNKWKSIPCSRVGRI NIVKTAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRACIV KTILSKKNKAGGITLPDFKRYY KATVTKTA/WSFHELGKTQLAT RTTVSTFQQIPGI*VQLRFDFSR DITLLSLLCR
9120	39488	B	9179	1	2034	
9121	39489	B	9180	1	2088	
9122	39490	A	9181	1	1870	MKAEIKMFFETNENKDTTYQN LWDTFKAVCRGKFIALNAHKR KQERSKIDTLTSPLKELEKQEQT HSKASRRQEITKIRAELKEIETQ KTLQKINESRSWIFESINKIDRPL ARLIKKKREKNQIDAIKNDKGD IITDPTEIQTTIREYYKHLYANK LENLEEMDKFLDTYTLPRLNKE EVESLNRPITGAEIVAIINSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKDGILPNSFYEASI ILIPKP
9123	39491	A	9182	1	1410	
9124	39492	A	9183	1	3996	

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9125	39493	A	9184	281	3030	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNEMKREGKF REKRIKRNKQSLQEIWDYVKRP NLRLISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RTPQRYSSRRATPRHIIVRFSKV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKKSPGPDGFTAEYY QRYKEELVPFLLKLFQSIEKEGI LPNSFYEASII
9126	39494	A	9185	1	2250	
9127	39495	A	9186	248	2385	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMLLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAEFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASIILI PKRGRDTTKKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIPGMQGWFNICKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLGIDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWYWYQNRDIDQ WNRTEPSEITPHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKLKLDPFLTPYTKIHPRWI KDLNVRPKTIKTLEENLGNTIQ DIGMGKDFMSKTPKAMAAKA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKK\TNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPSLAIREMQIKTTMRYHL

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9128	39496	A	9187	1	2229	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VQNFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKLENLEEMD TFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AEFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEASIILIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDKIQQPFML KTLNKLGIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRIKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPK\IGKTTLKFIWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWYWYQNRDIDQWNR
9129	39497	A	9188	1	2667	
9130	39498	A	9189	1	3033	MADMLTWESCLEESLQEESPL VTHCGPSCCISGQSPPSSARPSS VSSAISVLMLPQNRKLPPAWTS PGIFPTDLVVYSMSLPHALARY NCDVCKSMLPPRLYAPEEKAR TSPLCGTWYSPSLPLCGAWCKK NEKKRERERERKRQREDILSGA SSYKDTIHIQLRPPPYDVLQQIQ TTIREYFKHLYANKLENLEEMD KLLDTYTLPRLNQEEVESLNRLI TGSEIVAIINSLPTKKSPRPDGFT AEFYQRYKEE

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9131	39499	A	9190	1	950	MQAICTGQARALICMGGNFAL AMPDREASAVPLTQLDLAVHV ATKLNRSHLLTARHSYILPVLG RSEIDMQKNGAQAVTVEDSMS MIHASRGVLKPAGVMLKSECA VVAGIAQAALPQSVVAWEYLV EDYDRIRNDIEAVLPEFADYNQ RIRHPGGFHLINAAAERRWMTP SEIQTTIREY\YKHLYTNKL\ENL EEMDKFLDTYSLPRLNQEEVES LIRPITGSEIEAVVNSPPTKNSPG PDRFTAKFYQRY/K/EELVPFFL KLFLAAVPAPSSHGPFCCSRKA LRGSKTGSAYPSSSALRRVTVS EVVCLFAEAQLF
9132	39500	A	9191	1	3470	MASVSSATFSGHGARSLLQFLR LVGQLKRVPRTGWVYRNVQRP ESVSDHMYRMAVMAMVIKDD RLNKDRCVRLALVHDMAECIV GDIAPADNIPKEEKHRREEGNK CHKQKAMGKHLKEPHVLGQET KGLESTDVLLPLPAAGQDLGRE KKIREEAMKQITQLLPEDLRKE LYELWEDLEFESPSCLDSLSLCC SLKPQSESSPVLPEGCETLIQRL CAVGTGVTAALATRLCRASGL PAPHQWASELQRSRKKE
9133	39501	A	9192	1	3907	MAAWNLLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKLTTRKDIYTENPSV HHHHQRPKVDKTTKMGKKQN RKTGNSKMQSASPPPKERSSSP ATEQSWMENDFEELREEGFRRS NYSELREDIQTKGKEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRSLRSRCDQLEER VSAMEDEMNEMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
9134	39502	A	9193	3	3197	

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9135	39503	A	9194	1	3158	MVKGSIQQEELTILNIYAPNTG APRFIKQLLSDLQRDLDSHTLIM GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDIYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNYLSDHSAI KLELRIKNLTQSRSTTWKLNNL LLNDYWRKQERSKTDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKKEKNQID TIKNDKGD
9136	39504	A	9195	1	3285	
9137	39505	B	9196	1	1366	
9138	39506	A	9197	735	3541	RSFPRSRPSPFLLLSRYLRIHMV FSVLPFGLQNPKYLLSGSLQEK FRTPGINSHKTLDPNRVIIKVRR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITTDATEIQTTIREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPITGSEIEAIINSL PTKRSPGPDGFTAEFYQTYKEE LVPFPLKLFQSTEKEGILPNSFY EASIILIPKPGRDTTKKENFRPIS
9139	39507	A	9198	1	5356	MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSAMEDEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIYRTLHPKSIEYTFFS APHHTYSKIDHIVGS

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9140	39508	A	9199	1	2491	MGDFNTPLSTLDRSTRQEVNK DTQELNSALHQVDLIDIYRTLH PKSTEYTFFSAPHYTYSKIDHIV GSKALLSKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWKLN NLLLNDYWVNNEVKAEIKMFF ETNENKDTTYQNLWDTFKAIN KIDRPLARLIKKKREKNQIDAIK NDK\WDITTDPTEIQTTIREYYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPITGSEIEAI TNSLT\TKKSPGPDGFTAKFYQR YKEELVP\FLLKLFQLIEKEGILP NSFYEASIILIPKPGRDTT\KQKK NFRPISLMNIDAKILNKILANRI QQ\HIKKLIHHDQVGFIPG\MQG LFNICKSINVIHHINRTKDKNYM IIS/I*DAEKAFDKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAD IILNGQKLEAFSLKTGTRQGCPL SPLLFNIVLEVLARAVRQEKEIK GIRLGKEEVKLSLLADDMIVYL ENPIVSAPNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD MKDLFKENYKPLLNEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPEKMSIIDTGGW
9141	39509	A	9200	1	3083	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKL

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9142	39510	A	9201	1	4201	MRKKQSRKTGNSKKQSTSPPPK ERSSSPAMEQSWTENDFDELRE EGFRRSNYSKLQEEIETKGQEV ENLEKNLDKCITRITNIEKCLKE LMELKAKARELHEECRSLRSRC DQLEERVSVMEDEMNEMKQE GKFREKRIKRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLARQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
9143	39511	A	9202	715	6193	GQHHPDTKAWQRHNKKKENF RPISLMNIDAKILNKMLANQIQ QHIKKLIYHDQVGFIPGMQGWF NICKSINVIHHINRTKDKNHMII SIDAAKAFDKIQQPFMLKTLNK LGIDGTYLKIIRAIYDKPTASIIL NGQKLEAFTLKTGTRQGCPLSP LLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIISAQNLLKLIGNFSKVSGYTIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKR
9144	39512	A	9203	1	3682	KEGHYIMVKGSIQQEELTILNIY APNTGAPRFIKQVLSDLQRDLE SHTLIMGDFNTPLSTLDRSTRQ KVNKDTQELNSALHQADLIDIY RTLHPKSTEYTFFSAP\HHTYSK IDHILGSKALLSKCKRTEIITNCL SDHSAIKLELRIRKL\TQN\RSAT WKVNNLPPGMTYWV\HNGNE GQKLKMFFETQWE/HKDTAYQ NLW\DTFKAGCRGKFIALNAHK RKAGKDPKLTPLTSQLKK\LEK QEQT\HSKAS
9145	39513	A	9204	1187	1680	DSPCTIASTRSYSFICNRPLSVDI QLRCSCRNVRRLSTYC/LYLRQ LRIEGGNFVFTTKADNGPQQIIT *TNSFPVGNNAQTVKVRHHILT FFINLFGKEIGGPDHFNNGFTQP LPSGGTQPQHLSCVTIDGGNVT MRIHRNQPFINRTKQRLLLTDH ACDLLWLH
9146	39514	A	9205	3	293	ERSWSQLLFSTEQFWQQLPGTG SGRARQNISRKTPREHAGGYRR DNGNNWAVPHIQCNLVPR**K RPPVRAHRAPETLCASKALQEQ RYWVFELLR
9147	39515	A	9206	1	4509	
9148	39516	A	9207	1	507	

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9149	39517	B	9208	1	3448	
9150	39518	A	9209	1	2652	
9151	39519	A	9210	75	784	
9152	39520	B	9211	1	1968	
9153	39521	A	9212	1	298	LQGHLVGDYVSLSCLPFGIMGH GNWPLWVLTACLVLLLC*/WSL RRQ*IQQ*APSDQKRDFLVPHG A/VFDR*ISATCWSSINWPANCS RPSIAGWPKQAS
9154	39522	B	9213	167	362	
9155	39523	A	9214	959	1267	YHWHQLLSMVRQLMVLSWKK ISSWFMGPPIIRKSILAENSI*KN LV*VIILKLTEGISTLK*MAPQN TQY*MTVIKLFKWVARQTRLR SIMVCYSSTTTLLT
9156	39524	A	9215	370	555	
9157	39525	A	9216	1	1016	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEPFY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RLFARLSLDSALPDRTTIMNFR HLLEQHQLARQLFKTINRWLAE AGVMMTQGTLVDATIIEAPSST KNKEQQRDPEMHQTKKGNQW HFGMKAHIGVDAKSGLTHSLV TTAANEHDLNQLVQNELETAE RFRRQEDTQSKCLLSSIMLYIKN LSGPDVSELISPLSEGFNLCSSV VVAVIAAVLRRAPIHMPSGWW RSWNAESGAYNVTRSGDSYI/H G*LLYRSRKLPDPADEGALQK WWSVLPFFKRRLWF
9158	39526	A	9217	408	643	PGCGSGHSWHRHQCGPSCQSA TDCLSWSDASPDRVAALCSWS SWVPQ*WWHR/HKVP*VIMTP ASASQRLMVLNNWRAS
9159	39527	A	9218	626	760	
9160	39528	A	9219	1	2469	
9161	39529	A	9220	1	756	
9162	39530	A	9221	1738	1913	PTAWSPPRPTSMTSISWVICFME RSNLSQPMPATKERHSARSWPR WMWTG*SPSVPAR
9163	39531	A	9222	2403	2760	FRGDGILVSCPLVFSSAFSWRA ADGGKNRNVHPSV/VR*AGAL RPRTQSRIQ/SQRLNKVEKGGV KQFEHNQSCRQQVGVTIIKVVK QLADILPHGHFQFYAEVIGKLF RQRSARDAIRGSS
9164	39532	B	9223	1	3663	

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9165	39533	A	9224	1	1584	MELIEKHVSFGGWQNMYRHYS QSLKCEMNVGVYLPPKAANEK LPVLYWLSGLTCNEQNFITKSG MQRYAAEHNIIVVAPDTSPRGS HVADADRYDLGQGAGFYLNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMGG LGALVLALRNPDEYVSVSAFSP IVSPSQVPWGQQAFAAYLAEN KDAWLDYDPVSLISQGQRVAEI MVDQGLSDDFYAEQLRTPNLE KICQEMNIKTLIRYQRGAICSAD AATRGAKRESCRSGCGLLIAER PAKVEPGTASRQDNTAINIEYM KASIRARVEHPFRIIKRQFGFVK ARYKGLLKN\ETNWRCYSRWP/ HLFRADQMIRNPHDLYAPEVV HQKAKVTTSGYRFLPCCGFAN TFWGKTTADGTLIEHFGRRCQG WFEDDDGHREQCDFRFRFKNC PQCNAENDIAARRCRECDTVLV DPDDMLKAALRLKDALVLRCS GMSLQHGHDEKGEWLKITYYD EDGADVSERFRLQTPAQRTAFE QLFIRPHTRTPGI
9166	39534	C	9225	1	2127	
9167	39535	B	9226	1	1917	
9168	39536	A	9227	1671	2198	RAGAWASDPRQRGVVRNAALL PPDDRSDGRDAKTQSHRDG/VI SY/RAFDETILASGIVPRTPPIDGI DHPKNEADDMLRMGFIEDVETI /IGADPGRSSDRSVLCNHAGSDS SHYPPLYERAAGSAHSVQRDYP SGHQPELLDCLGYARTRSTDTG TPERWSSGHPDCDRRCSPWPGR
9169	39537	A	9228	642	746	
9170	39538	A	9229	1	2031	
9171	39539	A	9230	909	1058	
9172	39540	A	9231	2	268	WRCLLRQLKFIIKTVTSWICTG KLMLSTTSPLMMQMMVILLMP VLASKVKPKSTIN*LVSVSGNM NSKATALNLKVPPKIKPVLPSL
9173	39541	A	9232	63	463	FPATCWSSINWPANCSRPSIAG WPK/PGVMMTQGTLVDATIIEA PSSTKNKEQQRDPEMHQTKKG NQWHFGMKAHIGVDAKS\A*P TAWSPPRPTSMTSISWVICCME RSNLSQPMPATKGRHSARSWP RWMWTG

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9174	39542	A	9233	74	247	RNVMIKRRVLSSTSAS*LPPASA FCRLFSTPARWRSTACFTSGNR YRFLTVRLSGYW
9175	39543	A	9234	3	271	ASYWNRSFSPWGTYNRHPR*N RQCASRHCRGLHKQYQWPRIR S/WLNCTPAPHARDVLLWRPSS LPAGNADGPIRWRPCCVFTACS IGTT
9176	39544	A	9235	1	1048	MCSFRSQTFCSSSRFTFARVSVI HSANHRVLNDRSTIMRTRGQD PTLPEMRRVRLLEMADAMDMF CQGLRYGPLPAPVRQQAAIIIPC HRVVRGDGTLSGYRWGVSRKA QLVRREAENEERPINRGWPKQP SDDPKHFVMPTIIEAPSSTKNKE QQRDPEMHQTKKGNQWHFGM KAHIGVDAKSGLTHSLVTTAA NEHDLNQLGNLLHGEKQFVSA DAGYQGAPQREELAEVDVDW LIAERPGKVKTLKQNPRKNKTA INIEYMKASIRARVEHPFRIIKR QFGFVKARYKGLLKN\ETNWR CYSPWPTCFGWTK*YPSIPTCLL TTRTASLLKPPGVRTSVCWQQL

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9177	39545	A	9236	1	2493	MTQIFTGTLVEADPFHAVTLVA NHDTQPLQALEAPVEPWFKPL AYALILLRENGVPSVFYPDLYG AHYEDVGGAGQTYPIDMPIIEQ LDELILARQRFAHGVQTLFFDH PNCIAFSRSGTDEFPGCVVVMS NGDDGEKTIHLGENYGNKTWR DFLGNRQERVVTDENGEATFFC NGGSVSVWVIEEAANNRQYDY GAGHKIPVINYTDVHLRIERSCR FRADPRQQHELQLSSKLAVHD VLTNIYNRRYFFNSVESLLSRPV VKDFCVMLVDINQFKRINAQW GHRVGDKVLVSIVDIIQQSIRPD DILARLEGEVFGLLFTELNSAQ AKIIAERMRKNVELLTGFSNRY DVPEQMTISIGTVFSTGDTRNIS LVMTEADKALREAKSEGGNKH WYNLSDGAMEDALYEIASMRL FARLSLDSALPDRTTIMNFRHL LEQHQLARQLFKTINRWLAEA GVMMTQGTLVDATIIEAPSSTK NKEQQRDPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNQLGNLLHGEEQF VSADAGYQGAPQREELAEVDV DWLIAERPGKVRTLKQHPRKN KTAINIEYMKASIRARVEHPFRII KRQFGFVKARYKGLLKN\ETN WRCYSRWP/HLFRADQMILCPV FVHHIPRFFGTFFGATDTQTFTL TESVIHQPLVLTNFIAIDGNDFA
9178	39546	B	9237	1	3148	
9179	39547	B	9238	1	1680	
9180	39548	A	9239	191	470	

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9181	39549	A	9240	1	1675	MFARVSTTPVTRYEMYRKTRS TRLEDNNALSQSCKPLPFSEVT GSKGKADKEKVGDYVFCLKAQ GRYNGEPLTGTGKIGGMLALR GEGTPFPVQADFRSGNTRVAFD GVVNDPMKMGGVDLRLKFSG DSLGDLYELTGVLLPDTPPFET DGRLVAKIDTEKSSVFDYRGFN GRIGDSDIHGSLVYTTGKPRPK LEGDVESRQLRLADLGPLIGVD SGKGAEKSKRSEQKKGEKSVQ PAGKVLPYDRFETDKWDVMD ADVRFKGRRIEHGSSLPISDLST HIILKNADLRLQPLKFGMAGGS IAANIHLEGDKKPMQGRADIQA RRLKLKELMPDVELMQKTLGE MNGDAELRGSGNSVAALLGNS NGNLKLLMNDGLVSRNLMEIV GLNVGNYIVGAIFGDDEVRVN CAAANLNIANGVARPQIFAFDT ENALINVTGTASFASEQLDLTID PESKGIRIITLRSPLYVRGTFKNP QSG*WS/GTLLLSTKAKTIVAISI TTLKVTVMASVSLLPMNTKDS VSVQLMRNLIVPTLKLMQGKFF LKYLLPVKMQKFGPQV
9182	39550	A	9241	72	506	GHVAHLQPRAGGRQPARLHHP QGTDRVLHGQRGQQPGP/LLPS LSAWRPSTSTLKPASCGLRGPT SKRMSM\QDGGLPHHRAGAQP PVHPGQEAVG*C/EYWSASSRP VTQPGALMWRLWS\AGRPRPY LLSHSQHDPHSGQGGGEHP
9183	39551	A	9242	1	447	
9184	39552	A	9243	70	490	CGCDAETIILRINALAFIWKCGT EWICCFCRLALRELQQAVHAG LPQQAKILFDGGSEIGKIH*LRC AHCPLSS\GKPVVPAALMNRPT RGERRFAYWAPGWFFFSPVRR ATADCPSPPGPERVAASGPRWF APAGENPV

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9185	39553	A	9244	1097	1841	ANDGDLRSCVTLSCHMSHASE AADPPATTAFTDEHMSVKLRR TVGVACSVCPGWVTSGHPVNP AAS/GAKVLPGDTDIALPGPLPF ILSR\QLRDNTLILSDNGG\RILY FELLFPGEDGYRRCESLWLVRG GVAKLDQGHRLAALWQALSEE LRLTPHRYLATNSPQGPWWLL GWCERVPEADEVLPAPLPPYRV LTGLVDRIWRSEDVSAASGLHH DNRNAPSLSDQTRTDPPIRAHA SRYQRQKPDG
9186	39554	A	9245	456	928	EAATEPKHLHQLRHAALAQHR QAPRPQGRPLARPHQGQDQPD RLHHLRGGGRHGARGHLHQA GAGESAPAPKG/VTCPASPLGD VTGKPTSAWNTEKGRWAQHR GYPSPGPAAPLVLRSWPIPLFRP PPLLPLSSPAWILPSPLCHSLKA QSLVQATI
9187	39555	A	9246	1	1572	

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9188	39556	A	9247	1	2505	MAWRNSVNWQCKQEPGFLHR RHGRRKLTNGTTRRSLQNKEE DFYTSQPGFPALALGCCLRVNL LLGHRGISAGSSYRPITSTPCHL CKLGQEVFAKPLNLQDQCQQN LVMQVLKLVLNCLNFDFIGSSA DESADDLCTVQIPTTWRTMGL VGCDGVCCRTRWCQCLATAV VSGVGGGPWLLPACSSGPSMIS KRKKFVHKWAKDLVEPRHGLE NVWDLPRAMAGSYLMYKQRK WKIMEFGKWALQHKMTVKDIE RLQLYNKVKEQPVQVEGSGRA STIFWVLKTFKGGKSPCGAPGE CVAWTQCRILGWVQIHFKEHP ADRVVGLIKMPGLDFYFAADV CYAEKVAQEKGFLYRLTSRYR HYAAFERATFEQGKSTKLMML TDKQIADFQKHYQTEPERFQILP PGIYPDRKYSEQIPNSREIYRQK NGIKEQQNLLLQVGSDFGRKG VDRSIEALASLPESLRHNTLLFV VGQDKPRKFEALAEKLGSERAS MEFKRYEYNAAGDLTAVITPD GNRSETQYDAW\GKAVSTTQG GLTRSMEYDAAGRVISLTNENG SHSVFSYDALDRL\EDEGLVIL W\YYDESDRITHRTVNGEPAEQ CQYDGHGWLTDISHLSEGHRV AVHDGYDDKGRLTGECQTVEN PETGELLWQHETKHAYNEQGL ANRVTPDSLPPVEWLTYGSGYL
9189	39557	A	9248	481	857	PLAYLYRDPHVRRCVTASGPAP VYGIFQPGFSAPTG/IRKSVHGD HSYCKYAHSCSRQYRAPEPRLS RTSQCLFSHRSARCPLLDLMGR RYRRPECRLSPLLPAAPVPGLPP WTIYPRRLYRNSPR
9190	39558	A	9249	777	1229	GAGYSSARCGKHHARTGGAGR NILWRQLRRRGCRSTVDRSHH NQPGTWHRHQPGPRGPAKPAR PWRAGTHLPTGTASVRHPCLG QPLRAEPRPAVPDAPRNQNLPF PAPQTDSALPGAVRG*RAR*YH *SRTTTPPPDEHDHSWARACSP
9191	39559	B	9250	1	2681	

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9192	39560	A	9251	933	1828	VSRIHVLVWQPRMPAPPAVDW LTY/GSGIL/SGNKLVGTPLVEY TRDSLH/RETLRSFASMAGSNA AY/*LTSTDTPAGQLQSQH/LNS LVYDRDYGWSDNGD/LVRISGP RQTREYGYSA/TGRLESVRTLA PDLDI/RIPYATDPAGNRLPDPE/ LHPDMRADGGATGQKVEPEYT PARKAHLYHWTTGDCRWRLSA KTAIRVERGI**MGQPAY*GEPH HVYQPR*TWHWRWRQKGRKS ASGRRYLRPINPNNVGRENQRP TSPDGTHMAPISLMAWQPIQLR YRGHVRQRLSAVGERIYRYLPP
9193	39561	A	9252	1	1409	MECDASALLRYDSRQFIPLAID GLAKDVLGRRFALEGHPRLEAI ARAGDVVRFPADSELPDPYDG LIPGQESLKVHACVGLPLFAGQ NLIGALTLDGMQPDQFDVFSDE ELRLIAA\LAAGALSNALLIEQL ESQNMLPGDATPFEAVKQTQM IGLSPGMTQLKKEIEIVAASDLN VLISGETGTGKELVAKAIHEASP RAVNPLVYLNCAALPESVRKSE LFGHVKGAFTGAISNRSGKFEM ADNGTLFLDEIGELSLVLQAKL LRVGQYGDIQRVGDDRCLRVD VRVLAATNRDLREEVLAGRFR ADLFHRLSVFPLSVPPLRERGD DVILLAGYFCEQCRLRQGLSRV VLSAGARNLLQHYSFPGNVREL EHAIHRAVVLARATRSGDEVIL EAQHFAFPEVTLPTPEVAAVPV VKQSLREAT*AFQRETIRQALA QNRRKWTACARMLETSVANV HRLGKRLVLKK
9194	39562	A	9253	389	799	PQFLIPSVTPCMFIHPLDAK/AR DLRRGDKVKVVSRRGEVISIVE TRGRNRPPQGLVYMPFFDAAQ LVNKLTLDATDPLSKETDFKKC AVKLEKACPYDTLKLATLASG LSAGTPYFVARDIPCEMCEDIPC AKVCPS

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9195	39563	A	9254	588	1500	RHPPIPAKIGLHAVAQDRA\NN MQAGPNINEERMPGWRDPRNF IIVSDPYPTVSALAADL/TPEVSK FPGSELAEDQLNDESRELGFYL QKGLFEEYAWFGRGHGHDLAP FDDYHKARGLRWPVVNGKET QWRYSEGNDPYVKAGEGYKF YGKPDGKAVIFALPFEPAAEAP DEEYDLWLSTGRVLEHWHTGS MTLRVP*LHRAFPDAGLFI\YPL DAKARDLRRGDKVKVVSRRGE VISIVETRGRNRPPQGLVYMPFF DAAQLVNKLTLDATDPLSKET DWPHFSSTYNGPLLQGANKGIL VQQH
9196	39564	A	9255	1	1698	MEREQDSIIMDAATRRNLEITQ NLAGGAENTLASVLDCTVTPM GSRMLKRWLHMPVRDTRVLLE RQQTIGALQDFTAGLQPVLRQV GDLERILARLALRTARPRDLAR MRHAFQQLPELRAQLETVDSA PVQALREKMGEFAELRDLLER AIIDTPPVLSWMSGARWLTARP IICNYEVDRTIRHTKMNVGDVQ RLSVAVVVNYKTLPDGKPLPLS NEQMKQIEDLTREAMGFSEKR GDSLNVVNSPFNSSDESG
9197	39565	A	9256	590	910	SCSIQLSPWILPRTVMCVPGFTC ELLST*WLAKEPLKTVSWITIRS FTAETSTFGPTMTASMTFLPTY CSIIASLLSSFKLAAAILNSLPQI GRYITIGSGVRRNA
9198	39566	A	9257	1	854	MANRMILNETAWFGRGAVGA LTDEVKRRGYQKALIVTDKTL VQCGVVAKVTDKMDAAGLAF AIYDGVVANQHYCRQDSSEDF AEMSLIEGRRGLRRRPLWEFEI DTARQQLNLQFGTRDLVGFGV ENAPRGLCAAGCLLQYAKDTQ RTTLPHIRSITMEREQDSIIMDA ATRRNLEITQNLAGGAENTLAS VLDCTVTPMGSRMLKRWLHM PVRD/DPRVA*APANYWRIAGF HRRATAGTASGRRPGTYSGTSG FTNCSPTRSGPYAPRFPATAGA ACAVRNCR
9199	39567	B	9258	122	868	

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9200	39568	A	9259	2610	2897	PNLYLRFFFFFFLRQESHSVTQA GVQWCNLSSLQPLPPGFKQFSH LTG\LPKCWDYRSKRPRPANQT SILDVKEDPY*LHWPRSNRDIK LNLVANP
9201	39569	A	9260	2166	2426	VQPGGCGL*RQHGSYRPESRTA GGRHRG*RRLRRAFIDGGANSS GTGICRDAFNRISHWTGRTGRP DVDSGEHRKTAEQRRDGAVR
9202	39570	A	9261	846	1022	
9203	39571	A	9262	1	1339	MNALSKARQYVEEFDGNIASFI FSGKPGTGKNHLAAAICNELLL RERNLGESEIHTTSDHMVTATL PGETQTWPEDFRDVEQRQQVVI FQHLVGCVKVDGKYIQVCTFT VGGNYGGTCLRGDESLVIKKES DIEPLIVVTVVQQFHIGNGYVVI TITPSEGERYQGVVGLEGRIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTEVSPVLKKQLVLVPNPH YPGNKPNFKRVSVKIIGESASRR LQLSRGDIDIADALSDRFVSEAI TAKVEAAIKN*LSQYGILPEEW GGESQFVHVSAKAGTGIDELL\ DAILLQAEVLELKAVRKGMAS GAVIEFPSLDKG\RGP\VVTVLV REGTLHKGDIVLCGFEYGRVRA MRNELGQEVLEAGPSIPVEILGL SGVPAAGDEVTVVRDEKKARE VALYRQGKFREVKLARQQKSK LENMFANMTEGEVHEVNIVLK ADVQGSVEAISDSLLKLSTDEV KVKIIGSGVGGITETDATLAAAS NAILEGLFTLTSQDEFVIAPGFS TDPLEEQHSVVSGLLHKYHNR ALLLVKGGCAVNCRYCFRRHF PYAENQGNKRNWQTALEYVA AHPELDEMIFSGGDPLMAKDH ELDWLLTQVVHQHDVGRRVQ RLPFIHDALFHQQFFNQHQTTF GQVHLARFFVHREVDSILFRRIS VLKKMMSPHRVKDRCYCAQFI

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9204	39572	A	9263	922	2357	GKGNDEKKLVSDQ*MGTA*RQ RIHPIPSIIPLLW/YPEGPSVSRPE AGGYNSLLMVTHGKVINGGRG ILIESD\EPGDAR*SSGSCARHGL VFWLCSCRRCMPQTIEAIQHPN A/VAVNKIDRPEADPDRVKYVL SQYGILPEEWVGESQFVHGSAK AGTGIDELLDAILLQAEVLELK AVRKGMASGAVIESFLDKGRG PVATVLVREGTLHKGDIVLCGF EYGRVRAMRNELGQEVLEAGP SIPVEILGLSGVPAAGDEVTVVR DEKKAREVALYRQGKFREVKL ARQQKSKLENMFANMTEGEVH EVNIVLKADVQGSVEAISDSLL KLSTDEVKVKIIGSGVGVIEAES LDLRYYSVIYNLIDEVKAAMSG MLSPELKQQIIGLAEVRDVFKSP KFGAIAGCMVTEGVVKRHNPIR VLRDNVVIYEGELESLRRFKDD VNEVRNGMECGIGVKNYNDVR TGDVIEVFEIIEIQRTIA
9205	39573	A	9264	1	748	
9206	39574	A	9265	923	1387	PPNLARCSPSAMARQSPIRSPRR PLAPSPALRAPSPAPPHAARLA VPRQA*GLLLLALIAVSTHIEMI SNTLAMGWNSPLTTVLALLAC GFACFIEMGKIPFDVAASWIIMI WSQSSTCTAPTLKPLRSVTLMR LTPVSARDLVGYFATAVRLP
9207	39575	A	9266	352	478	CDPTQRKPLYWLQALRRGLPI WRNQRFRKAVR*MAMAPMFS
9208	39576	A	9267	54	811	HTTGGNPLYGI/SRQIAR*QSRV/ GPGFCQDYRDIHKLFKRQEVAP TSSGLMFRLMPWVLISSMLVLA MALPLFITVSPFAGGGDLITLIY LLALFRFFFALSGLDTGSPFAGV GASRELTLGILVEPMLILSLLVL ALIAGSTHIEMISNTLAMGWNS PLTTVLALLACGFACFIEMGKIP FDVAEAEQELQEGPLTEYSGAG LALAKWGLGLKQVVMASLFV DLFLPFGRAQELSL\ACLLTSLV VTLLKRLL

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9209	39577	A	9268	2	627	CGSIIAL/VAIFKSFFGHYLGTLE GLNGLVLKFGYKGDKTKVSLG KLNTISMIFIMGSTWVVAYANP NILDLIEAMGAPIIASLLCLLPM YAIRKAPSLAKYRGRLDNVPH AITRVDLKEDGKGLKIVRQSLP YGTASGTHGLYFCAYCARLHNI EQQLLSMFGDTDAIKAYQSFLA RSAFAVSQCIPVNTVYRAYSVI QNWIAITIRHV
9210	39578	A	9269	2648	3072	LSRTGTKTTFAIT/LEYAASIIAL VAIFKSFFGHYLGTLEGLNGLV LKFGYKGDKTKVSLGKLNTIS MIFIMGSTWVVAYANPNILDLI EAMGAPIIASLLCLLPMYAIRK APSLAKYRGRLDNVFVTVIGLL TILNIVYKLF
9211	39579	A	9270	467	614	VPLAVPYGRLWRTIFSPLPSSFR STR\E*YESMLGRFFERTACLQQ KQF
9212	39580	A	9271	1	846	MSYLVWPFIASLVLISLSLIPYW NSAVIDQVDLGSLALTGHDGILI TVWGG\ISTK\VFPLNFPPNVFSF G\VSK\RKK*KKDFGRDFTERKC SQIISRASMLMVAVVMFFAFSC LFTLSPANMAEAKAQNIPVLSH LANHFASMTGTKTTFSITLEYA ASIIALVAIFKSFFGHYLGTLEG LNGLVLKFGYKGDKTKVSLGK LNTISMIFIMGSTWVVAYANPN ILDLIEAMGAPIIASLLCLLPMY AIRKAPSLAKYRGRLDNVFSTV IGLLTILNIVYQLF
9213	39581	A	9272	95	456	RAISMSFRMERPCCLSLPSSLCIS STRVTASSPLSGCSSCTLLWISW GRMVRNCSNT/MQLQDLLLRA HLRPKPPMAKLLEPAEGFPGTS CLLEAEPSTIRDVVLIASQPASQ PASQQGSQI
9214	39582	A	9273	1	1241	

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9215	39583	A	9274	3	1608	SRGFPRREFSGPSIKKKVDAPTQ AQWPVHAVITNSTYDGLLYNT DWIKQTLDVPSIHLDSAWVPYT HFHPIYQGKSGMSGERGAGKVI FEPQ*AHRMLAALSQGSLILIKG EYDQEAFSEAFMRHSPSSPSYPI GG\SVETAAAMLRGNPGKRLIN RSVERALHFRKEVQRLREESDG WFFDIWQPPQVDEAECWPVAP GEQWHGFNDADADHMFLDPV KVTILTPGMDEQGNMSEEGIPA ALVAKFLDERGIVVEKTGPYNL LFLFSIGIDKTKAMGLLRGLTEF KRSYDLNLRIKNMLPDLYAEDP DFYRNMRIQDLAQGIHSRRVTA SVSSGSQANQQVNFIGDQSTAA LTLSVPSGDITVTNTAPQYMTA TLQDKNGNPLKDKEITFSVPND VASKFSISNGGKGMTDSNGVAI ASLTGTLAGTHMIMARLANSN VSDAQPMTFVADKDRAVVVLQ TSKAEIIGNGVDETTLTATVKD PSNHPVAGITVNFTMPQEGVYA MSLEYIILTFIALNGSRMWINSA REKRTQRND
9216	39584	A	9275	106	709	LRSAEDNDTREKNKQTNRSDS KLRLVETSGSPPTSSSQTPDPAF RYPKKY\CVEDCS\YRPE*PRITP DNRLLYGGGVVYGARDPDVVE RLVVPKLLKTFPQLKGVKIDYR WTGNFLLTLSRMPQYGRLDTNI YYMQGYSGHGVTCNHLAGRLI AELLRGDAERFDAFANLPHYPF PGGRTLRVPFTTKSAAYY\SLR DRLGV
9217	39585	A	9276	140	558	RKPHRQRGEKAGRNRSVDGCC EKAMSVIIVGGGMAGATLALAI SRLSHGALPVHLIEATAPESHA HPGFDGRAIALAAGTCQQLARI GVWQSLADCATAITTVHVSDR GHAGFGTLSRKITTWGL*QRSW ARWIWYPFAKNYHLGALTTVV ELQMGGKRLF
9218	39586	A	9277	3799	4086	
9219	39587	A	9278	3017	3184	
9220	39588	B	9279	1	1050	
9221	39589	B	9280	1	1455	
9222	39590	A	9281	374	506	RCIALIAWLTLPVLRVTLK*RW RVARR*RAACW*S*WHHSALA P
9223	39591	C	9282	47	406	

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9224	39592	A	9283	1	4749	
9225	39593	B	9284	507	3568	
9226	39594	A	9285	101	638	RQKYSDWSSALVPTAGEPTRH TQTTRAGIAHA\EADFAADILFL LCGKDISTAGGFSFV*LADNKQ HLMPVCFANHLTVKM/PHQSPV PDH/QALISHRIRSSRGSCSRYSA DNSVSRTPLSPTPGRSTMVIKCS PICRRKRKGSRVQAATSLTGDT SPANRALQRLLFPAPVLPMMPI TGS
9227	39595	A	9286	271	532	
9228	39596	A	9287	643	768	
9229	39597	A	9288	1	1948	MCSHAAGCTIPDVEHWTRINR KVPRLVSVLPNGPDYHPTVRAF LAGGVPEVMLHLRDLGLLHLD AMTVTGQTVGENLEWRPEPGA FRQCLREQDGVEPDDVILPPEK AKAKGLTSTVCFPTGNIAPEGS VIKATAIDPSVVGEDGVYHHTG RVRVFVSEAQAIKAIKRVVIVA CGFSPTRTAHAASDIDITNTVDL RNRRSQLRRGEIVQF/IPANKYR TSA*GS*LAHPTGSLCD*VGRL DIPLAANFVQR*SPPGISPTPV
9230	39598	A	9289	2166	2426	VQPGGCGL*RQHGSYRPESRTA GGRHRG*RRLRRAFIDGGANSS GTGICRDAFNRISHWTGRTGRP DVDSGEHRKTAEQRRDGAVR
9231	39599	A	9290	846	1022	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9232	39600	A	9291	1	1336	MNALSKARQYVEEFDGNIASFI FSGKPGTGKNHLAAAICNELLL RERNLGESEIHTTSDHMVTATL PGETQTWPEDFRDVEQRQQVVI FQHLVGCVKVDGKYIQVCTFT VGGNYGGTCLRGDESLVIKKES DIEPLIVVTVVQQFHIGNGYVVI TITPSEGERYQGVVGLEGRIRRT RRIRHKQSARCYNLRFKPTCAIT QTTPTEVSPVLKKQLVLVPNPH YPGNKPNFKRVSVKIIGESASRR LQLSRGDIDIADALSDRFVSEAI TAKVEAAIKN*LSQYGILPEEW GGESQFVHVSAKAGTGIDELL\ DAILLQAEVLELKAVRKGMAS GAVIESFLDKGRGPVATVLVRE GTLHKGDIVLCGFEYGRVRAM RNELGQEVLEAGPSIPVEILGLS GVPAAGDEVTVVRDEKKAREV ALYRQGKFREVKLARQQKSKL ENMFANMTEGEVHEVNIVLKA DVQGSVEAISDSLLKLSTDEVK VKIIGSGVGGITETDATLAAASN AILEGLFTLTSQDEFVIAPGFST DPLEEQHSVVSGLLHKYHNRA LLLVKGGCAVNCRYCFRRHFP YAENQGNKRNWQTALEYVAA HPELDEMIFSGGDPLMAKDHEL DWLLTQVVHQHDVGRRVQRL PFIHDALFHQQFFNQHQTTFGQ VHLARFFVHREVDSILFRRISVL KKMMSPHRVKDRCYCAQFICP
9233	39601	B	9292	1	2890	
9234	39602	A	9293	1	822	ITQYCDSFTICLSKGLGTPVGSL LVGNRDYIKRAIRWRKMTGGG MRQSGILAAAGIYALKNNVAR LQEDHDNAAWMAEQ\LRETG\ A\DVMRQDTNML\FVRVGEEN AAALGEIT*KP\RNVLI\NASPIV RLERDVPQRILVLGASGYIGQH LVRTLSQQGHQILAAARHVDR LAKLQLANVSCHKVDLSWPDN LPALLQDIDTVYFLVHSMGEAA IYRSSAGVASVSSVFRYCLRPSY DPRVFPCFLCCRALLVLPCRLIY SPLSFALVLSLAPIK
9235	39603	A	9294	1565	1825	SRMCVAIRSRNQRSCEITIAQPG NSSRAFSSARRVSISRSLVGSSSS SMLPPTCSSFARCRRPRSPPESS PTRLP*STPLKLKRPT

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9236	39604	A	9295	236	742	VATRCSRSPSPSLSPSLSLRVMIP TTSAYSFMITAKSSPAVLKLSN ASERVNVSGTISVLRICTPLFSA RLWLASTRFSRSLEST*PMMWS ISSLQTRNLECGCSATLFFRLCS SSWRSN/TNDVFTAVTLITERDG IPAQRRFQSARVPVYVTRPPAH RLPLPRRCHQK
9237	39605	B	9296	1	951	
9238	39606	B	9297	1	666	
9239	39607	A	9298	761	1162	IILGSMAIFTILILPIHEQGMFFHL FVTSFILLSSGL*FSLKRSFTSLV SCIPRYFILFVAIVNGSSLVIWLS VFLLFVYRNACDFCTLILYPETL LKLLISLRRFWAETLGFSKYTIM SSANRDNLTSSFPN
9240	39608	A	9299	82	160	
9241	39609	B	9300	64	477	
9242	39610	A	9301	408	507	LLPLFQNLLLVYSGI*LLPGLVW KGCMHPGIYP
9243	39611	A	9302	1	3141	MLLGLHSLAAFLQRESFSGKQS WGCQLAALLQRRITKMTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQRAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGTRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQRAVDLIS NVAGDRVTYRITKGEDLREQG YMGLHTVGRGSERSPVLLALD YNPTGDKEAPVYACLLGDIITY RNGKKVEVMNTDAEGRLVL
9244	39612	A	9303	1	983	MVRASGYLQTLDDFNHIVLKA SENGVPVYLRDVAKVQIGPEM RRGIAELNGEGEVAGGVVILRS GKNAREVIAAVKDKLETLKSSL PEGVEIVTTYDRSQLIDRAIDNL SGKLLEEFIVVAVVCALFLWHV RSALVAIISLPLGLCIAFIVMHFQ GLNANIMSLGGIAIAVGAMVD AAIVMIENA/R*TAGRVAAPAS* RHAG**NALAGQEGRLFGPLAL HQNVCDGGCGAAGDRSDPDPD GLLDPWQNSAGKQ*PAQSLFDS CLSSAVAESTALAENHAAGGG AFGADGSLAAQ*SSPGEFLPQIN EGDLLYMPCDAAQGIPQQRRR
9245	39613	A	9304	362	436	
9246	39614	A	9305	101	208	
9247	39615	C	9306	1	882	
9248	39616	B	9307	1	822	

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9249	39617	A	9308	668	826	VNSHSQLLQRE*NT*ESNLQGM *RTSSRRTTNHCSRK*KRIQTNG RTFHAHG
9250	39618	A	9309	497	1042	LPRIPTVLTSGVRRDGWYRRFG RRPSG*PGNWSSSPVEKSATRT LRITGTSAIPSEAITGSSAVVRR VPAGKTTAPTEIKSTPVSANSRS VLSVTLPDTSSSALPLVRLTASR ICSVSKLSSMMISAPAFRASSSS SRFSTSTSTGASGCSQDAFSTA WRTEPEAIIWFSLIRKASESPRR
9251	39619	C	9310	1	3447	
9252	39620	A	9311	570	647	
9253	39621	A	9312	1071	1323	RPPPHRLSGCYHPSHRRPVHGF HHA*RQRQFRR*TVDTLPADAP LPSPHPAHFRPL/TSIFCPVSTMA DNASM*RNSCCRLSARG
9254	39622	B	9313	1	2585	
9255	39623	A	9314	133	357	SSFFQFCEEIHW*LDGDGIESIN YLRQ*GHFHKIDPSYP*AWNVL PFVCVLFHFIEQWFVVLLEEVL HIPCKLYS

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9256	39624	A	9315	1	2680	MLVLPLFQPFMRILDHDDSSID HRPDGNRNATQRHNIGIQSLEV HDNKSNTQPQRQRNNRHQRRA HMPEKQRTDYRRDPLESPKAA AACLFPAIADPNTPPVFTPPASL PTTGM/FDSPPFRNDA*MVMRS LIRSMTVARAVIGVAICNKGLP ATMMALAAQHNIATVLVPGGA TLPAKDGEVNGKVQTIGARFA NGELSLQDARRAGCKACASSV RRSCQFLGTAGTSQVVAEGLGL AIPHSALAPSGEPVWREIARAS ARAALNLSQKGITTREILTDKAI ENAMTVHAAFGGSTNPLLHIPA IAHQAGCHIPTVDDWIRINKRV PRLVSVLPNGPVYHPTVNAFM AGGVPEVMLHLRSLGLLHEDV MTVTGSTLKENLDWWEHSERR QRFKQLLLDQEQINADEVIMSP QQAKARGLTSTITFPWQYAWIL HPDLDPETLLKLLISLRRFWAET PVGKNRITQMTNARHRTGFQG VTIHHTGVQFMGFITRKDSANS GVKQWTLFQQTHRFRHHIQRT FARFQHFLPGFNNGRQRLDVAS VFMEFTTGLMSLDTALNEMLS RVTPLTAQETLPLVQCFGRILAS DVVSPLDVPGFDNSAMDGYAV RLADIASGQPLPVAGKSFAGQP YHGEWPAGTCIRIMTGAPVPEG CEAVVMQEQTEQMDNGVRFT AEVRSGQNIRRRGEDISAGAVV
9257	39625	B	9316	1	2577	
9258	39626	A	9317	2	772	AFGASLAQDKPNTGTG*KSPSH P\LLRVLDIGKICHLARKVGAVS VVDNPFIRPALQNPLALRADLV LHSCTKYLNGHSDVVAGVVIA KDPDVVTELAWWANNIGVTG GAFDSYLLLRGLRTLVPRMELA QRNAQAIVKYLQTQPLVKKLY HPSLPENQGHEIAARQQKGFGA MLSFELDGDEQTLRRFLGGLSL FTLAESLGGVEKLISHAATMTH AGMAPKARAAAGISETLLRIST GIENGENLIADLENGFPA
9259	39627	B	9318	68	1895	
9260	39628	A	9319	1	636	
9261	39629	A	9320	1	942	

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9262	39630	A	9321	479	969	MPSTSQ*I/ISEDFVELNAARYR DEEIQRTPQRYSSRRPTQRHIIV RFTKVEIKEKMLRAAREKGGV AHKRKPIRLTADLSAETLQARR EWGPTFNILKEKNFQPRISYPTK LSFISEGETKSFTDKQMLRDFGT TRPPLKELLKEALNMERNNRY QPQQKHTKL
9263	39631	A	9322	1	652	MGKKQSRKTGNSKNQSASPPP KERSSSRAMEQSWTENDFDEL REEGFRRSNYSELKEEVQTHGK EDKNLEKKLDEWLARIINAEKS LKDLMELKTKARELCDECTSLS SRFDQLEDGVSVMEDEMNEMK SEGKFREKRIKRNEQSLQEIWD YVKKPNLCLIGVPESDRKNGTK LENTLQDIIQENFPNLSGQANIH IQEI\QRTPQRYSLRRATP\RHLI VRFTKVEMKEK\MLRAAREKG R\VTHKGKPIRLTTADLSAETLQ AR/RTEWGPIFNILKEKNF\QPRI SYPAKLSFISEGEIKYFIDKQML RDFCHHQGLPLKELLERKALK HGKGNNQ*PPPKERSSSRAMEQ SWTENDFDELREEGFRRSNYSE LKEEVQTHGKEDKNLEKKLDE WLARIINAEKSLKDLMELKTKA RELCDECTSLSSRFDQLEDGVS VMEDEMNEMKSEGKFREKRIK RNEQSLQEIWDYVKKPNLCLIG VPESDRKNGTKLENTLQDIIQE NFPNLSGQANIHIQEIPENATKIL
9264	39632	A	9323	403	410	VFLIRWGGKPLKRKLYFLHCSI TQALV*ACQGKYLG*IVGAKNI KYIDFFITASRYLRMLAQVFE*I LLLREVTRYS
9265	39633	A	9324	174	1252	

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9266	39634	A	9326	1	1049	MHRSDMSCPDKVDILDTTAFRI AINEVKHSKLTSVTVTKVLDMF ISRSSLFPIDDGLLDDGHSDQVG VLNSPTCYSAHQNGERIERFSR KVFVGGLPPDIDEDEITASFRRF GPLVVDWPHKAESKSYFPPKG YAFLLFQEESSVQALIDACIEED GK\LYLCVS*PLLSKDKPSSKYV PWNLSDSDFVMDGSQPLDPRK TIFVGGVPRPLRAVELAMIMDR LYGGVCYAGIDTDPELKYP\KA PGRVAFSNQQSYIAAISARFVQ LQHGDIDKRVEVKPYVLDDQM CDECQGARCGGKFAPFFCANV TCLQYYCEFCWANIHSRAGRE VHIPLVTESAVAAPRIHIPWT
9267	39635	A	9327	2	126	
9268	39636	A	9328	1	1327	IASNSWNASSSPGEAREDGPEG LDKGLDNDAEGVWSPDIEQSF QEALAIYPPCGRRKIILSDEGKM YGRNELIARYIKLRTGKTRTRK QVSSHIQVLARKKVREYQVGIK AMNLDQVSKDKALQSMASMS SAQIVSASVLQNKFSPPSPLPQA VFSTSSRFWSSPPLLGQQPGPSQ DIKPFAQPAYPIQPPLPPTLSSYE PLAPLPSAAASVPVWQDRTIAS SRLRLLEYSAFMEVQRDP*TRT SKHLFVHIRHTDRNPRRFFRTPP LGP\VDVR\QIYDPNFPEKKGGL KELYEKGPPNAF\FLVKFWADL NSTIQEGPGAFYGVSSQYSSAD SMTISVSTKVCSFGKQVVEKVE TEYARLENGRFVYRIHRSPMCE YMINFIHKLKHLPEKYMMNSV LENFTILQVVTSRDSQETLLVIA FVFEVSTSEHGAQHHVYKLVK
9269	39637	A	9329	2	339	
9270	39638	A	9330	1505	1876	TYGCASPSRKPRVMPLVTAQVP ITALRVNSSSIPAQSAVETTSNR PPTTGVPAFRPVRAAV*AVISPQ ISADPTTGGRA*LISAIPSQSVRH GSYSPRLML*RLDSEILLSSQPL TPVKHQRR
9271	39639	A	9331	1	1710	
9272	39640	A	9332	1	1191	

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9273	39641	A	9333	838	1365	STETLSPLPATPGEVTLRHLDV VSAEQQMFSGLVEKIQVTGSEG ELGIYPGHAPLLTAIKPGMIRIV KQHGHEEFIYLSGGILEVQPGN VTVLADTAIRGQDLDEARAME AKRKAEEHISSSHGDVDYAQAS AELAKAIAQLRVIELTKKAM*H RLEKHKSQSGNRLAFFCACDPS
9274	39642	A	9334	3	601	MLSAVGYQP/TLAEEMGVLQE RIPSTKTGSITSVQAVYVPADDL TDPSPATTFAHLDATVVLSRQI ASLGIYPAVDPLDSTSRQLDPL VVGQEHYDTARGGQFILARYQ ELESLL\AILGMNDLSEEDKLVV ARARKIQRFLSQPFFVAEVFTGS PGKYVSLKDTIRGFKGIMEGEY DHLPEQAFYMVGSIEEAVEKA
9275	39643	B	9335	681	1071	
9276	39644	A	9336	203	2189	VASSARRGLPVHGPAPLQGPGN SQDRL/ESGTNRCGLRGPLVKG GKGGRFPSARLIQTVKKGGTPS RDHA\IEPSGY\SVSAGVGE\RTR KGSVFAHEMPDCNVIDKVSLV YGQMTEPPGNCMRVALSGLTM AEKFRDEGRDVLLFVDNIYRYA LAG*ERFATVGR*ASN/AVGIQP TLAEKMGVLQERITSTKTGSITS VQAVYVPANDLTDPSPATTFA HLDATVVLSRQIASLGIYP\AVD PLDSTSRQLDPLVVGQEHYDTA RGG*SI\LQRF\QELKDFMALP/G LSDELSEEDKLVVARARKIQRF LSQPFFVAEVFTGSPGKYVSLK DTIRGFKGIMEGEYDHLPEQAF YMGDMAMTYHLDVVSAEQQ MFSGLVEKIQVTGSEGELGIYS GHAPLLTAIKPGMIRIVKQHGH EEFIYLSGGILEVQPGNVTVLAD TAIRGQDLDEARAMEAKRASG KVKPSIMQSLTPEKIAAILPLQF FPQPADFTGPYVMLTSRRNNRA LSRCDDQTLMPGLAIRGIRHRH QQAGVRILLNNAIEHVVDGEK VELTLQSGDTLQADVVIYGIGIS ADEPLAREANLDTANGIVIDEA CRTCDPAIFAGGDVPITSSLINV VDEIIHDILLTQPVATRYCIVKVI FEAVMILRDSGGAPFCSNGMAT

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9277	39645	A	9337	905	2319	SRQAQWKGVPSTFSVINYHSLQ KRTTNLTHRQLLNLLSTVLYCS CPSIQKLLLMLQTGQPSGVGLV DLPLKAMSRPALPNATAALPTG TRTQPPSTPLLTRLPSSHRLLLH SGF*AAALLGVSEMTIRRDLNN HSAPVVLLGGYIVLEPRSASHY LLSDQKSRLVEEKRRAAKLAA TLVEPDQTLFFDCGTTTPWIIEA IDNEIPFTAVCYSLNTFLALKEK PHCRAFPCGATPFSNPSIFSKRV NNFCRDIAFYYSAGVHVSKGV TCFNLKRWPVKQWAMSMAQK HVLVVDHSKFGEVGPVCMGDL KRFDIVVRECCPEDEYVKYAQT QRIKPDKVSRHPVIIRLREPGLE PVMEFHHPVLPQRTTESAVVHI AHTRKSWRPEHSAPVLIQTSPV ERGPQYIQCYQLSLTSEENNQP DTQTTTKPAQYSSILFLSKYPKV IVDAPDRSTQRGWSSGLATQSN EQACTTKCNSCTANWHQNTTT FNSTANPSTFKPPTSAALRVLSL WTGNHCDWCFIRYWRLTPNW QRFRRVGRTERATTHNRLQAF GGHTQGLSPGPRRWLHEQRFPT TSDTGGHTADDFRKLDPCIQGP YGSHRHSVKSEVNFKEKRYAF APAASFRYTVLIRFCAPPNTGRF LLTGTPLPMLSYRHSFHAGNHA DVLKHTVQSLIIESLKEKDKPFL YLDTHAGAGRYQLGSEHAERT
9278	39646	A	9338	98	596	YSGIIMAQSKLYPVVMAGGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQPRFIVAHQMRQLNELSENIIL EPAGRTTAPTIAPAALAANRHS PESAPLMLVLATDHVIANEDAV RAPVK\NAIPYPKKGKLVTFGIG LDGRVPRYNM
9279	39647	A	9339	2	437	LECPGRSTANCSPRARATSLLL LTHVHGESRDRAQEMVDLLAQ YEQHGLQLNSRELPDHLPLYLE YLAQLPQSEAVEGLKDIAPILAL LSARLQQRESRYAVLFDLLLKL ANTAIDSDKVAEKIA/VRSAR*Y AAGAGCCLGRRAG
9280	39648	A	9340	152	334	HLSPQYGSIPRVISRMGGKLIIM DHFHYGRDSILLSME*TLALDA NLQFLYVVLLPNYYL
9281	39649	B	9341	1	1401	

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9282	39650	A	9342	86	2063	
9283	39651	B	9343	1	885	
9284	39652	A	9344	1	101	MDDNITYTTFICNPLNLSPQRR MLIITGPNMGGKSTYMRQTALI ALMAYIGSYVPAQKVEIGPIDRI FTRVGAADDLASGRSTFMVEM TETANILHNATEYSLVLMDEIG RGTSTYDGLSLAWACAENLAN KIKALTLFATHYFELTQLPEKM EGVANVHLDALEHGDTMAFM HSVQDGAASKSYGLAVAALAG VPKEVIKRARQKLRELESISPNA AATQVDGTQMSLLSVPEETSPA VEALENLDPDSLTPRQALEWIY RLKSLGKTMPSTRYQKINAHH YRHIWVVGDIHGEYQLLQSRL HQLSFFPKIDLLISVGDNIDRGP ESLDVLRLLNQPWFTSVKGNH EAMALEAFETGDGNMWLASG GDWFFDLNDSEHQEAIDLLLKF HHLPHIIEITNDNIIYAITTCVGN ARRAHAVHFCGDVARLLTCQI NIYRGQFRRLPRTFHRRLLTKL RDLILRLSAGNLQCCPDRAWRD NIHPNTFLRDLFCQATAVVQNR RLRSRIGDRFLGAVERRFGNDL PSSPVEWLTDNGSCYRANETRQ FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDYISIMPKPDGLT AAKNLAEAFEHYNEWHPHRAN PITYQAVCANHYRTLNNGTMT NTG*QYNVYHIYLQPAESVAA APHVDHHRSEHGR
9285	39653	A	9345	1062	1179	PRFVPILAPYAPVRSVCLR*V*T DLPEYGHILFQPADR
9286	39654	B	9346	1	2439	
9287	39655	A	9347	136	629	RSVTPVTDIVKLLEFTRLRLPGY TKSIE*TNITFQCAIAAA*KNSVS TPRGGGTGTNGQALNQGIIVD MSRHMNRIIEINPEEGWVRVEA GVIKDQLNQYLKPFGYFFAPEL STSNRATLGGMINTDASGQGS/ LGVRAVLLGGDILDTQPLPVEL AETLGKSAE
9288	39656	B	9348	1	4653	
9289	39657	C	9349	584	819	

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9290	39658	A	9350	1	765	MQEWGRYTILSGCCNSALKGD VCLLYGFRVAGRRQASELQELT IGYRAQKNRVSSWCYCHFRQM AKAQHIKGFLNRLRKTAKK*GF QLVLLPFSANGK\AQHIKGFLN RLRKTAKKTRDFLTRMPKLGM TMVGVDPALVLCYRDEYKLAL GEERGEFNVLLANEWLASALES QPVATVSGESWYFFGHCTEVT ALPGAPAQWAAIFARFGAKLE NVSVGCCGMAGTYGHEAKNH ENSLGIYELSWHQAMQRLPRN RCLATGYSCRSQVKRVEGTGV RHPVQALLEIIK
9291	39659	A	9351	1	1710	
9292	39660	A	9352	1377	1712	IFRASLNQLLFCGLLAGRNHRQ RSVRALSQRKMVPTDRK*RCA RRAAR*PSARVL*SGE*TDRQH AD*PTIR*RRSWYLRPAVYASV RQSDRLYSDEYHW*PVRLQRY VRR
9293	39661	A	9353	203	1293	VASSARRGLPVHGPAPLQGPGN SQDRL/ESGTNRCGLRGPLVKG GKGGRFPSARLIQTVKKGGTPS RDHA\IEPSGY\SVSAGVGE\RTR EGNDFYHEMTDSNVIDKVSLV YGQMNEPPGNRLRVALTGLTM AEKFRDEGRDVLLFVDNIYRYT LAG*ERFATVGR*ASN/AVGYQ PTLAEEMGVLQERITSTKTGSIT SVQAVYVPADDLTDPSPATTFA HLDATVVLSRQIASLGIYPAVD PLDSTTRQLDPLVVGQEHYHTA RGG*SI\LQRF\QELKDFMALP/G LSDELSEEDKLVVARARKIQRF LSQPFFVAEVFTGSPGKYVSLK DTIRGFKGIMEGEYDHLPEQAF YMVGSIEEAVEKAKKL
9294	39662	B	9354	1	505	
9295	39663	A	9355	604	789	TMVASGSRRMTST*SRGSVNG CRTILRWKRHSSPLKIKRKQKS L*TMPSF*RLPAENSLFEI

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9296	39664	A	9356	1	1514	SVAVLRE*APKIRIQLATMPELA DASSDQQDNGAEMNLVYDRD TMARLGIDVLAANSLLNNAFG QRQISTIYQPMNQYKVVMEVD PRYTQDISALEKMFVINNEGKA IPLSYFAKWQPANAPLSVNHQG LWRAL\TIWFTLPTGKSLC\DPS AAIDRAMTQLGVPSTVRGSFAG TA\QVFQETMNSQVILIIAAIAT VYIVLGILYESYVHPLTILSTLPS AGVGALLALELFNAPFSLIALIG IMLLIGIVKKNAIMMVDFALEA QR\HGNLTPQEAIFQACLLRFRP IMMTTLAALFGALPLVLSGGDG SELRQP\LGITIVGGLVMSQLLT LYTTPVVYLFFDRLRLRFSRKP KQTVTDTRWQLWIVAFGFFMQ SLDTTIVNTALPSMAQSLGESPL HMHMVIVSYVLTVAVMLPASG WLADKVGVRNIFFTAIVLFTLG SLFCALSSTIRIILRFVSLLHMR WQFRDLTFWQMRFRTNTPITSG GSDDSLMNQSHQRSVSSSI
9297	39665	A	9357	3218	3337	
9298	39666	A	9358	252	771	RRCQILLSGSLHSSWRTLPGHV *QLASAHRPRF\R*LPGLEPGEL FVHRNVANLVIHTDLNCLSVV QYAVDVLEVEHIIICGHYGCGG VQAAVENPELGLINNWLLHIRD IIHGWAYGIHDGLLRDLDVTAT NRETLEQRYRHGISNLKRDVHF TTGRFIQQRTNRQRLRFAQA
9299	39667	B	9359	604	831	
9300	39668	B	9360	1	1104	
9301	39669	A	9361	242	337	LTVIHGVSAKTVILSSAVPIQ*K TVRRVSRR

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9302	39670	A	9362	2208	3411	LAADHRRRNAVQRPCNGGQSV QSTDEAAGRLSHADTHPGRPA RALPGDCRPETLLRTAGVAE*T KALYTLRSEKTRERPMDKQQA SDEKHRRFHDKESDFLA/FVNL WNY/LGEQQKALSSNAFRRLCR TDYLNYLRVREWQDIYTQLRQ VVKELGIPVNSEPAEYREIHIAL LTGLLSHIGMKDADKQEYTGA RNARFSIFPGSGLFKKPPKWVM VAELVETSRLWGRIAARIDPEW VEPVAQHLIKRTYSEPHWERAQ GAVMATEKVTVYGLPIVAARK VNYSQIDPALLHDTIELGTSPAF LITRWGFGRNLSRTSGGPRQEP RRKEIAMELVLKDAQSALTVSE TTFGRDFNEALVHQVVVAYAA GARQGTRAPKTRAAVTGGMPT LYAVGRLSRIPMDT
9303	39671	A	9363	79	559	TLSPGSINPFEKPNS*DSVPMTL/ RRFIEVRVFQQIHHMRQRPAHL W
9304	39672	A	9364	1	655	THWER/A/QGAVMATEKVTVY GFRIVAARKVNYSQIDPALCRE LFIRHALVEGDWQTRHAFFREN LKLRAEVEELEHKSRRRDILVD DETLFEFYDQRISHDVISARHFD SWWKKVSRETPDLLNFEKSMLI KEGAEKISKLDYPNFWHQGNL KLRLSYQFEPGADADGVTVHIP LPLLNQVEESGFEWQIPGL/RRE LVMPD*SCQTVTEFVPANSHSY

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9305	39673	A	9365	1	2082	MDIQEFPDLKGTTSLEILTLTRA GIRLLPSGMCQQLPRLRVLELS HNQIEELPSLHRCQKLEEIGLQH NRIWEIGADTFSQLSSLQALDLS WNAIRSIHPEAFSTLHSLVKLDL T\TSQLTTLPLAGLGGLMHLKL KGNLALSQAFSKDSFPKLRILE VPYAYQCCPYGMCASFFKASG QWEAEDLHLDDEESSKRPLGLL ARQAENHYDQDLDELQLEMED SKP\TPSVQ\CSPTPCPFKPCEYL FESWGIRLAVWAIVLLSVLCNG LVLLTVFAGGPAPLPPVKFVVG AIAGANTLTGISCGLLASVDAL TFGQFSEY/GLARWETGLGCRA TGFLAVLGSEASVLLLTLAAVQ CSVSVSCVRAYGKSPSLGSVRA GVLGCLALAGLAAALPLASVG EYGASPLCLPYAPPEGQPAALG FTVA\LVMMKLLLFSWFVGPLP YHQNWYCDLPRGDFEAVW\DC AHGEATWAWPHLRKTGLLYCP VAFLSFASMLGLFPVTPEAVKS VLLVVLPLPACLNPLLYLLFNP HFRDDLRRLRTPRRRTQGPP*PL CCGREDAGERASC\DSYPQALV APSLMWISFCEAS*SWAGPLEL ETYGFPSVTLISCQQPGAPRLEG THCVEPEGNHFGNPQPSLDGEL LLRAEGSTPASGGLSGGWRLSA LWLGLWLHTCKYPSPFFSSPLF PFLSPPSVNDGCF
9306	39674	B	9366	1	510	
9307	39675	A	9367	88	246	TPMRPMKSPMPTPVSRSGSSSK MG*SSASL*RSIPGLDAGKTPW PAGRSGTWA
9308	39676	A	9368	693	1041	AEGYSQCPNAREGHVDEENED SAPAAQKIP*I*ED*SPHVSQPVP EGEEECVKKQ/GRFSWNTSTS* RQT/TARKKLLADQAEARRSKT KEAHKSYEEHLQAKKEEIIKTL SKEEETKK
9309	39677	A	9369	1	1911	

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9310	39678	A	9370	1	921	MWRSIFLDSRYLLSSRRKILILLI HVTFSGIRALAVPFRLPVEKMS FIFMGDVIHRMLTATQYVAPL MANFNPGYSDNSTVVYFDNGQ QIRKLIKDGLIIRKPVTVHSRAR CRKNTLARRKGRHMGIEFACFC CVFLTPALICMVCAVRLLTRDP YLASGDQPLERATGEHASMHE Y\PGELG\QPPGLYPSSHPPGRA GTLRALSRQDTFDADTPGSRNS AYTEL*DSCVDMETDPSEGPGL GDPCE\GTPPARQGSWEDEEED YEEELTDNRNRGRNKARYCAE GWGPVLGRNKNELEGWGRGV
9311	39679	A	9371	3	740	ELFPFAAAAAAMSMLRLQKRL ASSVLRMWQRTNGLG*TPMRP M*SPMPTPRQQIPEAHQRWAD HP/LSLVTGPFPGSMPEKTPLA\ AGEGAGQHGALGKAGRGTSQ MPGMPGEGQHGLRRIEDFGAG LLQKDTGEI*RRSDRPHVFTAC YLEGEGGMLFQKQGGFFMGTL PQG*RQDKGPQRSFLADQA*RP QGLRTKESTESASEERLPGQRK EEINQRLYSKEGRRPRNKNLPL GSVHTWPLVIT
9312	39680	A	9372	1	2229	
9313	39681	A	9373	3	1560	SGPNSLKFYDWGETVPQPWPIF GLSPAFGFPLCFPRGLGETIFSSR PHIR/RNYPELQKRLNGWLSAA LKTARILTVCVAVMLLLSAWG LFDFWNWLQNGAGQKNP*NIP D/LRIRNSILFL/LSAVGWTVLA\ SLIENRLASDI\HGRPLP\SARTR TLLTLFRNALAVIISTITIMIVLS EIGVNIAPLLAGAGALGLAISFG SQTLVKDIITGVFIQFENGMNTG DLVTIGPLTGTVERMSIRSVGV RQDTGAYHIIPWSSITTFAN\FV RGIGSVGANYDVDRHEDADKA NQALRDAVEDDETRFTSESSPIL RCCQREGLGLKAVVQILLSHGR NGLPGEPASSQGLSAASSTPVF HLALQIDSAPDNIDWVEMLFNK NMVTERLQNVMVLEQCFSDSS SLYRFLTYSYLLAFNVWLLLAP VTLCYDWQVGSIPLVETIWDM RNLATIFLAVVMALLSLHCLAA FKSRVTASIPGCIKAHAVENVL TTKSKTRIYPEVVVQSGLQKQK GKGSVMFIEAAGL

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9314	39682	A	9374	3	276	VRQYR/LGN/MHQQRMAEMID ARQQQAFGEEGACWGGCPKHR VMLDASGKPGLNDLCAGYQRD VRHLPRYLKAMADLLAHGRPA SDIMHAHLLV
9315	39683	A	9375	102	916	RSLLAIFNHW*\KRDL\GKFLVW NIKW/AFAKFCRSAGQTSGRSVI VEHNGEIYACDHYVYPQYRLG NMHRQRMAEMIDSRQQQAFGE DKFKQLPAQCRSCNVLKACWG GCPKHRFMLDASGKPGLNYLC AGYQRYFRHLPPYLKAMADLL AHGRPASDIMHAHKKVFKRGT ACSGFQKGGPLFRSRTGYCPTL RKKAPCPKTGLLGKKWTPQRR NSSGKSCAKRRGDPPLLENRFN GSRVQRKPQWNSCTGHPENNF FPNYGGTPYPQRMWPL
9316	39684	A	9376	338	1155	SIFISIGNLAANDLSPSRIARLQK ILHSYVPEEIRDGNQVRVTSWD GRKWGELEGDTYDRVLVDVPC TTDRHSLHEEENNIFKRSRKKE RQILPVLQVQLLAAGLLATKPG GHVVYSTCSLSHLQNEYVVQG AIELL\PINTASRYRWKI*LTSEG FSWTHFVSSQSCPGWGAGNTK TSLA\ILALCTSAKCVGWT*YPP QSLKQEYQRVYSVGCTRNWKL GPVAEMHSRSCLHPVRVFLQFS AIRSRRFAVLLSNCGASAWFPT SLINPYPIS
9317	39685	C	9377	157	453	
9318	39686	A	9378	486	1195	ARPQQYEQVPGKAEASEWERG SSAPTGPGGHAAAAAGGVGGG EGSPPALHGRGARAG/GAGICM GLRQQLNR*AMDLTGAGGPAR AGAAGAVARGGGRHQGPGAG GRGRGLGFAAGTAEPRGAPHR PLQRALPPIRREPGERHRAPRAG AAPQCGSARPRQPRAPQSLRAG ALPEAHAQGQGPARTHPAEPGP AARRAQQSLCRHWD*GRGRPG PPDALRGGAASDFRLSARTPICR
9319	39687	A	9379	10	1278	

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9320	39688	A	9380	1	1305	MECVCVKEKEREEKEGKEEEE EDEAVAERGGKGERRGERRGE RKREKETYTEKNRYRDTKRDR DRERKEPYEIPSSLIGHGDPKDE LDRNLALKQVKTYWVIQFSKSI EVIEKRMAVLNEQVKEAEGSS AEYKKEIEELKELLPEITEKTED AKESQTTGNVAELALKATL\GG GSSVS/SIASRKPTDGASSSNCV TDISHFVRKKRKPEEQSPWKDD AKKVKQELEVNGGSGDAVPSG NEVLENMEEEAENRVESRAAV EGTVEAGATAESTAYMYDIPA MYQENTAVSKTDEVSDLIHKL AQTDLLAQERAGKRASPQDGG SAEGQAQSDRQEATKQRHKQE AGDRHYDKQMLEYQGAHELY SSREKRKEKKKKPPHGRLPPTP VALHGAKRRLLTKRLFNASPN KPKGHSTQFSVMSQAEQQPVL
9321	39689	A	9381	67	458	WDMANSGCKDVTGPDEESFLY FAYGSNLLTERIHLRNPSAAFFC VARLQ\QEGVKSGMYVVIEVK VATQEGKEITCRSYLMTNYESA PPSPQYKKIICMGAKENGLPLE YQEKLKAIEPNDYTGKGSEENE
9322	39690	A	9382	139	710	WDMANSGCKDVTGPDEESFLY FAYGSNLLTERIHLRNPSAAFFC VARLQDFKLDFGNSQG\KTSQT WHGGIATIFQSPGDEVWGVVW KMNKSNLNSLDEQEGVKSGMY VVIEVKVATQEGKEITCRSYLM TNYESAPPSPQYKKIICMGAKE NGLPLEYQEKLKAIEPNDYTGK VSEEIEDIIKKGETQTL
9323	39691	A	9383	1	731	MANSGCKDVTGPDEESFLYFA YGSNLLTERIHLRNPSAAFFCV ARLQLLIESPRMSRLAKFWPRT HAVILSKTERTSFWPLKPQKWE SGSDTPYSQTRKDFKLDFGNSQ GKTSQTWHGGIATIFQSPGDEV WGVVWKMNKSNLNSLDEQEG VKSGMYVVIEVKVATQEGKEIT CRSYLMTNYESAPPSPQYKKIIC MGAKENG\LRLKYQEKLKAIEP NDYTGKVSEEIEDIIKKGGTTKL
9324	39692	A	9384	41	333	MFCNTDLGT/LLCTDVVARGLD IPQVNWIVHYDHPDDPKEYIHR VVPAFVDLNVNGNEGKQKKRG GGGGFDYQKIKKVEKSKIFKHI SKKSSDSRQLSH

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9325	39693	A	9385	3	1852	SKQKPMNVGLSETQNGGMSQE AVGNIKVTKSPQKSTVLTNGEA AMQSSNSESKKKKKKKRKMV NDAEPDTKKAKTENKGKSEEE SAETTKETENNVEKPDNDEDES EVPSLPLGLTGAFEDTSFASLCN LVNENTLKAIKEMGFTNMTEIQ HKSIRPLLEGRDLLAAAKTGSG KTLAFLIPAVELIVKLRFMPRNG TGVLILSPTRELAMQTFGVLKE LMTHHVHTYGLIMGGSNRSAE AQKLGNGINIIVATPGRLLDHM QNTPGFMYKNLQCLVIDEADRI LDVGFEEELKQIIKLLPTRRQTM LFSATQTRKVEDLARISLKKEPL YVGVDDDKANATVDGLEQGY VVCPSEKRFLLLFTFLKKNRKK KLMVFFSSCMSVKYHYELLNYI DLPVLAIHGKQKQNKRTTTFFQ FCNADSGTLLCTDVAARGLDIP EVDWIVQYDPPDDPKEYIHRVG RTARG\LNGRGHALLILRPEELG FLRYLKQSKVPLSEFDFSWSKIS DIQ\SQLEKLIEK\NYFLHKSA\Q EAYKSYIRAYDSHSLKQIFNVN NLNLPQVALSFGFKVPPFVDLN VNSNEGKQKKRGGGGGFGYQ KTKKVEKSKIFKHISKKSSDSRQ

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9326	39694	A	9386	1	2703	MAQQATLCSMKGCMRALVAQ LKSESEDLQQTVQAKREVPKSK VPAAEKRESGPKQAAVNAAVQ RVQVLPDVDTLLHFATESTPDG FSCSSSLSALSLDEPFIQKDVEL RIMPPVQENDNGNETESEQPEE SNENQDKEVEKPDSEKDLLDDS DDDDIEILEECIISAMPTKSSRK AKKLAQTASKLPPPVARKPSQL PVYKLLPAQNRLQAQKHVSFTP GDDVPRVYCVEGTPINFSTATS LSDLTIESPPNELATGD/GVRA/S IQSGKSHKPFRVKK/IMDQVQQ ASSTSSGANKNQVDTKKKKPTS PVKPMPQNTEYRTRLPNNEDR VRGSFALDSPHHYTPIEGTPYCF SRNDSLSSLDFDDDDVDLSREK AELRKGKESKDSEAKVTCRPEP NSSQQAASKSQASIKHPANRAQ SKPVLQKQPTFPQSSKDGPDRG AATDEKLQNFAIENTPVCFSRN SSLSSLSDIDQENNNNKESEPIK EAEPANSQGEPSRQLSQQNLTK QASLSKNASSIPRSESASKGLNQ MSNGNGSNKKVELSRMSSTKS SGSESDRSERPALVRQSTFIKEA PSPTLRRKLEESASFESLSPSSRP DSPTRSQAQTPVLSPSLPDMSLS THPSVQAESSEKAKSEDERHVS SMPAPRQMKENQVPTKGTWR KIKESDISPTGMASQSASSGAAS GAESKPLIYQMAPPVSKTEDV
9327	39695	A	9387	2	193	QSSE*NIQGPCNVWSSR*RWER SKGRRHLSSASRPLSALSTLRFT SVSQHAAKRVVVIRPQGQ
9328	39696	A	9388	395	761	SMQKKPRPIAHRQRCRAAMAA/ GQQPQIPITTGTGVVYPGAITM ATTTPSPQMTSDCSST\SASPEPS LPVIQSTYGMKTDGGSLAGNQ MINGEDEMAMYDDYEDDPKS DYSSENEAPEAVSAN
9329	39697	B	9389	1	477	

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9330	39698	A	9390	167	890	LSGARSSQGRLPWGRGDAVSTS TSRRNPRTGASDERNNHEPGKN SPYLQAQ\VRIGGKGTARRKKK VVHRTATA\DDKKLQF\SLKKL GVNH\ISGIE\EVNM\FTNQGTSG STFNNP*KVQAISWAANTFHPL PGPCWRPKPADKKWLPQPSLN PSLGAG*S*LRFKGRLARSFLPP NNP\VDGKATHLPTG\KDDDD\ KVPRSLWRILMRLPKNEGKLEL RSTS*R*NLEEVT\GSRYFKIMT AF
9331	39699	A	9391	2	315	GAASLLRAGPGSSGSDP\PLSSR FVERRGALYRSPMNQENPPPYP GPGPTAPYPQYGWQGGPQEPP KTTVYVVEDQRRDELGPSTCLT ACWTALCCCCLWDMLT
9332	39700	A	9392	263	680	LLLPALVTSAPLPPAGLATCPCP RLAQLGIGRAAPQKRSPRRRNP EASRGRPPDGVWRAPLR/VPPT PRETEPQRRGDPGLRNPCLSQA SPGAPQFSGP/PPGSPGTRPVRA* SPPGPSWVGPGPLHLTSPLPNRL DNGRV
9333	39701	A	9393	2	537	SGARLLLTCSETGAASLLRAGP GSSGSDP\PLSSRFVESRGALYR SPMNQENPPPYPGPGPTAPYPP YPPQPMGPGPIGGPYPPPQGYP YPRIPTVRLAGWTSGSLLKTTV LLWVGRPKEEMKLGTIHLPSQP AGTGLCLLLSLGTWFTLTRTRP RPFLFLASSAANLLTGVPCPHLF
9334	39702	A	9394	3	470	PKAKKEAPAPPKAEAKAKALK AKKAVLKGVHNHT\QKKKIHTP LTFQRPKSLRLRRQPKYPRKSA PRRNKLDHYAIIKFPLTTESAM KKIEDNNTLVFIVDVKANKHQI KQAVQKLYDIDVAKVNTLIRPD GEKKAYVRLAPDYDALDVAN KIGII

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9335	39703	A	9395	1	1144	MLYQVLMVDTCGTRGEGAFLK YRKPACPTALGFMFPRSHGLTA DTVLVSSLSRWFLWRRLLLLLL LLLLNLPLQKAVHRKATPESAI ADCSGPRDCAPWVKFAMLELH SFKCPAGEYWSKDVCCKNCSA GTFVKAPCEIPHTQGQCEKCHP GTFTEKDNYLDACILCSTCDKG DFYGKKTAVHEALCDNIDTRT VMEEMRALVSQCNLYMAARK AERRRPNRALLENIAMYLTHM LKIFGAIEEESPLGFPVGGPGTN LNPIENGGMDKFLTTVSVLRKT HRVSNGQNSVCRSVSYWKPKC TFCSLTHITYIRYLELRLTLESTV MPYLQVLSEFREGVRKIAREKK VLEVLQLSDALR\VTSCLSLGSG LKTMKEPCLLF
9336	39704	A	9396	1	639	MDGDEKTSFICAVHNGIFREWK QTGTCSPIKKGQLLLRVECHGK IKAQGGQMYIKAALFTRAKTW NQPKCPS\MIDWIKKMWVHIY/ TCEYYTAIKKKIMSSVETWMEL EAIILSKLTQEQKSKFRTFSLYSS RVFQRTQDVPYHNKLNEEADK PTTNKKGLILNLRLVNTPIGRK NTGKLSAIKEKLLKRPKRKHLS KIYTLKNDSDLIKDKNI
9337	39705	B	9397	1	825	
9338	39706	A	9398	2	285	HEENRPFVCEH/AGCGKT/FAN KPSLTSDAVVH/DPGKKKMKL KVKKSREKRSLASHLSGYIPPK RKQGQGLSLCQNGESPNCVED KMLSAVPVLTLG
9339	39707	A	9399	2003	2344	PFVGVFWFLFFFFSVFVFTFVPP EYYVLPAPPPHRSVFLVFGKRV VFFFPLPC/CDFRSRLTPPFVCAP P\PPPLPFVSVPCVPSLSCGDVC AADKKNKKKFLNTTRWKKKT
9340	39708	B	9400	3	113	
9341	39709	C	9401	48	182	

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9342	39710	A	9402	2	752	VWWNSRRRPVKRRRLLASPYS ACSGRSAGFLDNCAMCAARLA AAAAAQSVYAFSARPLAGGEP VSLGSLRGKVLLIENVASL*GTT VRDYTQMNELQRRLGPRGLVV LGFP\CNQFGHQENAKNEEILNS LKYVRPGGGIEPNF\MLFHKSE VN\GAGAHPLFAFLREALPAP\S DDATALMTDPKLITWSPV/CRK DPGKIKFFLGPPGNFFEKFLGGP CTVLPLRRYSRRF\QTIDIEPDIE ALLSQGPSCA
9343	39711	A	9403	1	1128	
9344	39712	A	9404	7	378	ARCDHPTAFVVCYRFYPWPAG HVDAAVH*YVCARATDSFIAV WRTLLKGTIIILHESSIHDNFNLT SQKLWAFVPNKAPRTSGIICWP EIQSAFQGGGNLYFTIPIVDRNS TNYVLRQVRLLGN
9345	39713	A	9405	318	616	DPAGFPGCWKPLFYDLHYRSQ LHQLCLQAGRTPGQFGHQHRF WWQFCT*ELPSALQPLPEGNLV SCNEQSFGAPATGTNPGEPVHP AALGTWLYLLPPC
9346	39714	A	9406	1	145	MEYYAVIKKDEFMSFAGTWM KLETIILSKLTQE\QKPTPLMFSL ISGS

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9347	39715	A	9407	1	2052	MVLVVVAVVVVVLVVAVIVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATQALLNFLATCGYKVSKPKA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEK\TGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPLEMLTEGPLAFELA MATARAELSLAIHHCCLPPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEQGPPVTVQTHILRSHL
9348	39716	A	9408	2	350	YKVSKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIP\R*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9349	39717	A	9409	1	749	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYLGLKLSKGTRDLTTFLP VNEEKIE/P*LSTSNCSKLRCSRG TSRGSLG
9350	39718	A	9410	118	174	
9351	39719	A	9411	577	3018	

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9352	39720	A	9412	310	1964	TFRLTEPTQMRRNQKTNPHNM TKQGSSIPPQKNHTSSPAMDPN QEEIPDLP\EKNSGVNKIPRNPT YEGCEGPFQGELQTTAQQNKG GHKQTEDHSMLMDRKNQYCE NGHTAQAVPNPYTLLSQIPEDA EWFTVLDPKHAVFCIPVHPDSQ FLFAFEDPSNPMSQLIWTVLPQ GFRNSPHLFGQALAQDLSQFSY LDTLVLRYMDDLLLATHSETLC HQATQALLNFLATCGYKVSKP KAQLCSQQVKYLGLKLSKGTR TLSEERIQPILGYPHPKTLKQLT AFLGITGFCQIWIPSILTAKGDL WLSDNHLLKYQVLLLEGPVLQ LRTCATLNPATFLPDNEEKIEH NCQQVIAQTYATRGDLLEVPLT DPDLNLYTDGSSFVQKGLQKA GYAVVSDNGILESNPFTPGTST QLAELVALTWALEFGEGKRVN INTGSKYAYLVLHAHASIWRER EFLTSEGTPIKHQEAIRRLLLVV QKPEEVAVLHCWGHPKGKERE IEGNCQADIEAKRASRQDPPLE MLIERHLVWGNPLWETNPQYS
9353	39721	A	9413	3	370	RCCPCPRVHHMHISARAEIRPPP RPPPFLLLLVFLFQTGPCSHPGC SPPPAHPSCSSWPQWPG/CSSPV SVLLAKPAACLIAAAVSANPRL LFKPCCRTASNWAHRQVTLCQ WSELSSCFWPE
9354	39722	A	9414	191	1375	EWPEGGGRYSSVPSAVHHART CLAAELSGTSRPQEPRALPPETG VATAEAEKSNQPAAISK\PNGQ GAPLQR/RSPRLSPSPGAAQVPA LPMQDMSEGSSSPSPPGGHIWL ASLTPCSLALWNSCCQSPGSQP RGRDEGDCLVRATEPSATGPDP RRTRLCSISASLVVRNTPDPGIS DRRPGISDRRPGTSDRRPGTSDR RPGISDRRPGTSDRRPGTSDRRP GTSDRRPGTSDRRPGISDRRPGT SDRRPGISDRRPGTSDRRPGISD RRPGTSDRRPGTSDRRPGISRLP RDWIPAAAASRENSNSADARN RCSSPSRKCQTPTSHRMRGSAG SVGSSAGHTAGGTGLPTPSRCS QALQVFPAVLGKRGFLSWERS LKQRDIRGPDFSSTALI
9355	39723	A	9415	3	523	

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9356	39724	A	9416	1	846	MLCDFQDGSTSRHVNEPSNNPS PQPWSEDQGQASATVPCAKSV MHRLKKFTIEYLVMKFLKAVS HAIQMEMLAPKGPSPIPEDASV KEENICRAFSDALLYKIEDIDNK DWNNPQLCSDY/VKDNAYTSF QIQEMET\ILKELKFEVGGPLPL HFLRQASKAGKADVEQHTLAK YLMELTLIDYDMMHYHPSKAA TAASCLSQKVLGQGKWNLKQQ CYTGYTQNEVLEVMQHVAKN VLKVNENLTKFIAIKNKYASNK FLKISMIPQLNSKAIKDLAFPLM GGS
9357	39725	A	9417	72	1340	CPPFSVRVPPWAGLALLPSPSL MALLRRPTVSSDLENIDTGVNS KVKSHVTIRRTVLEEIGNRVTT RAAQVAKKAQNTKVPVQPTKT TNVNKQLKPTASVKPVQMEKL APKGPSPTPEDVSMKEENLCQA FSDALLCKIEDIDNEDWENPQL CSDYVKDIYQYLRQLEVLQSIN PHFLDGRDINGRMRAILVDWL VQVHSKFRLLQETLYMCVGIM DRFLQVQPVSRKKLQLVGITAL LLAPKYEKMFSPNIEDF\VYITD NAYPS\SQIREMETLILKELKFEL GRPLPLHFLRRASKAGEVDVEQ HTLAKY\LMELTLIDYDMVHY HP\SKVAAAASCLSQKVLGQGK WNLKQQYYHKDTQENEVLEV MQHMAKNVVKVNENLTKFIAI KNKYASSKLLKISMIPQLNSKA VKDLASPLIGRS

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9358	39726	A	9418	1	1875	EPEKQQLYDIPASPKKAGLHPP DSQASGQGVPLISVTTLRRGGY STLPNPQKSEWIYDTPVSPGKA SVRNTPLTSFAEESRPHALPSSS STFYNPPSGRSRSLTPQLNNNVP MQKKLSLPEIPSYGFLVPRGTFP LDEDVSYKVPSSFLIPRVEQQN TKPNIYDIPKATSSVSQAGKELE KAKEVSENSAG\QIPHGSPDGQ/ RSPSPEPDRLSGSSSDSRASIVSS CSTTSTDDSSSSSSEESAKELSL DLDVAKETVMALQHKVVSSVA GLMLFVSRKWRFRDYLEANID AIHRSTDHIEESVREFLDFARGV HGTACNLTDSNLQNRIRDQMQ TISNSYRILLETKESLDNRNWPL EVLVTDSVQNSPDDLERFVMV ARMLPEDIKRFASIVIANGRLLF KRNCEKEETVQLTPNAEFKCEK YIQPPQRETESHQKSTPSTKQRE DEHSSELLKKNRANICGQTLPN LEEKDKPILEQRLDENKDLGTM NPGPLIPQPSSQQTPERKPRLSE HCRLYFGALFKAISAFHGSLSSS QPAEIITQSKLVIMVGQKLVDT LCMETQERDVRNEILRGSSHLC SLLKDVALATKNAVLTYPSPAA LGHLQAEAEKLEQHTRQFRGT

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9359	39727	A	9419	1	2013	MGLKSWGGMGLGTAFGKGLR GEKAWCVSGRYHWRYSQWSG TLTQGPWVWRVHSLSDRVYDV PTQHRGPVVLKEPEKQQLYDIP ASPKKAGLHPPDSQASGQGVPL ISVTTLRRGGYSTLPNPQKSEWI YDTPVSPGKASVRNTPLTSFAE ESRPHALPSSSSTFYNPPSGRSR SLTPQLNNNVPMQKKLSLPEIPS YGFLVPRGTFPLDEDVSYKVPS SFLIPRVEQQNTKPNIYDIPKAT SSVSQAGKELEKAKEVSENSAG \QIPHGSPDGQ/RSPSPEPDRLSG SSSDSRASIVSSCSTTSTDDSSSS SSEESAKELSLDLDVAKETVMA LQHKVVSSVAGLMLFVSRKWR FRDYLEANIDAIHRSTDHIEESV REFLDFARGVHGTACNLTDSNL QNRIRDQMQTISNSYRILLETKE SLDNRNWPLEVLVTDSVQNSP DDLERFVMVARMLPEDIKRFAS IVIANGRLLFKRNCEKEETVQL TPNAEFKCEKYIQPPQRETESH QKSTPSTKQREDEHSSELLKKN RANICGQNPGPLIPQPSSQQTPE RKPRLSEHCRLYFGALFKAISAF HGSLSSSQPAEIITQSKLVIMVG QKLVDTLCMETQERDVRNEILR GSSHLCSLLKDVALATKNAVLT YPSPAALGHLQAEAEKLEQHTR
9360	39728	A	9420	3	645	DFHTN/K/RVCEEIPIILSKKLHN RRAGCVTHLTNQIQRGPVRGISI KLQEEEKERRDNYVPKVSALD QEIIEVDPDTKEMLKLLDFGSLS NLQQQKATRVYAVVQISAPMF LLWALPLSVAPLITDFKMFVTT SYLISLFLIINSSANPIIYFFVGSL RKKRLKESLRVILQRALADKPE VGRNKKAAGIDPMEQPHSTQH VENLLPREHRVDVET
9361	39729	A	9421	312	694	LTPAPRKNVTEKYYMCLGNDF HTN/K/RVCEEIPIILSKKLHNRR AGCVTHLTNQIQRGPVRGISIKL QEEEKERRDNYVPKVSALDQEI IEVDPDTKEMLKLLDFGSLSNL QVTRPTVGMNFKMPRGAV
9362	39730	A	9422	3	383	

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9363	39731	A	9423	304	1862	RMLEATSKMRKGVPSSIQ/SSQ GNSYTLIPSAKSDNLSDSSHSEI SSRSSIVSNCSVDSMSAALQDE RCSSQALAVPESTGALEKTEHA SGIGDHSQHGPGWTLLKPSLIK CLAVSSSVSNEEISQEHIIIEAAD SGSWEVGTSCSSSSHDNFQSLP NPKSWDFLNSYRHTHLDDPIAE VEPTDSEPYSCSKSCSRTCGQC KGSLERKSWTSSSSLSDTYEPN YGTVKRRVLESTPAESSEGLDP KDATDPVYKTVTSSTEKGLIVY CVTSPKKDDRYREPPPTPPGYL GISLADLKEGPHTHLKPPDYSV AVQRSKMMHNSLSRLPPASLSS NLVACVPSKIVTQPQRHNLQPF HPKLGDVTDADSEADATLGNK CKLLYMSDVRNPVPAVKDVLV QKYTSFNFFHPQEALDRRREEL ALPEGASGEACLSTRSLKRSGV QALAQQTHSRNFLPEKQPFSAQ AAGILHGSINHNTRGPCLLEGT KMMTGVLYRAYLLCIAYSRDLI VDEQIMNGLRKAI

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9364	39732	A	9424	1	1335	MTFKNPKYPFVSNLAKQKGMS VIKVNGKLQQSNPNRTTNGPDP SGMKVWVSPQGKNPQPTEVLA EGKGNTEWVVEEDTRNFGFGI QKHTDIGIKYDSSTGIYDLDFN VVLDRRASEEGITLTAALAADR ETPSENCLPSPVNPTAQGEEGIH PDPIIVLEQEDPTTAPHPQRLCQ QQQCQRPLCRLQPVWPHIVDLT PLTEIGSEEPVGELNFKHIRFEV SEDNMTFDASDQGPFFENYWQ LVLSATPGDVTWNGALGLHTP KSSSPDTCSAQQASQCWELSPG GRRIGTLLLPQESGASWLPPGV TSSLAAVRVIMNCGDKATPRN GGVRTLKKLSSLPLSKAGGKVL YGEINPEQEVQASLSFAALLES YGIFMETEFLVACLISQGGQLR NQDFSSSIYSLAPGPLDPSSVRA GAQRTAPPWGISPRSC/PVIKVN GKLQQSNPNRTTNGPDPSGMK VWVSPQGKNPQPTEVLAEGKG NTEWVVEEDTRNFGFGIQKHT DIGIKYDSSTGIYDLDFNVVLDR RASEEGITLTAALAADRETPSE NCLPSPVNPTAQGEEGIHPDPII VLEQEDPTTAPHPQRLCQQQQC QRPLCRLQPVWPHIVDLTPLTEI GSEEPVGELNFKHIRFEVSEDN MTFDASDQGPFFENYWQLVLS ATPGDVTWNGALGLHTPKSSSP DTCSAQQASQCWELSPGGRRIG
9365	39733	A	9425	56	235	
9366	39734	A	9426	1	515	
9367	39735	A	9427	138	830	AWAQLPSALGSTRVSPPPSARS QPPWRRRHK/CLLETEPLQGTD EDAVASADFSSMLSEEEKEELK AELVQLEDEITTLRQVLSA\KER HLVEIKQKLGMNLMNELK\QNF SKSWH\D\MQTTTAYKRTHDTL SHAGQKATAAFSNVGTAISKKF GDMSYSIRHSISMPAMRNSPTF KSFEERVETTVTSLKTKVGGTN PNGGSFEEVLSSTAHASAQSLA GGSRRTKEEELQC
9368	39736	A	9428	3	381	LLETEPLQGTDEDALASADFSS MLYEEEKEEVKAELVQLEDEIT TLRQVLSAKERHLVEIKQKLG MNLMNELKQ\NFSKSWHDMQT TTAYKKTHETLSHAGQKATA\A FSNV\GTAISKKFGDMRRK

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9369	39737	B	9429	79	426	
9370	39738	A	9430	1	570	
9371	39739	A	9431	1	1677	MLESVNVRLEDLITGPCWEAG WNAGYAFLVVAVEDFTIGKLF DKLEGTKLCLKNALPRVITQTE SHRQRLLQEAAANWHSWLIKV QKMKAVYHILNMCNIDVTQQC VIAEIWFPVADATRIKRALEQG MELSGSSMAPIMTTVQSKTAPP TFNRTNKFTAGFQNIVDAYGV GSYREINPAPYTIITFPFLFAVMF GDCGHGTVMLLAALWMILNER RLLSQKTDNEIWNTFFHGRYLI LLMGIFSIYTGLIYNDCFSKSLNI FGSSWSVQPMFRNGTWKTGTH DPHLAVLFKMGHVEGRDCVLR IVLAKIGYRNGFLRKIWNLASN KLTFLNSYKMKMSVILGIVQM VFGVILSLFNHIYFRRTLNIILQF IPEMIFILCLFGYLVFMIIFKWCC FDVHVSQHAPSILIHFINMFLFN YSDSSNAPLYKHQFNFGDVFV HQAIHTIEYCLGCISNTASYLRL WALSLAHAQLSEVLWTMVMN SGLQTRGWGGIVGVFIIFAVFA VLTVAILLIMEGLSAFLHALRL HWVEFQNKF\YVGDGYKFSPFS FKHILDGTAEE
9372	39740	A	9432	3	933	GTWPVSSAASIYAGTGGLG\SQI SMSCSTSFWGGLGSGGLATEM AGGLAEMGGIQNEKETMQSLN DHLDYLDRVRNLETENWRLES KIQEYLEKRPHVRDWGHYFKTI KELRAQIFANTVDNVHIILQIDN AQSSMRQELAMRQSVESNIHG LCKVIDDTNVTLLQLETEMGAL KEELLLMKKNHEEEVKGLQVQ IANSGLAVEVDAPKSQVLAKM EQLNRILLYLESKLAQNWAEG QRKVQEYKDLLNIRVKLEAEIA TYRRLLEDSEGLNLGDALDSSN SMQTIQKTTTRQIVDSKVVSEIS DTKVLRH
9373	39741	A	9433	3	698	

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9374	39742	A	9434	2	479	PRVRESTTVVTTQSAEVGAAET TLTELRRTVQSLEIDLDSMRNL KASLENSLREVEARYALQMEQ LNGILLHLESELAQTRAEGQRQ AQEYEALLNIKVKLEAEIA/TTY RRLLEDGEDFNLGDALDSSNS MQTIQKTTTRRIVDGKVVSETN DTKVLRH
9375	39743	A	9435	1	618	AEHLLKPLPADKQIETGPFLEA VSHLPPFFDCLGSPVFTPIKADIS GNITKIKAGYDTN\QPRFRTLKT ILEGEKEMYGAKGPKVGATLA LMWLKRGLRFIQVFLQSICDGE RDENHPNLIRVNATKAYEMAL KKYHGWIVQKIFQAALYAAPY KSDFLKALSKGQNVTEEECLEK IRLFLVNYTATIDVIYEMYTQM NAELNYKV
9376	39744	A	9436	1	1569	
9377	39745	A	9437	211	368	ERNSLSQLQWDNPTPPATRRPS HSSLRGEHAQ*GLLSFFERLSCT LSRFMPI
9378	39746	A	9438	1435	1703	
9379	39747	A	9439	1	913	MKNYNCWRRVFLFVVTPIPMG HIKHRQGPNKQQRGQKRDEQR MRKENRGHRKGCTWCGGGTE GTGWGKYEKSEVERGLVRYER KRRAYSGIQQYAAAALPTVYN QNLLTQQSIGAAGSQKEACAY AVMSLASRAPVYRSFDSEKAG DREVQRTMLELLNQLDGFQPN TQVKVIAATNRVDILDPALLRS GRIDRKIEFPMPNEEAR\ARIMQ IHSRKMNVS/TDTTLVALQMAL NVYNGKQAPYASCHIFELYQE DNGFLLEHTGFVSYDNPVSAQ AAIQSMNGFQIGMKRLKVQLK RSKNDSKPY
9380	39748	A	9440	3	438	
9381	39749	A	9441	1	247	AIAAIDSDSSDGSRQSEWKFWK GFTILDAIKNIYDSWEEVKMST LTEVWKKLIPTLMDSFEDFI\EE VTVDVWECTVLQTQI

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9382	39750	A	9442	93	726	TSLGLSLCPRQCKRCPHLSLQQ EEPDPANLEVDHDFFQDKVWP HLALRVP\AFETLKVQSAWAGY \YDYNTFDQNGVVGPHP\LVVN MYFATAFSGHGLQQAP\GIGRA VAEMVLKGRFQTIDLSPFLF\TR FYLG\EKIQ\ENNIILRHVCSGIG LPLACNPWLCLKSLVCWLPIFP KVLCPGLLSPSPVSSSSQAGHW HPIWAGQGTGSEAEGQ
9383	39751	A	9443	1	849	MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHS\DPEEIE KEEQAAAEKAVTKEEFQGEWT APAPEFTATQPEVADLSEGVQV PSVPIQQFPTDDWSTQPATENW SAAPTAQATEWKMQQQSTILE AESSPHQTPNLPAPWSRTSQPPE
9384	39752	A	9444	1	1575	
9385	39753	A	9445	1	2325	
9386	39754	A	9446	1	1149	
9387	39755	A	9447	85	1041	REIVTMSGALDVLQMKEEDVL KFLAA\GTHLGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWE\KL LLAA\RAIVAIENPADVSVISSQE ILGQKGCAESFAAATG\ATPICW ARFTPWNLSLTQIQGSPSGEPR AFLLVTDPQGLNHQPSHGGNL NV*PTLPLALVNPD/SPLRRYVD I\AIPCNNQGSSLQWGLMWW\M LASGSFCAMRGT\ISREHP\WEV\ MP\DLYFYRDPEEIEKEEPGCCL RSQVTKEEFQGEWTAPAPEFT\ VTQPEVADWSEGVQ\VPS\VPIQ QFP/TTEDWSAQPATEDWSAAP TAQATEWVGATTDWS

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9388	39756	A	9448	1	762	MGKVKVGVNGFGCIGRLVIRT ACNSGKVDIIAINDPFIDLSYMV YMFQYDPTHGKFHGTVKAENG KLVINGNPITIFQEPDPSKIKWG DAGTEYVMESTGIFTTMENAG AHLQWGAKRPQG\LQNIIPATT/ GAAKAVRKVIPELNGKLTGMA LRVPTANVSVVDLTYHLEKPA KYDDIKKVVKQASEGPLKGILG YTGHQVVSSDFNSDTHSSTFNA GAGTALNDHFVKLISWYDNEF GYNNRVVDLMAHMASKE
9389	39757	A	9449	93	660	DTMGKVKVGVNGFGRIGRLVT RA\AFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFHGTVK AENGKLVINGNPITIFQE\RDPSK IKWGDAG\AE\YVVESTG\VFTT MEK/ALGAHLQGGSQKGHSSL APSCLMPPMFVMGVN\HEKDD NSLK\IISN\ASCTTNCLAPLAK\ VIHDTLVSGEGLKDHRALP
9390	39758	C	9450	554	715	
9391	39759	A	9451	193	472	RRVGVWRRPQFQQSRCSHGPN QGSAPWLNPTGAFGKETDLLL\ DDSLVSIFGKRRL\KRFSMVG/D RMASKNALNAQPDGPGLTCSL APNIISQL
9392	39760	A	9452	1	864	GTRMGLAGVCALRRSAGYILV GGAG/WSVLAPRAAAARRCSE GEWASGGVRSFSRAAAAMAPI KVGDAIPAVEV\FEGEPGNKVK PGKSLFKGKKGVLFGVPGGPPP LGCS\KTHLAKGLWEQG*RLCK AKGKSRVVALF*VVNDALCDW AQWGQAPQGGKARFGLLAESP LGPFGK\ETDLL\LDESLVSHLL GIRRLK\RFS\MVVQDGIV\KAL\ NVEPDGTGLHLAAWAPNIIFTA LEALGPDLLPLPPPYSSPCPALC LGPLQFGNVGQISAINTLWVLR PKQKKKKKS
9393	39761	A	9453	1	239	QCCSGGTHGNPAIGDR\MQKQI LPWAPAQMKIRFMAPPERKYS VWIAAPILASLSTSSRMWISKQE YDESGPSIVHRKCF

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9394	39762	A	9454	2	801	ASAPRAQSLAFADPPPVHTRRQ LTMDDDIAALVVDNGSGMCKA GFAGDDAPRAVFPSIVGRPRHQ GVMVGMGQKDSYVGDEAQSK RGILTLKYPIEHGIVTNWDDME KIWHHTFYNELRVAPEEHPVLL TEAPLNPKANREKMTQIMFETF NTPAMYVAIQAVLSLYASGRTT GIVMDSGDGVTHTVPIYEGYAL PHAILRLDLAGRDLTDYLMKIL TERGYSFTTTAEREIVRDIK/EE AVLRRPGLRARDGHG\ASSSSL EKSYELPDGQVITIGNERFRCPE ALFQPSFLG\MESCGIHETTFNSI MKCDVDIRKDLYANTVLSGGT HQFPLPCRPGC*KKITALEP\AT MKI\RIIA\PPEAQSTPLWNRGAP IL\ASLVHLPAKMWDQKSREYD ESGPLPFVHRK\CFQLLPGEELR
9395	39763	A	9455	3	108	
9396	39764	A	9456	1	1430	MKFLIFAFFGGVHLLSLCSGKAI CKNGISKRTFEEIKEEIASCGDV AKAIINLAVYGKAQNRSYERLA LLVDTVGPRLSGSKNLEKAIQI MYQNLQQDGLEKVHLEPVRIP HWERGEESAVMLEPRIHKIAIL GLGSSIGTPPEGITAEVLVVTSF DELQRRASEARGKIVVYNQPYI NYSRTVQYRTQGAVEAAKVGA LASLIRSVASFSIYSPHTGIQEYQ DGVPKIPTACITVEDAEMMSRM ASHGIKIVIQLKMGAKTYPDTD SFNTVAEITGSKYPEQVVLVSG HLDSWDVGQGAMDDGGGAFIS WEALSLIKDLGLRPKRTLRLVL WTAEEQGGVGAFQYYQLHKV NISNYSLVMESDAGTFLPTGLQ FTGSEKARAIMEEVMSLL\QPL NITQVLSHGEGTDINFWIQAG\V PGA\SLLDDLYKYFFF\HHSHGD TMTVHGIQTQMECLLLLFWAV VSYV\VADME\EMLPRS
9397	39765	A	9457	2	631	
9398	39766	A	9458	1	406	PTVCERELCVFAFQTLGVMNE AADEIATGAQVVDLLVSMCRS ALESPRKVVIFEPYPSVVDPNDP QMLAFNPRQLKFMHTPHQFLL LSSPPAKESNFRAAKKLFGSTF AF/HLHGAMYGSGIYLSPMSSIS FGYSA
9399	39767	A	9459	7	257	

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9400	39768	A	9460	2	649	
9401	39769	B	9461	50	607	
9402	39770	A	9462	627	1665	EQAGQALSTAPVGDGHELLCE VGSSSFRDVLGTSMGLCGGY/G GAS/GMGGITAVTVNQNVLSPL NLEVDPNMQGMHTQEKEQVK TLNKSASFVDKVLFLEQQNKM LETNWSLLQQQKPAQSNMDN MFESYINNLLGQLEILGQEKLK LEAELGNMQGLCMFFVKEDFK KKYEDEINKPTEMENEFVLIKK DVDDAYMNKVELEFRLEGLTD EINFLRQLYEEEIPELQSQILDTS VVLSMDNSRSLDMDSIIAEIKY EELQTLAGKHWDDRRLTKTKIS EMNRNISRLQAEIEGLPQRPEQ RASLESVIADAEQRGELAIKDA KTKLSELEAAQQRAKQDMAHG
9403	39771	A	9463	2237	2656	LSCSLFSGFAGTRFFGTSILRLPL MYCPVNDSGTAIIASSGPSATTS PP*TPAPGPMSITWSAARIASSS CSTTITVLPRSRRWISVPNRRSL SRWCRPIDGSSSTYITPTRPAPI WLARRIRCASPPESVSAERESV
9404	39772	A	9464	3	2790	EFVLIKKD\VDEAYINKVELESR LEGLTDEINFLRQLYEEEIRELQ SWISDTSVVLSMDNSRSLDMNS VIAEVKAQYEEIANRSQAEAES MYQIKDEELQSLAGKHGDNLR CTKTKISEMNRNISRLQAENEG LKGQRAFLEAAIADAEQCGELA IKDANAKL/SELEAALQRAKQD MAWQLR\LMNVRLALDIEIATY KKLLEGEESRLESGMQNMSIHT KTTSGYASGLSSACGGLTSPGL SYGLGASSFSRT

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9405	39773	A	9465	2	1516	SAIPTSTPASTMSIRVTQKSYKV STSGPRAFSSRSYTSGPGSRISSS SFSRVGSSNFRGGLGGGYGGAS GMGGITAVTVNQSLLSPLV\LE VDPNIQAVRTQEKEQIKTLNNK FASFIDKVRFLEQQNKMLETK WSLLQQQKTARSNMDNMFESY INNLRRQLET\LGQEKLKLET\E L\GNMQGLVEDFKNKYEDEINK RTEMENEFVLIKKDVDVDEAY MNKVELESRLEG\LTDEINF\LR QLYEEEIRELQSQISDTSVVLSM DNSRSLDMDSIIAEVKAQYEDI ANRSRAEAESMYQIKYEELQSL AGKHGDDLRRTKT*DLLR*TRN ISRLQAEIEGLKGQRASL\EAAI ADAEQRG\ELAI\KDANAKL\SE LEAALQRAKQDMARHLR*VTR ELD*TFKLGPGTFEI\ATYRKLL EGEESRL\ES\GMQNMSIHTKTT GGYAGGLSSAYGGLTSPGLSYS LGSS\FGSGAGSSSFSRTSSSRAV VVKKIETRDGKLVSESSDVLPK
9406	39774	A	9466	1410	3244	PPCRRSHPRPPLRGEQKPRPSQP PFAVPAAPAPQV*\PQMIDLCNV GFQFYRSLEHFGGKPVKQEPIK PSAVWPQPTPTPFLPTPYPYYPK VHPGLMFPFFVPSSSPFPFSRHT FLPKQPPEPLLPRKAEPQESEET KQKVERVDVNVQIDDSYYVDV GGSQKRWQCPTCEKSYTSKYN LVTHILGHSGIKPHACTHCGKL FKQLSHLHTHMLTHQGTRPHK CQVCHKAFTQTSHLKRHMMQ HSEVKPHNCRVCGRGFAYPSEL KAHEAKHASGRENICVECGLDF PTLAQLKRHLTTHRGPIQYNCS ECDKTFQYPSQLQNHMMKHK DIRPYICSECGMEFVQPHHLKQ HSLTHKVLRGLWWGGRGLGK RSGALSRALGSRTPVPLCTLPR GGLQGEIQAQESEFSPVCNHSP GVIQAELKQGPSGVPEILPQLNS CPTKGTCRYYPEGSRLPSAGTI NKGPRLGFSRKGDHSLTSGAPL YVGKESKVHFRAYEDPGVKEH KCGICGREFTLLANMKRHVLIH TNIRAYQCHLCYKSFVQKQTLK AHMIVHSDVKPFKCKLCGKEF NRMHNLMGHMRLA\RNGKPLK RLYCPSKFTLKGNLTRHMKVK

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9407	39775	A	9467	1	1309	MRIQQLCGHLWQQKKISLELM SSFHKILKNKMGCGVTPDSKEL LKYLSYCNSYPLTGSPQEAPVS DVPLPVSKCSHCSVQLIMCLRP EHIPNSPGIKGQGIKQHEEKHPT LLHLDASHLMTCFVVEMTLYV LIAGFKSLCSIHSYPPRTLRHLC EKVWDSLLENERRHEKRGPAN FLHRLPAEHQWGIVQSSNIMAG LSARLQLFLEHRPFPVFELTAN GCPTKGLQGEIQAQESEFSPVC NHSPGVIQAELKQGPSGVPEILP QLNSCPTKGTCRYYPEGSRLPS AGTINKGPRLGFSRKGDHSLTS GAPLYVGKESKVHFRAYEDPG VKEHKCGICGREFTLLANMKR HVLIHTNIRAYQCHLCYKSFVQ KQTLKAHMIVHSDVKPFKCKK SFTAQGNSAPQEDAGSQGE/PV CLL/CPNWGQRKGRAWRHLRH
9408	39776	A	9468	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
9409	39777	A	9469	2	1844	
9410	39778	A	9470	3	772	VPNPYTLLSQIPEEAEWFTVLD LKDVFFCIPVHPDSQFLFAFEDP LNPMSQLTCTVLPQGFRDSPHL FGQALAQDLSQLSYLDTLVLQ YVDDLLLAACSETLCHQATQA LLNFLATCGYKVSKEKAQLCS QQVKYLGLKLSKGTKALSEECI QPILAYPHLKTLKQLREFLGITG FCRIW/NFQALLLERPVLQLCTC ATLNPVTFLPDNE\EEYNCQQII SQTYATRGDLLEVPLTDPDLNL YTDGSSFVEKGPQKA

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9411	39779	A	9471	1	6504	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
9412	39780	A	9472	2	1658	
9413	39781	A	9473	1	617	MCSWTAPVSSILTHPNWPVLR MAGLTGCASVAMKKKIEHNCQ QVIAQTFTTRGDLLEIPLTDPGL NLYTDGSSFVEKGLRKAGYAV VSDNGILESNPLTPGTSAQLAEL IALTWAPELEEGKRVKRKKAI WREREFLTSEGTPIKHQEAIRRL LLAVQKPKEVAVLHCRGH/QE GNCQVDIEAKRATRSQVARGH KICDFPSCSYR
9414	39782	C	9474	587	715	
9415	39783	A	9475	96	269	
9416	39784	A	9476	1	1398	
9417	39785	B	9477	1	1152	
9418	39786	A	9478	3	241	
9419	39787	C	9479	202	534	
9420	39788	A	9480	108	199	
9421	39789	A	9481	125	352	
9422	39790	A	9482	2	325	RRSLALSPRPDCGLQWHNLGSL QAPLPGFTPFSCLSLPSSWDYRR PPPRPANFLYFLVETGFHLVSQ/ SGLDLLTS\DPPASASQSAGITG VSHRARPQNLFFKVRCPE
9423	39791	A	9483	184	383	LGLQ\WRNLGSLQAPLPGFTPFS \CLSLPSSWDYRRPQPRPANFFF FVFFLVKTGFHLVSQG\G\LDLL TS*SHPASAFQSAG\IIGVSHRRP AITLQF
9424	39792	A	9484	1	416	MGRSFLGGGSTLMLLGGGQLH ILTPSFPSWTETGNYTCEFCGKQ YKYYTPYQEHVALHAPIRNSA KDDHRSASILSENRGSHQ/SHAS CHHHYHCHYYHQHHHCLHHH SYHHHHCHHHRGMWRNWDTV LWIHQTQPVQD

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9425	39793	A	9485	3	534	GRRQRRSRHLLHRRQDRQSAP GSGSKIPQK\KVKLAADEDDDD DDEEDDFDDEETEEAPVKKSIQ DTPARNAQKSDQNGKVSKPSS TPRSKGQESFKKQEKTPKTPKG PRSVEDIKTKMQASIEKAHGTV LGTTVGNIPLRGGNQEKFHGAA GVWFGKFGVQRKIQQKQLQKD VTSGS
9426	39794	B	9486	44	924	
9427	39795	B	9487	41	2197	
9428	39796	B	9488	67	1507	
9429	39797	A	9489	134	311	
9430	39798	A	9490	5	1545	EKIQINTI/KNDKGILPLDPTEIQI TIREYYEHLYAHKLENLEEIDK FLDIYTLPRLNQEELESLNRKPN TACSNLRDGSLLLGDGHGSSIQ AAIEVVGAGSVATKGRGRQDD TDPSNRYHRPPYSQEEKEQCITL LLSWCLGDSQGPQCRPQLSLQE LRREFTVSLHLARKLLSEVRGQ AHRFVSPPNAAGAGDGQTPNPF WPPLTDLAPQAESHLPGVNLYL LPLGEQLPDVSLTFQAWRRLSV KCTAVRAYQTTRVVETSSCRL HVKGASNASTHRSPKEVTQGT NKSERRTRETQRAIRERNMAGC CTCATDVLVTLQSLMEGLALQ PQRTRALLLGSASIKASCAVTII LMSENLGKGCSKKSEGMVRRY AKHKKQEIKPYYQRKSPSLERG QEEKKVGREDREGSENQYLYG PSNISEARNRLPECGRMGLGYV ARLFLGDRRSSTPSFASYDPSSL VTYGHRRSCRVSDIRVPRLGPN VGGPCKGTGIDLQCEREKKNEE
9431	39799	A	9491	32	2123	
9432	39800	A	9492	1	911	MSTLKGLIIKIIISVMIASEFILEE RIKTGLNAAKHCFAAPSQAASH TISRPIPMPIRSASACSTPTHTPQ DSLTGVGGDVQEAFAQSSRRN LRNDLLVAADSITNTMSSLVKE LNSEVGSETESNVDSEFARTQF EDLVPSPTSEKAFLAQIHARKP GYIHSGATTSTMRGDMVTG\DA NPYVQPEDENYENDSVRQLEN ELQMEEYLKQKLQDEAYQMPL VPTKKEIHMEDFLSSLPEGAIAQ CPRTFIPDCRRKGASYSQTDDES NMKTGDDGEPCGHTEEEDSSL AAASPKRGTTTPSSS

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9433	39801	A	9493	2	2233	
9434	39802	C	9494	477	737	
9435	39803	A	9495	2	746	GQATHFMAKEV*QWAHAHGIH WSYRVPHHPEAAGLIEWWDCL LKSRLQCQLGDNTLQAWGKVL QKAVYALNQCPIYGTVSPIDRI HGSRNQRVEVEVEVAPLTITPS DPLAKFLLPGLTTLCSAGLQVL VPEGGMLPPGDTTTIPLNRKLR LPPGHFGLFLPLSKQAKMRVTA LAVVIDLDYQDEISLPLHNGDK EEYARSTGDPLERLLVLPCPVIE VNGKLQQHNLGRTTNGPDPLG MKVWVSPPG
9436	39804	A	9496	70	532	HVALLMPLQNSRSFSGYGFAYP ARNTFSKTTIHGLKECLIHHHGI PSSIASDQGTRFLPKEV/RKWAH AHGIHWSYHVPHYPEAASP/HS DPLAKFLLPVPTTLCSAGLAVL VPEGGMLPPGDATMIPLNLSSR SHLGMPTTSLKVVRMCSKDKY
9437	39805	A	9497	51	408	CVPEPRTPSLGFQT/HPAAHAPG AQAPGSAH/DRLSSAGPGSRAA PRAPWRPWTIGYSESQPTVL\RP GQPWPGRGVSGSSAPSVPSALR GPPRSSRPSCCTWWCLWRCRH RDLGRDINFTL
9438	39806	A	9498	3	618	SSCAFSHRSSRPSRCHTVRRSTA PCAAS*HSSRAPKRHWALPGSS G*S/WRETPSTHW*P*TLPRWRT ALRPSQ*PRPRVFRVRKPCSSRP PTITRCALASAQ*SCAA\PTSSLA QRKSSRSPRRTATTWGTARRSR AHAVPAGRSPAPSASPAPPQAP RAWSAAAPASPSRLSSAGRGRQ AAPRAPWRLRGPPRSCRPTCCT WWCP
9439	39807	B	9499	215	293	
9440	39808	C	9500	1	1170	
9441	39809	C	9501	25	481	
9442	39810	A	9502	27	265	
9443	39811	A	9503	2	326	GRVGGRVGSDLGRGDMAKRT KKVGIVGKYGTRYGA/SRVRK MVKKIEISQHAKYTCSF\CGKT KMKRRAVGIWCCGSCMKTVA GGAWTYNTTSAVTVKSAIRRL KELKDQ

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9444	39812	A	9504	2	1125	RVGRPPLPPRPTHPRRKPLPPNN VTGKPGSAGIISSGPITTPPLRST PRPTGTPLERIETDIKQPTVPAS GEELENITDFSSSPTRETDPLGK PRFKGPHVRYIQKPDNSPCSITD SVKRFPKEEATEGNATSPPQNP PTNLTVVTVEGCPSFVILDWEK PLNDTVTEYEVISRENGSFSGK NKSIQMTNQTFSTVENLKPNTS YEFQVKPKNPLGEGPVSNTVAF STESADPRVSEPVSAGRDAIWT ERPFNSDSYSECKGKQYVKRT WYKKFVGVQLCNSLRYKIYLS DFLTGKFYNIGDQRG\HGEDHC QFVDSFLDGRTGQQLTSDQLPI KEGYFRAVRQEPVQFGEIGGHT QINYVQWYECGTTIPGKW
9445	39813	A	9505	2	385	REAGSGGNDNFARRRNFSG\RG G\FGG\SRGGVWIWVAVGDGY NGFG\NDGSNFG\GGGSY\NDF WENTNKSGLQNFGPHEGGEIFG GQKLLAPYGGWRPNTFAKPTK PQGG\YGG\SSSS\SSYGKWPEDF
9446	39814	A	9506	945	2313	TRVLLESRAGSQQSEGEASWQ RGYARPSCQAAISFPEHRRALR ALWAGDCRVADAGPGSSSSTPP SPPSLPKTSVSLGFLCFKKSLAA SCASGRERQLEA*VWASQPLSP TQWSEGQLGVRVWASQPLSPT QWSEGQ/PGGPSVGISTSLTYPV EGRT/GWGPECYVFCMLHRLPE QHDCTFDHMGRGREEAIMKM VKLDRKVGRSCQRIGEGGQED DVVASILVSMQPHSPRTPSPHLP YSKFKDFSSCNCARQGWKEMG ACVQRPSAVLGGTRPVSVQAK QPLPCFLLGASALGSCGTGLGV KDRDIDRIVVMSVMKILRGNQR PSGDEQARGQRAREGLGGLGV RRACREQWAVLCPLVHRNWV CVSSFLIASQSNSPQQQHNCCY ANNSPQQEEGMVGRQAETFLL GGVRNRKPWVGVGRGLQGSH QQHIQGAVSSPSSPKKGVSKRE
9447	39815	A	9507	3	684	

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9448	39816	A	9508	15	513	RIRLEGLWGSSKTMNLCSKCFA DFQKKQPDDDSAPSTSNSQSDL FSEETTSDNNNTSITTPTLSPSQ QPLPTELNVTSPSKEEYSQSENE ASPVKRPRLLENTERSEETSRSK QKSRRRCFQCQTKLELVQQEL G\MCRCGYVFCMLHRLPEQHD CTFDPHGAVAGR
9449	39817	A	9509	818	1455	SDYITRDGASFTKALLTWKNPV PNFFWKKDTFKLWGEVIRSTM WKT/DQSPSAAWMGGFGAQPP QGQAPPPVIPPPNQAGYGMASY QTQILPSPHILAVFMLPERGPNP DPKRGFLDLARKNLGNWVSTIT FLSRFPGVQVLQEFVVPGTMPL LRPLELPMHFNPHFSTALASLIA DELYLLPQLSVSQMGESFPSFD MMAICAQASTNRLWMP
9450	39818	A	9510	1	1132	MMEDDGQPRTLYVGNLSRDVT EVLILQLFSQIGPCKSCKMITEH TSNDPYCFVEFYEHRDAAAAL AAMNGRKILGKEVKVNWATTP SSQKKDTSNHFHVFVGDLSPEI TTEDIKSAFAPFGKISDARVVK DMATGKSKGYGFVSFYNKLDA ENAIVHMGGQWLGGRQIRTNW ATRKPPAPKSTQENNTKQLRFE DVVNQSSPKNCTVYCGGIASGL TDQLMRQTFSPFGQIMEIRVFPE KGYSFVRFSTHESAAHAIVSVN GTTIEGHVVKCYWGKESPDMT KNFQQVDYSQWGQWSQVLGN PKPSD\RYMANGWQVPPYELY GQPWNQQAFGV\DQSPSAAWM SGFGA\QPP\QGQAPPP\VIPPPN QAGYGM\ASYQTQ
9451	39819	B	9511	1	1212	
9452	39820	A	9512	1	1032	

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9453	39821	A	9513	17	976	SGRP/GGPGGPGMGKPRCF/RGE VFGIVIRGPGFPPGGRGRGR\GR GARGGKGPRIKGLGCPSTKLG\ RLVKDH*RSKFPWRRSIYSYSG PLKESE\IIDF\FLGGLLSKDEVFE RLCQVQEPEPVPGQRHQGSRHF VAI\GNYQWPTVGSGVLKCSQE /VWPTAHPVGPIILAKLLHSSPC AEGYWGEQSIGKAP/HTVPCQ/ VWTGRCGSVLVRPHPWHPRGS GIVSAPVA\KKLLMMAGIDDCY T\SARGCTATLG\NFAKAT\FDAI SKTYSYLTPDLWKETVFTKSPY QEFTDHLVKTHTRVSVQQTQA PAVAYNIGFLYKKNKVN
9454	39822	A	9514	1	866	
9455	39823	A	9515	1	1793	MAAAAVSGALGRAGWRLLQL RCLPVARCRQALVPRAFHASA VGLRSSDEQKQQPPNSFSQQHS ETQGAEKPDPESSHSPPRYTDQ GGEEEEDYESEEQLQHRILTAA LEFVPAHGWTAEAIAEGAQSLG LSSAAASMFGKDGSELILHFVT QCNTRLTRVLEEEQKLVQLGQ AEKRKTDQFLRDAVETRLRMLI PYIEHWPRALSILMLPHNIPSSL SLLTSMVDDMWHYAGDQSTD FNWYTRRAMLAAIYNTTELVM MQDSSPDFEDTWRFLENRVND AMNMGHTAKQVKSTGEALVQ GLMGAAVTSPRSRRGGWWPLG EMPYANQPTVRITELTDENVKF IIENTDLAVANSIRRVFIAEVPII AIDWVQIDANSSVLHDEFIAHR LGLIPLISDDIVDKLQYSRDCTC EEFCPECSVEFTLDVRCNEDQT RHVTSRDLISNSPRVIPVTSRNR DNDPNDYVEQDDILIVKLRKGQ ELRLRAYAKKGFGKEHAKWNP T\AGVAF\EYDPDNALRHTV\YP KPEE\WPKSEYSELDEDESQAP YDPNGKPERFYYNVESCGSLRP ETIVLSALSGLKKKLSDLQTQLS HEIQSDVLTIN
9456	39824	A	9516	3	176	FFFFFAETNSK*ITYQNIHIMVEI FQNSIFWDLYTKDKQIRGQEAA RREKRGLGRPL
9457	39825	A	9517	1485	1679	RVGDAGHDDPGKPGPPGAGHR PEG*TGAHSLRAGLPACRAEPA GPGRAREGSKAPGHCAEELLQ

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9458	39826	A	9518	1	232	FFFFETESCSVAQAGVQWCDLG SLQTLPTG/SSRHSPASAFRVARI TGARYHVRLIFVFLVQTGLHHL GQADFDLLTS
9459	39827	A	9519	1	2408	GTLVTKVAPVSAPPKVSSGPRL PAPQIVAVKAPNTTTIQFPANLQ LPPGTVLIKSNSGPLMLVSPQQT VTRAETTSNITSRPAVPANPQT VKICTVPNSSSQLIKKVAVTPV KKLAQIGTTVVTTVPKPSSVQS VAVPTSVVTVTPGKPLNTVTTL KPSSLGASSTPSNEPNLKAENSA AVQINLSPTMLENVKKCKNFLA MLIKLACSGSQSPEMGQNVKK LVEQLLDAKIEAEEFTRKLYVE LKSSPQPHLVPFLKKSVVALRQ LLPNSQSFIQQCVQQTSSDMVI ATCTTTVTTSPVVTTTVSSSQSE KSIIVSGATAPRTVSVQTLNPLA GPVGAKAGVVTLHSVGPTAAT GGTTAGTGLLQTSKPLVTSVAN TVTTVSLQPEKPVVSGTAVTLS LPAVTFGETSGAAICLPSVKPV VSFCWDHI\CKPVIGTPVQIKLA QPGPVLSQPAGIPTGSSS\KQLFS LFHVVQQPSGGNEKQVTTISHS STLTIQKCGQKTMPVNTIIPTSQ FPPASILKQITLPGNKILSLQASP TQKNRIKENVTSCFRDEDDIND VTSMAGVNLNEENACILATNSE LVGTLIQSCKDEPFLFIGALQKR ILDIGKKHDITELNSDAVNLISQ ATQERLRGLLEKLTAIAQHRMT TYKASENYILCSDTRSQLKFLE KLDQLEKQRKDLEEREMLLKA AKSRSNKEDPEQLRLKQKAKE
9460	39828	A	9520	1	637	MLSNVKRGRKLPNGTWAHDL VTPPTASLLLLLTEPAMPSVAFC HSILIVTKGGVKRTRVPPPNNSS GARTGNPLKVKHISFKTGDELIF LDPHTTQTFVDTEENGTGNDQT FHCLQSPQR\MNILNLDPSVALG FFCKEEKDFDNWCSLVQKEILK ENLRMFELVQKHPSHWPPFVPP AKP\EVTTTGAEFI\DSTEQL\EEF DL\EEDFEILSV
9461	39829	A	9521	3	176	
9462	39830	B	9522	1	792	

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9463	39831	A	9523	2	486	NGHVGLGVKCSKEVATAIRGAI ILAKLSIVPVRRGYWGNKIGKP HTVPCKVTGRCGSVLVRLIPAP RGTGIVSAPVPKKLLMMAGIDD CYTSARGCTATLGNFAKATFD AISKTYSY\LTPDLLKE\TVFTKS P*QELTDHLVKTHTRVSVQRT QAPAVATT
9464	39832	B	9524	1	2991	
9465	39833	A	9525	3	263	KHENWSTARQSLHACSRVTWQ NRLRLSNKWMPSHVLCLLPS/H MTLQPANLSSLLITPPEFGPKIA SPICTSCSVNFPRTLISPFSHC
9466	39834	A	9526	1022	1201	
9467	39835	C	9527	1	924	
9468	39836	A	9528	2	837	WKNCLEKRSMLTMHRILES*D* RQE/ILERHDAKYHSPKAEEKQ MKHKAGSQIVKKEEAKLALAL EGFCRFRNHHQTGFSPAGATQR GPLVAILSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGFPTGKRAWPPFRL FLPHKGFADWGPTINQDFRLLG QPSVARFLNFSQGPAGEGQSAV ARLPGHPFITQPYPILPGYAAAG MQALARRRPILMFDSLSSNFCH SSAYYHLFRRSNQAFKGTNNCL KKITPRPATHRSTVVIH
9469	39837	A	9529	3	1137	APAPSPVGSGSCCLSHMFFHPPS RANRAFVD\YAPMDEIQNAEIN SQVRRYLEGTLDEIDVRNPSVT TMLSQPGPPSPGHTPTHALLAS EPHVNGCKTVSTVHEDYSGSSE SSNDESDSEDTDSDDSSIPRNRL QSVVAVPKNSTLPMEETSPCSS RSSQSYRHYSDHWEDERLESRR HLYEEKFESIASKACPQTDKFFL HKGTEKNPEISFTQSSRKQIDNR LPELSHPQSDGVDSTSHTDVKS DPLGHPNSEETVKAKIPSRQQE ELPIYSSDFEDVPNKSWQQTTF QNRPDSRLGKTELSFSSSCEIPH VDGLHSSEELRNLGWDFSQEKP STTYQQPDSSYGACGGHKYQQ NAEQYGGTRDYWQANGLLGS
9470	39838	A	9530	1	1857	

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9471	39839	A	9531	1	989	MEDWKVRGHQEKTLAFEVQSF SCSERETTLVLLLRSPAVPQLLL HGLCGPDLSTKAAQCHFKAIW QSLGNTLGAVSDQATPGHVKS LPPGALISRQGRGQFCSVDAVF LLHDSPELPSSLPHGASLPLASS DKQAEQTWLGAVGSVQCTSIT ACPRDLEDRPHLTEHPPAGVHC GQNPCPCHLIFTLYSKSLPLDLA CRIWDVFCRDGEEFLFRTALGI LKLFEDILTKMDFIHMAQFLT\R LPEDLPAEELFGPSIATIQMQSR NKKWAQEPGHELEWPDRSFRP RVLACPMGSREHRLQPACSGST GQGHTKALFPETCCQSPIFQDA
9472	39840	A	9532	2013	2270	
9473	39841	A	9533	3	744	
9474	39842	A	9534	190	991	SVLSNKQNHCSQTAPPPPPPAA SGSRGWVWGLFWGLAAILEGS TGADWSQLPHSCCPSLLVPHVL SVVPLRPPHRDFPVEDVFTLPV YFSSDWLNEFWDALDVDDYRF VYAGPAGSWSPFHADIFRSFSW SVNVCGRKKWLLFPPGQEEAL RDRHGNLPYDVTSPALCDTHL HPRNQLAGPPLEITQEAGEMVF VPSGWHHQVHNLDDTI\SINHN WVNGFNLANMWRFLQQELCA VQEEVSEWRDSMPDWHHHCQ VIMRSCSGIKL
9475	39843	A	9535	1	885	MKRRAVMGPPQVQAWKALDL WESSQVMEGKAVVPMGRNPM MRKATQGQLENSPALEKLLPPL QGNVGFAFTKEDLTEVRDLLL ANKVPAATRAGAIGPCEVTVPA QNTGLGPEKISFFQALGITTKIS RGTTEILSDVQLIKTGDRVGAS EATLLNTPNISPFSFGLVIQQVF NNGSIYNPEVLDITEETLYSGFL EGVRNVAS\CLQTGYPPVASVP PSII/NGYKGCLALSVETDYTFPP AEKIKTFLADPSAFVAAAPVAT TATAAPAAAAAPTKFENEESEE LDEDMGFGLFD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9476	39844	A	9536	65	988	RTAVMPREDRATWKSNYFLKII QLLDDYPKCFIVGADNVGSKQ MQQIRMSLRGKAVVLMGKNT MMRKAIRGHLENNPALEKLLP HIRGNVGFVFTKEDLTEIRDML LANKVPAAARAGAIAPCEVTVP AQNTGLGPEKTSFFQALGITTKI SRGTIEILSDVQLIKTGDKVGAS EATLLNMLNISPFSFGLVIQQVF DNGSIYNPEV\LD\ITEETLHSRF LEGVRNVASVCLQIGYP\TVAS VPHSIINGYKRVLALSVETDYTF PLAEKVKAFLADPSAFVAAAPV AAATTAAPAAAAAPAKVEAKE
9477	39845	A	9537	1	993	MREIALTQTRQCGKKIGAKVGI RGSEVPAPAYWVAREDVGSGS GLGGGWYVPCAVLVDLEPVT MDSLRSGPFGLIFRPTTSSLKLIE NADKTFCIDNEALYDIYSRTLK LPTPTYGDMNHLLSATMSGVT MCLGFPGQLNADLQKLSVNMV PFPRLHFFMPGFAPLTSRGSQH YQALTVAELTQQMFYAKNMM AARDPRHGRYLTAAAIFQGRM PMREVDEQMFNIQDKNSSYFA DWFPDNVKTAVCDIPPRG\LKM SGSFIGNNAAIQELF\QCVSEQF TAMFRRKA\FLHWYTGEG\MDE \MEFT\EAESNMND\LVSEYQQY QDATAQGGGG
9478	39846	A	9538	231	881	SSLSGTKVGSLPFRLLHWMPVS YSSVTTRYYHRAGAEEGKDRII FVTKKDHETPSSAELVADDPND PYEEHGLILPNGNINWNCPCLG GMASGPCGEQFKSAFSCFHYST EEIKGSDCVDQFRAMQECMHK YPDLYPQEDEDEEEEREKKPAQ QAEETAPIEATATKEEE\DQVNE GHKALSTSPFGVDLLQKALSSP SKKVSFCCPVHYNIQNNLF
9479	39847	A	9539	1	804	

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9480	39848	A	9540	2	3337	SSLLEKMTSSDKDFRFMATSDL MSELQKDSIQLDEDSERKVVK MLLRLLEDKNGEVQNLAVKW LGVPLGAFHASLLHCLLPQLSS PRLAVRKRAVGALGHLATACS TDLFVELADHLLDRLPGPRVPT SPTAIRTLIQCLGSVGRQAGHRL GAHLDRLVPLVEDFCNLDDDE LRESCLQAFEAFLRKCPKEMGP HVPNVTSLCLQYIKHDPNYNY DSDEDEEQMETEDSEFSEQESE DEYSDDDDMSWKVRRAAA
9481	39849	B	9541	1	3178	
9482	39850	A	9542	190	284	LNAQPGTRRLWPAEIRPPPRRL GKGGQQVSHHPPISCFYCECEE KRLCVNTHVWTK*T
9483	39851	A	9543	62	280	
9484	39852	A	9544	1	1452	
9485	39853	A	9545	2	998	ITAGATPEERVICFVEYYLTAFH EGRKGALAKKPYNPIIGETFHC SWEVPKDRVKPKRTASR/PLLP AVMNTQWPMTLPKSYKLRFVA EQVSHHPPISCFYCECEEKRLCV NTHVWTKSKFMGMSVGVSMI GEGVLRLLEHGEEYVFTLPSAY ARSILTIPWVELGGKVSINCAKT GYSATVIFHTKPFYGGKVHRVT AEVKHNPTNTIVCKAHGEWNG TLEFTYNNGETKVIDTTTLPVY PKKIRPLEKQGPMESRNLWREV TRYMRLGDIDAATEQKRHLEE KQRVEERKRENLRTPWKPKYFI QEGDGWGILQSPLESTLMGLEV
9486	39854	A	9546	12	740	HFFLYKKLIPFVLKNCMFHFSP VRGTVVTNDRWGAGSICKHGG FYTCSDRYNPGHLLPHKWENC MTIDKLSWGYRREAGISDYLTI EELVQPLVETVFSAGNPLMD\IG PHLDGTI\SVVFEERLRQMGSW LKVNGEAIYETYT\WRSQ\NDT VTPDVWYTSKPKEKLVYAIFLK WPTSGQLFLGHP\KAILGAT\EV K\LLGHGQPLNWIFFGDKMGIM \VELP\QLT\IHQMPCKWG\WAL A\LTNVI
9487	39855	B	9547	1	627	
9488	39856	B	9548	47	504	

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9489	39857	A	9549	2	379	VDLVREFIERQ/HAKNRYYYYH RQYRRVPDITECKEEDIMCMYE AEMQWKRDYKVDQEIINIMQD RLKAFQQQSYRATQQGHPQAA SGGGSWRPLLQIFSLAASSASV RPGTSWQNCRPPGPDLGKQ
9490	39858	B	9550	49	707	
9491	39859	A	9551	3	1162	
9492	39860	C	9552	342	581	
9493	39861	A	9553	3	513	LLPHKPLAGFFKAYLPSEPPRV YVSSFWPQ/EYKPDTHQELFLQ EEIS/LLEDLNQVIENRLENKI/A FIRQHAIRVRIHALLLARGLDPF IGPRRDWLVYPAVTGAVAFGF VEGLDPSQEHPRFQGTQDNVSK DESTRKEQSVRLVGCGADDRK PRDLQILDRDRKGPELVQ
9494	39862	A	9554	1	1365	
9495	39863	A	9555	771	1536	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLCPTGSPQSLPPYAS IPPTPSPTIK/DPPSTQMV/QKET DKGVNNEPKSGNIPQLCRLQAV GGGEFGPARVRVPFSLSDLKQI KIDLGKFSDNPDGYIDVLQGLG QCFDLTWRDIMLLLNQTLTPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPDSGTYDTKE CKIVQSVEMSMEVMIAVMSVQ RQQGKQTQQQPLLVVVRSAEP AEESVPHKSSTRGAS
9496	39864	A	9556	220	249	P*N**PSTLTTGTGSTTT*QIRM KVN*MGN/DSPQGKNTPKMYS GEFSPVRVHVPFSLSDLKQIKID LGKFSDDPDGYIDVLQ
9497	39865	A	9557	2	385	
9498	39866	A	9558	84	849	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLCPTGSPQSLPPYAS IPPTPSPTIK/DPPSTQMV/QKET DKGVNNEPKSGNIPQLCRLQAV GGGEFGPARVRVPFSLSDLKQI KIDLGKFSDNPDGYIDVLQGLG QCFDLTWRDIMLLLNQTLTPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPDSGTYDTKE CKIVQSVEMSMEVMIAVMSVQ RQQGKQTQQQPLLVVVRSAEP AEESVPHKSSTRGAS
9499	39867	A	9559	66	197	RQWKG*KFVFQKM*DLGKYLQ RQLFCLSSLVQPPWPVPTEIYP
9500	39868	A	9560	1	2340	
9501	39869	B	9561	1	1776	

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9502	39870	A	9562	1	1349	
9503	39871	B	9563	107	769	
9504	39872	A	9564	329	2042	
9505	39873	A	9565	511	1631	HFGNHERTSKVMGNVPRKTKT PLRRILENWEQFDPQTLRKKRLI FFCSAAW\PPEGSINYNTILQLD LFCRKGKWSEVP*VQTFFSLRD NSQLCKKCDLCPTGSLQSLPPY PSIP\TPSPLNKDPPSTQMVQKEI DKRVNSEPKSANIPQL*PLQAV GGREFGPARVHVPFSLPDLKQI KTDLGKFSDNPDGYIGVLQGLG QFFDLTWRDI\MSLLNQTLTPNE RSATITAARELGDLWYLSQVN DRMTTEERERFPTGQQAVPSAD PH*DTESEHGDWCCRHLLTCVL EGLRKTRKKAVNFSVMSTVTQ GKEENPTAFLERLREALRKHTS LSPDSIEGQLILKIKFITRSAADI RKQTSKVHLRPGAKLKTPY
9506	39874	A	9566	15	178	
9507	39875	A	9567	3	826	RQLGTRNFLNGTKAKAFELSYL EKVPEGKDTVHKQSLLHHVGT MGGENFPDSSDLYSEIGAITRSA KDDFDQLQDNLCQMERRCIAS WDHLKAIAKHEMKPLLKQRMS ELLKDCAERIIILKIVHTRIINRF HSFLLFMGHPPYAIREVNINKFC RIISEFALEYRTTRERVLQQKQK RANHRERNKTRGKMITDSGKF SGSSPAPPSQPQGLSYAEDAAE HGEHEGCAENLVPLQESPAHTF SIVSAVFLLIP*HPVY*FKSVTPF LGKEQPL
9508	39876	A	9568	1	670	

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9509	39877	A	9569	1	2426	MPKPSLEAGSCPRLEFPVEDAQ PVIKGEEFTPPPPNSYLALGDIST EEWDLEVAQEYQERMPPQRAA LICVFSWNLGRSLPAPAMRRPC QNFCVALSTFAGDPEPESEAEP EAEAGAGQVADEAGQDIASAH EGAETEVEQALEQEPEERASLS EKERQNEGVNERDNCSASSVSS SSSTLEREEKEDKLSRDRTTGL WPAGVQDAGVNGQCGDILTNK RFMLDMLYAHNRKSPDDEEKG DGEAGRTQQEAEAVASLATRIS TLQANSQTQDESVRRVDVGCL DNRGSVKAFAEKFNSGDLGRV FNAPQGLGWSQVPRGQPTFTK KKKTIRLFWNRN/VGLLTGH/G KNNRRCREFLWSKLEPIKVDTS RLEHLFESKSKELSVSKASKLV RPLFILTSACPFLSFPWKAPLHS STRQLHRGLSAQERWRCSGIRG MECLNGKGPLESRNPAYRKSE GTRQTGAGDMKDGVWQGVPA TPDTPQGMCTVCTVSFAIMDGL NVNSVGPLPFHEVAEPLLDLKE GIDQLDYTLGFFFLVSMLSGGG LLGGSASAKAFELSYLEKVPEV KDTVHKQSLLHHVCTMVVENF PDSSDLYSEIGAITRFHSFLLFM GHPPYAIREVNINKFCRIISEFAL EYRTTRERVLQQKQKRANHRE RNKTRGKMITNCVRHCVRMFS GSSPAPPSQPQGLSYAEDAAEH
9510	39878	B	9570	164	346	
9511	39879	C	9571	160	339	
9512	39880	A	9572	54	212	SFPSVVLWKDLQNLKIQVPGLI LLGVGLISVPGGRI*LLRTGSRK PISQVCP
9513	39881	C	9573	48	185	
9514	39882	A	9574	2	551	ADRRGAVYPRSRDGGGVRGPC AMATSVLCCLRSCKDRGTGHIP LKDMLSVHMDTQHMGTDVVI VKNGRKIFGTGGCLASAPLHQN KSYFEFKIQSTGIWGIGVATQK VNLNQIPLGRDMHSLVMKNDG ALYHNNEEKNRLPANSLPQEG D/VVDDSAILDCQFSEFYHTPPP GFEKILFEQQIF
9515	39883	A	9575	3	655	

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9516	39884	A	9576	131	1066	SHSSSAAAHPLGLLPIAAQSLA VFIEPWSQASSRGQLQ/VSAPGI WGIGVATQKVNLNQIPLGRDM HSLVMRNDGALYHNNEEKNRL PANSLPQEGDVVLCWSNNGHS LCKEESLSPILPTSDGEERRRKR KKRKRKKRKQKQQQQQEAAA PAEADAEATAAEAAVEEAAAR KEEEEEGEEGEGNGEEEEEKAA AAARGDWSQQEKACKSSLQAI LFGHAKLEPGRLPRPTQCRVEA TVLVGTNSPLDNPLWSISWSLW QKPVGTSQQQPLGLWTREFPLE GHLLTRNETFTEATPLIPEIGML SQMMSEEHI
9517	39885	A	9577	1	2363	ELQRDIEKHSTGVASVLNLCEV LLHDCDACATDAECDSIQQATR NLDRRWRNICAMSMERRLKIE ETWRLWQKFLDDYSRFEDWLK SSERTAAFPSSSGVIYTVAKEEL KKFEAFQRQVHECLTQLELINK QYRRLARENRTDSACSLKQMV HEGNQRWDNLQKRVTSILRRL KHFIGQREEFETARDSILVWLTE MDLQLTNIEHFSECDVQAKIKQ LKAFQQEISLNHNKIEQIIAQGE QLIEKSEPLDAAIIEEELDELRR YCQEVFGRVERYHKKLIRLPLP DDEHDLSDRELELEDSAALSDL HWHDRSADSLLSPQPSSNLSLF ASLQPLRSER\SGRDTPG\SVDSI PL\EWDHDYDLSRDLESAMSRA LPSEDEEGQDDKDFYLRGAVG LSDVMIPESPEAYVKLTENAIK NTSGDHSALESQIRQLGKALDD SRFQIQQTENIIRSKTPTGPELDT SYKGYMKLLGECSSSIDSVKRL EHKLKEEEESLPGFVNLHSTET QTAGVIDRWELLQAQALSKEL RMKQNLQKWQQFNSDLNSIW AWLGDTEEELEQLQRLELSTDI QTIELQIKKLKELPESCWDHR\K AIILSINLCSPEFTQADSKESRDL QDRLSQMNGRWDRVCSLLEE WRGLLQDALMQCQGFHEMSH GLLLMLENIDRRKNEIVPIDSNL DAEILQDHHKQLMQIKHELLES

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9518	39886	A	9578	2	3248	ENAVGSWTDDLTQLSLLKDTL SAYISADDISILNERVELLQRQW EELCHQLSLRRQQIGERLNEWA VFSEKNKELCEWLTQMESKVS QNGDILIEEMIEKLKKDYQEEIA IAQENKIQLQQMGERLAKASHE SKASEIEYKLGKVNDRWQHLL DLIAARVKKLKETLVAVQQLD KNMSSLRTWLAHIESELAKPIV YDSCNSEEIQRKLNEQQELQRD IEKHSTGVASVLNLCEVLLHDC DACATDAECDSIQQA
9519	39887	A	9579	2	194	CSTSLMIREMQIKTTVRYHLTS ARMAIIKKSK\NSRCWHGCGEH GTLLHCCNLWKERNVSYVSA
9520	39888	C	9580	105	215	
9521	39889	A	9581	1	210	MNSHFLKEDIQMANKHMEKCS \TLLMIREMQIKPTVRYHLTSAR MPIIKKSK\NSRCWHGCGEHGT LLHC
9522	39890	C	9582	48	182	
9523	39891	A	9583	3	225	
9524	39892	A	9584	1	549	
9525	39893	A	9585	367	971	GVCLLGAPAGRRGSLLSLGSLR GQGSYLSKNVAVPSEATTVREL HP**TSLQRPPSDPGGWVVLGF P\CNQFGHQENRQ\NE\EILNSLK VRSGPGGGFEAQLHGSSRKCEV \NG\SGAHPLFAFLR\EALP\VPS DDGPRAL*PTPKLI\TWFSGVFA TIVAWNFFEKFL\VGPDGVPLR RYSR\AFQTIDIEPDIEALLSQGP
9526	39894	A	9586	1	129	
9527	39895	A	9587	1	406	PTVCERELCVFAFQTLGVMNE AADEIATGAQVVDLLVSMCRS ALESPRKVVIFEPYPSVVDPNDP QMLAFNPRQLKFMHTPHQFLL LSSPPAKESNFRAAKKLFGSTF AF/HLHGAMYGSGIYLSPMSSIS FGYSA
9528	39896	A	9588	2	634	SSNRSHIVKLPVNRRLKFMHTP HQFLLLSSPPAKESNFRAAKKL FGSTFAFHGSHIENWHSILRNGL VVASNTRLQLHGAMYGSGIYL SPMSSISFGYSGMNKKQKVSAK DEPASSSKSSNTSQSQKKGQQS QFLQSRNLKC\IALCEVITSSDL HK\HGEIWGCPPI/SDHVCTRFFF VYEDGQVGDANINTQEGGIHK EILRVIGNQTATG

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9529	39897	A	9589	3	3623	FGVCARGCLDSAGPWTMSRAL RPPLPPLCFFLLLLAAAGARAG GYETCPTVQPNMLNVHLLPHT HDDVGWLKTVDQYFYGIKNDI QHAGVQYILDSVISALLEDPTR RFIYVEIAFFSRWWHQQTNATQ EVVRDLVRQGRLEFANGGWV MNDEAATHYGAIVDQMTLGLR FLEDTFGNDGRPRVAWHIDPFG HSREQASLFAQMGFDGFFFGRL DYQDKWVRMQKLEMEQVWR ASTSLKPPTADLFTGVLPNGYN
9530	39898	B	9590	1	3839	
9531	39899	B	9591	1	513	
9532	39900	A	9592	1	233	KQELNEPPKQSTSFLVLQEILES ENKGDPNKPSGFRS\VKAPVTK VAASIGNAQKLPMCDKCGTVL QQASAAAFSLSV
9533	39901	A	9593	3	469	LTVARSEHKVWSPLVTGEGKR HPYKMNLASEPQEVLHIGSAHN RSAMPFNASPASSTTARVITNQ YNNPAGLYSSENISNFNN\ASSL VIDKESEVYKMLQEKQELNEHP KQSTSFWVLQEILESEEKGDPN KPSGFRSVKAPVTKVAASIGNA
9534	39902	A	9594	1	1146	MTTQQIDLQGPGPWGFRLVGR KDFEQPLAISRVTPGSKAALAN LCIGDVITAIDGENTSNMTHLE AQNRIKGCTDNLTLTVARSEH/ KKVWSPLVTEEGKRHPYKMNL ASE\PQEVLHIGSAHNRSAMPFT ASPASSTTARVITNQYNNPAGL YSSENISNFNNC/ALESKDWLPA GVEANSRPLDHA\QPP\SSLVID KRILKVYKMLQEKQE\LNE\PPK QSTSFLGFCQEIL\ES\EEKGDPN KP\SGFRSV\KAPVT\KVA\ASIG KCSRKFAFCVDKCWHLGFLGV F\LKLR\DRHRHP*VFMCCT\DC GHQT*KQKGPFLLWMDQ\IYCE ESMAPGSEVNTHPEG\YESGST VFPPSGAQQDLDPLFLPAGLLL KLFLLKCSGPLSLS
9535	39903	A	9595	65	353	

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9536	39904	A	9596	1	1974	MNGVPVGAQKRVDKEEVKNG AIAELFSEDWSDCAYKANEVSR IRPLEESELLYPILGQSKLFVLSG EWSQSSEEASEEVAVTLIYQLA ESPTVICAQIWQGCAKQALEKL EEKRTSQGDPKESPTMLPTFLL MNLLSLAGDVALQQLVHLEQA VSGELCQRRVLREEQEHKTKDP KEKNTSFETTMEEELGLVGAA DDTEAELIRGFCKMELLDGKQT LAAFVPLLLKVYNNSGLYSNPD LSAAASPTLGKFCMISTTFCNSQ PHLLFTMLEKSPLPIVRSNLIVA TGDLAIHFPNLVDPWTPHLYAH LQDPAQPVWKTVGLVMT\HLIL KDMVKVKGQSKAL/RKMLGNF DCFGDKLSDESIFSSFLSVMGKL QHGAKPEGKAIIDEFEQKLQAC HARGLDGIEELEINQAGSQRAP TAKKPSTVCRHQPLASAASDN DFVTPEPRRTTHRHPNTQQRAS EKKPKVVFSSDESSIKTEVEGLG YNIKLRVATQRLSFVWVMNIA EGESAVLVTVAWPECEVAVMG SLGSAARGTGKRLQGEGNLQL NFVTIATKLEVSWTELGGGCVS ALFASVGTKREKAGFYQGCSF ASNIMKRGRVKEVEDVQKRLI KMTVEFNLAWSSLPPHMAMN GDQGGDRVTHESFLRCMTLMR
9537	39905	A	9597	785	5049	ACRSRMAPQMYEFHLPLSPEEL LKSGGVNQYVVQEVLSIKHLPP QLRAFQAAFRAQGPLAMLQHF DTIYSILHHFRSIDPGLKEDTLEF LIKGVYGSGVVSRHSQELPAIL DDTTLSGSDRNAHLNALKMNC YALIRLLESFETMASQTNLVDL DLGGKGKKARTKAAHGFDWE EERQPILQLLTQLLQLDIRHLW NHSIIEEEFVSLVTGCCYRLLEN PTINHQKNRPTREAITHLLGVA LTRYNHMLSATVKI
9538	39906	C	9598	134	382	
9539	39907	A	9599	117	235	KIAAPQLHVFLPFLFFCMRPFAF WQPLPEPLELRP\RLSD
9540	39908	B	9600	1	732	
9541	39909	C	9601	1	420	
9542	39910	B	9602	110	928	

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9543	39911	A	9603	1	868	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSLRLSEMPRKQGD YRTRIWKFEDGLSNVLVIQLNK LIICVMCLDLALKGLRVLLVEG NDPQGTASMYHGWVPDLHIHA EDTLLPFYLGEKDDVTYAIYFT CWPGLDIIPSCLALHRIETELMG KFDEGKLPTDPHLMLRLAIETV AHDYDVIVIDSAPNLGIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDD PTGNRTVQLTWQPLPEPLEL\C*
9544	39912	A	9604	1036	1119	
9545	39913	C	9605	1	513	
9546	39914	A	9606	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
9547	39915	A	9607	1	286	
9548	39916	A	9608	1	1674	
9549	39917	B	9609	531	744	
9550	39918	A	9610	1	818	YNRAMFHPHAVNKIALSLNNK NP\RSKVLFLELLAAVCLVRGG HKLFYLAFDNFKEVCGEKQRFE KLMEHFRNEDNNIDFMVASMQ FINIVVHSVEDMNFRVHLQYEF TKLGLDEYLDKLKHTESDKLS\ VQIQAYLDNVFDVGALLEDAE TKNAALERVEELEENISHLSEK LQDTENEAMSKIVELEKQLMQ RNKELDVVREIYKDANTQVHT LRKMVKEKEEAIQRQSTLEKKI HELEKQGTIKIHKKGDGDIAILP VVASAHCPWGQKW

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9551	39919	A	9611	1	937	MALLTLKQQQNEDLQDISHFTT TRTPRQGTPVQKEKSEETRLEW ARRMLRRDQHSTKGKVVKRM RGFLVGLVYCDKQSGALESLLC LWNVSGNTTLSSLVEIGSKAAL GLVCGEKQRFEKLMEHFRNED NNIDFMVASMQFINIVVHSVED MNFRVHLQYEFTKLGLDEYLD LLDTKSTDRKQTLLHYISNVVK EQYHQVSLFYNELHYVEKAAA VSLENVLLDVKELQRGMDFTK REYTMHDHNTLLKEFILNNEGK LKKLQDDAKIAQDAFDDVVKY FGENPKTTPPSVFFPVFVRFVKA YKQAEEE/NMELRKKQEQALM EKLLEQEALMEQQDPKSPSHKS KRQQQELIAELRK\RQVK\DNR HVYEGKDGAIEDIITVSLENVLL DVKELQRGMDFTKREYTMHD HNTLLKEFILNNEGKLKKLQDD AKIAQDAFDDVVKYFGENPKT TPPSVFFPVFVRFVKAYKQAEE
9552	39920	C	9612	47	286	
9553	39921	A	9613	1	423	

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9554	39922	A	9614	1	2015	MPSVSKAAAAALSGSPPQTEKP THYRYLKEFRTEQCPLFSQHKC AQHRPFTCFHWH/FPQTRRRRR\ PLGRRDGTFNYSPDVYCSKYNE ATGVCPDGDECPYLHRTTGDT ERKYHV\RYYKTGTCIHETDAR GHCVKNRLHCAFAHGPLDLRP PVCDVRELQAQEALQNGQLGG GEGVPDLQPGVLASQAMIEKIL SEDPRWQALLPVALLRHRVAH FSDANFVLGSYKTEQCPKPPRL CRQGYACPHYHNSRDRRRNPR RFQYRSTPCPSVKHGDEWGEPS RCDGGDGCQYCHSRTEQQFHP EGPVRESGVRGVFCVQSRRPW LQTPVSGTQLKWSWHHVGHSR TINPEGDKPSRLGPAPENIKRGN DFACDGRADAAGMAPHVCVFP IYKSTKCNDMRQTGYCPRGPFC AFAHVEKSLGMVNEWGCHDL HLTSPSSTGSGQPGNAKRRDSP AEGGPRGSEQDSKQGVRAHGV YVFEQNHLAVFAAVHPPAPSVS SSVASSLASSAGSGSSSPTALPA PPARALPLGPASSTVEAVLALE PTPSSPTSSAVQGVAGELGMGS GGQGCWSHVVGALAAVPAWT HSGDLEWDPSTIRTRVNVGGGP AARPAMTLAREPQLLVVGGCP TRNCSGPAASPQQLLDDAGQG GRGERDSSQRPLRPQTTHRQDT
9555	39923	A	9615	2	609	IHSLCVSPCLSPCHCLSLSPASLL VSFFCCLFLMTLFPSLCVCGSLP VHLLPSL/HFLSQVLNEYFHNV CELDLVFNFYKVECFPLKSPVV PESKEIGSQVDGQSRMEQRSPA HTNRENDIAREGGSEETHSKPG KGNLEFRFRCSHLQLGECPIPP WQKERTIAQGPEPEARAAVPA GRHDTRHAVNAGCALIGSLRRP WGGA
9556	39924	A	9616	60	277	
9557	39925	B	9617	43	354	
9558	39926	A	9618	3	309	GGGQGRPGAGGQGRSDGGGQ GSPGGGSQGSPGGSGGVGQGS RGGQGKPGGGGGQGSPDGGGR PLAGGASGRRGSRGQAQ/CPISV SATHLAF
9559	39927	A	9619	36	363	

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9560	39928	A	9620	1	512	MLMPGLSACVRDCVAFLQAVV LGDPSPAAQCQDTWTLAASAD GTCKAVGTEDGSVYFISVYDKE SPQVVHKAFLSESSVQHVVYD QQGIFLLVGTAEGKVFIINANSS SSFQIIGFT/DGGQRHFTDIHSVS FRNRHSGSDGAFLASRSREKQV GDVHTAYITATSFHNLC
9561	39929	A	9621	1	822	MKLGV/QVVITDHEKLDQIRQR ESD\ITKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVRR VLK/RIAKASGATILSTLANS\KA HTSASIILRGANDIMCGEMERSL HDALCVVKRVLESKSMVPGGG AVEAALSIYLENYATSMGSQKE LAIAEFARSLLVIPNTLAVNAA QDSTDLVTKFRAFHNEAQVNP EHKNLKWIGLDLSNGERGDNK QAGMFEPTIVKVKSLKFATEAA ITILRIDDLTKLHPESKDDKHGG YEDAVHSGALND
9562	39930	B	9622	625	1162	
9563	39931	A	9623	202	402	
9564	39932	A	9624	350	652	SAGGYPDGQGVHPGPPELFAAL GRLGHTLREHGHHLLRYHRPG HMGRRPLPCRMGHREPGSLH* QDCPRAWQWCWPHRPGHLQD VPPPGIHLQRLSQPGP
9565	39933	A	9625	83	1503	SWNTPYNHWATKQ/LSSHYSR GGAKYEGEAVKQSLVESYTHP NSNETERSANIDTVMNWFTKE DFDFVTLCYREPDNVGHRFRPE AENRKLMIQQIDRTIRPWDDHR EEETQCQQDPLSNYIKFMDLVK FDIVGYGGFGMPLPKLGQEEAL YQALKNAYPHLHIYKKEGFPEH FHLAKHDRVLPIVMYANFGYSI NGISLLYFYTHLCDKYFNVHFF HEPLSLWRAQTTPSLSHRYISLV RHMDATNLDASEAQLPGSPYP DSAPGPANLDSTQDLPQRRLSW PYPRPRPPNAHPGPALQPAPRTL LLTLPPGPAPSLPPRTALGPPPL QSRPGFRPVSRQRCGPAHFMAP EENAGTELLLQSFERRFLAART LRSFPWQGGGGRAERPAGLAG VQGQTGWVSVLKPPALLPREFL GSPRSGPRDPVPVPGAWPKSLA PLLPRELAAEDEGVSTALGGQT RARCGVQFTIIFTTF
9566	39934	B	9626	1	1177	

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9567	39935	A	9627	1	283	
9568	39936	A	9628	1	708	MPKGKEAKGKKLALAPAFVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTCFVKWPRYIRLQW QRSILYKQLK\PETKQEKKWRL LAQAE/SVGKGDLPMKRLPVFR AGVNTVTTFVDNKKAPLVVTT HDMDPIELTVFLPVLCHKMGA TCCIIKGKARLGCLVHRKTYTT VDFTQVNSEDKGALAKLVEAI GTNYNARYDETHCHWDGNVL GPKSVAHIAKLEKAKAKELAT
9569	39937	A	9629	1	836	GTRPKMPKGKKAKGKKVAPAP AVVKKQEAKKVVNPLFEKR\PK NFGIGQDIQPKRDLTRFVKWPR YIRL\QRQRAILYKRLKEPPAIN\ QFTQAL\DRQTATQLLKLAHK\ YRP\ETKQEK\KQRL\LARAEKK AA\GKGDVPTKRPPV/LFRAGV KQPSPPLVE\NKESFSLVVISH\D VDPIELVVFLP\ALCRKMGVPY CIIKGKARLGRLS\HKKTCTTVA FTQVNSEDKGALAKLVEAIRTN YNDRYDEIRRHWGGNVLGPKS VARIAKLEKAKAKELATKLG
9570	39938	A	9630	3	119	
9571	39939	B	9631	1	711	
9572	39940	B	9632	97	942	
9573	39941	A	9633	1	588	
9574	39942	A	9634	1	1029	
9575	39943	A	9635	1	1031	MADQKEARHSASQWKCFVGFL SFRGHMQVAWEADRCKGPGRP LLAEALQDLWPSPRRSQRDPVP ERPCRRPQQSPLPRFGSLSAPLH RENNFIKDFPQLADGLLVIPLPV EEQCRGVLSEPLPDLQLLTGDIR YDEAMGYPMVQQWRVRSNLY RVKLSTITLAAGFTNVLKILTKE SSREELLSFIQHYGSHYIAEALY GSELTCIIHFPSKKVQQQLWLQ YQKGFLGEPKKILGSSLPRRTQF LWKNNHLITKQTVSILSCGEAFI LRKGQQISFSSDSQLLSELEFLR PGAGDQSLPTHLVKVIPFPPQFS L/LCEMGTFILFCNINCAWGRG RGERYSQSC

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9576	39944	A	9636	3	4091	FASASAVSAAASSSSFATAATA AAARSTAAPPAMAAAGARLSP GPGSGLRGRPRLCFHPGPPPLLP LLLLFLLLLPPPPLLAGATAAAS REPDSPCRLKTVTVSTLPALRES DIGWSGARAGAGAGTGAGAA AAAASPGSPGSAGTAAESRLLL FVRNELPGRIAVQDDLDNTELP FFTLEMSGTAADISLVHWRQQ WLENGTLYFHVSMSSSGQLAQ ATAPTLQEPSEIVEEQMHILHIS VMGGLIALLLLLLV
9577	39945	A	9637	2	398	SDARVDALNKIKIWERIKKHLE GHSTNLSLDIAKLKEQIFEASQA HLTLMPGTGVLEGAADRLSAS NPLKWIKTLGSSVISMMIVLLIC VVCLCVVCRCRS*LLREVAHRD KAAFAFIALQIKEGEHVGNST
9578	39946	A	9638	201	495	WKKTLMPGTGVLEGAAN/GLA AINPLKWIKTLGDSVISMMIVLL IC/VCLCIVCRCRSRLLREVAHC DKATFAFIISEKMWYFGFCFCN NSLRVIASSCIH
9579	39947	A	9639	3	409	GIYILHQKKTWEK\LLLAACAIV AIENPADVSVISSRKTGQKATPL FAAVTGATLVAGCFTPRTFSNQ ISAAFREPQLLVVTDPRADHQP LTEASYINLPTIALC\TDSPLHYV GLAIQCNNKGAHSGGLTCNLS
9580	39948	A	9640	3	438	
9581	39949	A	9641	288	489	SFRPLSVLGDCVVRGPTKPSGK CSPASRSLFVRRHILLLHPQGLH NLDQNKATPPPQPL\GHQTCAC
9582	39950	C	9642	23	411	
9583	39951	A	9643	1	209	SPSTTAVCCPPRPSIDFHSSGSSR VSAALLIQ/QRFPLPLWIGLKAR HCSCGLRQRQVSWQETEEDGK AG

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9584	39952	A	9644	28	925	PEAGTRSWREPDPEDLRRFLLS AACRSFPQWLPGGGGGQVSSC SDTDVPYLLLAVKSEPGRFAER QAVRETRRKPTS\GIRLLFLLGS PVGEAGPDLNSLVAWESRRYS DLLLWDFLDVPFNQTLKEP/VL WLPGWAGPCPTGSFVLRAQDD AFVHTPALLAHLRALPPASARS LYLGEVFTQAMPLRKPGGPFY VPESFFEGGYPAYASGGGYVIA GRLAPWLLRAAARVAPFPFED VYTGLCIRALGLVPQAHPGFLT AWPADRTADHCAFRNLLLVRP LGPQASIRLWKQLQDPRLQC
9585	39953	A	9645	1	1612	MIFVVIILMVVLSPEGGSGLDSS PFLSEANAERIVQTLCTVRGAA LKPYPPTGPNFRYSHGVPPHLF AYFPPGSTVSQDNSFISPQLQHI FERVRQSADFMPRWQMLRVLE EELGRDWQAKVASLEEVPFAA ASIGQVHQGLLRDGTEVAVKIQ YPGIAQSIQSDVQNLLAVLKMS AALPAGLFAEQSLQALQQELA WECDYRREAACAQNFRQLLAN DPFFRVPAVVKELCTTRVLGME LAGGVPLDQCQGLSQDLRNQIC FQLLTLCLRELFEFRFMQTDPN WANFLYDASSHQVTLLDFGAS REFGTEFTDHYIEVVKAAADGD RDCVLQKSRDLKFLTGFETKAF SDAHVEAVMILGEPFATQGPYD FGSGETARRI\QDLIPVLLRHRL VSP\PEGDLWPWHRKL\AGAFL ACAHLRDHIACRDHKPGHLPPL LGQSPARRSHCRQPPHQRGTPG WIPHDSLHGGFSPQSRPYPAVV PLIPSPSALGQRSPLGLPSLAWL SSLAQELRIPGAGELPTSCPRSC TSPLESEVSEN
9586	39954	A	9646	930	1123	GVRRDGSSASVTVGQPCRDTSL AFETVAGPYLA*KT*TSGKPGS D*RASKVAGGVQNGTRTTAT
9587	39955	A	9647	719	1346	

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9588	39956	A	9648	1	823	MKKVLIAALIAGFSLSATAAETI RFATEASYPPFESIDANNQIVGF DVDLAQALCKEIDATCTFSNQA FDSLIPSLKFRRVEAVMAGMDI TPEREKQVLFTTPYYDNFALFV GQQGKYTSVDQLEGKKVGVQ NGPTHQKFIMDKHPEITYVSDE SYQNAKL\DLQNGCAARAAPG SRRYGGWTIQASTARPSDVLLT ADSVSFAVRSRGAAATAYHRC CLSGVMVNAATACEHSTASQG RASRTVTDSADPHPRSVRRRAS FRRSGRGFCGTVR
9589	39957	A	9649	583	730	
9590	39958	C	9650	333	439	
9591	39959	A	9651	2	171	
9592	39960	A	9652	1	826	MGGLFWRSALRGLRCGPRAPG PSLLVRHGSGTIMGVFVAVGTI PVPSRVPCIEADTLKPGGPSWT RERTLVAVKPDGVQRRLVGDV IQRFERRGFTL\VGMKMLQAPE SVLAEHYQ\DLRRKPFPPCPSSR YMSSGPVVAMVWEGYNVVRA SRAMIGHTDS\AEAAPG\TIKGV DFSVHISRNVIHASDSV\EGAQR EI\QLWF\QSSELVSWA\D\GGQH SSIHPGLRLRAALTTPSPTQDPT YPPLARTPSPTSKPALSPNPLTS PVSPLAPPQAQREF

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9593	39961	A	9653	144	1650	NCETTTKGSAILRNVDPSTLLPL RRAGSSPGLM\PVEEEMEIDEEK QMKGFLDDSERMAFLVSLHLG AAERWFILQMEVGEPLSHENKS FLRRSQGIYDSLSEIDILSAVLC HPKQGQKSVRQYATDFLLLAR HLSWSDAILRTRFLEGLSEAVT TKMGRIFLKVAGSLKELIDRSL YTECQLAEEKDSPGNSSQVLPT ACKRNNEEAMGNELSSQQQTE EHQHVSKRCYYLKEHGDPQEG LHDHLGQSTGHHQKAHTNNVA ATKKVVQQLQLEAGLNSVKVS QAATEPQTIISPPNALQEPSGIE WEQFPKAQIPSEPQENLCPFVST MNSIKGLHEDYQGNAGKVLST VPGRRYALQNLGTAIVQGEER KQSSLCPGEEGKRHELRSGSHS LVMKHAMVLFNVGFETKDQIH LPTRLGMAEVETLCIYAKQLPH KLIAKLRLLKGTRPLSLNNEHIL THPGLEGWLHTEFFRILSINNKY HLSAYLVQSIVLHVMGFHRKT
9594	39962	A	9654	8	440	VFERSTPPTLETVRSKQEWETR LNGVRIMKKNVRDQFNSHIQL VRNGAKLSSLPQIPTPTLPPPPSE TSCFRCFNPVPLWLLGCPSPLG RQTGEDPGEAADPVPTVQ*GPD DQHSSADQDSTYHHGRPDHGG TYPVGCCTTGRT
9595	39963	C	9655	89	389	
9596	39964	A	9656	1	184	
9597	39965	B	9657	1	942	
9598	39966	A	9658	424	614	NDGPDWGGRRRETDVNRKRGF KISKTLYLYSDIYSCHVHFYYIG NVCIESLYSNVRK*NYVYY
9599	39967	A	9659	1	717	
9600	39968	A	9660	103	374	
9601	39969	A	9661	1590	2051	SYPVSEERSQAEQPSSNPYSHFT STPIRDRLHASGVSTQSLSGSSD ALLHWAGHNAHGYAQCRSPLL VFPNPEPCPFPAQPAFLTPSWLP WQK*PWLGFPCQPPRSTHAPCR LHPTSP\GLGGVKASAETPRPQP VD/ETGEDPGEAADPVPTVQ

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9602	39970	A	9662	1	2912	MAQALPWLLLWMGAGVLPAH GTQHGIRLPLRSGLGGAPLGLR LPRETDEEPEEPGRRGSFVEMV DNLRGKSGQGYYVEMTVGSPP QTLNILVDTGSSNFAVGAAPHP FLHRYYQRQLSSTYRDLRKGV YVPYTQGKWEGELGTDLVSIPH GPNVTVRANIAAITESDKFFING SNWEGILGLAYAEIARPDDSLE PFFDSLVKQTHVPNLFSLQLCG AGFPLNQSEVLASVGGSMIIGGI DHSLYTGSLW\YTPI
9603	39971	A	9663	1	902	MSAKEKGKFENMAKADKVHY VREMKTYIPPKQETKKKFKDPN APKRPPFS/SEYCPKIKG\EHPGQ STGDVAKKLGEMRTNSAADDK WPYEKKAAKLKEKYRKDTAV YRAKGKPDAAKKGDVKAEKS KKRKNEKDEEDEEEDEEEDEE DDDNEYADNECTGFSGFVYKT FNSPVHNSLFLNVEIHALGFDEL LESIFCILLVVEVFSLQKGVAML EEVVVNGERSGRSLPWLPAAPS LPVPVPLGLRHPPSQSDNHSLQ LTFLTALRLLRPRLGAVLEETV EDGRTKTNLPDENSVPFSPET
9604	39972	A	9664	146	733	LNMGKGDPKKPRGKMSSYAFF VQTCREEHKKKHPDASVNFSEF SKKCSERWKTMSAKEKGKFED MAKADKARYEREMKTYIPPKG ED/TKKKFKDPN\APKRPPSAFF LF\CSEY/RAPKIKGEHPG\LSIG\ DVAEETGEEMW\NNTAADDKQ PYEKKAAKLKEKYEKDIAAYR AKGKPDAAKKGVVKAEKRSTR PRIPDL
9605	39973	A	9665	30	359	
9606	39974	C	9666	418	555	
9607	39975	B	9667	550	1717	
9608	39976	B	9668	1	1705	
9609	39977	B	9669	328	484	

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9610	39978	A	9670	5	1215	IIVLPKMSMPVVSAQLTITSIPP WAVE/WGNVTLSVQGIPQNLIS YNWLRGATTNQVTRILNFNFFS HGYTLGPAHTGRETGRADGSLI IIDVRASDNGIYTLHLISSGE\KV AIMLCYLSLLVAPWHFHKTPR WRFPWGPRAASQRASCSQPQS WSSGCSK/VSQAALYIQKIPEQP QKNQDLLLSVQGVPDTFQDFN WYLGEETYGGTRLFTYIPGIQR PQRDGSAMGQRDIVGFPNGSM LLRRAQPTDSGTYQVAITINSE WTMKAKTEVQVAEKNKELPST HLPTNAGILAATIIGSLAAGALL ISCIAYLLVTRNWRGQSHRMAT TEKPELGPAHDAGDNNIYEVM PSPVLLVSPISDTRSINPARPLPT PPHLQAEPENHQYQQDLLNPDP APYCQLVPTS
9611	39979	A	9671	1	558	EGGLRTPSNPYHVDISQTKPCH *TNHCIQKEYSKNYGKYEEGNE MFFKEFNQYLTSALNITLESSIL LQIKHIIRNCLLSVEPAISTKHLP \YQSFQLFGFDFMVDEELKVWL IEVNGAPACAQ*ACTSLCFYKW EVGSAVGIVCGYKCSHFDCCEG GCHSDRRPLGGLYLAGGFAESL PFLFPRV
9612	39980	A	9672	1	534	MVGVDVTFKVISREERQTQRL GSSSPKRCPLEQEFEHEYSSFFG RNCLLSVEPAISTKHLPYQSFQL FGFDFMVDEELKVWLIEVNGA PACAQSPAKSL/CATSSSLFLSPP PWTCQQHSRQPTALAELLSCH GWTRGAGQACLWAFVLSVTC VWNPHHHYHHHHQPYRGWLL LYQNIL
9613	39981	A	9673	624	805	SGGHPGHWLPPNPMASPGATT PVGEG/ELQYASLSFQMVKPWD SRGQEATDTECSEIKIHR

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9614	39982	A	9674	1	1005	MENRRKVKGEWIAVPQPVKEL RGVLNAATTLSKTREILRGKCF QLTSPTGNEPSHLSWTPRKRSR DGHPGCPDPLAASGARPLRSSS AFAAAAADSGSTVQVWDKGV LRVADVWSTIEPVTHVNLGWA AKVGPIISHGSAVISAFSKEGMF RIFSERKTLLAKLRDFQNTQLR KLFSEMEKAAGRSQSGVSFGQ KGLGDRACEEMSENPQKGRKK PKAPQEVSFRENGNWKTP\SIFF SPKTPRKKKSFS\KEELMS\SD\L EETRWQAPSIPKRKKSTPKEET VNDPLE\AGHK\SGSKKKRKFS K\EEPV\SSGPEEAAGKSSSKKK KKFHKASQED
9615	39983	A	9675	1	2742	
9616	39984	A	9676	1	405	MADIPQEARQYRHKQAYAYSI QGEGVEDDDERIVRFHTRWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGR/VLKDSDKFDAN DPILKDQTQEWSGSATFTGSVF LAFGCYSK
9617	39985	A	9677	3	642	GKGLFDDEDEESDLFMEAPQD RQAGASVKEESSSSKPGKKIPA GAVSVFLGDTDVFGAASVPSLK EPQKPEQPTPRKSPYGPPPTGLF FFSAPHSKPSKTRKVQSTADIFG DEEGDLFKEKAVASPEATVSQT DENKARAEKKVTLSYSKNLKP SSETK\TQKGLFSDEEDSEDLFS SQSASNLKGASLLPGKLPTSVS WFDDEDEEDNLLGVQ
9618	39986	B	9678	175	1422	
9619	39987	A	9679	1	3096	MVTHQQPAARKPNMTSKKPKP MGPKAHGIFSGTRKNNLEIYMD QTRTGIAKTKLSKNNKSGGMT LPDFKLYYKAIVAKIACGGSMY NSDTDEDEETEPSSSGQQIIENSI TMNKMKLLKAKMKNMNLSKK HITQVSDEEEDDDGCDLFADSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDAVGRVDEEPTT VSYEDDRRGKNQDAYTEGGLS TIKTVNCSSSL\PSGEAKLRKTL/ KEKKERRTPSDDE
9620	39988	A	9680	1	2925	
9621	39989	A	9681	2	688	
9622	39990	A	9682	1	1005	
9623	39991	B	9683	1	588	

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9624	39992	A	9684	1	2763	
9625	39993	A	9685	2	1075	NSDEELLFSHKLQKDNDPDVDL FAGTKKTKLLEPSVGSLFGDDE DDDLFSSAKSQPLVQEKKRVV KKDHSVDSFKNQKHPESIQGSK EKGIWKPETPQ\AHQVSLHLKP NEPSTRIGKIQANLAINPAALLP T\AASQIS\EVKPVLP\ELAF\PSS EHRRSHGL\ESVPVLPGSGEAG VSFDLPAQADTLHSANKSRVK MRGKRRPQTRAARRLAAQESS EAEDMSVPRGPIAQWADGAISP NGH*PQLRAASGEDSTEEALA AAAAPWEGGPVPGVDTSPFAK SLGHSRGEADLYDSGDIFSRAP GSQ/SVERPNPRQRSRDLPPPGW KQRPRSGKQPRKRPSP*QPKHP LPKGRTSSPW
9626	39994	A	9686	1	4086	VTPRAAWLGLGFRGSAVLGLC WQPRSPPSRAAGMMNRTTPDQ ELVPASEPVWERPWSVEEIRRS SQSWSLAADAGLLQFLQEFSQQ TISRTHEIKKQVDGLIRETKATD CRLHNVFNDFLMLSNTQFIENR VYDEEVEEPVLKAEAEKTEQE KTREQKEVDLIPKVQEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVELILEPKDLYIDRPLP YLIGSKLFMEQEDVGLGELSSE EGSVGSDRGSIVDTE
9627	39995	A	9687	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
9628	39996	A	9688	1	3654	
9629	39997	A	9689	1	5127	
9630	39998	A	9690	1	3663	

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9631	39999	A	9691	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
9632	40000	A	9692	1	3489	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNPTQSRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIPLNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKTDRPLARLIKKKR EKNQIDTIKNDK
9633	40001	A	9693	1	3235	
9634	40002	B	9694	1	3300	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9635	40003	A	9695	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
9636	40004	B	9696	1	3420	
9637	40005	A	9697	1	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSASEPPSAPIPKAQV SSTEKLRNCIDDLKPFPALASEL SRRAKALQIAGFPPMKVPRDTI SKVCLDKTVGKLCHSGEESRK CTLICNNKHYPIQDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAKYSSLEAKLCQIESKYL ILLQEMKTPVCSEDQGPTREVI AQLLEDALQVESQEQPEQAFV KPHLVSEYDIYGFRTVPEDDEE EKLVAKVRALDLK
9638	40006	A	9698	1	4371	

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9639	40007	A	9699	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKL\GIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGQ
9640	40008	A	9700	1	4449	
9641	40009	A	9701	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
9642	40010	B	9702	1	2858	
9643	40011	A	9703	1	3354	
9644	40012	B	9704	288	3301	
9645	40013	A	9705	1	3457	
9646	40014	A	9706	1	4794	
9647	40015	B	9707	1	3384	
9648	40016	A	9708	1	3345	
9649	40017	A	9709	1	3780	
9650	40018	A	9710	1	3720	
9651	40019	A	9711	1	3894	

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9652	40020	A	9712	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
9653	40021	A	9713	1	3780	
9654	40022	B	9714	1	3855	
9655	40023	A	9715	1	3345	
9656	40024	A	9716	965	4362	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFFSAPHHTYSKI DHIVGSKALLSKCERTEIITNYL SDHSAMKLELRIKNLTQNCSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTNQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREKNQIDT
9657	40025	A	9717	1	3921	
9658	40026	A	9718	1	3988	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNL
9659	40027	A	9719	32	583	GPHGAFTHGRR/RFGRDPYEGP RRTGKRKQKSARGCIVDANLSI LNLVIVKKGEKDIPGLTDTMVP CHLGPKRASRICKLFSLSEDDD VHQCVVRKALNKEGKKPRTKA PTTKYLVTPHVLQHEWWHIAL KKQRIKENKEVAAEYAKLLAK RMKEAKEKHQEQIAKRRRLSSL RASTSKSESSQK
9660	40028	A	9720	318	605	

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9661	40029	A	9721	1	649	MGLKGQGVEGGLLRQSGSVSL QPLSREDLGRSQSESLGPEFQGL WEWLPVERVERENLSDYCVLG QRPMHLPNMNQLASLGKTNEQ SPHSQIHHSTPIRNQVPALQPIM SPGLLSPQLSPQLVRQQIAMAH LINQQIA/S*PAPGSPASSSHQPA VPEPS/IPSPEQLSQSQPTLPWKS LQISTSKSEMS*RGPVCPKLSLQ EWHSTAHRNLKTWKKD
9662	40030	A	9722	15	272	KPQWPGIPSGPPPPGSCFKC*KS GHWAKECLQPRIPPKPCPICAGP HWKSDCSTHLAATPRAPGTLA QGSLTDSFPDLLGLAAEG
9663	40031	A	9723	96	531	VQPADLLRPLHTDTCNIWCQRP GTEGLLRETGPLSS/PLTP/MRRS TYDLRSSDQPKEHLTDFKSGSC FKCRKSGHWTKECQQPRIPPKP CPICAGPHWKSDCPSCPAATPR APGTLAQDSLTDSFPTDPKGSLI DYFPDLLCLVAED
9664	40032	A	9724	3	567	GRLQTGADPAWRVHGTWRSTS AADAIDQMWP\PVMRTWRLNE RHYGGLTDLGKAETAAKHGEA QVKIWSNISKDRRYADLTDDQL SSCESLKDTIASALPFWNKEIVP QIKEGKWVLIAAHGNSLRGIVK HLEGLSEEAIMELNLLTGIPIVC KLDKSSKPIRCMEFLGDEGTLC KAMEAVAAQGKAKK
9665	40033	A	9725	2	801	GGVPHPQPAAMAAYKLVLIRH GESAWNLENRFSGWYDADLSP AGHEEAKRGGQALRDAGYEFD ICFTSVHLY\AIRTLWTVLEMPL\ SEMWLPVVRTWRLNERHYGG LTGLNKAETAAKNGEAQVKIW RRSYDVPPPPMEPDHPFYSNISK DRRYADLTEDQLPSCDRLKDTI ATALPFWNEEIVPQIKEGKRVLI AAHGNSLRGIVKHLEGLSEEAI MEL\NLPTGIPIVYELDKNLKPI KPMQFLGDEETVRKAMEAVAA QGKAKK

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9666	40034	A	9726	3	573	VAPVVQVWKEMHKLLPFSPDS V\VTHGDISIDSGIFDQDKLIGRI DVGRVGIACGCQDVAIVWNYL AACSVDRNTCRIMRPNCRPEVE ETPGLKEEKELSQPKEGEATDL KKEVEKISSSEEEETVNLKEEVE KIPPPEEETMDLKEEKEEIPPPEL RDQKLMHVLKDLEPVSAVPHK DSLFHGQLTTVPV
9667	40035	A	9727	2	685	TLYCRVFLLDGTEVSVDLPKHA KGQDLFDQIVYHLDLVETDYF GLQFLDSAQVAHWLDHAKPIK KQMKIGPAYALHFRVKYYSSEP NNLREEFTRPKITKMDFKKSKL TLVVVEDDDQGREQEHTFVFR LDSARTCKHLWKCAVEHHAFF RLRTPGNSKSNRSDFIRLGSRFR FSCFS/ERENAHSTGNSPALRER PGDGSVSREGRWVDEGWPQRP GGRGQNALCSVP
9668	40036	A	9728	1	419	MSKFGRATRGLRKPEVGDVIRT IVRAGLAMPGPPLGPVLGQRRA SINQFCKEFNERTKDIKEGIPLL TKIFLKPDGTFEIKIGQPTVSYF VKAAAGIEKGARPT/DLSSEEFA AFQKEQAIFLAAQKKADLATQ EEAAKK
9669	40037	A	9729	97	826	SQLPRIMSKLGRAARGLRKPEV GGVIRAIVRAGLAMPGPPLG\N VLGQRGVSINQFCKEFNERTKD IKE\GIPLPTKIL\VKPD\RTFEIKI GQPTVSYFLKAAAGIEKG\ARQ TGKEVAGLVTLKHVYEIARIKA SGLRAFALQDVPLSSV\VRSIIGS ARSLGTSRGERTSSSEELAAFQ KERAIFL\AAQK\EADFGLPKKE AAKEIDPLPHQLPDFQKEVSLQ KLCPRGGRRSHQYDDGFHDFE
9670	40038	B	9730	273	418	

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9671	40039	A	9731	69	1565	RRRRFQASGAAAMLSSRAEAA MTAADRAIQRFLRTGAAVRYK VMKNWGVIGGIAAALAAGIYV IWGPITERKKRRKGLVPGLVNL GNTCFMNSLLQGLSACPAFIRW LEEFTSQYSRDQKEPPSHQYLS LTLLHLLKALSCQEVTDDEVLD ASCLLDVLRMYRWQISSFEEQP HFQDGLVQLRVGVVCRHYPEK WEAASWTSQNCGADDAHELF HVITSSLEDERDRQPRVTHLFD VHSLEGHPLTLDHCLHHF\TQSE SVRDVVCDNCTKIEAKGTLNG EKVEHQRTTFVKQLKLGKLPQ CLCIHLQRLSMVQP\GTPLKRHE HVQFNEFLMMDIYKYHLLGHK PSQHNPKLNKNPGPTLE/HAGW AGSPHTSSESARGPQNTDFYEW RLLPIFIANAVSADALPSPSCSR LQLLHIPLPADGQLSSTMGDMA LWDTLFIYRRSPPSARNPLSTSN QWLWVSDDTVRKASLQEVLSS SAYLLFYERVLSRMQHQSQEC
9672	40040	A	9732	1	1393	PLQLQPRHIGAQIQLGPLLQRV QAIRLGSFHMVLSLW/VMQSAR VEILEPPPRLQRMYGKAWRISL CPQGLSTVMRSELTASSTPQVQ EILPPQSPEYLGPKGITERIHKIM HVKGLAKLPANRNQPSPGVSG KRLVNCVSASAVDSEPAAVPEP DVCAGIVIKKQCFPVIARCNKT KQVDSIPHRAYAKPSPFFPAVV VVTSESKDPRVKQNPTHPLLAE GSNAAHFHKTKISQSLKWLPVG YLNSTTYEYRDLTKGLSLLCSL LLGVEADIPSMAGLHVRHLMQ VPQQPCIAFAVSSPLHQGGKET EDAWSFHIPSTIHRWPTSPSVQL SSLRASTQLLCLHINLAKCFIWG ILAQVLSCHHHRITQFVGMLTF VCAGDSSKLSPDIRTLVRRLTS YLVSASVLLKSKQMALCSASRI LDVSVSPGDHVASEARARCAP DLVAPRPMPHQNQGSLEWTEE
9673	40041	A	9733	44	282	FSCLILHDAFPCLILHDAFPCSL CSVTGSLVLSRVPLRGTHQKSA IATSTKIALSNM/KILKHHTDAY FKKQQLFFDVSKK

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9674	40042	A	9734	3	381	EQQGQR/SQWWRGAARVSRTV KRVLCE/VVECPLKSACPDVDM YWAALQRLASLLKADGNLVT MAALHSHYMVGSKKFFGLHPE KETVEKAMQEAGCQVQRCA/SI SCSETCSINDGICFVAACKGPSV
9675	40043	A	9735	2	209	CRHSTQHCVS/HHGHSQYK/DS HQHYSHYHHHNHPHHHHQSPY LHHHHYDCHLHHHHHNDHYH RHISVYDI
9676	40044	A	9736	197	3348	RVVQTDMIKGMLETSLLKISLD QAFIRICLNSTCFRPKGKLVIK/C EKSINSASLVSTSQRISCRPKTHI SKNYGNNFLNSSLLTQKQEVH MREKSFQCNESGKAFNYSSVLR KHQIIHLGAKQYKCDVCGKVF NQKRYLACHRRCHTGKKPYKC NDCGKTFSQELTLTCHHRLHTG EKHYKCSECGKTFSRNSALVIH KAIHTGEKSYKCNECGKTFSQT SYLVYHRRLHTGEKPYKCEEC DKAFSFKSNLERH

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9677	40045	A	9737	1	1665	MAGACWLMAFQYWVLKLLVV KSA/SWPRQSSLKWNWNFKGC QDLETWGKKETRKFYGYRRNE EAQKYSCRIPRKPD*WCHCWQ W**WLMAFQYWVLKLLVVKS AYGLVKALSNGIGISKVAKTW KPGGKKRLENFMAIEEMKKHR STHVGFPENLTNGATAGNGDD GLIPPRKSRTPESQQFPDTENEE YHRDFSKLCLGSAANGVVHVE VKMCVYNGKGERQEEKMKGLI SMNLVVEEEMKKHESNNVGLL ENLTNGVTAGNGDNGLIPQRKS RTPENQQFPDNESEEYHSLGDK SKTSFQNSNNNNNKQQEQQQQ NPTFSNTRKLTKLYKAPIPPSIIL SGCPNINDSNWQEIEHGMQTA GLPTRPLSHGLQQKGAAFRCLG CKCSEPFTGSLILQKAKTNTQK WQATYPKSQNEQLVPSVGKSY RCSTPAQPMKTAVGHKPCKAT GAELPKALGAQPLHPCALDVG QGFKKGNFGAVGLNGLLGLEF HGVSGVLLVGPGDGGLISEGVV REDLMCGVWSAGTWSVGTAE RCLEKPGALHVIEGPLDSWDGP VMPNGPVKSRQSSCLDGPGRC CSEILTGQSHGNKKPARASSKS SQSINDRPLAVLTNQYQCEQLA SERQPSSNSCSIRIDSA
9678	40046	A	9738	1	115	RRTARGPQQTSTDGLGTSPCRN ASEHTADILELSTLIV*RRQ*ICL CLDFLYY/LIPEGRCFCRACDLV HNF\DTIILQQHRTLTSQGVDDF LKAKATFKASDFIDALVLSKVA SPRILIQGGRMGA*DQVSDQAS VYGRCSSSGAEAAKRPKSAWL\ LLGYDSRASGLY*ILYNLTKHP D/YRECCQPVMQES*S*RRTAR GPQQTSTDGLGTSPCRNASEHT ADILELSTLIV
9679	40047	A	9739	1	506	MVIVGLAAGVLLVGPGDGGLIS EGVVREDLMCGVWSAGTWSV GTAERCLEKPGALHVIEGPLDS WDGPVMPNGPVKNHKGEQQE VPSKHPQMALEICLCLDFLYY/L IPEGRCFCRACDLVHNF\DTIILQ QHRTLTSQGVDDFLKAKATFK ASDFIDALVLSKVASPGS

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9680	40048	A	9740	1	380	KFSRPSVNMLRIVKPCITRG/YP NLKSVNKLIYKHGRGKINKKRI ALTDNTLIDQSHGQYGIICIEDLI HELY\LWPFKLSSPQSGMKKKT THFVENGAAANREGQIHRLLIR MNCGVYRDYFSNLVS
9681	40049	A	9741	3	279	
9682	40050	B	9742	23	197	
9683	40051	A	9743	2	402	CGDRGALRPPSCAGRSGPGPPR PPRPPRPLPWHPAPPAHGAPLA RPGARARRSEKPPSEKPRLRRSS PRAQEEGPGEPPPPELALLPPPP PPPPTPA\PRRPRRP\PGPGRAAG ALGDVPEAAEAYLERVPPSSC
9684	40052	A	9744	1	660	
9685	40053	A	9745	1	1035	
9686	40054	A	9746	1	2575	MRAAGGAMLCGKQGRWDPEG EGAHPGFIPKLACSSQGVFRQL HLRTAVTAAVSRHFPQPSWRY DPGPQFLGEKSGFKPRCPGVAV CQFQSMNAFIHWFRNKAWASS CDRIKIPVPPEATFVEPNCLPGEI GQLLRQLQSGRNLKEWLREQF CDHPLEHCEDTRLHDAAYVGD LQTLRSLLQEESYRSRINEKSV WCCGWLPCTPLRIAATAGHGS CVDFLIRKGAEVDLVDVKGQT ALYVAVVNGHLESTQILLEAGA DPNGSRHHRSTPVYHASRVGR ADILKALIRPAACDRSVSITADT HFRYLIKVVPAMFRSRKAIPFLS SCTAWRCADELQFIQPVPLVDT SGSGKTVSNVITESHNSDNEED DQFVVEAAPQLSEMSEIEMVTA VELEEEEKHGGLVKKILETKKD YEKLQQSPKPGEKPSATGWHG ECLGTRNRAQGALVGWGWLY SERHSGMLRAITLKYKGGGRQ GIQA/AWKSETFRSRAAPENPL GRWGFALLSKIIS*RQVL\KLHF SLSPQARVNSRFPGSGKAGLGL WMEGARPSGHVPKERVVAGK RPQVPTKAHHTCVRETAGNQE GNGEGALQQEQRLGVAEAGSN GEGALQQEHRITDCAVEPLKAE LAELEQLIKDQQDKICAVKANI LKNEEKIQKMERSLFESAWKKE KDIVSKEIEKLRTSIQTLCKSAL

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9687	40055	A	9747	2	1739	MKGLYTDAEMKSDNVKDKDA KISFLQKAIDVVVMVSGEPLLA KPARIVAGHEPERTNELLQIIGK CCLNKLSSDDAVRRVLAGEKG EVKGRASLTSRSQELDNKNVRE EESRVHKNTEDRGDAEIKERST SRDRKQKEELKEDRKPREKDK DKEKAKENGGNRHREGERERA KARARPDNERQKDRGNRERDR DSERKKETERKSEGGKEKERLR DRDRERDRDKGKDRDRRRVKN GEHSWDLDREKNREHDKPEKK SASSGEMSKKLSDGTFKDSKAE TETEISTRASKSLTTKTSKRRSK NSVEGDSTSDAEGDAGPAGQD KSE\VPETPEIPNELSSNIRRIPRP GSARPAPPRVKRQDSMEALQM DRSGSGKTVSNVITESHNSDNE EDDQFVVEAAPQLSEMSEIEMV TAVELEEEEKHGGLVKKILETK KDYEKLQQSPKPGEKERSLFES AWKKEKDIVSKEIEKLRTSIQTL CKSALPLGKIMDYIQEDVDAM QNELQM\YHSENRQHAEALQQ EQRITDCAVEP\LKAELA\ELEQ LIKD\Q\QDKICAVKANILKNEE KIQKMVYSINLTSRR
9688	40056	A	9748	93	800	RANLPTQPYCHCGLAPAALTRI VGGSAAGRGEWPWQVDLWLR RREHRCGAVLVAERWLLSAAH CFDVYGDPK/QWAAFLGT/HVP ERRGGAVERVARIYKHPFYNL YT/FDYDVALLELAGPVRRT/SL VRPICLPEPA/HATPDGTRCVIT GWG/YGS/TGAQLQKAAVRLLS EQTCRA/LYPVQISSRMLCAGF/ LQGGVDSCSGDAGGPLACREPS GAPVPGQPRTCTAPARWPRRSA LSPAPL
9689	40057	A	9749	107	378	NLVP*LRSGD/SPLGDQSPVLLIF TP*ERSTYNLKSSD*PAQETS/PP ISNPDPTEN/PDCSTHLAATPRA PGTLAQGSLTDSFPDLLSLAAE D
9690	40058	A	9750	2	286	

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9691	40059	A	9751	215	631	GTQSCNQKVLNSANNLQELGIG PKFQMRLKPQLAPMQPNRGTS LGRSIPCPPVLCSMRKIHLRPQV LRPTSPRNISPILNRVSEVSDHA GTPALVLHP*RQVPLFWGRGK YPNPFSLCLYPFSAFLGGKKHP TPSPSP
9692	40060	B	9752	1	933	
9693	40061	A	9753	1	2283	MLPNRLGSSETITDAELRVTLT VEELNGLRAVQDMFVKQILKA ARSLRVITIPNLKYPGTQTLRKA AAPDPNTTGLIFLEKLCEIAAAI ASYVAVPSLEINHRKKANPNLL LRRSGSGSVSLQLLAEKIWEGV REPWARVLVLWEWLPDQNPLS GLTKSNSTSRHELPHGRAIQLH LSGWELWSEPSNLLDLVVTGDI ENTSLAPEDPTFLTMPSGSHCPE SPSDGPGLSSLVALVWFLVED WLSRKRLESEPAELPLGKAGEV VFDTLPLPSRRTHFSGFLGHFCY SFSDGYSTNRAAPDGSSTKAEK HGSCRKQPPYTLQCRDKAGLR VHGNSPVSAYGWLFSEERPGKP TRTPFSWEGDPPGLLTADETSL VVHLELPVFPSFLKRAGNSRHS GMGSPLEAEEAYSTVVMADVS QYPVNEPLVAAVVCQEPERAQ PDVHFFQ/CLRLGGHAGGVAAR PLPAAETPPLQRRPSVRA*SAP* SGARAADDPRRTHS\QAEEAQR PEPDILNHVFDDVESF/VSRLQK SAEAARVLEHR/KRGRRSRRRA AGEGLLTLR/AKPPSEAEYTDV LQKIK/HAFSLLARLRGNIADPS/ SSELLHFLFGPLQMIV/QPSGGP EFASSVRRPHLT/RDAVALLRD NVTPRE/RRLWTSLGDSWTRPG LELSPEEGPPY/IPEFFSGWEPPV TDPQSAPGRTQLRNSYSTSGGA
9694	40062	B	9754	1	930	
9695	40063	A	9755	76	247	QLKTDTAQLPRKLFVESHNYH CSWPGLQSGLPHYSGYHTSSS* LYLSDPADIHPISP
9696	40064	C	9756	95	301	
9697	40065	A	9757	352	545	DILNHVFDDVESFVSRLQKSAE RPGCWRRRTRPQKPAPGVAG* RGTWRGI*TPPDLFQMSPLSP
9698	40066	B	9758	406	602	
9699	40067	A	9759	1	543	

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9700	40068	A	9760	2	138	LDDFVGRMLTLMGCPIPEC/PR VPSPLREGRKTQAALSVRRGRS HRR
9701	40069	A	9761	1	417	
9702	40070	A	9762	830	1029	YLPHLSLRLLPCPPPLPLSKPNS LP*LRPSLLQRDYLSIFILILNMP SISSTTMLLYGQKEISSLH
9703	40071	B	9763	40	980	
9704	40072	C	9764	419	700	
9705	40073	A	9765	271	1185	
9706	40074	A	9766	2	1655	RGRRSRRRAAGEGLLTLRAKPP SEAEYTDVLQKIKYAFSLLARL RGNIADPSSPELLHFLFGPLQMI VNTSGGPEFASSVRRP\LVTSD\ AVALL\GNNVTPRENELWTSLG DSWTR/LRA/EELSPEEGPPYRP EFFSGWEPPVTDPQSRAWEDPV EKQLQHERRRRQQSAPSGRCQ WVTGDLEPESEPQLESETAGK WVLCNYDFQA\RNSSEAVRSSS GDVL\EVL\DDSR\KWWKVRDP AGQEGYVPYNILTPYPGPRLHH SQSPARSH\DSTPPPPPAPAP/VP/ LPPALARPRWDRPRWDSCDSL NGLDPSEKEKFSQMLIVNEELQ ARLAQGRSGPSRAVPGPRAPEP QLSPGSDASEVRAWLQAKGFSS GTVDALGVLTGAQLFSLQKEEL RAVSPEGG\ARVYSPVTVQRSL LEDKRES\SELEAVMEKQKEEG GRRGGNGGHLTCQAPFAKSDE APWENGPPQTLPNSGSRSSEGW PICSGPGLPPLPVDRLNDPCCSP SGEDLDWLGVGRAWRQSTESA SRPPRGCSGALSIVILRPSPINMP PCLAKKKK
9707	40075	C	9767	565	762	
9708	40076	A	9768	1	401	SPLRPLLLALALASEPCAQGAC PASADLKHSDGTRTCAKLYD\C SDPYYENCCGGAELSLESGADL PYLPSNWANTASSLVVAPRCEL TVWSRQGKAGKTHKFSAGTYP RLEEYRRGILGDWSNAISALYC RCS

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9709	40077	A	9769	1	1489	MPQLLQNINGIIEAFRRYARTEG NCTALTRGELKRLLEQEFADVI VKPHDPATVDEVLRLLDEDHT GTVEFKEFLVLVFKVAQACFKT LSESAEGACGSQESGSLHSGAS QELGEGQRSGTEVGRAGKGQH YEGSSHRQSQQGSRGQNRPGV QTQGQATGSAWVSSYDRQAES QSQERISPQIQLSGQTEQTQKAG EGKRNQTTEMRPERQPQTREQ DRAHQTGETVTGSGTQTQAGA TQTVEQDSSHQTGRTSKQTQEA TNDQNRGTETHGQGRSQTSQA VTGGHAQIQAGTHTQTPTQTVE QDSSHQTGSTSTQTQESTNGQN RGTEIHGQGRSQTSQAVTGGHT QIQAGSHTETVEQDRSQTVSHG GAREQGQTQTQPGSGQRWMQ VSNPEAGETVPGGQAQTGASTE SGRQEWSSTHPRRCVTEGQGD RQPTVVGEEWVDDHSRETVILR LDQGNLHT\SVSSAQGQDAAQS EEKRGITARELYSYLRSTKP
9710	40078	A	9770	2	3031	
9711	40079	A	9771	6288	6584	TAVSLPAPLFSDLQIPPRKRSLK ETVMAPENLTN*RAPPQSSARV FQ*EALYVPGP*ALDPPEVCSSY SSVCGLHQLSHSSSESSSTLGSL LGSFQML
9712	40080	A	9772	884	1032	ESRPNTTTRLRKTSSWSFQS*TA TQTKGPRDPGASMTKPGATSER SASG

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9713	40081	A	9773	1	1457	RSAQKEKTAAKEQQGEKTEVL SSDDDAPDSPVILEIPSLPPSTPP STPTYKKSLRLSSDQIRRLNLQE GANDVVFSVTTQYQGTCRCKA TIYLWKWDDKVVISDIDGTITK S\DALGHILPQLGKDWTHQGITS LYHKIQLGQLVMPLDARPERP MDGMKVRAFMERLLFVRRGT DKRWSVRMYVTCSQSSNLNEE IYINQVVIQANMKLQLWAMRT DDARGLSSLGDTEPSPCPSVVP GLQPKPAPVCAGDALLQAQIPG VLLGTLFSGAAFYSGLYGGSEQ FLDHLLHPARAAPPPPLVGPGP APRVPGSPSAPELAGPAVWRFA AAASRGVVVAASGWGRGGEA SQTFQTGKEPGGTRHPTRMPLG STGCIFPGTLEKSQGYERYNAM RADPALCFLEKVGMPDEKSLSA EQGVTDGTSDIPERARQNEEQL TSFGLLWPTPQGSTDHIDNHPR ERYPEMRWELDVPLPDIDYMEI PVDWWDA
9714	40082	A	9774	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
9715	40083	A	9775	1	897	
9716	40084	A	9776	486	800	CLQLSWLSLGQAQVHWLGRA VHTAFCMD*VLLFGESFGFLVR LTPGILLGLL*P*KQGHCHSVSL GEVRI/CGIIS*TFITSWAFSVLQ GKASAQPVKVSTQNSRY
9717	40085	C	9777	332	497	

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9718	40086	A	9778	1	6504	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
9719	40087	A	9779	1	5421	
9720	40088	B	9780	124	273	
9721	40089	A	9781	84	493	IHANNCS*L*KAALNFVLLLLQ KRL*GEKHLTLSETGREGNKVG GVGS*VTGTGQETELGSLGRCH SPLSVLHLLPFFS/ILLGRTHLNA LLIRDYFASSCKYL*EVLLSLSD GSG*NLMSVWMAGNSSAEYVR
9722	40090	A	9782	1	5954	MDGMTEACIKGGIEACYAAVS CVCTLLGALDELSQGKGLSEGQ VQLLLLRLEELKDGAEWSRDS MEINEADFRWQRRVLSSEHTP WESGNERSLDISISVTTDTGQTT LEGELGQTTPEDHSGNHKNSLK SPAIPEGKETLSKVLETEAVDQP DVVQRSHT\VPYPDITNFLSVDC RTRSYGSRYSESNFSVDDQDLS RTEF\DSCDQYSM\AAEKDSGRS DVSDIGSDNCSLADEEQTPRDC LGHRSLRTAALS
9723	40091	A	9783	1	2217	
9724	40092	A	9784	1	1360	
9725	40093	A	9785	1	777	MNIKNPIAAQHLDNLPIVKASSI GMTWGLVRNGVSAPTQKSCIRI HILARCTGAVAFEKLYFKSPAN QAHARKVGKQVQDCYIGRDIV AKAGAIIHLNVGKGTPVCCPLL EEGINSEVWTTEGQYGRAK\NA RPVQVKLKDSTSFPYQRQYPLR PKA/LTKGFQKIVKDLKAQGLV KPCSNPCSTPILGVQKPNRQWRI EALKLQIVLQMEPQMQSMTKI YHGPLGRPASPCSDVNDIEGNP TKEISTAPPLLCPNSAGSS
9726	40094	A	9786	1	415	

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9727	40095	A	9787	1	451	MVHFISRLLYSDGLDVPGDPIQ DSDDAALSVSPHCSPDSRVSTT KHLWVSPRLLRVAVRVKNIDIT NFSSSW\NDGLAFCALLHTYLP AHIPYQELNSQDKRRNFMLAFQ AAESVGIKSTLDINEMVRTERP DWQNVMLFVI\AIYKYFET
9728	40096	A	9788	3	605	DEWPPERIIQYNEPTTWH/EDGL WGYRTRFYMINQIIW/LQAILEII TNKTDRALTILAQQETQMRNAI NQNRLALDYLPAAEGGICGKF NLTNCCLHVDDQGQVVEDIVR DMIKLSHVPMQVWHGFDPGA MFGKWFPVLGGFKTLIIGVILVI GTCLLLPCLLPVLLQMIKSFIAT LVHQNASEQLYYMNHYRSVLQ EYMGS
9729	40097	A	9789	3	876	GAGGGFGSPMDIFDMFF\GGGG RMHRERRGKNVVHQLSVTLED LYNSATRKLALQKNAICDKCE DRGGKKGGVEYCPNCRGTGM QIRIHQIGPGKVQQIQSVCVECQ GHGEQISPKDRCESCNGRKILR EKKILEFHIDKGMKYGQKITFH GEGYQEPGLEGEDIIIVLDQKD DAVFTRQGEDLFMCQIVKHGDI KCVINEGMPIYPRPYEKGRLIIE FKVNLPENDFLSPDKLSLLEKL LPKRKEVEETDEMDQVELVDF DPNQERWHHYNGEAYEDDEH
9730	40098	A	9790	199	410	
9731	40099	A	9791	134	1369	KMVKETTYYDVLGVKPNATQE ELKKAYRKLAL\KY\HPDKNPN EGEKFKQISQAYEVLSDAKKRE LYDKGGEQAIKEGGAGGGFGS PMDI\FDMFFGGGGRMQRERRG KNVVHQLSVTLEDLYNGATRK LALQKNVICDKCEGR/SGRFKE QGAVRSACPNCRGTGMQIRIHQ IGPGM\VQQIQSVCMECQGHGE RIRPKDRCKSCNGRKIVREKKIL EVHIDKGMKDGQKITFHGEGD QEPGLEPGDIIIVLDQKDHAVFT RRGEDLFMCMDIQLVEALCGF QKPISTLDNRTI\VITSHPG\QIVK HGDIKCVLNEGMP\IYRRPYE\K GRL\IIEFKVNFPENGFLSPDKLS LLEKLLPE\RKEVEETDEMDQV EL\VDFDPN\QERRRHYNGEAY EDDEHHPRGGVQCSDLLMGPV

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9732	40100	A	9792	3	337	GYSQAPRKR/GGECSSLSQPFSK AQPDAASLEPPSLETPAGRTPA TLTQGSPPAAVREPLSPGHNAK ARLRSRPARPPWIPDPDPPGHFV TDFCAPESLQGETRTSRSFQLL
9733	40101	A	9793	1	346	SGS*QLQMCSGLPAHTQDETHI SSCGQLDLALPPLLPPLPPSPLN TLPPQGLCTC
9734	40102	A	9794	1	1110	MEGEEAAGAAGPDPVGHRKKC GFHPVCEREAPSTFAAVMIHLV VQYIGEICRYLLKQPVREAERR HRVRLAVGNGLRPAIWEEFTER FGVRQIGEFYGATECNCSIANM DGKVGSCGFNSRILPHVYPIRL VKVNEDTMELLRDAQGLCIPC QAGEPGLLVGQINQQDPLRRF\ NGYVSESATSTKIAHSVFSKGD SAYLSRDALMMDELGYMYYR DRSGDTFRWRGENVSTTDVEG ELSRL\LGQTDVAVYGVAVPGK LGLQGVVLRHGVEGKAGMAA VADPHSLLDPNAIYQELQKVLA PYARPIFLRLLPQVDTTGTFKIQ KTRLQREGFDPRQTSDRLFFLD LKQGHYLPLNEAVYTRICSGAF
9735	40103	B	9795	28	376	
9736	40104	A	9796	3	461	VRQCRGIRDPYRFKKRTELFIA AEGIHTGQFVYCGKKAQLNIGN VLPVGTMPEGTIVCCLEEKPGD RGKLARASGNYATVISHNPETK KTRVKLPSGSKKVISSANRAVV G/VVSGSS*MLRAVGEHAVSAG GQPVARLGPWNSITCCSKTWV
9737	40105	A	9797	1	701	MQEVPGMFERNYPHPAITFKPS VPVSRSLDYAPLPGGVFRDPYW FKKRTELFIAAEGIHTGQFVYC GKKAQLNIGSVLPVGTMPEGMI VCCLEEKPGGRSKLSWASGNY ATAISHNPETKKTRVKLPSGSK KVVSSANRAVVGVVAGGGRT DKPILKACQAYHKYKAKRNW WPRVWDVAMNPMEHPFGGGN HQHIGIPSAI/SRDDPAGCKMGL IAARQTGRLWGTKTVQEKEN

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9738	40106	A	9798	1	910	QCGGIRRTGPVAMGRVIRGQR KGAFSVFRAHVKHRRGAARLR AVDFAERHGYIKGIVK/DAERW PGREGKGRPAGTPHSRRLCPQD IIHDRGR\GAPLA\RVVFRDPYRF KKRTELF\IAAEG\IHTGQF\VYC GKK\AQ\LNIGNVLPVGT\MP*\G TIVCCLEEKPGD\RGK\LARASG NYATVIS\HNPETKKT\RVKLPS GSKKVISSANRAVVGVVAGG\G \RIDKPIFEGWPGRYHKYKAKR NC*PRIRGV\AMNPVEHPF\GGG NHQHIGK\PST\IRRDAP\AGRKV GLIA\ARRTGRLRGTKTVQEKE
9739	40107	A	9799	1	405	LEISIMAASISGYTFSAVCFHSA NSNADHEGFLLGEVRQEETFSIS DSQISNTEFLQVI\KVIGWYRFR RNTQQQMSYREQVLHKQLTRI LGVPDLVFLLFSFISTANNSTHA LEYVLFRPNRRYNQRISLAIPN
9740	40108	A	9800	1	232	
9741	40109	A	9801	1	420	
9742	40110	A	9802	3	1272	EISIMAASISGYTFSAVCFHSAN SNADHEGFLLGEVRQEETFSISD SQ\ISNTEFLQVIEIHNHQPCSKL FSFYDYASKVNEESLDRILKDR RKKVIG\WYRFRRNTQQQ\MSY K\EQVLHKQLT\RILGVPDLVFL LFSFISTANNSTHALEYVLFRPN RRYNQRISLAIPNLGNTSQQEY KVSSVPNTSQSYAKVIKEHGTD FFDKDGVMKDIRAIYQVYNAL QEKVQAVCADVEKSERVVESC QAEVNKLRRQITQRKNEKEQE RRLQQAVLSRQMPSESLDPAFS PRMPSSGFAAEGRSTLGDAEAS DPPPPYSDFHPNNQESTLSHSR M\ERSVFMPRPQAVG\SSNY\AS TSAGFEVFLGSGADLPPPQRAA GDSGEDSDDSDYENLIDPTEPS NSEYSHSKDSRPMAHPDEDPRN
9743	40111	A	9803	3	513	GAYGGGYGACDNYNGYGYGF GSDRFGRDLNYCFSGMSDHKY GDGGSTFQSTTGHCIY\VHIEIGP DGRVTGEADVEFATHEDAVAA MSKDKANMQHSYVEPFLNCAA GASGTAYGSQMMGGMGLSIQS SYGGPASPQLSGGYGGGYGGH SSMSGFDQVLQENSCDFQSDIA
9744	40112	B	9804	73	1127	

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9745	40113	A	9805	1	3647	MRVRHVGQAALELLTSVRESR ATSAFQVSPYEDEPCRPCNCDP VGSLSSVCIKDDLHSDLHNGKQ PGQCPCKEGYTGEKCDRCQLG YKDYPTCVSCGCNPVGSASDEP CTGPCVCKENVEGKACDRCKP GFYNLKEKNPRGCSECFCFGVS DVCSSLSWPVGQVNSMSGWLV TDLISPRKIPSQQDALGGRHQVS INNTAVMQRLAPKYYWAAPEA YLGNKLTAFGGFLKYTVSYDIP VETVDSNLMSHADVIIK
9746	40114	B	9806	141	236	
9747	40115	B	9807	66	266	
9748	40116	A	9808	1	330	
9749	40117	A	9809	1	792	
9750	40118	A	9810	129	311	
9751	40119	A	9811	3	538	
9752	40120	B	9812	96	536	
9753	40121	A	9813	1	2090	MSSNQKSPTKTSKSPGTANVLD VNNSTLMFVGGLGGQIKKSPA VKVTHFKGCLGEAFLNGKSIGL WNYIEREGKCRGCFGSSQNEDP SFHFDGSGYSVVEKSLPATVTQ IIMLFNTFSPNGLL\LYLGSYGT KDFLSIELFRGRVKVMTDLGSG PITLLTDRRYNNGTWYKIAFQR NRKQGVLAVIDAYNTSNKETK QGETPGASSDLNRLDKDPIYVG GLPRSRVVRRGVTTKSFVGCIK NLEISRSTFDLLRNSYGVRKGC LLEPIRSVSFLKGGYIELPPKSLS PESEWLVTFATTNSSGIILAALG GDVEKRGDREEAHVPFFSVMLI GGNIEVHVNPGDGTGLRKALL HAPTGTCSDGQAHSISLVRNRR IITVQLDENNPVEMKLGALVES RTINVSNLYVGGIPEGEGTSLLT MRRSFHGCIKNLIFNLDHGFVD SVEQKRFCGVPSCARESARGRA QAQDTAQELQSESACDKRSPQP PGKGKHMYGGVLQPQSLFQKN LLLFYDEVLDLQPNGKEKEFSV GANHNAFMVVHWGVCGFCLF PSGEWLASPFCVHPQITIHPPDR FQASVTDEGYLFLAKPTQPAPA CPLDPIRPLLLGHAQQPLLTDQ HTDAAVTPSSAVTARAANYCA GGRNERKKTGREKRHLTGGPC VALRTFTVLHISSHHQVDGIRA GYVQRDGLQPTNRQIVM

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9754	40122	A	9814	1	8705	MRGGVLLVLLLCVAAQCRQRG LFPAILNLASNAHISTNATCGEK GPEMFCKLVEHVPGRPVRNPQ CRICDGNSANPRERHPISHAIDG TNNWWQSPSIQNGREYHWVTI TLDLRQVFQVAYVIIKAANAPR PGNWILERSLDGTTFSPWQYYA VSDSECLSRYNITPRRGPPTYRA DDEVICTSYYSRLVPLEHGEIHT SLINGRPSADDLSPKLLEFTSAR YIRLRFERIRTLNADLMTLSHRE PKELDPMLPR
9755	40123	A	9815	1	564	MGDLEDKLVPFIGELPRHLDQN SEQLKQVVQRELKELHETCQQ HQLCQASTSGEPKERDKEEGK DSKPRSLRFTWSMKTTSSMDPN DMMREIRKVLDANNCDYEQKE RFLLFCVHGDARQDS/LPCQWG DGKSCQVGPRLS\LNGV\RFKRI S\GTSYCPLKNIA\SKIA\NELKP VKKSQIYQVQGRYIHI
9756	40124	A	9816	2	451	ANAHGFIMELQDGYSTETGEK GAQLSGGQKQRVAMARALVR NPPVLILDEATSALDAESEYLIQ QAIHGNL\QKHTVLIIAHRLSTV EHAHLIVVLDKGRVVQQGTHQ QLACPRAGFYGKLVQRQMLGL QPAADFTAGHNEPVANGSHKA
9757	40125	A	9817	1	498	MVKY/YLGQGVLRSSW/DQVV PA/FWQRYRNPVQRYLTEDIVH RENQTMTTFTWNINHARPMVV EERCVYCVNSDNSGWTEIRREA WVSSSLCGVSRAVWEFGLAQF KSNVTKTLKGFEYILAKLQGEA ASKTLIKTAREAKEKAKETALA ATEKAKDLASKAATKKQQQ
9758	40126	A	9818	3	231	
9759	40127	B	9820	94	375	
9760	40128	A	9821	45	439	

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9761	40129	A	9822	304	1557	DRQNVMEQFNPGLRNLINLGK NYEKAVNAMILAGKAYYDGV AKIGEIATGSPVST\ELGHVLIEI SSTHKKLQRESLMENF\KKFHK EIIHELEKKIEL\DVKYMNATLK RYQTEHKNKLESLEKSQAELK KIRRKSQGSRNALKYEHKEIEY VETVTSRQSEI\QKSIADGCKEA LLERERGASCFPGLNKHCGFA/ NTHIHYYHLQSAELLNS\KLPR WQETCVDAIKVP\EKIMNMIEEI KTPASTPVSGTPQASPMIERSNV VRKDYDTLSKCSPKMPPAPSGR AYTSPLIDMFNNPATAAPNSQR VNNSTGTSEDPSLQRSVSVATG LNMMKKQKVKTIFPHTAGSNK TLLSFAQGDVITLLIPEEKDGWL YGEHDVSKARGWFPSSYTKLL EENETEAVTVPTPSPTPVRSFSG
9762	40130	B	9823	1	1128	
9763	40131	A	9824	1	434	
9764	40132	A	9825	92	319	SIPPYPIPPPVDRKEID*LEGMQT SGLFQQTSG*EEGVGSIMASGR PPHPEPLKADFICKREVRLAFSI ACIWMR
9765	40133	A	9826	1	851	
9766	40134	A	9827	227	305	LVIFSIFNLVG*NISDCIILICQLK
9767	40135	A	9828	66	808	YCWQSQGAKPRDLLGPDLIPLN HSPRVSHLLCHRHIRKAGGVFV ADEIQVGFGRVGKHFWAFQLQ GKDFVPDIVTMGKSIGNGHPVA CVAATQPVARAFEATGVEYFN TFGG\SPVSCAVGLAVLNVLEK EQLQDHATSVGSFLMQLLGQQ KIKHPIVGDVRGVGLFIGVDLIK DEATRTP\ELKRHVYLVSRLKE NYVLLSTDGPGRNILKFKPPMC FSLDNARQVVAKLDAILTDME EKVRSCENR
9768	40136	A	9829	3	597	

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9769	40137	A	9830	1	3281	MGFHHVGQAGLKLLTSGTPQL LALVQHWVPGARLVEELPHEL VLVLPYTGAHDGSFATLFRELD TRLAELRLTGYGISDTSLEEIFL KVVEECAADTDMEDG/TLRAA PMHRHCWPRRNPTAQDAATGD SAG\DGEPAGSAPETDQGSGPD AVGRVQGWALTRQQLQALLL KRFLLARRSRRGLFAQIVLPALF VGLALVFSLIVPPFGHYPALRLS PTMYGAQVSFFSEDAPGDPGR ARLLEALLQEAGLEEPP
9770	40138	A	9831	1	684	RTRGPPPQSRSGGRRRRIPLYLP TSCIKELVAGGVAVESWPGRD AAQLLLCSCLLSPPPVMTETRE PAETGGYASLEEDDEDLSPGPE HSSDSEYTLSEPDSEEEEDEEEE EEETTDDPEYDPGYKVK*RLGG GRGGPSRRAPR\AAQPPAQPCQ LCGRSPLGEAPPGTPRCTGTSCC MPGVRCRQSPHTGSLAEGVGW EEGAEEIGVVTVVMGDGVLPV CVVLEVDV
9771	40139	A	9832	1	670	MESDIGRKGGKDPEAGPEHSSD SEYTLSEPDSEEEEDEEEEEEET TDDPEYDPGYKVKQRLGGGRG GPSRRAPRAAQPPAQPCQLCGR SPLGEAPPGTPPCRLCCPATAPQ EAPAPEGRALGEEEEEPPRAGE GRPAGREKEEEEEEEGTYHCTE CEDSFDNLGEL\TGTSCCMPGV RCRQSPHTGSLAEGVGWEEGA EEIGVVTVVMGDGVLPVCVVL
9772	40140	A	9833	3	512	
9773	40141	A	9834	3	815	MLYSRGPQPMGHGPVLVCGLL GTGCTAGAQELREAYTSISSQID QAEERISEIEDKLNEIKREDKITE KRMKRNEQSLQEIWDYVKRPN LRLIGVPKSDVENGTKLENTLQ DIIQENFPNLARQANVQIQEIQR TPQRYSSRRATPRHIIVRFTKVE MREK\MLRAAREKGRVTHKGK PVRLTADLSAETVQARREWGPI FNILKGKNFQPRISYPAKLSFISE GEIKYFTDKQMLKDFVTT/RPA LKELLKEALNMERNNWYQPLQ KHAKL

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9774	40142	A	9835	1	561	MVNGRIPQAPSQFSHLARLHPA PSPNSDPSPFLAELLLMPSVIGL TPSYPSRFSSESTFLQEAFPDLC QAEDPVYANGGLNYSYRGYGA LSSNLQPPASLQTGNHSNGPTD L\SMKGGAFTTSTTPTPTPSSTST SRPVPTAQLSPTEISAVRQLIAG YRESAAFLLRSADELENLILQQ NRPRRHL
9775	40143	A	9836	2	226	KGVQFQFSSYG*PVFPTPFIK*G VLSPLFVFLRFLKDQMVVDV*H YF*GLCSVPLVYISVLVLVPCCF FFTVAL
9776	40144	A	9837	2	350	YKVSKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIP\R*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9777	40145	C	9838	213	365	
9778	40146	A	9839	1	1923	

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9779	40147	A	9840	1	2091	MVLVVVAVVVVVLVVAVIVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATQALLNFLATCGYKVSKPKA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEK\TGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPLEMLTEGPLAFELA MATARAELSLAIHHCCLPPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPQV REHEACHHLGSGLPPFWKWPT TILGALGARTPGNTGSTYTFIGY TYTSPVIFILSWQYVYFHGLYY
9780	40148	A	9841	1	1284	

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9781	40149	A	9842	1	1522	MVAPGSVTSRLGSVFPFLLVLV DLQYEGAECGVNADVEKHLEL GKKLLAAGQLADALSQFHAAV DGDPDNYIAYYRRATVFLAMG KSKAALPDLTKVIQLKMDFTA ARLQRGHLLLKQGKLDEAEDD FKKVLKSNPSENEEKEAQSQLI KSDEMQRLRSQALNAFGSGDY TAAIAFLDKILEVCVWDAELRE LRAECFIKEGEPRKAISDLKAAS KLKNDNTEAFYKISTLYYQLGD HDCSFSEFRDVLNLDQDHKR\C FAHYKQVKKLNKLIESAEELIR DGRYTDATSKYESVMKTEPSIA EYTVRSKERIC\HCF\SKDEK\PV EAI\RVCSEVLQMEPDNVNALK DRAEAYLIEEMYDEAIQDYETA QEHN\ENDQQIREGLEKAQRLL\ KQSQKRDYY\KILGVKRNAKK QEIIKAYRKLALQWHPDNFQNE EEKKKAEKKFIDIAAAKEVLSD PEMRKKFDDGEDPLDAESQQG GGGNPFHRSWNSWQGFNPFSS GGPFRFKFHFN
9782	40150	A	9843	5	519	LTCQEEHKKKHPDSSVNFVEFS KKCLERWKTTSAKEK/SKFEEK AKSDKARCDREIKNYIPPKCKK GRPPSAFFLFCSEHRPKIKSGHP GLFVVETAKKLGEMWSGQSAK DKQPYEQKAVKLQERYEKGIA AYRAKGKSEAGKKGSKKNKPE DEEEEEEKEDEDEEEEGEDEE
9783	40151	A	9844	1	3140	YSIATVLAAEEKLDPRRDEAKR LRPQRNFNITFTHGTVFRPLTLE STFFNSALLFTTIKQDLPPLPKTI ITNAFHRFRNHHQTGFKLSAAN QRGPLAATLSGPGGEGQSAVA RLTGEKKNHPGAQYANRLSPR VGRFINAAGTTGFPTGKRARSD SSLAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFY

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9784	40152	A	9845	2	604	FLELPPAAAAAVLSASPGALER EARSPRSPQTADTSPRPRAPAC APSRARAMPSDRPFKQRRSFAD \RCKEVQQIR\DQHPSKIPV\IIER YKGEKQLPVLDKTKFLVPDHV NMSELVKIIRRRLQLNPTQAFFL LVNQHSMVSV\STPIADIYEQEK DEDGFLYMVYASQETFGF*ASS PCLSAHLPLTHPRLCPPPGPAHP
9785	40153	A	9846	3	303	RDQHPSKIPVIIERYKGEKQLPV LDKTKFLVPDHVNMSELVKIIR RRLQLNPTQAFFLLVNQHSMVS VSTPIADIYEQEKD\EDGFL\YM VYGLPGKPFGF
9786	40154	A	9847	254	2110	
9787	40155	A	9848	234	1904	
9788	40156	A	9849	5	189	
9789	40157	A	9850	1	1546	MASASSQPSLAVGFSSFDPGAP SCTASSASGILSPTASEVPYASG MPIKKTGHRGVDSSGETTYKKT TSTALKGAIQLGITYTVGSLSTK PERDVLMQDFYVVESIFFPSEGS NLTPAHHYNAFRFKTYAPVAF RYFRELFGIPPDDYLCSLCSEPLI ELCSSGASGSLFYVSSDDELIIK TLQHKEAEFLQKLLPGYYLNLS QNPRTLLPKFFGLYCVQTGGKN IRIVVMNNLLPRSVKMHIKYDL KGSTYKRRASQKEREKPLPTFK DLDFLQDIPDGLFLDADTYNAL CKTLQRDCLVLQSFKIMDYSL WLSIHNIDHAQREPLSSDTLQV SIDTQRLAPQKALYSTAMEFIQ GEARLGDTMEADDHMGGIPAQ NSKGERLLLYIGIIDILQSYTFLK KLEHSWKAVVHDGDAVSVHR PGFYAERFQHFMCNAVFKKIPL KPSPSKKFRSGLSFSLHTGSSGN SCITYQPLVSEEHKSQVIKVQVE PGVHLGRSDVLPQTSE\PPLEEIT

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9790	40158	A	9851	233	2051	AGPGAGSTCLREARRGRGGGP QNAGSVKRRWEDSIPRRGRTGL KESQAAEGEGAAKMASASSGP SSSVGFSSFDPAVPSCTLSSASGI KRPMASEVPYASGMPIKKIGHR SVDSSGETTYKKTTSSALKGAI QLGITHTVGSLSTKPERDVLMQ DFYVVESIFFPSEGSNLTPAHHY NDFRFKTYAPVAFRYFRELFGI RPDDYLYSLCSEPLIELCSSGAS GSLFYVSSDDEFIIKTVQHKEAE FLQKLLPGYYMNLNQNPRTLLP KFYGLYCVQAGGKNIRIVVMN NLLPRSVKMHIKYDLKGSTYK RRASQKEREKPLPTFKDLDFLQ DIPDGLFLDADMYNALCKTLQ RDCLVLQSFKIMDYSLLMSIHNI DHAQREPLSSETQYSVDTRRPA PQK\ALYSTAMESIQGEARRGG TMETDDHMGGIPARNSKGERL LLYIGIIDILQSYRFVKKLEHSW KALVHDGDTVSVHRPGFYAER FQRFMCNTVFKKIPLKPSPSKKF RSGSSFSRRAGSSGNSCITYQPS VSGEHKAQVTTKAEVEPGVHL GRPDVLPQTPPLEEISEGSPIPDP SFSPLVGETLQMLTTSTTLEKLE
9791	40159	A	9852	30	298	EPFIFLFIYLFIYLFFETESRPVIQ AGVQWCNLSSLQPLPTGFKQFS \CLSPLTSWDYRHPPPCPANFCS FSRDGVSPCWPGWSQTPDLR
9792	40160	A	9853	3	938	
9793	40161	A	9854	208	870	LGMAGRLFTVNLQSPLNPSTLL AEVCVEQCTLMDSKMKPLWIM YSNEEAGSGGRVSVSLKRDDD LWQDMLTMQTIRLMDVPDTIA NIQLNNRNMDGGNEEFTLSCA GYCVATYVLGIGDRHSDNIMIR ASGQLFHIDFCHFRQRVPFILTY DFVHVIEQGKTNN/SEKFERFRG YCERA\YTILRRHGLLFLHLFAL MQAAGLPELSCSKDIRYLKDSL VHPL

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9794	40162	A	9855	1	790	VEELSKKLADSDQASKVQQQK LKVGQLGEWVWPLDKGGKLFS KLWGRGGLVYKWFLLIYKISY ATGIVGYMAVMFTLFGLNLLF KIKPEDAMDFGISLLFYGLYYG VLERDFAEMCADYMASTIGFY SESGMPTKHLSDSVCAVCGQQI FVDVSEE/EDH*EHRCS/CFHEF CIRGWCIVGKKQTCPYCKEKV DLKRMFSNPYPLLGSLLGVGCG KKVLASVTCIWVLLGPSLLPPT RTCQTMNNKKIMKVMMRIKR MMTDTMAS
9795	40163	A	9856	1	1005	FRGRAVKMAAVVEVEVVGGA AGERELDEVDMSDLSPEEQWR VEHARMHAKHRGHEAMHAEM VLILIATLVVAQLLLVQWKQRH PRSYNMVTLFQMWVVPLYFTV KLHWWRFLVIWILFSAVTAFVT FRATRKPLVQTTPRLVYKWFLL IYKISYATGIVGYMAVMFTLFG LNLLFKIKPEDAMDFGISLLFYG LYYGVLERDFAEMCADYMAST IGFYSESGMPTKHLSDSVCAVC GQQIFVDVSEEGDH\ETTYRLSC NHVSHEFCIRGWCIVGKKQTCP YCKEKVDLKRMFSNPWERPHV MYGQLLDWLRYLVAWQPVIIG VVQGINYILGLE
9796	40164	A	9857	28	267	LNIGKGDSKKPRGKMSSYAFFV QTCREEHKKQHPDASVNFSEFS YKKDIAAY*AKGKPDAAKKGFI KAEKSKKKKEEEED
9797	40165	A	9858	1	194	MGKGDPKKLRGKMSSYAFFVQ TCQEEHKKQQPDASVNFSEF/S KKCSERWKTMSAKEKSEDMA KL
9798	40166	A	9859	241	958	HQIFILFFRKITKHGQRRSLRSPR GKMSS\FAFF\VQTCREEHKKRH PDASVN\FSEFSKKC/SQRGWKT MS\SKEKGKF*RYGQKRDKAR YER\EMKTYYPS\KGGDQKRSF KDPNAPQGGPPFGPSFLF\CSEY RPKIKREDHPGLSIGDVAKKLG EMWELTLLQ/SDKQPYEKKAA KLKEKYEKDIAAYRAKGKPDA AKKGVVKAEKSKKKKEEEEDE EDEEDEEEEEDEEDEEDEEEDD

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9799	40167	A	9860	2536	2909	KSGVPGSRFSSSDKSDTGVTGL FSTYFLKSDFQLQLIDISASTAS KSLFSAVLFQEYILSFGLSEIISIL SSAVCWREAPKLSMVGCLAAG GKLTGC*AAGCLATDGRTETL DAAPAAAALSAV
9800	40168	A	9861	5	1752	KCTICLRNS/IAVCCGCGQGLSG YLNGEGADGAERGGGGSGVEC LRAPVCGQAASSLAASQLAAG GQAANHAQLRCLSPADCALML FIQVEVLTNSIAMVSVHLEKQP LKLVLGELGFRSPAGEEQATPV VGGEGLGCIEDSAAVAEGGIAI GGIVGINTALQEVLKPHTIKMQ RNNAQLSRRKEPKEGLCGERG QDRMSRAKGSSSKGKELPPGCR RVTMKPLLVRETQEGQAAERG AEEQLQTLGPFAVYRDSPSKNF YKRDKMLKGLEEAKVNFVWR TNEGFLEEDAGQEFGIQKAVTP ALCPSRKAEVPLSCLTLKLSED GKAKKAPYNTGPLGLLHLSMC SHSRKGFEQLWQLNSGKLLQG PRDSVEGSARRAETAVHCPAVL HFAPALLLAALRCQRDLESAAA PSHTRSCQHPRLLSGAVQTAGF SNPPKVVIQIKWNFLVMLLNFP GSTKLIARLKQQMNYKEMASQ RLTQSMLPHRSRLIGAGPCNRC VHPEPVIVTLFGQKVFARIIKKN QTCLLCSQIWCAHYQQGWICA WLAGFGKIYIFSTIGVIDTLSSG HIHLQPNCTARDSASWESPA
9801	40169	A	9862	1	668	MWRLVIQDAKDENGVLVGNR VLAHSSLAVLSCLALNNRRISG WTP/CGPSGSPPGFMGRRGTST/ RLPTG**CPEGQPPRCPCG*ASG CASSPAECRMPATHLPGNSGRV PFPPGPVNYSPLRLQAPEQVTG S/SPWPFS/RPVLGPLPLEGS\PPP F/RLPPRPRPAGVAAGSSWGHS AASVRRSPGRRPEGESIHPRPPA SRLPWLRATREEEAGAPKLGED SYPNF

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9802	40170	A	9863	2	624	FMGRRGTSTPFPLADNAPRGSP PGAHVVGGWDPDLRRAPVTGF SCSGSCSQRGAADWESFPRSPP CRASGCASSPAECRMPATHLPG NSGRVPFPPGPVNYSPLRLQAP EQVTGS/SPWPFS/RPVLGPLPLE GS\PPPF/RLPPRPRPAGVAAGSS WGHSAASVRRSPGRRPEGESIH PRPPASRLPWLRATREEEAGAP KLGEDSYPNF
9803	40171	A	9864	51	225	
9804	40172	A	9865	1	276	AFAAIPTNTLLLEQKALDEPAE TESVSKDNTL*PPVETPTTLPRA AGRETKYANLSSPTSTVSESQ/P D*AWSNSPSTCKIQNITEKRGGS L
9805	40173	A	9866	3	441	QTNFKGCSKVTSSKLNMSLLW TPTGR*GCDRKVEQGPPGDLGT AAVRPKSLAISSSLVS/ACSASK TQGTDLKTSSHPEMLHGMAPQ QKHGQQYKTKSSYKAFASIPYK HIAFGTEDS/STTLPRAAGRETK YANLSSPTSTVSESQAD
9806	40174	A	9867	123	417	SLDLDLFTVSGLLSLDSSGILTR NLEVSAN*VWVGSLLTVGTNV KIRGLASEPPAETVSFSSKFLFN KLLFSRFSSSILKENEKERKNER HRGSNSV
9807	40175	A	9868	153	1624	TTRRKSMNPTLSGKYLEDNSDL FSEQALDEPAKTESVSKDNTLE PPVELYFPAQLRQQTEELCATID KVLQDSLSMAPSLSPTKQASSS LAYMNVERTPSPTLKSNTMLSL LQTSTSSSVGLPPVPPSSSLSSLK SKQDGDLRGPENPRNIHTYPST LASSALSSLSPPINQRATFSSSEK CFHPSPALSSLINRSKRASSQLS GQELNPSALPSLPVSSADFASLP NLRSSS/APSCQSAHPGAPAQSL SSAPT\CGSGTLPSRLGKSESTTP NHRSPVSTPSLSISLTRTEELISP CALSMSTGPKNKKSKTPTTLPR AAGRETKYSKSNDYLTLNAGS QQERDQAKLTCPSEVSGTILQE REFEANKLQGMQQSDLFKAEY VLIVDSEGEDEAASRKVEQGPP GGIGTAAVRPKSLAISSSLVSDV VRPKTQGTDLKTSSHPEMLHG MAPQQKHGQASAYKGEESNEE DWTILKSSRMTNPRKLSDNKI
9808	40176	A	9869	1	762	

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9809	40177	A	9870	1	537	
9810	40178	A	9871	490	681	MGLVLLHVGKLGSSWLRNGSQ ETAGQIISPLSSWHDTGAGAAL DFSPGLSCLPVR*GSRRAAPH
9811	40179	C	9872	258	527	
9812	40180	A	9873	1	2865	MLPAFEHQTPSSSAFGLLNLQQ WFVRGSRAFGHRLKAALSGSL LLKFSDSDWLPCSSACRGPIVG LHLVIVYVKSHQNAYRHKNIQL KQTLLSCNTTKVRSFIIEVSETR NPPAGTNSGHILGTCPGYRYAK GKETGKEIIKGPQNPPGYRLCPL QAVGGGEFGPTQVHVPFSLSDL KQIRVDLGKFSDDPDRQYPLRP EAHEGLQDILRYLKVQGLVRK CSSPCNTRILGVQKPKGQWRLV QDLRFINEAVIPL
9813	40181	A	9874	3	177	
9814	40182	A	9875	255	1299	AAVFPLWCWRTRGKCHSLEWR PCTVCSWPDSPPKVSAGQALCG SETLPLTQTPDIQVPATLESGHP ANLL\VSAAWKSRKSLIFSWTW GTVISLGPRTPHFSEITIIPLPWS HGSSITFQVTFPRFHVTTEMTIQ LNVSSPVALENATSLSVLKNQS LRFVYVTDSNPPARLSWTWEG QALNLSQSSESAVLELPPVESC DGGEFVCQAQHPLGSQHVSISL SVQSDSVISIEEGVLQTLGFTLIR GILMGTSCTFICGFTWICCTSPVI PKPGTQSCFSTRDSATLPDACG SPGPKRVWMCSESHQPLCAVP DEDEQELHYAVLHFHKVQPQE PKVTDTEYSEIKIHK
9815	40183	A	9876	27	385	ASTTTGSGTSTAAARCTAWSPG PLVTAVEKFEAEAAALGQRIST LQKGSPDPLQVRMLNDQLMLL ERTFLNPRAFPEERYYSHVLWA /PSHGLRSHIPG\LSNACSRARDT ASGSEAWAEG
9816	40184	A	9877	160	480	
9817	40185	A	9878	19	433	GLDHGWAGDRWRTRPVVGAG EGRAPRLNSPSGQIRSPGPGDLS IYDNWIRYFNRSSPVYGLVP\GF SSHQAVARTAGSVILRLSDSFFL PLKVSDYSETLRSFLQAAQQDL GALLEQHSISLGPLVTAVEKFE AKAAAL

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9818	40186	A	9879	1	996	MALSKERSTVTRTQWARKTML QGETIQISESVSTYLRPYSVSGT VLGTNMSKTSARIYPTYHTAFD TFDYVDKFLDPGFSSHQAVART AGSVILRLSDSFFLPLKVSDYSE TLRSFLQAAQQDLGALLEQHSI SLGPLVTAVEKFEAEAAALGQR ISTLQKGSPDHVLWA/PSHGLRS HIPG\LSNACSRARDTASGSEA WAEVQRQLSIVVTALEGSVEAL HEVLQLPAALRACPPLRKALAV DAAFREGNAARLFRLLQTLPYL PSCAVQCHVGHARREALARFA RAFSTPKGQTLPLGFMVNLLA WMDSGKHGTCARPTGCPWTER RELCS
9819	40187	A	9880	66	744	RAHEDRERSGVQIRTQSWNGG KREKDFLHQSG\LETLLMKGC WRKSKTSARIYPTYHTAFDTFD YVDKFLDPGFSSHQAVARTAG SVILRLSDSFFLPLKVSDYSETL RSFLQAAQQDLGALLEQHSISL GMHSPDPEVRMLNDQLMLLER TFLNPRAFPEERYYSHVLWA/PS HGLRSHIPG\LSNACSRARDTAS GSEAWAEVQRQLSIVVTALEG AAATLRPVADL

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9820	40188	A	9881	2	2241	PRVRRMQWTKVLGLGLGAAA LLGLGIILGHFAIPKKANSLAPQ DLDLEILETVMGQLDAHRIREN LRELSREPHLASSPRDEDLVQL LLQRWKDPESGLDSAEASTYE VLLSFPSQEQPNVVDIVGPTGGI IHSCHRTEENVTGEQGGPDVVQ PYAAYAPSGTPQGLLVYANRG AEEDFKELQTQGIKLEGTIALTR YGGVGRGAKAVNAAKHGVAG VLVYTDPADINDGLSSPDETFP NSWYLPPSGVERGSYYEYFGDP LTPYLPAVPSSFRVDLANVSGF PPIPTQPIGFQDARDLLCNLNGT LAPATWQGALGCHYRLGPGFR PDGDFPADSQVNVSVYNRLEL RNSSNVLGIIRGAVEPDRYVLY GNHRDSWVHGAVDPSSGTAVL LELSRVLGTLLKKGTWRPRRSI VFASWGAEEFGLIGSTEFTEEFF NKLQERTVAYINVDISVFANAT LRVQGTPPVQSVVFSATKEIRSP GPGDLSIYDNWIRYFNRSSPVY GLVPSLGSLGAGSDYAPFVHFL GISSMDIAYTYDRSKTSARIYPT YHTAFDTFDYVDKFLDPGFSSH QAVARTAGSVILRLSDSFFLPLK VSDYSETLRSFLQAAQQDLGAL LEQHSISLGPLVTAVEKFEAEA AALGQRISTLQKGSPDPLQVRM LNDQLMLLERTFLNPRAFPEER YYSHVLWAPSHGLRSHIPG\LS
9821	40189	A	9882	1	1962	
9822	40190	A	9883	1	166	MEYYAALKKDEFMSFVGTWM KLETIILSKV\CQGQKVKHHMFS LTGALLVRGPWA
9823	40191	A	9884	1	378	
9824	40192	A	9885	1	681	
9825	40193	A	9886	1	3174	MEYYAAIKNDEFMSFVGTWM KLETIILSKLLQGQKTKHRMFSL IGSIIVKVPSSLQAHLQLSGKEV DVNSEVHVQEMAEARKDDVV TVTDAEKALDKIQHLFMVKTLS KIGIQGTYLNVIKAIYDKPTANII LNGEKLKAFPLRNETRQGCPLS PLLFNTVLKVLARAVRQEKEIK GIQIGKEEVILSLFADDMIVHLE NPIVSAQNLLKLIDNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASER
9826	40194	B	9887	1	352	

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9827	40195	A	9888	3	430	FFFFLPVAGLRRPRPRLGPVPPR PRVPPPQDRAATMKKFFQEFKA DIKFKSAGPGQKLKESVGEKAH KEKPNQPAPRPPRQGPTNEGTD GSRCCPQP/WLEQKQSRAWGPH IAGHHPKPGEKGTSSRSHRQRE PRGPRDQRGI
9828	40196	A	9889	1	1062	MKKFFQEFKADIKFKSAGPGQK LKESVGVWGRPNGLMSVKGN CECGNLWLLYPEVAALAAEAE GPEVGSVEDQRRQQGYFVRLG SLSARIRHLAYEHSVGKLRQSK HRAQDTLAQLQETLELVDHMP CGVTPTAPARPGKVHELWGEW RQRPP/REPPPE\QAELETLVLAR SLTHELQGTVEALEFSVWGLPA GAQEKVAEVRRSVDALQTAFA DARCFRDVPAAALAEGRGRVA HAHACVDELLELVVQAVPLPW LVGPFAPILVERPEPLPDLADLV DEVIGGPDPRWAHLDWPAQQR AWEAEHRDGSGNGDGDRMGV AGDICEQEPETPSCPVKHNPDA RAGLLTHGPVEAG
9829	40197	A	9890	11	285	
9830	40198	A	9891	2	138	FFFLGFHVFYSIPLIPRDNSF*GV FSSLDLITAVFVTLAELRSVT

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9831	40199	A	9892	121	2320	EMAFQKAVKGTILVGGGALAT VLGLSQFAHYRRKQMNLAYVK AADCISEPVNREPPSREAQLLTL QNTSEFDILVIGGGATGSGCAL DAVTRGLKTALVERDDFSSGTS SRSTKLIHGGVRYLQKAIMKLD IEQYRMVKEALHERANLLEIAP HLSAPLPIMLPVYKWWQLPYY WVGIKL\YDLVARKANCLKSSY VLSKSRALEHFPMLQKDKLVG AIVYYDGQHNDA\RMNLAIALT AA\RYGAATANYMEVVSL\LKK TDP\QTGK\VHVSGARCKGCPST GQEFDVRAKCVINATGPFTDSV RKMDDKDAAAI\CQPSAGVHIV MPGYYSPESMGLLDPATSDGR VIFFLPWQKMTIAGTTDTPTDV THHPIPSEEDINFILNEV\RNYLS CDVEVRRGDVLAAWSGIRPLV TDPKSADTQSISRNHVVDISESG LITIAGGKWTTYRSMAEDTINA AVKTHNLKAGPSRTVGLFLQG GKDWSPTLYIRLVQDYGLESEV AQHLAATYGDKAFEVAKMAS VTGKRWPIVGVHLVSEFPYIEA EVKYGIKEYACTAVDMISRRTR LAFLNVQAAEEALPRIVELMGR ELNWDDYKKQEQLETARK\FL YYEMGYKSRSEQLTDRSEISLL PSDIDRYKKRFHKFDADQKGFI TIVDVQRVLESINVQMDENTLH EILNEVDLNKNGQVELNEFLQL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9832	40200	A	9893	1	2020	MLKPLMGGGAHRRAAAGARK WDGTAIIASTSGLEVLWVTTSR SKTVESVGLAKPGQHNDARMN LAIALTAARYGAATANYMEVV SLLKKTDPQTGKVRVSGARCK DVLTGQEFDVRAKCVINATGPF TDSVRKMDDKDAAAI\CQA\SA GVHIVMPGYYSPESMGLLDPAT SDGRVIFFLPWQKMTIAGTTDT PTDVTHHPIPSEEDINFILNEVR NYLSCDVEVRRGDVLAAWSGI RPLVTDPKSADTQSISRNHVVDI SESGLITIAGGKWTTYRSMAED TINAAVKTHNLKAGPSRTVGLF LQGGKDWSPTLYIRLVQDYGL ESEVAQHLAATYGDKAFEVAK MASVTGKRV/WPIVGVRLVSDF PYIEAEVKYGIKEYACTAVDMT SRRTRLAFLNLQAAEEALPRLL ELMGRELNWDDYKKQEQLET ARKFLYYEMGYKSRSEQLTDR SEISLLPSDIDRYKRRCHKFDAD QRGFMTVVEVQRVLESINVQM DENTLHEILNEVDLNKNGQVEL NEFLQLMSAIQKGRVSGSRLAI LMKTAEENLDRRVPIPVDRSCG GLYFCVRNWWVLGLTDFKNE AADPSGVKLQTFTVSVTALKV ARLELFVSPGGLVVLLGSGVKL QIFAPNMAMHNKAAPPQIPDTR RELAELVKRKQELAATLAKFG
9833	40201	A	9894	2	593	ISSAVEFETSQLSGLWTEQSAA RSRGENIVCGPQGPRG/GPWVP AEPTGSPVVSEEPLDLLPTLDLR QEMPPPRVFKSFLSLLFQGLSVL LSLAGDVLVSMYREVCSIRFLF TVVSLL\NLFLSAFWLGLLYLVS PLENEPKEMLTLSEYHERVRSQ GQQLQQLQAELDKLHKEVSTV RAANSERGAKLVFQRLNEGFV

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9834	40202	A	9895	1	1105	MRRSSRPGSASSSRKHTPNFFSE NSSMSITSEDSKGLRSAEPGPGE PEGRRARGPSCGLLFQGLSVLL SLAGDVLVSMYREVCSIRFLFT AVSLLSLFLSAFWLGLLYLVSP LENEPKEMLTLSEYHERVRSQG QQLQQLQAELDKLHKEVSTVR AANSERVAKLVFQRLNEDFVR KPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPP TVILEPHVFPGNCWAFEGVQGQ VVIQLPG/HECTLSDITLQHPPPS VEHTGGANSAPRDFAVFFLLSF FTHQGLQVYDETEVSLGKFTFD VEKSEIQTFHLQNDPPAAFPKV KIQILSNWGHPRFTCLYRVRAH GVRTSEGAEGSAQGPH
9835	40203	A	9896	10	395	VEPGKRLIDRIVETICSCFQGPQ TDEGVQLQIIKALLTAVTSPHIEI HEGTILQTVRTCYNIYLASKNLI NQTTAKATLTQML/NHARSDSG KVSTENGDAPRERGSSLSGTN\ DGAQEVVKDILEDVVT

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9836	40204	A	9897	1	1698	MLGTSVEDIAQFLHQEERLDST QVGDFLGDSARFNKEVMYAYV DQLDFCEKEFVSALRTFLEGFR LPGEAQKIDRLMEKFAARYIEC NQGQTLFASADTAYVLAYSIIM LTTDLHSP/PDLEMHQPAGARS ADRNRCEDALPVWIWA*KRRE PEGPHIGRRRVHGPWPR*FGEW RSG*KTDGQLPRIGW*DQLAEC GCSCGQDFYWVYQTGWKCNS* LCPLAVCCVHG*TGFPPPSSHV QLAEDCGDIILQHESDPTTVVS NMACDWRSLQ*DKL*MLGTSV EDIAQFLHQEERLDSTQVGDFL GDSARFNKEVMYAYVDQLDFC EKEFVSALRTFLEGFRLPGEAQ KIDRLMEKFAARYIECNQGQTL FASADTAYVLAYSIIMLTTDLH SPQILKCISQLELAQLIGTGVKT RYLSGSGREREGSLKGHTLAGE EFMGLGLGNLVSGGVDKRQM ASFQESVGETSSQSVVVAVDRI FTGSTRLDGNAIVDFVRWLCA VSMDELASPHHPRMFSLQKIVE ISYYNMNRIRLQWSRIWHVIGD HFNKTSCDRLRELHVSEVFTVI TETRETKGPRDTPIFIETLVKVK DAEDQLGARVGYIELDLNSGKI LESFRPEERFPMMSTFKVLLCG AVLSRIDAGQEQLGRRIHYSQN DLVEYSPVTEKHLTDGMTVRE LCSAAITMSDNTAANLLLTTIG
9837	40205	A	9898	1	492	
9838	40206	A	9899	1	3555	
9839	40207	A	9900	1	4145	MFVLKVGCPSLLLRDPRRSLLH YTCFTSVPVLVQVGCNPNEDV AIFAVDSLRQLSMKFLEKGELA NFRFQKDFLRPFEHIMKKNRSP TIRDMAIRCIAQMVNSQAANIR SATIFQHHFPAAIDSFQDAVKCL SEFACNAAFP\DTSMEAIRLIRF CGNYL\SERPRVLLEYTSDDMN VAPGDRVWVRGWFPILFELSCII NRCKLDVRTRGLTVMFEIMKS YGHTFEKHWWQDLFRIVFRIFD NMKLPEQLSEKS

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9840	40208	A	9901	1	5477	MQESQTKSMFVSRALEKILADK EVKRPQHSQLRRACQVALAWK LLLIAPLAVGKATPVKMWSNK VEQLTVMNMHSAEQETDEIKA EIEKQRLGTAAPPKANFIEADK YFLPFELACQSKSPRVVSTSLDC LQKLIAYGHITGNAPDSGAPGK RLIDRIVETICSCFQGPQTDEGV QLQIIKALLTAVTSPHIEIHEGTI LQTVRTCYNIYLASKNLINQTT AKATLTQMLNVIFTRMENQVL QEARELEKPIQSK
9841	40209	A	9902	2	740	TGWEGRAEAEVPQDDRREPRH S/IEVEEEDQKLVSASLEPIGG/P PDCPQKPQ\PQCPLSPSKKWGC DLCL*QHKLAQKWRREISTSVP SQPGLGPGRTADTGPSLPT\TPA GQEAGRTPAPPAWSAFDLDST VVKMEKGWICS*KYTRSQASC SELPRRLGRAGPTEELGMPTQE VAPLPARG*GPESLPL/ASRQEF LSGRTVRVKLGLPLPLTEGKIV LPGGEGGSPHVCPSPWIIERRTA DQGVVAE
9842	40210	A	9903	1	1376	MPSSSVGPARPSLRGSSEQLAW LRGIFSYRSSPPPSPQQSSPNQTR SRQHYAPSVFEKYTASVTVGSK EVTLNLYDTAALAGPWPALHS WRPLRGAGCGALEAKPYTKQ WAALGPPMVPGLLRYLLWSLQ TLATPGQRPREGPHAHTPRAEA TAGQEPARDPKGSARNPEPQRP RGKGVRAAPKQGVRGMSIPAQ PHASTRAGSERRSE\QRRLLSSF TGSCDSDLLKFNQLKFRKKKLK FCKSHIHDWGLFAMEPSGDPLE SAWIHARNAPTTTPSQTPHPPPR EAGNPNPPPRAPEARGPGHDKA AQKACVHGGPNTQHPRPQPEP AVPPAALAPPPKHQLSSQASSPS RLGRAAERPHKTQQRQTPTHT GPRAAATAEHAPQALPPPAPAP HYNRTRPAQLRNPPTPKKGSEE PAQPTKHTPATPAKRDPKGGG ARRRPARPLQPHSGGEEDEKES

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9843	40211	A	9904	724	2076	KLCPCLYHFFHTNVQRHAPFVA NPFLLTHIQISTKHPAIVGTTELL LCVGGVQRVLQLAPQRLQLLA QVPALLLRLGPGHTLRLQVLLG LGQGCLSLPQGFQQLGPGPTLV FCPLPELLEEDAVGEALATDAD ALQDPVAAKLVQHQPWLQLPG LGKQPPPLPVSQLEVGRAVPLH HPQGALLLLALLEGLQSLLPRV HSPFLHDTFRRHRPVPASLQLN SFEQLCITTPQKLQQLFNHTMF VSPPAVNVQANPAGLLALLDEE CWFPKATDKSFVEKVAQEQGG HPKFQ\RPRHLRDQADFSVLHY AGKVDYKANEWLMKNMDPLN DNVAALLHQSTDRLTAEIWKD VEGIVGLEQVSSLGDGPPGGRP RRGMFRTVGQLYKESLSRLMA TLSNTNPSFVRCIVPNHEKRAG KLEPRLVLDQLRCNGVLEGIRI CRQGFPNRILFQEFRQ
9844	40212	A	9905	2	480	VGCMGCSKGPWRQAFQVDVH VSDLALPQCRLQTGMRGAFGK PQGTVARVHIGQVIMSIRTKLQ NKEHVIEALRRAKFKFPGRQKV CSAAAPFSHLCPRPPDSVLSIAP *IHISKKWGFTKFNADEFEDMV AEKRLIPDGCGVKYIPSRGPLD KWRALHS
9845	40213	A	9906	1	485	SDEYDQLCSEALVGAQICAKK YIVKCCGKNGFHIRVRLHPFHV ICINRMLACAGTDRLQTGMGG AIGKP\QGTVARILIGQVIMSIRT KLQNKEHVIEALRRAKFKFPGR QKIHISKKWGFTKFNADEFEDM VAEKRLIPDGCGVKYIPSRGPL DKWRALHS
9846	40214	A	9907	198	452	DYYLEGLINHIVHHDHFLNLQN HSSNLPVAEICYR*RYRKKVQQ RIIIAKDYTTELFSNR*LFN

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9847	40215	A	9908	2	1968	SYLHCKWATMEELEKDPRIAQ KIKRFRNKQAQMKHIFTEPDED LFNPDYVEVDRILEVAHTKDAE TGEEVTHYLVKWCSLPYEEST WELEEDVDPAKVKEFESLQVLP EIKHVERPASDSWQKLEKSREY KNSNQLREYQLEGMNWLLFN WYNRKNCILADEMGLGKTIQSI TFLSEIFLRGIHGPFLIIAPLSTIT NWEREFRTWTEMNAIVYHGSQ ISRQMIQQYEMVYRDAQGNPL SGVFKFHVVITTFEMILADCPEL KKIHWSCVIIDEAHRLKNRNCK LLEGLKLMALEHKVLLTGTPLQ NSVEELFSLLNFLEPSQFPSETA FLEEFGDLKTEEQVKKLQSILKP MMLRRLKDDVEKNLAPKQETII EVELTNIQKKYYRAILEKNFSFL TKGANQHNMPNLINTMMELRK CCNHPYLINGAEEKILEDFRKT HSPDAPDFQLQG\MIQA\AGKL VLIDKLLPKLIAGGHKVLIFSQM VRCLDILEDYLIQRRYTYERIDG RVRGNLRQAAIDRFCKPDSDRF VFLLCTRAGGLGINLTAADTCII FDSDWNPQNDLQVPEGRIQKV WEQMSWPRAQPQDNAAAACL QDFGSQLGVQSEETGPFHNRQK QDSGNSHTAPRGRESFIKPPSSR DLLPLKIQKEGPATNYNS
9848	40216	C	9909	223	402	

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9849	40217	A	9910	1	1710	MFEKAARQEWIQVAKSVTRVA MSSYTFQKNPDLISVGEDVEKK LELSYAAVTMAWGQYGDYGY PYQQYHDYSDDGWVNLNRQG FSYQCPQGQVIVAVRSIFSKKE ADSVSRASATGPDSGQFFLLER VGTCKTTAEAQPQRDDPYLVT RTVEGLSRTVEGVGRGLTQAA AGEGAGAVEAAW/NSLCGPFSS TPMASDEETEAIRGHETRPDDT AKNSGAIQQHSQCSWPLYY/RA PHSVKRYQTCSNNGLVAGFQS RYFESVLDREWQFYCCRYSKR CPYSCW/LSLAADQTLMTPGVG EAPRKCSSFRKGNRTIEPALTGP KSPTYSVGMPSLKLRPNDSHPS AVLLLPNFWLTTEYPGHYGEE MDMISYNYDYYIRGATTTFSAV ERKEERRERKGIGDKKHTEPTV LVWAAIPHYLRLGNLRTIEIYFH SSGSWKVQDQVDPEEEPARQN HRDRVPCHTPPLGGQEGDSQPV VMRAKDHYELEKQKALGQVE DEEDLCQQQRLPEQTYGSEEAP QEAKKNLGSPEPNSQAGAQKPI SMATNRAVFDVTCNFSPHWLQ CLQSRSLSPEDPGL
9850	40218	B	9911	101	1237	
9851	40219	A	9912	1	622	NLSDRHRGSHLESQHFQRLKQE DLLSPRIQDQPGQHWETLSHINI VVIGHVDSGKSTTTGHLIYKCG GIDKRTIEKFEKEAAEMGKGSF KYAWVLDKLKAER\ERGITIDIS LWKFETSKYYVTIIDAPGHRDFI KNMITG\TSQADCAVLIVAAGV GEF\EAGISK\NGQT\REHALPG/ YSQKRYEEIVKEVSTYIKKIGYT PDTVACVP
9852	40220	A	9913	1	762	VVQTQISKTADELISYWGTSFPP PFAASLTLYELEYCITIDISLWK FETSKYYATVIDAPGHRDFIKN MITGTSQADCAVLIFAAGVGEF EAVTFAPVNVTTEVKSVEMHH EVLSEALPGDNVDFDVKNVSV KEVHHGNVAGQISAGCAPVLD CHMAHIACKFAKLKKKTGSTS GKKLEDGPTFLKSGDAAIVDM VPGKPMCVESFSVYPPLSRFAV CDMRQTVAVGVIEAMDKMAA\ GAGKVTMSAQKAHNAK

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9853	40221	A	9914	1	618	MVQARPGAHPTLLPGPTAAWV SGFSGGGSDLTGAREAQERGR WSPTESSSASVSPVAKVSKFTLS SELEGGDYPKERERTGGGPGRP PDWTPHGTGA\LQSPHPRTAPA PHPTPCPGRPRDAGQRSPGAPA WSPRVHRPTPSLLPPRRWTAAA LWAAWQRPLPASQPGRGTSPG NPGPGRTPPSPQEVGSPGHIHIS LRTGFPPTL
9854	40222	C	9915	3	406	
9855	40223	A	9916	1379	2096	NGGGCGAARGGAAPGEGTRRG ACWATRGLPGTGRSAAAPARR GERQQLAMDVFLMIRRHKTTIF TDAKESSTVFR/ELKRIRRGQSS KRPPDEQRL\YK\DDQLLD\DG\ KTLGECGF\TSQNRHRPQAPAT VGSGLPASSAASSTDDTFEALCI EPFSS\PPEL\PDVDGRPQGFGEG SAQLNKAVQVETPQEGPIFPQL KGDLGSLPGCCLFFPPLPGMGP TPCGLLLGLVLGSSCAVLSPRS
9856	40224	A	9917	1	695	MAHAGRTGYDNREIVMKYIHY KLSQRGYEWDAGDVGAAPPG AAPAPGIFSSQPGHTPHPAASRD PVARTSPLQTPAAPGAAAGPAL SPVPPVVHLALRQAGDDFSRRY RGDFAEMSSQLHLTPFTARGRF ATVVEELFRDGSVNREMSPL\V DNIALWMTEYLNRDLHTWIQD NGGWPWDFLIGATTPVTIPYLP YHSTEECQLINVKGTAEFKIPFA KPDEMIQAKIIDGC
9857	40225	A	9918	3	422	CSLKNWREVLALLLTYSGTEKF PELC\DLMEKVMVLNRSLEQLR GPH/GGSAVLGQQSPPFPFPRIV VGATLHSKETSSYRLGSQPSHQ VPTPSPRPRVFTPQSSPAMPLAP SHPSPYQGPRTQNISDYRAPGP QAIQPLPL
9858	40226	A	9919	1	849	

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9859	40227	A	9920	3	868	NSSPPFPFPRIVVGATLHSKETS SYRLGSQPSHQVPTPSPRPRVFT PQSSPAMPLAPSHPSPYQGPRT QNISDYRAPGPQAIQPLPLSPGV RPGPQDSWKEAPAPRGNLQRN KLPETFMPPAPITGPS/IM/RPHP* ATRDSSLTAPLSPV*VMLPQEF QENS\PAGDKDNVFPSLGKPPSP PCVQVMVDGPHSSR/PCAEGD WVQVPGVLTAEKGRLLISPTLL *WEQCDCESLGTSP*GSHEKDS LPLWPFSLLLYQQLQHLPPEKM ERKELPPEHQSLKSSFEALLQRC
9860	40228	A	9921	1	307	MKLKELERPAVQAWSPASQYP LYLATGTSAQQLDSSFSTNGTL EIFEVDFRDPSLDLKHRGVLSA LSRFHKLVWGSFGSGLLESSGV IVGGGDNGMLILYNVTHILSSG KEPVIAQKQKHTGAVRALDLN PFQPPEDIKALSWNRQAQHILSS AHPSGKAVVWDLRKNEPIIKVS DHSNRMHCSGLAWHPDIATQL VLCSEDDRLPVIQLWDLRFASS PLKVLESHSRGILSVSWSQADA ELLLTSAKDSQILCRNLGSSEPC PRLVFISQVTTESEFLMRSAELQ EALGSGNLLNYCQNKSQQALL QSEKMLWQFLKVTLEQDSRMK FLKLLGYSKDELQKKVATWLK SDVGLGESPQPKGNDLNSDRQ QAFCSQASKHTTKEASASSAFF DELVPQNMTPWEIPITKDIDGLL SQALLLGELGPAVELCLKEERF ADAIILAQAGGTDLLKQTQERY LAKKKTKISSLLACVVQKNWK DVVCTCSLKNWREALALLLTY SGTEKFPELCDMLGTRMEQEGS RALTSEARLCYVCSGSVERLVE CWAKCHQALSPMALQDLMEK VMVLNRSLEQLRGPHGVSPGP ATTYRVTQYANLLAAQGSLAT AMSFLPRDCA/PAARDIYAPSTN YCSSYEPHP*ATRDSSLTAPCLQ SASAPAT*EDGKEGAAPRASVL EEQL*GASPTLLPVCN*LKDKK

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9861	40229	A	9922	3	2751	SVSWSQADAELLLTSAKDSQIL CRNLGSSEVVYKLPTQSSWCFD VQWCPRDPSVFSAASFNGWISL YSVMGRSWEVQHMRQADKISS SFSKGQPLPPLQVPEQVAQAPLI PPLKKPPKWIRRPTGVSFAFGG KLVTFGLPSTPAHLVPQPCPRL VFISQVTTESEFLMRSAELQEAL GSGNLLNYCQNKSQQALLQSE KMLWQFLKVTLEQDSRMKFLK LLGYSKDELQKKVATWLKSDV GLGESPQPKGNDLNS
9862	40230	A	9923	363	543	
9863	40231	A	9924	2	737	EAETEYFVRCIKHMFTNHIVFQ LFHLLTFQFDCTNTLNDQLLEK VTVQMEPSESYEVLSCIPAPSLP YNQPGICYTLVRLPDDDPTAVA GSFSCTMKFTVRDCDPNTGVPD EDGNDDEYVLEDLEVTVSDHIQ KVLKPNF\AAAWEE\VGDT\FEK EETFALSSTKTLEEAVN\NIITFL GMQPCERS\DKVPENQD\SHSL YLAGIFRGGYDL\LVRARLALA DGVTMQVTVRCKHRTPVDIILA
9864	40232	A	9925	327	464	GSPTTRPAKPLTLSSGHLRSRPR WAEGPQYHLP*ISAPRAKLGV MM
9865	40233	A	9926	2	1179	WQPDIGPYGGLLNVVVDGLFII GWMYLPPHDPHVDDPMRFKPL FRIHLMERKAATVECMYGHKG PHHGHIQIVKKDEFSTKCNQTD HHRMSGGRQEEFRTWLREEWG RTLEDIFHEHMQELILMKFIYTS QYDNCLTYRRIYLPPSRPDDLIK PGLFKGTYGSHGLEIVMLSFHG RRARGTKITGDPNIPAGQQTVEI DLRHRIQLPDLENQRNFNELSRI VLEVRERVRQEQQEGGHEAGE GRGRQGPRESQPSPAQPRAEAP SKGPDGTPGEDGGEPGDAVAA AEQPAQCGQGQPFVLPVGVSSR NEDYPRTCRMCFYGTGLIAGH GFTSPERTPGVFILFDEDRFGFV WLELKSFSLYSRVQATFRNAD APSPQAFDEMLKNI\QSLTS
9866	40234	A	9927	287	537	TGKFPSC/CLLSFYGTGLIAGHG FTSPERTPGVFILFDEDRFGFVW LELKSFSLYSRVQATFRNADAP SPQAFDEMLKNIQSLTS
9867	40235	A	9928	1	3651	

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9868	40236	A	9929	1	3720	MEEMFGGGAADDYGKAGPPE DEGDPKAGAGPPPGPPAYDPY GPYCPGRASGAGPETPGLGLDP NKPPELPSTVNAEPLGLIQSGPH QAAPPPPPPPPPPAPASEPKGG LTSPIFCSTKPKKLLKTSSFHLL RRRDPPFQTPKKLYAQEYEFEA DEDKADVPADIRLNPRRLPDLV SSCRSRPALSPLGDIDFCPPNPG PDGPRRRGRKPTKAKRDGPPRP RGRPRIRPLEVPTTAGPASASTP TDGAKKPRGRG
9869	40237	A	9930	503	739	QGWRRRRPISKISESRNMQNFL HALSNCLPEGGA*DRCSSRLEE GRQLPPLLLGSLQVAKKSGGTG WMVRCSQCLFLG
9870	40238	A	9931	1	1148	MGGKGDDSWVISATPLGKCCA AVPLGGNPTLRVDQLWRKQRP PLQQCTASAPGGWVTSLMGAG THAANTGFQLVWSSKRPMYKV LQAFFGVQRSDRSAMNGQGFS KCVGMPITHTRQQADLGRGPE ETEDKKQQSRGSDELRSEGEEP EPYLLRTSK\VKDKERILKAARE MKQIIYNGAPIHLAADFSVETL QAKKEWCDIFKVLKKKTFYPK MVLTAGPSHPQSVISVSFTGLA NAASLTMSPDLHGQPGFAGLSS VAAVDWQWALLRPSPPQGRM GLLPICQATQGPQLCVASPSDK EGFLLLFGKEIARLTNKGGARL YKCDIVQGVCCEDPLATLDWE LRPDLEQGERPTPERHKPFLLG KSFSAPLIKICRYEWQMF
9871	40239	A	9932	333	689	NSFLTCILPPVSI*TDLLQPSAQ WKQLSLARRNVHSTRLAGARR CAASGPSPVAAHCYHPVSGHSR LLHGCQHGHWGSWQVPEVPPG SPFSLAPVWKRRQTALPAILHL PVEHYYPEL

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9872	40240	A	9933	84	933	PLTSPEAFSNRCGLRGPP\PCVP VGRLQF\NDVSSLGICLPDSSCC SSWHGPHSLHH/HVQACKASIR ASGTAASANCAFSRYHVHCSIA FQIKVLHNLIVLTVIIPAAEHMA WGPGIAQPNPPHRASGHSSWGP EVGPKLSTTAILVGTYPQVPPV GLETGPPSLFQPLPISTHTAWNT ENCPANATVIAHPTLAAQGTKN PPTLLVHHCHYQHLSLKDDGT RRENSLKLGEGKVILQTEGIQK GMDPTMEYATNYWKKLQLWK RRQTALPAILHLPVEHYYPEL
9873	40241	A	9934	1	627	MESLDTETSTWGECHRKIRGM VPQVKELAEEEEAPPDGAVAE YRREKQKYEALRKQQSKKGTS REDQQIIIKNLPCTNHCIWQSTH EHIPALSDLSGKRAKQVIPVKG GEHYERTLALLNQFKSKLTQAI AETPENDIP\ETEV\EDDEGWMS HVL\QFEGKSRKSGKVPSMQDS DTFEIYDPRNP/LVNKRREGKK AKSLMREKKERRLK
9874	40242	A	9935	1	371	PMRPAFTRVEMARVLMERNQY KERLMELQEAVRWTEMIRASR EHPSVQEKKKSTIWQFFSRLFSS SSSPLRPKRPYPSVNIHYKSPTE GCSV\AAGFSPPPCHLHCDVCPL PRLFPQDLEVTPG
9875	40243	A	9936	2	186	
9876	40244	C	9937	109	408	
9877	40245	C	9938	161	341	
9878	40246	C	9939	303	439	
9879	40247	C	9940	201	419	
9880	40248	C	9941	122	307	
9881	40249	A	9942	3	80	YNPAPYKEKTITL/PCPRKLGPP QGS/S*NGPPSSSSSSQCSVSFND PHLPEGQVQAAR*WAPPGIL
9882	40250	C	9943	249	427	
9883	40251	A	9944	90	244	TVVPHDPCGTDAHVCETHMD MCPSHSVMLCGWLTFAEFRGA MGEGGRESFLLNQASFCY*CSQ AGFSSNLWRCSRAGRGNTADE LWCHMTLVAQMPTYVKHTWT CVPATVLCSVAGSPLLSSGVQW GREGGKASS
9884	40252	C	9945	4	204	
9885	40253	C	9946	340	497	
9886	40254	C	9947	158	184	

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9887	40255	A	9948	200	386	LFYTME*IMAFLLSSSSSPGRPF* RILGGAKVYAGMQRYSFFLIGS RIITYLGIFGRELYFC
9888	40256	B	9949	47	622	
9889	40257	A	9950	1	630	
9890	40258	A	9951	1	782	
9891	40259	A	9952	1	677	MHGLGRWDACPQDEMSESGQ SSAAATPSTTGTKSNTPTSSVPS AAVTPLNESLQPLGDYGVGSK NSKRAREKRDSRNMEVQVTQE MRNVSIGMGSSDEWSDVQDIID STPELDMCPETRLDRTGSSPTQ GIVNKAFGINTDSLYHELSTAG\ S*VIGDVDEGADLLGNNDRKK VYTSVQTRPPQACTFSVRLVES THAELVGIEGRLYHKIHPLRVH GAVGYSVLT
9892	40260	C	9953	202	366	
9893	40261	A	9954	1	2429	MKEGGWGCDPVGRGVTSGHV LQMKLLPFRQKKAHIMEIQLNG GTVAEKVAWAQARLEKQVPV HSVFSQSEVIDVIAVTKGRGVK GVTSRWHTKKLPRKTHKGLRK VACIGAWHPARVGCSIARAGQ KGYHHRTELNKKIFRIGRGPHM EDGKLVKNNASTSYDVTAKSIT PLGGFPHYGEVNNDFVMLKGC IAGTKKRVITLRKSLLVHHSRQ AVENIELKFIDTTSKFGHGRFQT AQEKRAFMADGLSLSPAASDS DYPPGEMFLDSDVNPEDPGAD GVLAGITLVGCATRCNVPRSNC SSRGDTPVLDKGQGEVATIANG KVNPSQSTEEATEATEVPDPGP SEPETATLRPGPLTEHVFTDPAP TPSSGPQPGSENGPEPDSSSTRP EPEPSGDPTGAGSSAAPTMWLG AQNGWLYVHSAVANWKKCLH SIKLKDSVLSLVHVKGRVLVAL ADGTLAIFHRGEDGQWDLSNY HLMDLGHPHHSIRCMAVVYDR VWCGYKNKVHVIQPKTMQIEA SAGQGPGEGKRLLLASSSPASSI RKSTRPTHDST\KSFDAHPRRES QVRQLAWIGDGVWVSIRLDST LRLYHAHTHQHLQDVDIEPYVS KMLGTGKLGFSFVRITALLVAG SRLWVGTGNGVVISIPLTETVV LHRGQLLGLRANKTSPTSGEGA RPGGIIHVYGDDSSDRAASSFIP

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9894	40262	A	9955	9	452	KIKVLSKNSQVTDFPVPTLLND GQCLGYNSTPYKEKAITL/PCPR KLGPPQGSFKTA/APSSSSPSFNF FNGSQNSVTNFWSSCFH*KVLI LKTNNLKLPHAKKKTKVV/LQ NILLSF*RFYDALLSLTSLLLLN LNGQLKQTVMRPFFHH
9895	40263	A	9956	1	3223	ATATPSTTGTKSNTPTSSVPSAA VTPLNESLQPLGDYGVVSKNSK RAREKRDSR\NMEVQVTQEMR NVSIGMGSSDEWSDVQDIIDST PELDMCPETRLDRTGSSPTQGI VNKAFGINTDSLY\HELSTAGS\ EVIGDVDEGADLLGEFSGMGK EVGNLLLENSQLLETKNALNV VKNDLIAKVDQLSGEQEVLRG ELEAAKQAKVKLENRIKELEEE LKRVKSEAIIARREPKEEAEDVS SYLCTESDKIPMAQ
9896	40264	B	9957	176	658	
9897	40265	A	9958	2	5671	AGGPCVRSSRELWTILLGRSAL RELSQIEAELNKHWRRLLEGLS YYKPPSPSSAEKVKANKDVASP LKELGLRISKFLGLDEEQSVQLL QCYLQEDYRGTRDSVKTVLQD ERQSQALILKIADYYYEERTCIL RCVLHLLTYFQDERHPYRVEY ADCVDKLEKELVSKYRQQFEE LYKTEAPTWETHGNLMTERQV SRWFVQCLREQSMLLEIIFLYY AYFEMAPSDLLVLTKMFKEQG FGSRQTNRHLVDETMD
9898	40266	A	9959	1	404	MVDQEAIFGCKNRNNCSHLEPP VSRLEGGAFVRDLLSPTQYLLA SCPYQYDGSFVIQQIPSSNLFMV VVDSSCLCESVAPITMAPIEIRYI LLC\EVHSLPRKPENARECGGA PSL\QAQTVLLLLPLLLMLFSR
9899	40267	A	9960	1	1374	
9900	40268	A	9961	102	205	

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9901	40269	A	9962	1	1527	MVPDAAVLAQLAIRARVNRRW PTGLSAPHLCGAACSRCRHAAI AKYFGDALPACAKGCDHCQNP TAVRRRLEALERSSSWSKTCIG PSQGNGFDPELYEGGRKGYGG FSRYDEGSGGSGDEGRDEAHK REWNLFYQKQMQLRKGKDPKI EEFVPPDENCPLKEASSRRIPRL TVKAREHCLRLLEEALSSNRQS TRTADEAD\FRAKAVELEHETF RNAKVANLYKASVLKKVADIH RASKDGQPYDMGGSAKSCSAQ AEPPEPNEYDIPPASHVYSLKPK RVGAGFPKGSCPFQTATELMET TRIREQAPQPERGGEHEPPSRPC GLLDEDGSEPLPGPRGEVPGGS AHYGGPSPEKKAKSSSGGSSLA KGRASKKQQLLATAAHKDSQS IARFFCRRVESPALLASAPEAEG ACPSCEGVSGTPDWPQRSTQGR KMEPGDIRLPLPRLRSASGRGQ APARPETRAPLKSSPPLQRTHG KGKRPRFPARRTQRASLRRGHA PQPIPPS
9902	40270	A	9963	2	99	
9903	40271	A	9964	115	1360	ENGQLHMVNLALDGVRSSLQK PRPFRLFPKGFSVELCMNREDD TARKEKTDHFIFTYTREGNLRY SAKSLFSLVLGFISDNVDHIDSLI GFPEQIAEKLFSAAEARQKFTEP G\AGL\RALQKFTGGLWEVWVL CSLCFLLWKLPDICCKLGDEHE LLEHLTNEALSRY*PVTTCR*IV SVLF*RLIQQDYRVMKRGLENL TLLDLSCKFSSKL*IILMLEEWP *RSCSSFSGTGLKVRLLVPSLIFL DSTI*YFACANWEFDHSNCKTE GWADQVLQIFLPCG*CSFSS*FQ VSYPTSRETAESCFRSTLSLVQN MHDEAAQRFCEKFPFL*SFLPFI CILKAVRLF*KLQFYKEKAPDC HGPVLKHEAISSQESKKSKKRP FEESETEQNNSSQPSKQKYVCL AVEDWDLLNSY

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9904	40272	A	9965	3	1026	DNVDHIDSLIGFPEQIAEKLFFA AEARQKFTEPGAGLRALQKFTE AYGSLVLCSLCLRNRYLVISEK LEEIKSFRELTCLDLSCCKLGDE HELLEHLTNEALSSVTQLHLKD NCLSDAGVRKMTAPVRVMKR GLE\NLTLL\DLSCNP\EITGGRA LGYPLFLFRGNLN\CFRDISGDR GSRDIKTL\KHKLQTHIGLVHSK VPLKEFDHSNCKTEGWADQIV LQWERVTAEAVKPRETSEPIAA AQRFYGKRSRAEAPLK\CPLAD TH\MNSS\EKLQ\FYKEKAP\DCH GP\VLKHEAISKPRSPKKSKKRP FEESETEQNNSSQPSKQKYVCL AVEDWDL\LNSY
9905	40273	A	9966	1	289	VKHCLHRPILWDPWKTSGIQQ VLTPL*KAMEKLEAILLIICSLE AIGLITLPSLSMTQFLQLHVECC YVSPDQTPYFIDVETEAMKDEV TVHNPHG
9906	40274	A	9967	1	1413	MVVPPNIAELKNLEVLNFLNNQ IEKLPTQISRLQKLKHLNLGFLS PCNSMNRLNISPQGFGSLPALE VLDLTYNNLNENYLPGNFFYLT TLCALYLSDNDFEILPPDIGKLT KLQILSNRDNNLISLPKEIRVLT QLKELHIQGNRLTVLPPELGSR GGSGSRFSAETATGGAQNAPPS VLGSAGTIFK\QRRNPSPAALRG GSVAA*PSPAAAKYGKDQREH LPTAAGDGVGWEPTRDIQVGS ATAQALSQANAARGRLSTAQA AGSLHVECCYVSPGQTLYFTDV EIEAMKDESRGISILYKHRHLK VPLDQKLPKSKGHQPDGYGQH DHKPQMTSLTRNIATLR
9907	40275	A	9968	1	619	MNRLNISPQGFGSLPALEVLDL TYNNLNENYLPGNFFYLTTLCA LYLSDNDFEILPPDIGKLTKLQI LSNRDNNLISLPKEIRVLTQLKE LHIQGNRLTVLPPELASSSRCGP LSHPYAGKRIPRNAVFKFEQNT\ PWHTPPKKAGREMLLDVTGFP EAATSKPPAFLHRRRGRGSWNP RSRSSSLQRTPWPPGSREAEYPP ASGA

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9908	40276	A	9969	810	1672	GLPSVTMSKSLKKLVEESREKN QPEVDMSDRGISNMLDVNGLF TLSHITQLVLSHNKLTMVPPNIA ELKNLEVLNFFNNQIEELPTQIS SLQKLKHLNLGMNRLNTLPRG FGSLPALEVLDLTYNNLSENSL PG\NFFYL\TTL\RALYLSDN\DF EILPPDIG\KL\TKLQILSLRDNDL ISLPKEIGELTQLKELHIQGNRL\ TVVPPEL\GNLGF*LGQKQVFK AENNPWVTPIADQFQLGVSHVF EYIRSETYKYLYGRHMQANPEP PKKNNDKSKKISRKPLAANNR
9909	40277	C	9970	120	347	
9910	40278	A	9971	2	10018	LCVSPVTAGRPARSLREMEVEQ EQRRRKVEAGRTKLAHFRQRK TKGDSSHSEKKTAKRKGSAVD ASVQEESPVTKEDSALCGGGDI CKSTSCDDTPDGAGGAFAAQP EDCDGEKREDLEQLQQKQVND HPPEQCGMFTVSDHPPEQHGM FTVGDHPPEQRGMFTVSDHPPE QHGMFTVSDHPPEQRGMFTISD HQPEQRGMFTVSDHTPEQRGIF TISDHPAEQRGMFTKECEQECE LAITDLESGREDEAGLHQ
9911	40279	A	9972	2	5196	APLDGEVELLQQKLREKLDEFN ELAIQKESADRQVLMQEEEIKR LEEMNINIRKKVAQLQEEVEKQ KNIVKGLEQDKEVLKKQQMSS LLLASTLQSTLDAGRCPEPPSGS PPEGPEIQLEVTQRALLRRESEV LDLKEQLEKMKGDLESKNEEIL HLNLKLDMQNSQTAVSLRELE EENTSLKVIYTRSSEIEELKATIE NLQENQKRLQKEKAEEIEQLHE VIEKLQHELSLMGPVVHEVSDS QAGSLQSELLC
9912	40280	A	9973	1	8277	GEFGSEKKTALHEKEETLRLQS AQAQPFHQEEKESLSLQLQKKN HQVQQLKDQVLSLSHEIEECRS ELEVLQQRRERENREGANLLS MLKADVNLSHSERGALQDALR RLLGLFGETLRAAVTLRSRIGE RVGLCLDDAGAGLALSTAPAL EETWSDVALPELDRTLSECAEM SSVAEISSHMRESFLMSPESVRE CEQPIRRVFQSLSLAVDGLMEM ALDSSRQLEEARQIHSRFEKEFS FKNEETAQVVRKHQ
9913	40281	A	9974	1	393	

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9914	40282	A	9975	2	153	
9915	40283	A	9976	184	790	KFTKHISMNQEDLDPDSTTDVG DVTNTEEELIRECEEMWKDME ECQNKLSLIGTETLTDSNAQLSL LIMQVKCLTAELSQWQKKTPE TIPLTEDVLITLGKEEFQK\RGQ DLEMVLSTKESKNEKLKEDLER EQRWLDEQQQIMESLNVLHSE LKNKVETFSESRIFNELKTKML NIKEYKEKLLSTLGEFLEDHFPL
9916	40284	C	9977	23	217	
9917	40285	A	9978	25	100	
9918	40286	A	9979	1	2850	
9919	40287	A	9980	108	1132	HPHQVETSRDVAGEQSHAVAF MSTGISQADVCRLEWFSAPNLK GRPRKKKPCPQRRDSFSGVKDS NNNSDGKAVAKVKCEARSALT KPKNNHNCKKVSNEEKPKVAI GEECRADEQAFLVALYKY\MK ERKTRIERIPYLGFNQINLWTMF QAAQKLGGYETITARRQWKHI YDELGGNPGSTSAATCTRRHYE RLILPYERFIKGEEDK\PLPPIKP RKQENSSQENENKTKVFGTKRI KHEIPKSKKEKENAPKPQDAAE VSSEQEKEQETLISQKSIPEPLPA ADMKKKIEGYQEFSAKPLASR VDPEKDNETDQGSNSEKVAEE AGEKGPTPPLPSAPL
9920	40288	B	9981	177	3543	
9921	40289	B	9982	63	374	

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9922	40290	A	9983	1	2023	MGGGSWAPTGLCPLQSLLAMS PEKRKLAAQEGQFTEPRPEEPP KEKLHTLEEFSYEFFRAPEKDM VSMAVLPLARARGHLWAYSCE PLRQPLLKRVHANVDLWDIAC QIFVDILPHQPACTSAVVGVSV YPQSVSAWSCPSTVLLDSHT\IL RYMGDYPSRQAWPTLELTDQIF TLALQHPALQDEVYCQILKHLT HNSDRHSEERGWQLLWLCTGL FPPSKGLLPHAQKFIDTRRGKLL APDCSRRIQKVLRTGPRKQPPH HVEVEAAEQNVSRICHKIYFPN DTSEMLEVVANTRVRDVCDSI ATRLQLASWEGCSLFIKISDKVI SQKEGDFFFDSLREVSDWVKK NKPQKEGEEASVELGEGVAGW VEGALAASVRPMPIHPSIRSRVS LGCGNNQALGPGGAPVTLPYQ VYFMRKLWLNISPGKDVNADT ILHYHQELPKYLRGFHKCSRED AIHLAGLIYKAQFNNDRSQLAS VPKILRELVPENLTRLMSSEEW KKSILLAYDKHKDKTVEEAKV AFLKWICRWPT\FGSAFF/EGEG KPCPTPGPPTQAASAQPSPSRPS VNQHTSWQTSEPSYPDVILIAIN RHGVLLIHP\KTKDLLTTYPFTK ISSWSSGSTYFHMALGSLGRGS RLLSET\SLGYKMDDLLTSYVQ QLLSAMNKQRGSKAPALAST

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9923	40291	A	9984	428	2502	VSKEIVYNKLLPYAERLDAESD LQLAQIKCNLGRAVQLQELWP GGLFWTRKLS/TRAGPLALSSLE LSPSGDPRVVTEPVKYSSRPPCH FPTGLPGSLPSLYVLRICFSRSV RVVVFPPGGPWVAQGPRPRGR ETWGFTMLLRYIRLYGRKFSKE DHVLFIKLLYELVSIPKLEISMM QGFARLLINLLKYFPADATAEM LEEWRPLMCPFDVTMQKAITY FEIFLPTSLPPELHHKGFKLWFD ELIGLWVSVQNLPQWEGQLVN LFARLATDNIGYIDWDPYVPKG GPSKLVQKHLAGLFNSITSFYH PSNNGRWLNKLMKLLQRLPNS VVRRLHRERYKKPSWLTPVPDS HKLTDQDVTDFVQCIIQPVLLA MFSKTGSLEAAQALQNLALMR PELVIPPVLERTYPALETLTEPH QLTATLSCVIGVARSLVSGGRW FPEGPTHMLPLLMRALPGVDPN DFSKCMITFQFIATFSTLVPLVD CSSVLQERNDLTEVERELCSAT AEFEDFVLQFMDRCFGLIESSTL EQTREETETEKMTHLESLVELG LSSTFSTILTQCSKEIFMVALQK VFNFSTSHIFETRVAGRMVADM CRAAVKDWGKPGDLWNLGIQ WHVPSSEEVSFAFYLLDSFLQP ELVKLQHCGDGKLEMSRDDIL QSLTIVHNCLIGSGNLLPPLKGE
9924	40292	A	9985	2	5396	AESDLQLAQIKCNLGRAVQLQE LWPGGLFWTRKLSTYIRLYGR KFSKEDHVLFIKLLYELVSIPKL EISMMQGFARLLINLLKKKELL SRADLELPWRPLYDMVERILYS KTEHLGLNWFPNSVENILKTLV KSCRPYFPADATAEMLEEWRP LMCPFDVTMQKAITYFEIFLPTS LPPELHHKGFKLWFDELIGLWV SVQNLPQWEGQLVNLFARLAT DNIGYIDWDPYVPKIFTRILRSL NLPVGSSQVLVPR
9925	40293	A	9986	1	477	VREFPGRRFRGCCGALRPRYKR LVDNIFPEDP\GYVCIAMEALDQ LLMACHCQSINLFVESFLKMVA KLLESEKSNLQILGTNSFVKFA NIEEDTPSYHRSYDFFVSRFSEM CHSSHDDLEIKTKIRMSGIKSLQ GVVRKTVNDELQANIWDPQH

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9926	40294	A	9987	1	2371	AGGARLRPARGRPPRLLPPRPG PCRPPPVPAPTVNERRAPPRAG WERRSDAGLSRGARPAEMYGV CGCCGALRPRYKRLVDNIFPED PEDGLVKTNMEKLTFYALSAPE KLDRIGAYLSERLIRDVGRHRY GYVCIAMEALDQLLMACHCQS INLFVESFLKMVAKLLESEKPN LQILGTNSFVKFANIEEDTPSYH RSYDFFVSRFSEMCHSSHDDLEI KTKIRMSGIKGLQGVVRKTVN DELQANIWDPQHMDKIVPSLLF NLQHVEEAESRSPSPLQAPEKE KESPAELAERCLRELLGRAAFG NIKNAIKPVLIHLDNHSLWEPK VFAIRCFKIIMYSIQPQHSHLVIQ QLLGHLDANSRSAATVRAGIVE VLSEAAVIAATGSVGPTVLEMF N\TLLRQLRLSIDYALTGSYDGA VSLGTKIIKEHEERMFQEAVIKT VGSFASTLPTYQRSEVILFIMSK VPRPSLHQAVDTGRTGENRNR LTQIMLLKSLLQVSTGFQCNNM MSALPSNFLDRLLSTALMEDAE IRLFVLEILISFIDRHGNRHKFSTI STLSDISVLKLKVDKCSRQDTV FMKKHSQQLYRHIYLSCKEETN VQKHYEALYGLLALISIELANE EVVVDLIRLVLAVQDVAQVNE ENLPVYNRCALYALGAAYLNLI SQLTTVPAFCQHIHEVIETRKKE APYMLPEDVFVERPRLSQNLDG
9927	40295	A	9988	1	662	IPGSTISWSPAAARGLSVCRCCR LHPASAMDLFGDLPEPERSPRP AAGKEAQKGPLLFDDLPPASST DSG/SSLQALPGSGGPLLFDDLP PASSGDSGSLATSISQMVKTEG KGAKRKTSEEEKNGSEELVEK KVCKASSVIFGLKGYVAERKGE REEMQDAHVILNDITEECRPPSS LITRVSYFAVFDGHGGIRASKF AAQNLHQNLIRKFPKGDVISVE

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9928	40296	A	9989	3	1145	KEAQKGPLLFDDLPPASSTDSA VAALGTTPSPVTLWFLQTRRGS KIWRNSLDYQSKVGAEPWCHE RQQKADRFLGKRGRVPASSVIF GL\KGYVAERKGEREEMQDAH VILNDITEECRPPSSLITRVSYFA VFDGHGGIRASKFAAQNLHQN LVRKFPKGDVIS\VEKTVKRCLL DTFKHTDEEFLKQASSQKPAW KDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLS KEHNPTQYEERMRIQKAGGNV RDGRVLGVLEVSRSIGDGQYK RCGCHLCAPTSRRC\QLTP\NDR FI/LVWPCDGLF\KVFTPEEAVN FIL\SCLEDEKIQTREGKSAADV RLRSSPATRLANKAVAAGARP DNVTV\MVVR\IGH
9929	40297	A	9990	2	419	
9930	40298	A	9991	2	1842	CLRLIAAAPPI/AIEPATTSSLALF LLLQRDQSSRTRGLPEEKEEVT MDTSENRPENDVPEPPMPIADQ VSNDDRPEGSVEDEEKKESSLP KSFKRKISVVSATKGVPAGNSD TEGGQPGRKRRWGASTATTQK KPSISITTESLKSLIPDIKPLAGQE AVVDLHADDSRISEDETERNGD DGTHDKGLKICRTVTQVVPAE GQENGQREEEEEEKEPEAEPPV PPQVSVEVALPPPAEHEVKKVT LGDTLTRRSISQQKSGVSITIDD PVRTAQVPSPPRGKISNIVHISN LVRPFTLGQLKELLGRTGTLVE EAFWIDKIKSHCFVTYSTVEEA VATRTALHGVKWPQSNPKFLC ADYAEQDELDYHRGLLVDRPS ETKTEEQGIPRPLHPPPPPPVQPP QHPRAEQREQERAVREQWAER EREMERRERTRSEREWDRDKV REGPRSRSRSRDRRRKERAKSK EKKSEKKEKAQEEPPAKLLDDL FRKTKAAPCIYWLPLTDSQIVQ KEAERAERAKEREKRRKEQEE EEQKEREKEAERERNRQLEREK RREHSRERDRERERERERDRGD RDRDRERDRERGRERDRRDTK RHSRSRSRSTPVRDRGGRR
9931	40299	A	9992	1400	2959	
9932	40300	C	9993	169	430	

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9933	40301	A	9994	2	199	STSR/KMTELEEVTLNGKPLQA LRVTDLKAALEQRGLAKSGQK SALVKRLKGVRSRRCWGVGGE RTR
9934	40302	A	9995	1	4033	MWRRKHPRTSGGTRGVLSGNR GVEYGSGRGHLGTFEGRWRKL PKMPEAVGTDPSTSRKMAELEE VTLDGKPLQALRVTDLKAALE QRGLAKSGQKSALVKRLKGAL MLENLQKHSTPHAAFQPNSQIG EEMSQNSFIKQYLEKQQELLRQ RLEREAREAAELEEASAESEDE MIHPEGVASLLPPDFQSSLERPE LELSRHSPRKSSSISEEKGDSDD EKPRKGERRSSRVRQARAAKLS EGSQPAEEEEDQETP
9935	40303	A	9996	3	6305	ELEEVTLDGKPLQALRVT\DLK AALEQRGLAKSGQKSALVKRL KGALMLENLQKHSA\PHAAFQP NSQIGEEMSQNSFIKQYLEKQQ ELL\SSRLEREAREAAELEGKSS SISEEKGDSDDDKPRKGERRSS RVRQARAAKLAEGSQPAEEEE DQETPSRNLRVRADRNLKTEEE EEEEEEEEEDDEEEEGDDEGQK SREAPILKEFKEEGEEIPRVKPE EMMDERPKTRSQEQEVLERGG RFTRSQEEARKSHL
9936	40304	B	9997	99	332	
9937	40305	A	9998	3	236	YIFTILNTLQGVFILLFGCLMDR KIQEALRKRFCRAQAPS/SHHLP GELLPSDPQLCIQEHVRRHSMA LLRGHGHSQKL
9938	40306	B	9999	1	3099	
9939	40307	A	10000	355	858	RASSAAWGPSRKTSASSSAFSSS CWSSS*QS*SYSSSSLS\HGQGE RERQEGPEGRPAAVPHREQRG AEERLEHHPG*DAMLWCH*LH RLVPSAGGEHGSRPLLHGELPG LRAQRHHAFVENGLL*KGEDV VR*Q*ARAGHGGDVHPHHADP GHGLLHDPLPAHPPDW

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9940	40308	A	10001	3	1478	GRALTSRRRACQGASEAAGSPA QVTTSTGHHQHRSHQHRSPPA QVTTSTGHHQHRSPAQATTSTG HHQHRPPPAQVTTSTGHHQHR SPAQATTSTGHHQHRSH\HTGH HQHRS/HTSTGHHQHRSPAQAT TSTGHHQHRPPPAQVTTSTGHH QH\GHQHRPPPA/HGHHQHSSPP A/HGHHQHRPPPA/HGHHQH\G HHQHSSPPA/HGHHQHR\HHQ\P GHHQHRSP/HSTAHHQH\GHHQ HSSPPA/HGHHQHHQH\GHHQH SSPYQH\GHHQHRPPPA/HGHH QHRSH\HTAHHQHRSHQH\GHH Q\PGHHQHRSPAQATTSTGHTS TGHHQHRP/HTSTGHH\HTGHH QHRSHQHRSPPAQATTSTAHH QHSS/HTSTGHHQHRSP/HSTGH HQHSSPPA/HGHHQHSSPPAQA TTSTGHHQHRESPAVAAAADPS ALSAARRGSPGPAAAPQSRGTR GGGAPAKWWGSALGLGWAGR ARARLGRPLRPILGAMPPAPRT PRERREHGEVE
9941	40309	A	10002	5	341	PPRRRGQKRRQK/REEGERERG ERKRPRDRKEERKG/RRTKRQG GTETRESRPNGDGPQAKRKKQ TAGQREREEGEQRSSRQRGAA ERERGRETTHITCLLVPCWWEP NGRLCL
9942	40310	A	10003	1	582	MLAQRGGRSVVQCIAVSKLSV TQRSFVTLIMDEEALGNCGGSS GSQTCEKAVCIHNLPFLTSHAF QSGFPPHQSPEASLPKMVSDAQ TARLSLESMRELGFHISESAGFP APVSGYEHSNPSRPGVMPSGTS HWKQRSQKVEDNRTEMVKGIQ GDT\VKHQQHLPRINGN*LAYM TAKSRTWLPVQQDPGPQTI
9943	40311	A	10004	1	332	MEYYAAIKNDEFMSFVGTWM KLETIILSKLSQGQKTKHHIFSLI EAQAQVSPPPPYPAPQELTQPL LQQPRAPEAPAQQ/PPGSLLTAT VRLSASPGPGLIFDQLLPRCGF

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9944	40312	A	10005	1	1108	MLAQRGGRSVVQCIAVSKLSV TQRSFVTLIMDEEALGNCGGSS GSQTCEKAVCIHNLPFLTSHAF QSGFPPHQSPEASLPKMVSDAQ TARLSLESMRELGFHISESAGFP APVSGYEHSNPSLSTTNLSGPSR RRQPPVSPLTLSPGPEAHQGFSR QLSSTSPLAPYPTSQMVSSDRS QLSFLPTEAQAQVSPPPPYPAPQ ELTQPLLQQPRAPEAPAQQPQA ASSLPQSDFQLLPAQGSSLTNFF PDVGFDQQSMRPGPCLSSTGAS GAT\GSRELQDSFHLRPSPYSNC GSLPNTILPEDSSTSLFKDLNSA LAGLPEVSLDVDTPFPLEEELQI EPLSLDGR\HMLSDSSMGLLDP SVEETFRADRL
9945	40313	A	10006	1	691	MRERARPPRGCLAPPLPPG/E/S GADGQPAPRGRGTAGG/ELAA AGCGARAAMHRGAVPSAEPVP ASP/DGRWQWAGEGRPCNAAG GSRT/GAGCGWPAPAGWGPAP SSAASCPASGGATHRGASAAPG GGGGGRAP/GPDALEQRRAGAP PNAPGTPGSPEESSLRMRRESA AGAPAVGMAAATSLGQALGPR VPRSPYRTAVVLSSRSAFGYFSL ITLARYTLGCLSHSDITLFEC
9946	40314	A	10007	1	1065	MADKRAGTPEAAARPPPGLAR EGDARTVPAARAREAGGRGSL HPAAGPGTAFPSPGRGEAASTA TTPSLENGRVRDEAPETCGAEG LGTRAGASEKAEDANKEEGAIF KKEPAEEVEKQQEGEEKQEVA AEAQEGPR/PPEPWCPN/C/MDP LEAIQWEAEAVSAQADRAYLP LERRFGRMHRLYLARRSFIIQNI PGFWVTAFLNHPQLSAMISPRD EDMLCYLMNLEVRELRHSRTG CKFKFRFWSNPYFQNKVIVKEY ECRASGRVVSIATRIRWHWGQE PPALVHRNRDTVRSFFSWFSQH SLPEADRVAQIIKDDLWPNPLQ YYLLGDRPCRARGGLARWPTE TPSRPYGFQSG
9947	40315	A	10008	2	433	
9948	40316	A	10009	125	289	TRKSGCLKIRFHVFLFLYRNPG MDVADAYVTFVRHSQDVLRD KVNE\EMYI\ERLF
9949	40317	A	10010	1	774	
9950	40318	A	10011	1	1749	

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9951	40319	A	10012	1	1175	MFASCYMRNIPKRVIEFGTCLW RTCKNCLSSLEFKMPFPPHPRSV TYNLKQERCRLSLDASLSCMLS IEDSQIPNTRLECCKGLSRCTSV ASTCPLVTFSFCLFSPKMEQYS KDDSEKTLKGWFSPGQVFVLD EYCARNGVRGCHRHLCYLRDL LERAENGAMIDPTLLHYSFAFC ASHVHGNSQQMHVYLSGLPPN TDPEGSKTPSPPEPEAKKDTKK ESKKRKDSKTQANQELKRSLTS NLP/ICEPTQ/W*TFPKYQIYQLT SL*ASHKCLLFRHRHGWLLY/ID ADNGSGTSEDLFWKLDALQTFI RDLHWPEEEFGKHLEQRLKLM ASDMIESCVKRTR\IAFEVKLQK TSSIQQIFRVPQFNMAPCFNVM GLMAKGSIQPKL\CSMEMGQE
9952	40320	A	10013	1	3951	MLDPSSSEEESDEIVEEESGKEV LGSAPSGARLSPSRTSEGSAGSA GLGGGGAGAGAGVGAGGGGG SGASSGGGAGGLQPSSRAGGG RPSSPSPSVVSEKEKEELERLQK EEEERKKRLQLYVFVMRCIAYP FNAKQPTDMARRQQKISKQQL QTVKDRFQAFLNGETQIMADE AFMNAVQSYYEVFLKSDRVAR MVQSGGCSANDSREVFKKHIE KRVRSLPEIDGLSKETVLSSWM AKFDAIYRGEEDPRKQQ
9953	40321	A	10014	1	457	VAAVAATALKGGGARNARVL RGIFAGATA\NKAS\HNRTRALQ N/HTASPEGKEEP\EPLIPGTGKY IPQKRGAKNPHENCGNLPWAIG FPCGILLFDPSPKR/RKLDKDRV\ KQMKARQNMRVSNTG\EYES\Q RFRASSQS\APSP\DVGSGVSGV QT
9954	40322	A	10015	464	863	TPAAVESSPSIPLAPRLLYTG*PL QP/GPRGQGCVPRIVPCCPKP/V CAPRPPWPRRSQRLRSAGLSPL CAAAAPPVPAGSHGTPGRVWA PLSNSACCTCCRHPS*LHPGTLD PGRWQAR*GPALPRGPLPGSPP
9955	40323	A	10016	1	300	PKILVGASKVVLL\SAHKLGFIG DTLSRQAK\AVDVASRVTHYSN LL\CDFL\QGIVATTKAAALQYP IAFPGPKDMVERVKELGHS\TQ QFRRVLGQLAAA

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9956	40324	A	10017	3	291	ARI/VFAIISFYFMPCCPLTA/SSF YLLSGLLDAFDGHALALLIKFC VRGSESHKMIDLSGNP/VLRIYY TS/RVGSVGLFR/MGLWVTAPIA LLKSLISVIT
9957	40325	A	10018	1	344	VLIRARLSDNPAVRGSESHKMI DLFCYPVLRIYYTSRPALFTLCA GNELFYCLLYLFHFSEGPLVGS VGLFRMGLWVTAPI\ALLKSLIS VIHLITAARNMA\ALGRQQDRA KKK
9958	40326	A	10019	1	469	MVRSCFVDDRRKRCNFNRQAS EVLNEYFYSHVSNPYHSEEAKE ELAKKCGITVSQVSNRFGNKKI RYKKNIGEFQEEANIYAVKTAV SVTQGGHSSTS\SPTPPSCAGCG GSFNISGSGDMFLGMPGLNGDS YSASQALESGDASPAQSEMPK MGT
9959	40327	A	10020	232	1728	PGGGRGGAGRGPQGPPPAMDE RLLGPPPPGGGRGGLGLVSGEP GGPGEPPGGGDPGGGSGGVPG GRGKQDIGDILQQIMTITDQSLD EAQGQKTPPLNCP\RKKPVLFS GRGEIKEKTG\LSIRSSQEEEPVD PQLMRLDNMLLAEGVAGPEKG GGSAAAAAAAAASGGGVSPDN SIEHSDYRSKLAQIRHIYHSELE KYEQACNEFTTHVMNLLREQS RTRPVAPKEMERMVSIIHRKFS AIQMQLKQSTCEAMMMLRSRF LDARRKRRNFSRQATEVLNEYF YSHLSNPYPSEEAKEELAKKCG ITVSQVSNRFGNKKIRYKKNIG KFQEEANIYAVKTAVSVTQGG HSSTSSPTPPSSAGSGGSFNISGS GDMFLGMPG\LNGDSYSASQ/V WESLRHSMGARGVIGG*TFGG RARCYSPR\EMRANGSWQEAV TPSSVTSPTEGPGSVHSDTSNLI LPLRVTGVGALTRRLEEDAGFQ RTNPNTGEAQDREGPMGSSPP
9960	40328	A	10021	337	830	IPRLPGSIQLSFVGAFGQTSKSLF FLCVFILLLFQFFLCSVYVPMCT E/RRINIPIGPCGGMCLSVKGRC EPVLKEFGFAWPESLNCSKFPP QNDHNHMCMEGPGDEEVPLPH KTPIQPGEECHSVGTNSDQYIW VKRSLNCVLKC/GYDACLYSRS AQEVT\DIWMA

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9961	40329	A	10022	1	1561	MAWRGAGPSVPGAPGGVGLSL GLLLQLLLLLGPARGFGDEEER RCDPIRISMCQNLGYNVTKMPN LVGHELQTDAELQLTTFTPLIQ YGCSSQLQFFLCSGYVPMGTEK INIPIGPCGGMCLSVKRRCETPS LK\EFGFA\WP\ESLNCSK/YPHP QND\HNPHVPWKGPGDEEVPLP HKTPIQP\GEECHSVGTNSDQYI WVKRSLNCVLKCGYDAGLYSR SAKEFTDIWMAVWASLCFISTA FTVLTFLIDSCRFSYPERPIIFLS MCYNIYSIAYIVRLTVGRERISC DFEEAAEPVLIQEGLKNTGCAII FLLMYFFGMASSIWWVILTLT WFLAAGLKWGHEAIEMHSSYF HIAAWAIPPVKTIVILIMRLVDA DELTGLCYVGNQNLDALTGFV VAPLFTYLVIGTLFIAAGLVALF KIRSNLQKDGTKTDKLERLMV KIGVFSVLYTVPATCVIACYFY EISNWALFRYSADDSNMAVEM LKIFMSLLVGITSGMWIWSAKT LHTWQKCSNRLVNYT
9962	40330	A	10023	496	664	FYKAVPSIHQLDVPQTHQP*ST GLVQKVYSRSKHVSL*PKYYY VQLVPKLDHLIFY
9963	40331	A	10024	1	954	
9964	40332	A	10025	127	481	GRTREATWRVYSVAVGVSRSQ IIRIAREFADNADKTHGRSMIIV GAGLNHWYHLDMNYRGLINM LIFCGCVGQSGG/GWAHYVGQ EKLRPQTGWQPGVCLDWQRPA RHMNSTSYFLLVP
9965	40333	B	10026	161	234	
9966	40334	A	10027	3	199	DDFLDLAESPNASDTESSDEIPL KAGPGTLIMATGVQDFNRTEFD RLNAIKGHLEI\ALLEKHFFT
9967	40335	A	10028	37	455	LRTHLLPRLSQSSPVSSLPRALL RPPGQLELWAVPAGPGPLL\AA DASQNLTQHMEALASQSRGRV DMSDGHLAVLSPIEEELRKLRE ETNAEMLRQELDRERQRRMEL EQKVQEVLKARTEEQMAQQPP KGQAQASNGA

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9968	40336	A	10029	1	1721	DKIRFRGHKRDDFLDLAESPNA SDTECSDEIPLKVPRTSPRDSEE LRDPAGPGTLIMATGVQDFNRT EFDRLNEIKGHLEIALLEKHFLQ EELRKLREETNAEMLRQELDRE RQRRMELEQKVQEVLKARTEE QMAQQPPKGQAQASNGAERRS QGLSSRLQKWFYERFGEYVED FRFQPEENTVETEEPLSARRLTE NMRRLKRGAKPVTNFVKNLSA LSDWYSVYTSAIAFTVYMNAV WHGWAIPLFLFLAILRLSLNYLI ARGWRIQWSIVPEVSEPVEPPK EDLTVSEKFQLVLDVAQKAQN LFGKMADILEKIKNLFMWVQP EITQKLYVALWAAFLASCFFPY RLVGLAVGLYAGIKFFLIDFIFK RCPRLRAKYDTPYIIWRSLPTDP QLKERSSAAVSRRLQTTSSRSY VPSAPAGLGKEEDAGRFHSTKK GNFHEIFNLTENERPLAVCENG WRCCLINRDRKMPTDYIRNGV LYVT\ENYLCFESSKSGSSKRNK VIKLVDITDIQKYKVLSVLPGSG MGIAVSTPSTQKPLVFGAMVH RDEAFETILSQYIKITSAAASGG
9969	40337	A	10030	18	573	
9970	40338	C	10031	71	205	
9971	40339	C	10032	190	243	
9972	40340	A	10033	18	283	
9973	40341	A	10034	1	190	
9974	40342	A	10035	1	135	
9975	40343	C	10036	90	137	
9976	40344	B	10037	272	560	
9977	40345	A	10038	3	422	
9978	40346	A	10039	205	1090	
9979	40347	A	10040	1	2142	

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9980	40348	A	10041	15	1524	FPGRRFRAEGERTECAEPPRDEP PADGALKRAEELKTQANDYFK AKDYENAIKFYSQAIELNPSNAI YYGNRSLVYLRTECYGYSL*D ATRAIELDKKYIMGYYRRA\AS NMALGKFRAALRDYETVVKV KPHDKDAKMKYQECNK\IVKP KAFERAIAGDEHKRSVVDSLDI ESMTIEDEYS*PKLEDGKVTISF MKELMQWYKDQKKLHRKCAY QILVQVKEVLSKLSTLVETTLK ETEKITVCGDTHGQFYDLLNIFE LNGLPSETNPYIFNGDFVDRGSF SVEVILTLFGFKLLYPDHFHLLR GNH\ETDNMNQIYGFEGEVKA KYTAQMYEEFSEVFEWLPLAQ CINGKVLIMHGGLFSEDGVTLD DIRKIERNRQPPDSGPMC\DLLW SDPQPQNGRSISKRGVTCQFGP DVTKAFLEENNLDYIIRSHEVK AEGYEVAHGGRCVTVFSAPNY CDQMGNKAS\YIHLQG\SDLRP\ QFHQF\TAVP\HPNVK\PMAYAN
9981	40349	A	10042	94	188	VIEHLVSQDGLDFL/NLVICPPR PPKVLGLQA
9982	40350	A	10043	419	495	EPTNENSPIALSR*VNSQKISMK AV
9983	40351	A	10044	1	265	EMESRSIA\RMECSGSISAHCKL RLPGSHHSPASVSRVAGTTGTC HHARLIFLYF/LLETGFHCVSHD GLHLL/NLVICPPRPPKVLGLQA
9984	40352	A	10045	3	706	ADAWAWPHC/CTVLL*CLGFA GVLFGWPSLVFVFKNEDYFKD LCGPDAGPIGNATGQADCKAQ DERFSLIFTLGSFMNNFMTFPTG YIFDRFKTTVARLIAIFFYTTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIIKLLYEK GISLR/VLLHLHLCLQYLACSTH FPPDAPGAHPIPTAPQLQLWPV PWEWHHKGREGNS

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9985	40353	A	10046	1	1413	MKRGNGSRRRRRLLSENNGVF HIESFAQHPKDEKSRKLLGPIEH WTFVVEKGKGKPEETGTVSMV LEDGEVEADIKQGSVVGCCNV PPDAARERAEKAYMDGEQPTLI LLLWDLKKQIPVHKGTHSVGR HQTELLPNNGGGVVRFFYTTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIIKLLYEK GISLRASFIFISVCSTWHVARTF LLMPRGHIPYPLPPNYSYGLCP GNGTTKEEKETAEHENRELQSK EFLSAKEVSTYTNAFAFTQFGV LCAPWNGLLMDRLKQKYQKE ARKTGSSTLAVALCSTVPSLAL TSLLCLGFALCASVPILPLQYLT FILQVISRSFLYGSN\GRFLTLAF PSEHFGKLFGLVMALSA\VVSL LQFPIFTLIKGSLQNDPF\YVNV MFMLAILLTFLPPLSGISGMPYL
9986	40354	B	10047	316	395	
9987	40355	A	10048	1	1614	RMQQQAVMHYMQQQQQQQQ QQLGGPPTPAINTPVHFQSPPPV PGEVLKVGPVLACPPPCPH*SQ PPLEPLPYLSETYGNKFAAHISP AQ\ALRNPHQPPPQGCELDTCC PPPLATVLP/ISPMAMLHIGSNPE REVSEELASGHAACRARAHCC ASETMPNTVLLARVGWVCKGS REGGTHCGSEPGESGVTSSSCP ADLTQKRELTGTASLYPCAFEY PTPPSFSPSLPAAPLPASLFLVLT WAG*KANDL*/VRFLRGRVMG LGGQQLT\RLSALLQKSRELEN HSRRLEMTNKQLWLRIQVWS* TWTSLVTLTLNLAPGPKGQYFR MFCFGNKQSSASLSNTYQLEVL FCETLILAPTLLAPSSLMAHLEL ALKAIVTLKVPHVTSVQWAWP MQAHSTSTLTSLAQQVVKQEL PSEEGPGEALMLGAEVPDPEPL PALPPQAPLPLPTQPPSPFHHLD FSHSLSFGGREDEGPPGYPEPLA PGHGSPFPSLSKKDLDLMLLDD SLLPLASDPLLSTMSPEASKASS RRSSFSMEEGDVL

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9988	40356	A	10049	1	1651	GGVTAGARAPARGSVTAEAAA RAGRGSGRGADGGREGRTGRA SLVARGRSRPGAGGGHSLRAR HPNLRQVAGA/GGARAADRLT FRAREPAPAATMASRIGLRMQL MREQAQQEEQRERMQQQAVM HYMQQQQQQQQQLGGPPTP AINTPVHFQSPPPVPGEVLKVQS YLENPTSYHLQQSQHQKVREY LSETYGNKFAAAHISPAQ\ALR NPHQPPPQGCELDTCCPPPLAT VLPISPMAMLHIGSNPERELDD VIDNIMRL\TMSLGYINPEMQM PNTVLLARLPLSSSHLNVYSSDP QVTASLVGVTSSSCPADLTQKR ELTDAESRALAKERQKKDNHN LIERRRRFNINDRIKELGMLIPK ANDLDVRWNKGTILKASVDYI RRMQKDLQKSRELENHSRRLE MTNKQLWLRIQELEMQARVHG LPTTSPSGMNMAELAQQVV\KQ ELPSEEGPGEALMLGA\EGP\DP EPLPALHRQAPLPLPTQAPSPFH S/HWDFSHSL\SFGG\RVDDWSP GLPRTPGAGAWLPIPQPVQEGS GPHAPGRLTATAGL
9989	40357	A	10050	2	76	TPLAPPPKPVRRRLKSRR*IKAR S
9990	40358	A	10051	3	206	
9991	40359	A	10052	1	492	

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9992	40360	A	10053	2	2395	KQTELRRSGSRDVTGALLVAA AVASEAVGSLRVAEGGPNTLLL QVLR\SW\PWCNKATQTMEERK VKRRSPKSFSAHCTQVVNVQK KMSIPV\SKS\TGFSNPASQVNFT SRPKVKKEVMK\EKTKPQGLEE GQRHSSQLPIQHSFLT\DVSRCS RKMERGLLSL\LNDFHSWKTFK HFGN\ECSI\EQMEHVSGELQEK LARLNLELYGELEELPEDKRKT ASDS\NLDRLLSDCREMIPAFRT FLKRHDKTIVTKMLSLPELLLY PSRRFEEYLNLLYAVRLHTPAE HVDRGDLTTAIDQIKKYKGYID QTLSEVNRYLIRVQDVAQLHCC DEEISFSLSVACRSVDSASPESL PEMQNSQATLALLNQNLHFNKI TRLYEHIHDLSLFLFNDALLVSS RGTSHTPFERTSKTTYQFIASVA LHRLLIENIPDSKYVKNAFILQG PKYKWICATEIEDDKFLWLSVL RNAIKSSMEKACGLVFTGQFMF DTMGMTNILNNQDTAQALADG LMELSKEDSKCGKKIKDVEGN VIPTKCDPKTTFSLFMKERNVV EDNSWDTKSRLSKNDLNFEALI NLERILQKDSAEKRARVVRELL QSERKYVQILEIVRDVYVAPLK AALSSNRAILSAANIQIIFCDILQ ILSLNRQFLDNLRDRLQEWGPA HCVGEIVTKFGSQLNTYTNFFN NYPVILKTIEKQWETFSERSSSS
9993	40361	A	10054	2	296	
9994	40362	A	10055	2	369	
9995	40363	B	10056	82	2483	
9996	40364	A	10057	2	3343	YDVVLDAIDTMQRVAWHIND MKRKHEHAVRLQEIQSLLTNW KGPDLTSYGELVLEGTFRIQRA KNERTLFLFDKLLLITKKRDDT FTYKAHILCGNLMLVEVIPKEP LSFSVFHYKNPKLQHTVQAKSQ QDKRLWVLHLKRLILENHAAKI PAKAKQAILEMDAIHHPGFCYS PEGGTKALFGSKEGSAPYRLRR KSEPSSRSHKVLKTSETAQDIQ KVSREEGSPQLSSARPSPAQRNS QPSSSTMISVLRAGG

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9997	40365	A	10058	32	483	LKGHADAVLAAGTEAVKCHLL LGRHLLRLMASSGIHHKIVN*R QYAKFSHG*IQKF**WQHRQQF RGKETEMASAVDLPVTLTETEA NFPPEYEKFWKTVENNPQDFTG WVYLLQYVEQENHLMAARKA FDRFFIHYPYCYGYWKKYADL
9998	40366	A	10059	1	1090	MRQKRKEEKELFHNKDCEKKE KNSWERMRHTGTEKMASESET PTGAISQYKERMPSVTHSPEIM DLSELRPFSKPEIALTEALRLLA DED/WDKQLHALEQLLASCYS GTRHTTSSFHCGHQGMWWHPE AWRC/LATAEPQREPGKSTISSH SSLWN*Q/LHSHKLQSVPGLKV KNLRSGVSRAAVVCLSDLFTYL KKSMDQELDTTVKVLLHKAGE SNTFIREDVDKALRAMVNNVT PARAVVSLINGGQSHLHIAVRR CTAQHLSDVLEFMEPERILSAA KDMAERILPAAAKFAQDSSQET RYYGRKMLFFMMCHPNFEKM LEKYVPSKDLPYIKDSVRNLQQ KVCGKSLFYKQLYKQSLFLHP
9999	40367	A	10060	36	203	
10000	40368	A	10061	1	798	MKFQYKEDHPFEYRKKEGEKI RKKYPDRVPVIVEKAPKAR/RA *SGQEEVPSAL*PYCCLP/DGAG LGTCS/HAMPEPPTHSMGTCAA RASPTSTTPCSTAPSPIDRE\EQT TQGLRNASARRGTGRQLHLQ/S PVWDPLGEASWAPESSGNVESI SSSGIVNIPISTLCLAQGFSRFVN APIDTLYLAALVGPWRTFMSSS GIVNTPIGTLYLAQGMVHYHKS PFPTCLVQMSKIESLPKEKGAQ GVAAGLPSSLAPTCPPPDPSMK LHNN
10001	40369	A	10062	164	605	ALLKQHLRTVHRSAPPIRGHCC VSSSWT*G/AGKLSLEHTEEPSD VPSHLLYRWSISSAITEVFQALA SS\IPPRSQ*MSTPRR\NESTRHSP GPSIEEVKECMQDDN*YLQGTS YAPAGSQSYSAKLCFQVLKRN TCPPEKPNPASER

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10002	40370	A	10063	3	2480	RPITGAEIVAIINSLPTKKSPGLD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQ/R LHAKNS/RIN*VLM/ETYFKIIRA IYDKPIANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRAHIA KSILSQKNKAGGITLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEITPHTYNCLIFDKPEK NKKWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQNI GMGKDFMSKTPKAMATKDKID KWDLIKLKSFCTAKETTIRVNR QPTKWEKIFATYSSDKGLISRIY NELNQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAIIKKSGNNRCWRGCGEIGTL LHCWWDCKLVQPLWKSVWRF
10003	40371	A	10064	317	582	STVCCFLLRFIGGGFRHIPLSVD LWIHYIKILKETLDPGDPETNNT IRGYVEH*Y*NVFYDINNYSDV DNRAHES*AGSLTSIPLLKK
10004	40372	A	10065	41	434	GDLQPTAALWEPLSGLAKAGA RSLSLQGGVGGEARARTRAAR GACGPAAAPGGHGLGGHALGA AGR/RLLALGRLGTCSLPCLSLP PSPWAPVPPEPPR*VPPHAPGRP VPSATQRLRSAGAQRRTGRQL
10005	40373	A	10066	67	459	LRDCKYTHRHCVSSSRFINTPIN TLCLAQGL*VHQSTLCI*LLWV GGLGGNFCVQYSVSN*SDGDV ENLCI*LRDCKCTNQHPVKTGH FGSTNQQDVGWGQIKRIKAGLP EPASGNSLGSPSTLWELCSLQ

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10006	40374	A	10067	2481	2882	IPQGNYRVIARNAKTQRGGNLT LTKPS/GIGRRGENSSISSWQRQ QKGKKETGSQRKRQRGRDKKL ERKRDRHRSQREGKKERKRQR RSQRERWK**RKNSVPIPLKAR VNFSLPTQGNSLLDLNPYLPLK QLKK
10007	40375	B	10068	52	5199	
10008	40376	A	10069	1510	2454	
10009	40377	B	10070	97	3414	
10010	40378	A	10071	164	620	PPTGCGTGPIGCSGPGTGPVPVP VAP\PFPQEGARTQPGSAGA\PG ARGLRRAETLVALGAVGPGLP TPPPPPPPAPQSQAPGGPEAQPF GSRVCVLASCCAHRPRPAPSAP PAPPAPPESTVRPAPPTRPGESS YSSISHAFTATNFPFGTA
10011	40379	A	10072	1	513	MATLAGEGRPAGWVPWISLLA VGVLIIWKLWPAPPIGGELQFA FVCFLLGNVYEAFEHWKRLLN LLCRSEAAMKK/HATRLWINLI SILHHQLGEIPADFFVDIVSQHN FLTSTLQVFFSSACSIAVDATLR KKAEKFQAHLTKKFRWDFAEE PEDCAPVVEELPEGIEMG
10012	40380	A	10073	1	1642	MDYIRTDLTTAAPSPPRRLGPPP PGEQPPSGSGHVRPPGARPPHR GGGRGGGGGDPAAPPARGGGG GGKARPPGGGAAPCEPGCQCR APMVSVSSERHPLYNRVKTGQI ANCALPCHNPFFSQDERAFTVF WIGLWSVLCFVSTFATVSTFLID MERFKYPERPIIFLSACYLFVSV GYLVRLVAGHEKVACSGGAPG AGGAGGAGGAAAGAGAAGAG AGGPGGRGEYEELGAVEQHVR YETTGPALCTVVFLLVYFFGMA SSIWWVILSLTWFLAAGMKWG NEAIAGYSQYFHLAAWLVPSV KSIAVLALSSVDGDPVAGICYV GNQSLDNLRGFVLAPLVIYLFIG TMFLLAGFVSLFRIRSVIKQQD GPTKTHKLEKLMIRLGLFTVLY TVPAAVVVACLFYEQHNRPRW EATHNCPCLRDLQPDQARRPD YAVFMLKYFMCLVVGITSGVW VWSGKTLESWRSLCTRCCWAS KGAAVGGGAGATAAGGGGGP GGGGGGGPGGGGGPGGGGGSL YSDVS\TGLTWRSGTASSVSYP

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10013	40381	A	10074	3	475	HSSLNSVDKARALEADNGELE VNIRDWYQKQGPGASRDYSHY YTTIQDLRDKILGATIENSRIVL QIDNARLAADDFRTKFETEHAL RMSVEADINGLRRVLDELTLAR TDLEMHIEGLKEELAYLKKNHE EEISTLRGQVGGQVTV*VDSAP GTDL
10014	40382	A	10075	39	1323	NGMWSNWNPLIPQRWEEKFQS PSRHRGSSSRGVSLSS\SGGYSGI LSGSNGLLAGNEKLTMHNLNN CLASYLDKVHALEAANSKLEF GLSVWVLDEVTLARTDLEAQI KGLKEELAYLKKKHEEEINALR GQVGDQVHILSDRQSQYEIMA KQNWKDAEAWFTSWTEELNQ EVTGHIEQLQISRSEVTDLQCTL QGLEIELHSQLSVKAPLEGTLA ETEACFGAQLVQIQALISSIEAQ LGDVRADGEWQNQEYQRLLE QEIATYRSLLEGQEDHYNNLST SKVQIPECTVSNVPVASVCLQT LEPHSLASNPGSSTYSVTFGQYI NLSVSPFLLLEATIAGAKKAAT GNNSTQFSPPAERQLCIFTCPRT IPLTTASHAGSYGPKLVKYTSL RPLPMAAPTESNPALPSSRATA HRLLPAPGHFPSGL
10015	40383	B	10076	133	180	

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10016	40384	A	10077	1	2182	MSVDKAELCGSLLTWLQTFHV PSPCASPQDLSSGLAVAYVLNQ IDPSWFNEAWLQGISEDPGPNW KLKVSNLKMVLRSLVEYSQDV LAHPVSEEHLPDVSLIGEFSDPA ELGKLLQLVLGCAISCEKKQDH IQRIMTLEESVQHVVMEAIQEL MTKDT\P\DSLSPETYGNFDSQS RRYYFLSEEAEEGDELQQRCLD LERQLMLLSEEKQSLAQENAGL RERMGRPEGEGTPGLTAKKLLL LQSQLEQLQEENFRLESGREDE RLRCAELEREVAEL\QHRNQAL TSLAQEAQALKDEMDELRQSS ERAGQLEATLTSCRRRLGELRE LRRQVRQLEERNAGHAERTRQ LEDELRRAGSLRAQLEAQRRQ VQELLGQRQEEAMKAEKWLFE CRNLEEKYESVTKEKERLLAER DSLREANEELRCAQLQPRGLTQ ADPSLDPTSTPVDNLAAEILPAE LRETLLRLS/LLENKRLCRQEAA DRERQE/EKLQRHLEDAN\RAR HG\LETQ\HRLNQQAAYSELRA QVEDLQKALQEQGGKTEDAISI LLKRKLEEHLQKLHEADLELQR KREYIEELEPPTDSSTA\RRIEEL QHNLQKKDADLRAMEERYRR YVDKARMVMQTMEPKQRPAA GAPPELHSLRTQLRERDVRIRH LEMDFEKSRSQREQEEKLLISA W\YNMGMALQ\QRAGE\EPAPA
10017	40385	A	10078	1	687	
10018	40386	A	10079	1	1104	
10019	40387	A	10080	1	677	MAAAGGGGGGAAAAGRAYSF KVVLLGEGCVGKTSLVLRYCE NKFNDKHITTLQASFLTKKLNI GGKRVNLAIWDTAGQERFHAL GPIYYRDSNGAILVYDITDEDSF QKVKNWVKELRKMLGN\ETCL CIVGNKIDLEKERHVSIQEAESY AESVGAKHYHTSAKQNKGIEE LFLDLCKRMIETAQVDERAKG NGSSQPGTARRGVQIIDDEPQA QTSGGGCCSSG
10020	40388	A	10081	1	1467	
10021	40389	A	10082	2	244	
10022	40390	A	10083	1	257	
10023	40391	A	10084	1	558	
10024	40392	B	10085	41	618	
10025	40393	A	10086	1	591	

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10026	40394	A	10087	128	851	KMEKEKGNDDGIPDQENSLDFS EHFNQLELLETHGHLIPTGTQSL WVGNSDEDEEQDDKNEEWYR LQEKKMEKDPSRLLLWAAEKN RLTTVRRLLSEKATHVNT\RDE DEYTPLHRAAYSGHLDIVQELI AQGADVHAVTVDGWTPLHSA CKWNNTRVASFLLQHDADINA QTKGLLTPLHLAAGNRDSKDT LELLLMNRYVKPGLKNNLEET AFDIARRTSIYHYLFEIVEGCTN
10027	40395	A	10088	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDQEAVI DGRRKPEESRTTSHICRCRS
10028	40396	A	10089	2	461	
10029	40397	A	10090	2	749	
10030	40398	B	10091	1	1077	
10031	40399	A	10092	1	1114	MPQNSLEECALELGKKSLQEN VNNFPKTKLFQFLKLTNWILPKI TKFKPIEGAENVFTDGSSNGKA SYFGLKGKVFQTPYTAAQKVE LVAVIEVLTAFDMPVSMISDST YVVHSTQLTENAQLRLHTDEQ LMTLFSQLQTAVR\CFAVMGIP ASRKTDNVPGYTIQTLATFFSM WNIKHITGIPYNSQGQAIVGRIN LSLKQRLQKQKEGNREYRTPQ MQLNLALLALIFLSLSKGQMLS AAEQHLQKPPAKTEAEQLIWW RDTKTRSWEIGKIITCGRGYAC VSPGQNQQPIWTPSRHLKPYHE PDAK\KRFREDPEDPPSCSHVKT DAEEDPNCHEQHPSNTAIHLRS DQEAVTDGRRKPEESGTTSHNE
10032	40400	A	10093	239	783	RRAPGTAPDAGPELRS\LHNLL GPACIFLRKGFAENRQPVQLRE AFREFDKDKDGYINCRDLGNC MRTMGYMPTEMELIELSQQIN MNLGGHVDFDDFVELMGPKLL AETADMIGVKELR\DAFREFDT NGDGEISTSELREAMRKLLGHQ VGHRDIEEIIRDVDLNGDGRVD FEAPFPGSSN
10033	40401	A	10094	1	304	
10034	40402	A	10095	3	154	
10035	40403	B	10096	126	251	
10036	40404	B	10097	122	2916	

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10037	40405	A	10098	3	2433	LAELSSLSVLRLSHNSISHIAEG AFKGLRSLRVLDLDHNEISGTIE DTSGAFSGLDSLSKLTLFGNKIK SVAKRAFSGLEGLEHLNLGGN AIRSVQFDAFVKMKNLKELHIS SDSFLCDCQLKWLPPWLIGRML QAFVTATCAHPESLKGQSIFSVP PESFVCDDFLKPQIITQPETTMA MVGKDIRFTCSAASSSSSPMTF AWKKDNEVLTNADMENFVHV HAQDGEVMEYTTILHLRQVTF GHEGRYQCVITNHFGSTYSHKA RLTVNVLPSFTKTPHDITIRTTT MARLECAATGHPNPQIAWQKD GGTDFPAARERRMHVMPDDD VFFITDVKIDDAGVYSCTAQNS AGSISANATLTVLETPSLVVPLE DRVVSVGETVALQCKATGNPP PRITWFKGDRPLSLTERHHLTP DNQLLVVQNVVAEDAGRYTCE MSNTLGTERAHSQLSVLPAAG CRKDGTTVGIFTIAVVSSIVLTS LVWVCIIYQTRKKSEEYSVTNT DETVVPPDVPSYLSSQGTLSDR QETVVRTEGGPQANGHIESNGK ASVTVKQSSAVTVSLGAGGGL QVFTGQVPGIRWGKLGEVEGG VCPRDASHFPEPDTHSVACRQP KLCAGSAYHKEPWKAMEKAE GTPGPHKMEHGGRVVCSDCNT EVDCYSRGQAFHPQPVSRDSAQ PSAPNGPEPGGSDQEHSPHHQC
10038	40406	A	10099	1	164	
10039	40407	A	10100	368	566	

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10040	40408	A	10101	3	1160	RDQRGYRDDRSPAREPGDVSA RTRSGGGGGRSATTAMPPPVPN GNLHQHDPQDLRHNGNVVVA GRPSCSRGPRRAIQKPQPAGGR RSGRGPAAGGLCLQPPDGGTC VPEEPPVPPMDWEALEKHLAG LQFREQEVRNQG\QARTNSTSA QKNERESIRQKLALGSFFDDGP GIYTSCSKSGKPSLSSRLQSGM NLQICFVNDSG\SDKDSDADDS KTETSLDTPLSPMSKQSSSYS\D RDTT\EEESESLGWTWDFLYKG KRNLQAEAKMALAMAKPMAK MQVEVEKQNRKKSPVADLLPH MPHISECLMKRSLKPTDLRD\LI MGQLQVIVNDFISQ\IKSLNEEW VQLLLI\QDELHTEQDAMLVDIE DLTRHAESQQKHMAEKMPAK
10041	40409	A	10102	1	506	RGPRTEPQDPCCPRAAAGARPS GPG/QDLPRLRLPGSPGAPGAG GGAGTAAGRKGPGLPEEAAAD GAWRLGEGWAAASEEPAPPGP HTSQRGASPPQPGWARAAGLS NQPTKDRIFGGSHKAAPQASAD SPTSLQCGAAGHCPKASRRALG DNPETEATSSLSPTEWLQ
10042	40410	A	10103	1	429	MGSRLNWMEVIPEQCTYLHVLI KCMFFWNRQHRGGIQEKAALK QRTPRIFHEKNTPCYLLVQE*H RSNAFGEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEETLFSNM
10043	40411	A	10104	4	122	
10044	40412	A	10105	53	619	ILVWSIVPEGKILWGTKQQRRD SRTQRLLKKSPWRAKQSVWEE/ ERKKKNKEEKEEKEKKEKEKK EKEKEKKRKKKRKKKKKKKK KKKKKKKKKKKKKKEEEEEEE EDEEEEEEEEEKKKKEKEEKVK EKKKEEKK/QEEKEEEN/EEEEK EEEEKEEKSSSSKYSLLDSVPTL LISLWVILNTLPELLQPA
10045	40413	A	10106	2821	4680	
10046	40414	A	10107	18	1535	
10047	40415	A	10108	3	1494	
10048	40416	A	10109	3	617	
10049	40417	A	10110	3	1142	
10050	40418	B	10111	1	2151	
10051	40419	B	10112	1	1461	
10052	40420	A	10113	1	1248	
10053	40421	A	10114	2	1624	

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10054	40422	A	10115	1	1416	
10055	40423	A	10116	1	2262	
10056	40424	A	10117	1	1791	
10057	40425	B	10118	1	1497	
10058	40426	B	10119	1	1599	
10059	40427	A	10120	1	1722	
10060	40428	A	10121	1	3168	
10061	40429	A	10122	1	1083	
10062	40430	A	10123	1	589	MGAIYDKPTANIILNGQKLEAF PLKTGIRQGCPLSLLLFNIVLEV LARAIRQEKEIKVIQVGKEEVK LSLFADDMIVYLEDPIISAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKE\KEDTNKWKNIPCSWVG RINIVKMAILPKPYVES
10063	40431	A	10124	1	1566	
10064	40432	B	10125	1	2406	
10065	40433	A	10126	1	2478	
10066	40434	B	10127	69	1259	
10067	40435	B	10128	225	997	
10068	40436	A	10129	2	1124	
10069	40437	A	10130	1	2058	
10070	40438	A	10131	258	823	TLMQKSSAKYWQTESSSTSKSL STMIKWASSLGCKAGSIYANQ* M*SSI/YTNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTELEKTTLKFIRNQ KRACIAKSILSQTKLEASRYLTS NYTTRLQ
10071	40439	A	10132	1	1512	
10072	40440	A	10133	1	992	
10073	40441	B	10134	1	2019	
10074	40442	A	10135	1	1203	
10075	40443	A	10136	1	1578	
10076	40444	A	10137	1	2956	
10077	40445	A	10138	1	1983	
10078	40446	A	10139	1	3156	
10079	40447	A	10140	1	3325	
10080	40448	A	10141	1	1870	
10081	40449	A	10142	1	1446	
10082	40450	A	10143	1	2310	
10083	40451	A	10144	1	1293	
10084	40452	A	10145	1	1038	
10085	40453	A	10146	1	1713	
10086	40454	A	10147	1	2271	
10087	40455	A	10148	1	3654	
10088	40456	A	10149	1090	1647	

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10089	40457	B	10150	1	1248	
10090	40458	A	10151	1	1884	
10091	40459	A	10152	1	1140	
10092	40460	B	10153	1	1545	
10093	40461	A	10154	1	3300	
10094	40462	A	10155	1	1824	
10095	40463	A	10156	1	1023	
10096	40464	A	10157	1	2169	
10097	40465	A	10158	1	2661	
10098	40466	A	10159	1	1104	
10099	40467	A	10160	1	1668	
10100	40468	A	10161	1	1945	
10101	40469	A	10162	1	3303	
10102	40470	A	10163	1	1382	
10103	40471	A	10164	1	399	MPPVDASRDLRELNPLSSYKAK PNEYLLLVQVLFLNRNTKEGLI RLLARYPDDLQQTESQIMSELP FTIASKRIKYPGIQLTKDVEDLF KENYKPLLSK\KEDANKWKNIP CSWIGRINIVKMAVLPKKKIWV
10104	40472	A	10165	1	2218	
10105	40473	B	10166	1	2562	
10106	40474	A	10167	1	3169	

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10107	40475	A	10168	1	2105	MKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAHKR KQERSKIDNLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK WDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLKLFQSIGKEGILPNSFYE ASIILIPKPGRDTTKKANFRPISL MNIDAKILNKILAKRIQQHIKKL IHHDQHINKAKDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFK\E NYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKGFCRFRN HHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINAAGTT GFPTGKRAVSATQLMDFADFG TTIKQDFRLLGQTSVDRLLQLS QGQAVKGNQLLPVSLVKRKTT LAPNTQTASPRALADSLMQLA RQVSRLESGQ
10108	40476	A	10169	1	1689	
10109	40477	A	10170	425	1333	
10110	40478	A	10171	1	2274	
10111	40479	A	10172	1	3828	
10112	40480	A	10173	3	3130	
10113	40481	A	10174	1	960	

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10114	40482	A	10175	746	2470	TLMQKSSIKYWQNESSSTSKSL STMIKWASSLGCKAWFNIRKSI KVIQHINRAKDKNHMIISIDAEK AFDKIQQPFMLKTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLIRNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLLKEN YKP\LLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKNWKKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSKWIKDLNVRPK TIKTLEENLGITIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKL KSFCTAKEATIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFA KEDIYAAKKHMKKCSPSLAIRE MQIKTTMRYHLTPVRMAIIKKS
10115	40483	A	10176	1	3492	
10116	40484	A	10177	1	3139	
10117	40485	A	10178	637	2760	
10118	40486	A	10179	2	3932	
10119	40487	A	10180	1	1865	
10120	40488	A	10181	1	5754	
10121	40489	A	10182	959	1615	
10122	40490	A	10183	701	6973	
10123	40491	A	10184	3	3319	
10124	40492	A	10185	1	3296	
10125	40493	A	10186	1	2296	

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10126	40494	A	10187	1614	2615	TLMQKSSIKYWQTESSSTSKSL STMIKWASSLGMQGWFNICKSI NVIQHINRTKGKNHMIISIDAEK AFDKIQQPFLLKTLNKLGIDGT YLKIIRAIYDKPIANIILNGQKLT FEKFPLKIGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLAKE EVKLSLFADDMIVYLENPIVSV QNLLKLISNFSKVSGYKIYKIDV QKSQAFLYTNNRQTESQIMSEL P\FTIASKRIKYLGIQLTRDVKDL FK\ENHKPLLKE\IKEDTNKWKN IP\CSWVGGRINLVKMAIL\PKVI YRFNAIPIKL\PMTFFTELEKNYF KVHMEPKKEPVLPSQS
10127	40495	A	10188	141	401	
10128	40496	A	10189	1	156	MQFPKTKTKKKEEEEEEEEEEE EEEEEEEEE\EEEEEEEEEEEGEE EKEEII
10129	40497	A	10190	1	1446	

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10130	40498	A	10191	272	2722	ETSCPLVRVHYAEAITGRCTAP EDEGSLGQKPPARRSNNRTEGA WGKRQLMSSP/STEPRVCLTIEG QEIDFLLDTGAAFSVLISCPGRL SSTSVTIQGILGQPVTRYFSHLL SCNWETLLFSHAFLLMPERPTG LLGRDILAKAGAIIYMNMGNKL PICCPLLEEGINPEVWALEGQFG RAKNAHPVQIRLKDPTTFPYQR QY/PLRPEAHKGLQNIVKHLKA QGLVRKCSSPCNTPILEVQRPRL VQDLRLINEAVISLYPVVPNPYT LLSQIPEEAEWFTVLDLKDAFF CVPLHSDSQFLFAFEDPTNHTS QLTWMVLPQGFRDSPHLFGQA LAKDLGHFSSPGTLVLQYVDDL LLATS*EALCQQATLDLLNFLA NQGYKVSMSKAQLCLQQVKY LGLILAKGTRALSKE*IQPILAY PRPKTLKQLREFLGITSFCRLWI PGYSETARPLYTLIKDTQRANT HLVEWESEAETAFKTLKQALV QAPGLSLPTGQNFSLYVTERAG IALGVLTQTRGTTPQPVAHLSK ETDVVAKGWPHCLRVVAAVA VLVSEAIKIIQGKDLIVWTTHEV NGILGAKGSLWLSDNCLLRYQ ALLLEGPVLQICTCMALNPATF LPEDGEPIKHDCQQIIVQTYAAR DDLLEVPLTNPDLNLYTDGSSF VENGI/RKVSDVTILESKPLPPGT SAQLAELVALTWALELGKGKR

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10131	40499	A	10192	1	2529	MTQEPSAIMREVPEMVNILKGT GDIHNTEIQNDNGKVGMTKCM AKPKDELRNLKLILSESLESAQR QGVSKQEKVLQCRRAQDLQPT MPEPPIPSMGSCAARASPTSATP CSRAPSPTDHPTAAKCRRMAR YWQAAPPAALVLDQLGEASW APESANLVGKWRTFVSSSGTA NAPISTLSKQTTGLYQSAGCGW GQNLGAKYRAPVGQLKATSTA ARLKTRVSGFLGKGSLTTPDSS ELGPLDPTDHTSQLTWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLILQYVDDLLLATSLEALCQ KATLDLLNFLANQGYKVSRLK AQLCLQ\SEIARPLYTLIKETQR ANTHLVVSEPEAVI/AFETLKQA LVHAPALSLPIGQNFSLYITERA GIALGDLTQTCGTTPQPVAYLS KEIDVVAKGWPHCLRVVAAVA ILVSEAIKIMQGKDLTVWTTHD VNGILGAKGSLWLSDNHLLRY QALLLEGLVLQICTCVALNTAT FLPEDGEPIEHDCQQIIVQTYAT RDDLLEVPLTNPDLNLYTDGSS VVENGIRRAGYAIVSDVTILESK PLVPGTSAQLAELVALTRALEL GKGKIINVYTDSKYAYLILHAH AAIWKEWEFLTSGNPHGCHRE VMELLHMVQETKEVGVLHYQS HQNGKERGEQQRKQLAEASAA FLWGRALDLQPTMPEPPIPSMG
10132	40500	A	10193	1	197	
10133	40501	A	10194	1	259	
10134	40502	A	10195	1	295	
10135	40503	A	10196	1	439	
10136	40504	A	10197	1268	1420	
10137	40505	A	10198	1	389	
10138	40506	C	10199	1	298	
10139	40507	A	10200	2	90	
10140	40508	A	10201	3	1252	
10141	40509	A	10202	2	82	WMKLETSKLT*EQKTKHCMFS LISGS
10142	40510	A	10203	149	244	
10143	40511	A	10204	485	668	
10144	40512	B	10205	1	598	
10145	40513	C	10206	422	784	

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10146	40514	A	10207	3	899	IYNHLIFDKPDKNKQWGK\DSL FNKWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMGKDFMTK TPEAMATKAKIDKWDLIQLKSF CTANETVIRVNRQPTEWEKIFAI IYPSDKGLISKIYKELYEKKTNN LIKKWAKDMNRHFSKEDFYEA KKHEKSSSLLGQGVTKGGCCLP MNLLGTYRSEENPSEYQRRQLI KTLRVCKPSSSYFLTSDFLDTPS FSCEPTQTNELQGCSLRFRVAT AAGPVQVRGARLPSFAAPERGL AQIPRQMDSKI
10147	40515	A	10208	3	352	APGRRRRLCQPAGGPGAWPGS AVPGSVSPAPDARSPISGPSRAL RRHLRPSAAGGPGLEIPTHDPH LPGVDYKEGRP\PSGKAGRGGP\ PGKGSPSASGARALGVPAAAA TPRASTL
10148	40516	A	10209	1	510	
10149	40517	A	10210	73	327	
10150	40518	A	10211	1	957	MWSTCKLHGQGAKYILCAAEL SWGAASCLHGSTMSLTVVSMA CVG\AWPLMGGQDKP/FLSARP STVVPRGGHVAF/RCHYRRGFN NFMLYK/EDRSHVPIFHGRIFQE S/FIMGPVTPAHAGTYRC/RGSR PHSLTGWSAPSNP/LVIMVTGN HRKP/SLLAHPGPLLKSGETVI/L QC/WLSA/PSDPLDIVIT/GWENP CLSHVL*S*SHS*ELPADDGEKH GQMQREPKTG*NPSSSWPSPTE/ PSSKSGICR/HLHVLIGTSVVIFL FI/LLLFFLLYRWCSNKK\DSDE QDPQEVTYAQL/NHCVFIQRKIS RPSQR/PKTPLTDTSVYTELPNA
10151	40519	A	10212	351	637	AWIGDMGLDWRYGLRVEISA WSGDMGLEWRYGL\REGMFN DTLRLIGEHHDGVSKANFSISR MKQDLAGTYRCYGSVTHSPYQ LSAPSDPLDIVII
10152	40520	A	10213	1	1314	
10153	40521	A	10214	1	1008	

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10154	40522	A	10215	3	1080	GQDKPLLSAWPSLVVPLGHVIL RCHSYLGFNNFSLYKEGVHRKP SLLAHPGRLVKSEETVILQCWS DVRFEHFLLHREGKFKDTLHLI GEHHDGVSKANFSIGPMMQDL AGTYRCYGSVTHSPYQLSAPSD PLDIVITGLYEKPSLSAQPGPTV LAGESVTLSCSSRSSYDMYHLS REGEAHERRFSAGPKVNGTFQ ADFPLGPATHGGTYRCFGSFRD SPYEWSNSSDPLLVSVTGNSRY LHALIGTSVVIIPFAILLFFLLHR WCANKKNAAVMDQEPAGNRT VNSEDSDEQDHQEVSYA*LDH CVFTQREITRPSERPKTPPTDTS MYIELPNAEPRSKVVFCPRAPQ
10155	40523	A	10216	3	1379	
10156	40524	A	10217	352	1825	
10157	40525	A	10218	1	1497	MGLEWRYGPGGADMDLEWRY GPGVEMWVWSGDMGLEVEIR AWSGDMGLEWRYEPGDGDMG LEWRYGPGGGQDKPLLSTWPS LVVPPEHVTLRCHSNLGFNNFS LYKDDGVPVPELYNRIFWKSLF MGPVTPSHTGTYRCRGSHTHSP SGGSAPSNPLVIVVTGFRRKPSL LAHPGPLVKSEETVILQCWSDV MFEHFLLHREGTFNHTLRLIGE HIDGVSKGNFSIGRMTQDLAGT YRCYGSVTHSPYQLSAPSDPLD IVITGLYEKPSLSAQPGPTVLAG ESVTLSCSSRSSYDMYHLSREG EAHERRLPAGPKVNRTFQADFP LDPATHGGTYRCFGSFRDSPYE WSKSSDPLLVSVTGNSSNSWPS PTEPSSETGNPRHLHVLIGTSVV KLPFTILLFFLLHRWCSNKKNA SVMDQGPAGNRTVNREDSDEQ DHQEVSYA*LDHCVFTQRKITP PSQRPKTPPTDSSMYIELPNAES RSKAVFCPRAPQSGLEGIF
10158	40526	B	10219	114	1944	

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10159	40527	A	10220	20	1138	AGARPPVCTGSTMSLMVIIMAC VGFFLLQGAWPQEGVHRKPSF LALPGHLVKSEETVILQCWSDV MFEHFLLHREGKFNNTLHLIGE HHDGVSKANFSIGPMMPVLAG TYRCYGSVPHSPYQLSAPSDPL DMVIIGLYEKPSLSAQPGPTVQ AGENVTLSCSSRSSYDMYHLSR EGEAHERRLPAVRSINGTFQAD FPLGPATHGGTYRCFGSFRDAP YEWSNSSDPLLVSVTGNPSNSW PSPTEPSSKTGNPRHLHVLIGTS VVKIPFTILLFFLLHRWCSDKKN AAVMDQEPAGNRTVNSEDSDE QDHQEVSYA*LDHCVFTQRKIT RPSERPKTPPTDTSMYIELPNAE PRSKVVFCPRAPQSGLEGIF
10160	40528	A	10221	1	1334	MSLMVVSMACVGLFLVQRAGP HMGGQDKPFLSAWPSAVVPRG GHVTLRCHYRHRFNNFMLYKE DRIHIPIFHGRIFQESFNMSPVTT AHAGNYTCRGSHPHSPTGWSA PSNPVVIMVTGNHRKPSLLAHP GPLVKSGERVILQCWSDIMFEH FFLHKEGISKDPSRLVGQIHDG VSKANFSIGPMMQDLAGTYRC YGSVTHSPYQLSAPSDPLDIVIT GLYEKPSLSAQPGPTVLAGESV TLSCSSRSSYDMYHLSREGEAH ERRFSAGPKVNGTFQADFPLGP ATHGGTYRCFGSFRDSPYEWSN SSDPLLVSVTGNPSNSWPSPTEP SSETGNPRHLHVLIGTSVVIILFI LLLFFLLHRWCSN\KKNAAVM DQESAGNRTANSEDSDEQDPQ EVTYTQLNHCVFTQRKITRPSQ RPKTPPTDIIVYTELPNAESRSK
10161	40529	A	10222	50	492	RARHRVTRPSIRKHSGHIRRILC LTCSSGVFLQGLRAGSRGTGPG LRTGWRLSPRAPRRRLHTPSAS SP*CSQ*RGPSAGTAAGARRRW RCRGQLRHPAGTSPPGRRWTG TACGPPAAPPAPWHSSWSCPHS GAGPPWSPACRTASL

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10162	40530	A	10223	3	3159	QAEFAAASTTPALGSDGVRVT MDSALTARDRVGVQDFVLLEN FTSEAAFIENLRRRFRENLIYTYI GPVLVSVNPYRDLQIYSRQHME RYRGVSFYEVPPHLFAVADTV YRALRTERRDQAVMISGESGA GKTEATKKLLQFYAETCPAPQR GGAVRDRLLQSNPVLEAFGNA KTLRNDNSSRFGKYMDVQFDF KGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEEETL RRLGLERNPQSYLYLVK
10163	40531	A	10224	1	2810	MLNGCAHAHPIFPTRILSECPRG MLRAGFHLNRREALPPSRSHIS AAVLAPGALLSWGPDHPLELY GLHSHQDPPTGYEGVKGAPVG GHILSYLLEKSRVVHQNHGERN FHIFYQLLEGGEEETLRRLGLER NPQSYLYLVKGQCAKVSSINDK SDWKVVRKALTVIDFTEDEVE DLLSIVASVLHLGNIHFAANEES NAQ\VTTENQ\VKYLTRLLSVE GSTLREALTHRKIIAKGEELLSP LNLEQAAYARDA
10164	40532	A	10225	1	416	FRGVARQLRTSAMTMPVNGAH KDADLWSSHDKMLAQPLKDSD VEVYNIIKKESNRQRVGLELIAS ENFASRAVLEALGSCLNNKYSE GYPGQ\GSPANFAVYTALVEPH GRIMGLDLPDGGHLTHGFMTD KKKISATSI
10165	40533	A	10226	135	840	GSPANF/AV/YTALVETHGCIMG LDLPDGGHLTHGFMTDKKKIS ATSIFFESMPYKGGPHNHTIAG VAVALKQAMTLEFEVYQHHV VANCRALSEALTELGYQTVTG CSDKHLILVDLHSIKGTDGRRA EKVLEACSIACNKNTCPDDRNT LRPSGLRLGNPALTSLGLLEKG FQKVAHFIHRGIELTLQIQSNAG IRATLKEFKERLAGHKYQGCV QALQEEVESFTLFPLPGLPDF

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10166	40534	A	10227	2	1355	QLRTSAMTMPVNGAHKDADL WSSHDKMLAQPLKDSDVEVYN IIKKESNRQRVGLELIASENFAS RAVLEALGSCLNNKYSEGYPG QRYYGGTEFIDELETLCQKRAL QAYKLDPQCWGVNVQPYSGSP ANFAVYTALVEPHGRIMGLDLP DGGHLTRGL\MTDKKKISATSIF F*SMPYKANPETGYINYGQLEE NARLFHPKLIIAGTSCYSRNLEY ARLRKIADENGAYLMADMAHI SGLVAAGVVPSPFEHCHVVTTT THKTLRGCRAGMIFYRKGVAV ALKQAMTLEFKVYQHQVVAN CRALSEALTELGYKIVTGGSDN HLILVDLRSKGT\DGGRAEKVL EACSIACNKNTCPGDRSALRPS GLRLGTPALTSRGLLEKDFQKV AHFIHRGIELTLQIQSDTGVRAT LKEFKERLAGDKYQAAVQALR EEVESFASLFPLPGLPDF
10167	40535	A	10228	2	243	GTACNPAWPPPGLAPHLTHYA DLLPGSPFHVALPPPESELWETP DVSLITG\PRLGQTPVTEAVSGR RGIAIAYEDEGSG
10168	40536	A	10229	1	1194	MESMFSSPAEAALQRETGVPGL LTPLPDLDGVYELERVAGFVRD LGCERVALQFPDQLLGDAVAV AARLEETTGSKMFILGDTAYGS CCVDVLGAEQAGAQALIHFGP ACLSPPARPLPVAFV/LSSTFCG LGALCQGL*GPEPRPQSACGAA \GEPACAHALDTGKTQDEGAR AGRLRARRRYLVERARDARVV. GLLAGTLGVAQHREALAHLRN LTQAAGKRSYVLALGRPTPAK LANFPEVDVFVLLACPLGALAP QLSGSFFQPILAPCELEAACNPA WPPPGLAPHLTHYADLLPGSPF HVALPPPESELWETPDVSLITGD LRPPPAWKSSNDHGSLALTPRP QLELAESSPAASFLSSRSWQGL EPRLGQTPVTEAVSGRRGIAIA
10169	40537	A	10230	35	429	KEKRYLVYLGCCDLPEK*ESV* TNPVQPIELSAMMAYPVAALSP HVA/RLNT*MTNVTEKLSF*S*L T*I*V*PHVFSGYCTGQCRSS*A SSSSSSSSSSSSSSSSSSSSSSS SSSASDK*WAEASPRVR

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10170	40538	A	10231	73	393	RTQAPKLSQGGPRCIPPPKLCL MESMFSSPAEAALQR\ETGVPG LLTPLPDLGRSVALQFPDQLLG DAVAVAARLEETTGSKMFILG\ DTAYGSCCVDVLGAEQAGAQ
10171	40539	B	10232	191	367	
10172	40540	A	10233	131	1681	RTQAPKLSQGGPRCIPPPKLCL MESMFSSPAEAALQRET\GVPG LLTPLPDLDGVYELERVAGFVR DLGCERVALQFPDQ\LLGDAVA VAARLEE\TTG\SKMFI/LGVDT AYGSCCVDVLGAEQAGAQALI HFGPACLSPPARPLPVAFVLSST FCGLGTLCQDLWGPKPRPQSAC GAA\GEPACAHALEALATLLRP RYLDLLVSSPAFPQPVGSLSPEP MPLERFGRRFPLAPGRRLEEYG AFYVGGSKASPDPDLDPDLSRL LLGWAPGQPFSSCCPDTGKTQD EGARAGGLRARRRYLVERARD ARVVGL\LAGTLGVAQHREAL AH\LRNL\VQAAG\KCSYVLALG RPTPAKLANFPEVDVFVLLACP LGALAPQLSGSFFQPILAPCELE AACNPAW\PPPG/LWVPHLTH/Y IADLLPGSPFHVALPPPESELWE TPDVSLITGDLRPPPAWKSSND HGSLALTPRPQLELAESSPAASF LSSRSWQGLEPRLGQTPVTEAV SGRRGIAIAYEDEGSG
10173	40541	A	10234	3	605	AAAREAAGRDMLAADLRCSLF ASALQSYKRDSVLRPFPASYAR GDCKDFEALLADASKLPNLKEL LQSSGDNPQTGPGDLVSLDFYP QKVLTNPQVQ/WECRSFEKDSK S*LGLLTRLFLHRTSCLKLST/SD PANAKFYETKGERDLIYAFHGS RLENFHSIIHNGLHCHLNKTSLF GEGTYLTSDLSLALIYSPHGHG WQH
10174	40542	A	10235	197	895	LGLLTRLFLHRTSCLKLST/SDP ANAKFYETKGERDLIYAFHGSR LENFHSIIHNGLHCHLNKTSLFG EGTYLTSDLSLALIYSPHGHGW QHSLLGPILSCVAVCEVIDHPD VKCQTKKKDSKEIDRRRARIKH SEGGDIPPKYFVVTNNQLLRVK YLLVYSQKPPKRASSQLSWFSS HWFTVMISLYLLLLLIVFCGLL ALQDRGLPQVCPQIPCGWRPPS EGSQVFETQPGL

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10175	40543	B	10236	1	1059	
10176	40544	B	10237	226	522	
10177	40545	A	10238	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPKEHLTNFKSAA ED
10178	40546	B	10239	101	397	
10179	40547	A	10240	2	253	LQEFGTRKDPPTTSGPQTDQAR EHLTNFKSSA/CQIPWNSGPRLS E*LLPRSSRLSS*RLT/RAQSPW KPTGQSQMLWVTLTVEGT
10180	40548	B	10241	1	409	
10181	40549	C	10242	1	462	
10182	40550	A	10243	1	861	
10183	40551	C	10244	1	140	
10184	40552	B	10245	1	1773	
10185	40553	B	10246	1	320	
10186	40554	C	10247	1	420	
10187	40555	A	10248	273	485	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQPKEHLTNFKSG P\TENRTVQL\TWQPLPEPLELW PKAL
10188	40556	A	10249	508	558	
10189	40557	B	10250	76	358	
10190	40558	C	10251	83	414	
10191	40559	B	10252	1	1111	
10192	40560	C	10253	1	411	
10193	40561	B	10254	1	1054	
10194	40562	B	10255	57	229	
10195	40563	B	10256	1	222	
10196	40564	A	10257	230	1272	LLCSSACKCLMLGLHFVIVGNI CATLKEKYSSMLHLDVTMKKN GEKRTRLQKRKKGMPPHPAYE DLNIAAITLPANVVLHQPSGFRT SGQLDPVWWSLDTDAHEIWCQ DPGLGSGDFPWEITPLSSYSLLH EKDPPTTSGPQTDQPKKHLTNF KSKTKETGFIHGPKTPAPVTDW EGSLPLVFNHCRDTSLIIHPCFK GVRPRRDACLGPSPLAASPAFL EKGQDLINLAFKVYNNRKKLQ FLASTVRQTAATSPAHKNFQMP EPQRPGVPPEPPPTGACYMCRK\ SGHW\TRNAGSPGFLLSRVPSV WDPTENRTVQLTWQPLPEPLEL WPKALCLTDSFPDLLGLAA

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10197	40565	A	10258	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL\DPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
10198	40566	A	10259	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGIDGTY FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSEITPHIYNYLIFD KPDKNKQWGKGSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGMDFMSKTPKAMAT KDKIDKWDLIKLKSFCTAKETT IRVNRQPTKWEKIFTTYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSPSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCW\WINWMKKTWH IYTMEYYASIKKNEFMSFAGA* MKLETII
10199	40567	A	10260	1	347	TNKIDRPLARLIKKKREKKQID AIKNDKGDITTDPTETQTTIKEY YKHLYANKLENLEEMDKFFDT YTLPRLNQEEVESLNRPIAGSEI EAIINSLPT/KKSPGPDGFTAKFY QRE

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10200	40568	A	10261	31	809	KPRLENYVKNAEASGADAINW KKGY/LVMEDEMNEMKREGKF REKRIKRNEQSLQEIWDYVKRP TLHLIDVPETLNAHKRKQERSK TDTLTSQLKELEKQEQTHSKAS RRQEITKIRAELKEIETEKTLQKI NESRSWFFERINKIDRPLARLIK KKREKNQIDAIKNDKGDITSDP TEIQTTIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVES LNRPITGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
10201	40569	A	10262	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
10202	40570	B	10263	1	2265	
10203	40571	A	10264	1	2832	
10204	40572	A	10265	1	2757	

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10205	40573	A	10266	1	2114	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTRPVLK ELLKEALNMERNNWYQPLQKH AKNMPNSIILIPKPGRDTTKKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGMQGWF NIHKSINVIQHINRTIDKNHMIIS IDAEKAFDKIQQLFMLKTLNKL GIDGTYLKIRIKYLGIQLTREVK DLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAISNKLPMTFFTELEKTTL NFIWNQKRARIAKSILSQKNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWGKDSLF NKWCWENWLAVCRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPSLAIREMQIKT TMRYHLTPVRMAIIKKSGNNR QTESQIMSELPITIASKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVK/T WPYCPSPQMYMSPTWQPKTLQ LWRQPKYPWKGTHRRKK
10206	40574	A	10267	1	2952	MLLNQGRKLPRVFAEETLKFK GTSNKPQTLEQISTSIIAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLFEQTLNYLQEFLFTP QWHLECQQERTVHSPGKAAEA REPSVIDRHLIQESSNWHLVGA ALGQSFQRKEQAAIFAVLQPLL VIPRQTGSGVDLQKTPTDLQQR GLIVRRKTNKQKGIVHNSTTRE QNWTENEFDKLTEGGFKRWVI TNSSELKEHVLTQCKEDKNLEK SAIKLELRIKNLIQN
10207	40575	A	10268	1	1797	

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10208	40576	A	10269	1	1751	MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIMKMAILP KVIYRFNAIPIKLPMPFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTKDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK IFTTYSSDNGLISRIYNELKQIYK KKTNNPIKQWAKDMNRHFSIE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAIIKKSG NNRNHLDFKHIRILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA
10209	40577	A	10270	1	4729	
10210	40578	A	10271	1	1428	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10211	40579	A	10272	1	2718	MALFRVGMTTRRLGHANKFTR DLLVKRLLLYEFVVEIIPGLRTK TTLVGPLETGYTSSDSVNSPHF MLDIALSHNVKSTQLLLRPWR NIDCSRNHKNAKKEEQMGDDE INRQQECSSSPAMEQSWTENDF DELREEVFRRSNYSELQEEIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQEITKIRAELKEIE TQKTLQKINESRSWFFEKINKID RPLARLIKKKREKNQTDTIKND KGDIITDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPITGSEIEAIINSL PTKKSPGPDGFTAEFYQRYKEE LVPFLLKLSQSIEKERILPNSSYE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KLISKFSKVSGHKINVQKSQAF LYTDNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIPCSWVG RINIVKMALLP\RFSAIPIKLPMT FFTELEKTTLKFIWN/QKRARIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNYLIFDKPDK KKEWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKMNSRWI
10212	40580	A	10273	396	1227	SLGRNSTSQKRVGANIQHS*RK EFSTQNFISSQTTLHK*RRNKIL YRQANAERFCHHQACPKTAPE RSTK\LERNNRLPARLIKKKREK NQIDATKNDKGDITTDPTEIQTT IREYYKHLYANKLENLEEMDK FPDTYTLPRLNQEEVESLNRPIT GSEIEAIIKSLPTKKRPGPDRFTA EFYQRYKEELVPFLLKLFQSTE KEGILPNSFYEASIILIAKPGRDT TKKENFRPISLLNIDAKILNKILA NRIQQHIKKLIHHDQVGFIPGM QGWFNI
10213	40581	A	10274	1	2168	
10214	40582	A	10275	1	1845	

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10215	40583	A	10276	1	2877	MENDFDELREEGFRQSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERVSAME DEMNEMKGEGKFREKRIKRNE QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLYTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPITGAE
10216	40584	A	10277	1	1689	MIFSIDAEKAFDKIQQPFMLKTL NKLGIDGMYLKIIRAMYDKPA ANIILNGQKLEAFPLKTGTRQG CPLSPLLFNIVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPITSAQNLLKLISNYSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYTFSAIPIKLPMTFFTELEK TTSKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPDKNKQWGKDS LFNKWCWENWLDIWRKLKLD PFLTPYTKINSRSIKDLHVRPKTI KTLEENLGDTIQDIGMGKDFMS KTSKAMATKAKIDKWDLIQLK SFCTAKETTIRVNRQPTEWEKIF AIYSSDKGLIFRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEAI YAAKRHMKKCSSSLAIREMQIK TTLSLPAQVSVV/RHGLSFCWD SRG\CGKSGLFLAYSINPFPQSH WDQEQVM
10217	40585	A	10278	1	2142	

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10218	40586	A	10279	1	1722	MIISIDAEKAFDKIQQRFMLKTL NKLGIDGLYLKIIRAIYDKPTAN IILNGQKLEALPLKTGTRQGCPL SPLQFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLLADDMIVYL ENPIVSAQNLLKVISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWYQKRARITKSILSQRNK AGDITLPDFKLYYKATVNKTA WYWHQNRHIDQWNRTKPSEIT LHIYNYLFFDNPDKNKKWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKYFMT KTPKAMATKAKIDKWDLIKLK SFCTGKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKKHMKKCSPSLAIREMQI KTTMRYHLTPT/RLIVIGIEECLR GKEKLETLYYWNSDTDHQV*W LGWP*WKSDHKKEQPSF

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10219	40587	A	10280	1	2076	MDKFLNTYTIPRLNQEEVESLN RSITGSEIEAIINNLPTKRSPGPD GFTPEFYQRYKEELVPFLLKLF QSIVKEGFLPNSFYEGSIILITKS GRDTTKKENLRPISLMNINAKIL NKILANQIQQHIKKLIHHEQVDF IPGMQGWFNIRKSINVIQHINRT NDKNHMIISIDAEKAFDKIQQLF MLKTLNKLGIDGTYLKIIRAIYD KHTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAIS QEKEIKGIQLGKEEVKLSLFAD DMIVYLENPIVSAQNLLKLIGNF SKVSGYKISVQKSQAFLYTNKR QTESQIMSELPFTIVSKRIKYLGI QLTRDVKDLFKENYKPLLNEIQ DETNKWKN\CSWVGRINIVKM VILP/KELEKTTLKFIWNQKRAR IAKTILSQKNKAGGITLPDFELH YKATVTKTACYLYQNRDIDQR NRTEPSEIMPHIYNYLIFDKSDK NKKWGKDSLFNKWCWENWLA ICRKLKLDPFLPPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMSTKAKID KWDLIKLKSFCTAKETAIRVNR EPTEWEKIFAIYSSDKGLISRIYN EFKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAANRHMKKCSSS LAIREMQIKTTQVGGSEEKSAS ELGNKLIELDQSEEWRGKED

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10220	40588	A	10281	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD
10221	40589	A	10282	1	1996	

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10222	40590	A	10283	1	1778	MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IIPNGQKLEAFPLKTGTTQGCPF SPLLFNIVLEVLARVIRQEKEIK GTQLGKEEVTLSLFADDMIVYL QNPIVSAQNLLKLIGNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFKWNQKRACIAKSILSQKNK AGGIMLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPDQNKQWGKDS LFNKWYWENCLAICRKLKLDP FLTPYTKINSRWIKDLNVRLKTI KALEENLGNTIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKPK SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRNYNELKQIYK KKTIGPIKKWAEDMNRHFSKE DTYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMVIIKKSG NNRCWRGCGETGTLSHCWWD CKL/IQPLW/RFLRD*GPKTGGD S*MIQVKY*PQQKKKGCPNA
10223	40591	A	10284	3	2875	

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10224	40592	A	10285	1	1838	MIIPIDAEKAFDKIQQPFMLKTL NKLGIHGMYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LPPLLFNIVLEILARAIRQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGKDSLF NKWCWENWLAICGKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNLIELKSFC TAKETTISVNRQPTEWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPIKKWAKDMNRHFSKEDIY AANRHMKKCSSSLAIREMPIKT TMRYHLTPVRMAIIKKSGNNRC WRGCGEIGTLSHCWWDCNLVQ PLWKAVWRFLKDLELEIPFDPA ISLLG/IYPKDYKSCCYKDTCTQ STFTCRQHLPL
10225	40593	A	10286	1	2046	

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10226	40594	A	10287	1	1700	MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIQIQEIQRMPQRYSS RRATPRHIIVRFTKVEMKEKMS RAAREKEIQTTIREYYKHLYAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAEFYQRQSESQI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTFFTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKW\CWENW\LAICRKLKLD PFLTPYTKINSRWIKDLNIRPKTI ETLEENLGITIQDIGMGKDFMS KTSKAMSTKAKIDKWDLIKLKS FCTAKETTIKVNRQPTKWEKIF ATYSSDKGLISRIYNELKQIYKK K\TNNPIKKWVKDMNRHFSKE DIYAAKRHMKKCSSSLAIREMQ IKTTMRYHLTPV
10227	40595	A	10288	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ

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10228	40596	A	10289	1	2019	MDTIKNDKGDITTDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRK\AFDKIQQAFTLKTLNK LVIDGTYRKIIRAICDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVLDRAIRQEKEITCIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGRINIMKMAILPKVIYR FNAIPIKLPVAFFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSLFN KWCWENWLDIWRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTL EENLGNTILDIGMGKDFMSKTP KAMATKAKIDNWDLIKLKSFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELKQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLTPVRMVIIKKSGNNR PPLSKEQPPIFRLSIILATTRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
10229	40597	A	10290	1	3144	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
10230	40598	A	10291	1	2274	
10231	40599	A	10292	1	2250	
10232	40600	A	10293	1	822	

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10233	40601	A	10294	1	2605	MKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAYKR KQERSKIDTLTSQLKELEKQEQ SHSKAGRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTNPTEIQTTIREYYKHLYA NKLENLEEMDTFLDTYTLPRLN QEEVGSLNTPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL PGRVPTKKENFRPISLMNIDAKI LNKILANRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHIN RAKDKNHMIISIDAEKAFDKIQ QPFMLKTLNKLGIDGTYFRIIRA IYDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYNFYVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEIMPHIYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQDI GVGKDFMSKTPKAMATKAKID
10234	40602	B	10295	111	2440	

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10235	40603	A	10296	1	1795	MIISIDAEKAFDKIQQPFMLKTL NKLSIDGTYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFAHDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSGVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKGACITKTILS\QKNK VGGITLPDFKLYYKATVTKTA WYWYQ\NRDIDQWNRIKPSEIM PH\IYNYLIFDKPEKNRQWGEDS LFNKWCWETWLAIWRKLKLDP FLTLYAKIN*RWIKDLNVRPKTI KTLEENLGIT\IQD\IGMGKDFM SKTPKAMATKAKIDKWDLIQL KSYCTAKENTIRVNRQPTKWE KIFATYSSDKGLITRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKKCSSSLAIRE MQIKTTMRYHLTPVRMAIIQKS GNNRTKRTIYRRNDDDDDNDD NDDDSLMSLSRTEIPFSSYSELN VVLHKPRPEPSASTILLLHTA
10236	40604	A	10297	1	2851	
10237	40605	B	10298	1	3220	

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10238	40606	A	10299	1	2047	MENDFEELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTQKCLKELMELKTKARELR EECRSLRSRCDQLEERVSAMED EMNEMKREGKFREKRIQRNEQ SLQEIWDYVKRPNLRLIGVPET LHPRDEAHLKNLIDAIKNDKGD ITTDPTEIQTTIREYYKHLYANK LENLEETDKFLDTYTLPRLNQE EVESLNRPITGSEIVAIINSLPTK KSPGPDGFTAEFYQRYKEEL/PD KQLQQSLRIQNQCTKITSILIHQ QQTNREPNHE*TPIHNCFKENKI PRNPTYKGCEGPLQGELQTTAQ GNKRGYKQMEEHSMLMGRKN QYHENGHTAQGNLQIQCHPH* ATNAFLHRIGKNYFKVHMEPK KSPHRQVNPKPKEQSWRHHTT *LQTILQGYSNQNSMVLVPKQR YRSMEQNRALRNNAAYLQLSD L*QT*EKQEMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKR*T*NHKNPRRKP RHYHSGHRHGQGLHV*NTKSN GNKSQN*QMGSN*TKELLHSK KKKNY*QTEQATCKMGENFHN LLI*QRANIQNLQ*TQTNLQEKN KQPHQKVGKGHEQTLLKRRHL CSQK\NHEKMVTITGHQRNAN QNHNEIPSHAS*NGNH*KVRKQ VLERMCRNRNTFTLLVGL*TSS

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10239	40607	A	10300	1	2704	MYSHVITVCRHVKNGDILLLNR QPTLHRPSIQAHRARILPEEKVL RLHYANCKAYNADFDGDEMN AHFPQSELGRAEAYVLACTDQ QYLVPKDGQPLAGLIQDHMVS GASMTTRGCFFTREHYMELVY RGLTDKVGRVKLLSPSILKPFPL WTGKQHINRTKDKNHMIISIDA EKAFDKIQQPFMLKTLNKLGID GTYLKIIRAIYDKPTASIILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKSIQLGKE EVKLSLFADDMIVYLENPTVSA QNLLKLMSNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSGLP FTITSKRITYLGIQLTRDVKDLF KENYKPLLKEIKEDTNKWKNIP CSWVGRINIVKMAILPKVIYRF NTIPIKLPMTFLTELEKTTLKFI WNQKRAHIAKSILSQKNKAGGI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMPHI/Y YNYLIFDKPEKNKQWGKDTLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKT PKATATKAKIDKWDLIQLKSFC TAKETTIRVNRQPTEWEEIFAIY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMVIIKKSGNNRC
10240	40608	B	10301	1	3345	

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10241	40609	A	10302	248	2623	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMLLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAEFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASIILI PKRGRDTTKKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIPGMQGWFNICKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLGIDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAG\GIT\LPDFK LYLQGLQ*PKTAWYWY\QNRD IDQWNRTEPSEITPHIYNYLIFD KPEKNKQWGKDSLFNKWCWE NWLATCRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLGI TIQDIGVGKDFMSKTPKAMAT KAKIDKWDLIKLKSFCTAKETA IRVNRQPTTWEKIFATYSSDKG LISRIYNELKQIYKKK\TNNPIKK WAKDMNRHFSKEDIYAANKH MKKCSPSLAIREMQIKTTMRYH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10242	40610	A	10303	1	2467	MGDFNIPLSTSDRSTRQKVNKD TQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNNL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TEIRAELKEIETQKTLQKMNES RSWFFEKINNIDRLLARLIKKKR EKNQIDAIKNHKGDITTNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEQVESLNRPI TGAEIEAIINSLRTKKSPG\PGGF TAEFYQRYKEKLIVLEVLARAI RQEKEIKGIQLGKEELKLSLFAD DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYSNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEV KEDTNKWKNIPCSWIGRINIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTLKFIWNQKRS\RIAKSIL SQKNRAGGITLSDFKLYYKATV TKTAWYWYQNRDIDQWNKTE PSEIMPHIYNYLIFDKPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDTGM GKDFMSETPKAMATKDKIDKW DLIKLKSFCTAKETTIRVNRQPT
10243	40611	A	10304	2	2480	
10244	40612	A	10305	1	4793	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVNNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
10245	40613	A	10306	1	4320	

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10246	40614	A	10307	1	3229	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLQ PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNL\WDAFKAV CRGKFIALNAHKRKQERSKIDT\ LTSQLKELEKQEQTHSKASRRQ EIT\KIRAELKEIETKK\TLQKINE SRSWFFERIKKTDRPLARLIKKK REKNQIDTI
10247	40615	A	10308	1	3392	MGDFNTPLSTLDRSRRQKVNK NTQELNSALHQVQLIDIYRTLH PKSTEYTLFSAPHHTYSEIDHVV GSKALLSKCKRTEIITNCLSDHS AIKLELRIKKLTQNCSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYPNLWDTFKAVC RGKFIALNAHKRKQERSEIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFEKINKIDRPLARLIKKKRE KNQIDSIKNDK
10248	40616	A	10309	1	4137	MGKKQNRKTGNSKKQRASPPP KEHSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITDIEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAMEDEMNEMKQ EGKFREKRIKRNEQSLQEIWDY VKRPNLPPIDVPESDRENGTKL ENTLQDVIQENFPNLARQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
10249	40617	A	10310	1	5195	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIHIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE IMKIRAELKEIETQKTL\QKINE\ SRSWFF\ERINKIDRPLARLIKKK REENQID\AI

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10250	40618	A	10311	1	2958	MKQEGKFREKRIKRNEQSLQEI WDYVKRPNLHLIGVPESDREN GTKLENTLQDIIQEDFPNLARK ANIQIQEIQRTPQRYSSRRATPR HTIVRFTKVEMKEKMLRAARE KGRVTHKGKPIRLTADLSAETL QARRELNQEEVESLNKPVTGSE VVAIINSLPTKKSPGPDGFTAEF YQKYKEEPVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKILAN RI\QQHI\KK
10251	40619	A	10312	5211	7687	TDTSQKKTFYAAKRHMKKCSS SLAIREMQIKTTYHAGPDGFTA EFYQRYKEELVPFLLKLFQSIEK EGILPNSFYEASIILIPKPGRDTT KK\ENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSIN\VIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKLGIDGTYFKIIRAIYDNPT ANIILNGQKLEAFPLKTGTRQG CPLSPLLFNIVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADNMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQTE SQIMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSG\EGRINIVKMAIL PKNWKKTTLKFIWNQKRARIA KSILSQKNKAGGITVPDFQLYY KATVTKTAWYWYQNRDIDQW NRKEPSEIMPHIYDSLIFGKPDK NKQWGKDSLFNKWCWEDWLA ICRKLKLDPFLTPCTKINSRWV KDLNIRPKTIKTLEENLGNTIQD IGMAKDFMSKTPKAMATKAKI DKWDLIKLKSFCTRIAKEPTIRV NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSSSLAIREMQIKTTMRYHLT PVRMAIIKKSGNNRCWRGCGE TGTLLHCWWDCKLAQPLWKS

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10252	40620	A	10313	1	4525	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH HKSTEHTFFAAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN LLLNNYWVHNEMKAEIKMFFE TNKNKDTTYQNLWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKQLEKQEQTHSKASRRQEI TKIRGELKEIETQKTLHKINESR SWFFERINKIDRLLARLIKKKRE KNQIDAIINDKG
10253	40621	A	10314	1	1185	MEDIKRTQNKLSEMKATLAEM KNTLDGINDHGRDSRRKIRKLQ DNGGDDPTGNTQRKKNLINGP SLSVHIGEKRGGRRSWAETLTP LQTKALRLGPTTPSARRKCGIV PNLQTRKTEAYRYPDTHPGETP VGTAVLSIQKPKLESVIDVRVN MSSFHPEPELQPTQTSVLPDQD ATVAGSTTKFPEEQEARQGRVR ERPATRERPVPGGVSVPGLHHI HFLRGPSLPLASLTRITVLEAVV CFFSVWSIVGLSGFHTYLISSNQ TTNEDIKGSWSNKRGKENYNP YSYGNIFTNCCVALCGPISPRT/ LSHTGQRPTPIECEPHLNLVTSA ETLLASKPD/PTEEGTSSPTRRS QQHPPMASPCTGPRSHRVTCTL EKREEEEGVGQRLSPLCKPRL
10254	40622	A	10315	44	302	GLLGPGPPTAC*CGPHCGIHPES SPQSWCLCHSHRSSRAPPLARL SGDRHPGWRTWGGRDARSVA RGQWWCLVEPVLPFSTRSAFW

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10255	40623	A	10316	3	2182	IRDPGKKPVMLFLHGGSYMEG TGNMFDGSVLAAYGNVIVATL NYRLGVLGFLSTGDQAAKGNY GLLDQIQALRWLSENIAHFGGD PERITIFGRYSQPGLSYHIAFGPV VDGDVVPDDPEILMQQGEFLN YDMLIGVNQGEG\LKFVEDSAE SED/GAFDFTVSNFVDNLYGYP EGKDVLRETIKFMYTDWADRD NGEMRRKTLLALFTDHQWVAP AVATAKLHADYQSPVYFYTFY HHCQAEGRPEWADAAHGDELP YVFGVPMVGATDLFPCNFSKN DVMLSAVVMTYWTNFAKTGD PNQPVPYDTKFIHTKPNRFEEV VWSKFNSKEKQYLHIGLKPRL WSRFRGVLYQVFHDTICEKEAP KSSLLRKQTQPPKKQSSPAVHL RCTMDPVMMTVSPPPAHRHRR RGSPTRCAHCPVAWAPDTDDE KPHQYPAICSYHWDVPEDWEG FQHTQGTWVPWSQDAPESPPQ TIRFQPTVEERPLKTGIWSELGL RAYVYPVNPPPPSPEAPSHKNG RIVYDARDMRRRLRELTREVE ALSGCYPLASGSSTAEETSKNW VYRSLTGSQKMSQLHRVPFFD QEDPDSYLEEEDNLPFPYPKYP RRGWGGFYQRAGLPSNVGLW GHQGGILASLPPPSLYLSPELRC MPKRVEARKCQDLGDSILLLLG SFILLNVWINVVTLLWKHLKSS
10256	40624	B	10317	37	241	
10257	40625	A	10318	2	815	
10258	40626	A	10319	1	943	RAGGQGVG*GWGPPSVPCSVH GGKGL/PPEEGPGQVTHLEF\GR GDGLLTPWWPLTGDGRGPSA/S LASQRTCSQ*GMWLPAAQPSPS HPGPAGTVGQSHLHL*GLLGPG PPHCLLMRPTLRDSSRVFTSKL VSVPQPQVQQGPTTRKTVWRS ASWMENLGRKGCQVCSTWPM VVPGGACTSIWEWEADRVTPG GHRGSSCSHSAAGGANAAPHG PRGRPGGHAAAGGRHSTDGRS SCSPRPPDPGAARPQSAVHTDY RSPSLGTFPLAQPFGESKSDQSA PGIRGQKAPLAVARRGQQTPRP RGQARGRGRGTRPR

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10259	40627	A	10320	39	621	SCPEEEESSLLSPGTSWPLHAW ACSAAQVTGRERVVADWPGY HPGGPTAPHWRAGPLSDKTRPS RDVGTWDTGRAGCPPPPGRNP GPPDQRKALGVVVTSFGSQLG NGTPNSCLSPRQCWIQRLGGSS RTGPPPPGSVPEAAVSCPGHHT LFGLRSGAGKIQG*LLGPGWEL GQAGTEPPLPLAPPPPHRSCG
10260	40628	A	10321	1	496	AAATYVQNQSEDCLYLNLYVP TEDGPLTKKRDEATLNPPDTDI RDPGKKPVMLFLHGGSYMEGT GNMFDGSVLAAYGNVIVATLN YRLGVLGFLSTGDQAAKGNYG L\LDQIQALRWLSENIAHFGGDP ERITIFGSGAGASCVNLLILSHH SEGLFQKAIAQSGT
10261	40629	A	10322	1	4304	MLPVWFTDNLGAAATYVQNQ SEDCLYLNLYVPTEDGPLTKKR DEATLNPPDTDIRDPGKKPVML FLHGGSYMEGTGNMFDGSVLA AYGNVIVATLNYRLGVLGRYS QPGLSYHIAFGPVVDGDVVPDD PEILMQQGEFLNYDMLIGVNQG EGLKFVEDSAESEDGVSASAFD FTVSNFVDNLYGYPEGKD/DW ADRDNGEMRRKT\LLALFTDH QWVAPAVATAKLHADYQSPV YFYTFYHHCQAEGRPEWADAA
10262	40630	A	10323	1	2765	MDVGFSRTTVQTLSRSHCKNIK QKISQWEGRANGISNPEKWCPK DFGVRYNCHQEIRLKKNPIAER KSKNLDVTSRENVGLDINENTK SHDQSENENKKHEYDDTHFFK NESESNWVCSRVKEIESCKEDV LDPETSLPPGNFYTSQILWKKIE ALPPDKLLNLALEHCDSSEKEL NFRVLDSSYGITKSLENIYSEPE GQECGPSINPLPKPRRTFRYLSE SGVTPYKERNCDKKYCENNSC AQSSLASSQEPE
10263	40631	A	10324	2	597	RWLIPKVMRIYDTQKKMDREA SQAALQKMLTLLMLPPTFGDLL REEYIGDNGDPQTLQAQFQEM MADSMFVIPALQVAHFQCSRA PVYFYEFQHQPSWLKNIRPPHM KADHVKFTEEEEQLSRKMMKY WANFARNGNPNGEGLPHWPLF DQEEQYLQLNLQPAVGRALKA HRLQLW\KKALPQKIQELEEPE ERHTEL

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10264	40632	A	10325	2	1766	PGQPLGEQQRVRRQRTETSEPT MRLHRLRARLSAVACGLLLLL VRGQGQDSASPIRTTHTGQVLG SLVHVKGANAGVQTFLGIPFAK PPLGPLRFAPPEPPESWSGVRDG TTHPAMCLQDLTAVESEFLSQF NMTFPSDSMSEDCLYLSIYTPA HSHEGSNLPVMVWIHGGALVF GMASLYDGSMLAALENVVVVI IQYRLGVLGFFSTGDKHATGN WGYLDQVAALRWVQQNIAHF GGNPDRVTIFGESAGGTSVSSL VVSPISQGLFHGAIMESGVALLP GLIASSADVISTVVANLSACDQ VDSEALVGCLRGKSKEEILAIN KPFKMIPGVVDGVFLPRHPQEL LASADFQPVPSIVGVNNNEFGW LIPKVMRIYDTQKEMDREASQA ALQKMLTLLMLPPTFGDLLREE YIGDNGDPQ\TLPKRKF\QKMM ADS\MFVIPALQVAHFQ\CS\RAP VYLPTSSQH\QPSWLKNIRPPH MKADHGDELPFVFRSFF\GGNY IKFTEEEEQLSRKMMKYWANF AR\NGNPNGEGLP\HWP\LFDQE EQYLQLNLQLAVG\RALKAHRF \QFWKKALPQKIQ\ELEEPEERH
10265	40633	A	10326	2	435	ILAEFGSLHLEFLHLTELSGNQV FAEKVRNIRKVLRKIEKPFGLYP NFLSPVSGNWVQHHVSVGGLG DSFYEYLIKSWLMSGKTDMEA KNMYYEALET/HKLGPEAFWF NSGREAVATQLSESYYILRPEV VESYMYLWRQTHNTK
10266	40634	A	10327	3	583	

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10267	40635	A	10328	1	1299	MHLNQLPPILSRLGAVGFFGSM KAHLVSVSRQVRNIRKVLRKIE KPFGLYPNFLSPVSGNWVQLPI PGSVAAGEMPASYPYRHRAPE VRRVCEALPHHVSVGGLGDSF YEYLIKSWLMSGKTDMEAKN MYYEALEAIETYLLNVSPGGLT YIAEWRGGILDHKMGHLACFS GGMIALGAEDAKEEKRAHYRE LAVQITKTCYESYAR\SDTKLGP EAFWFNSGREAVATQLSEE/YT YILRPEVVESYMYLW\RQTHNP\ SYR\EWGWEVVLALEKYCRTE AGFSGDSKTCYSRHPQPRTTSR QSFFLAETLNRCLVSACNGPDT GLEARDTAESETVISPAVKGSR GEKAMVRETDKPAKCIGKKSK NGKSDLKAASKMDAQFRSLCF EEVTPLWFEKVLEMNGPASPSV SPGGLSLEVWSLVMWHKDARP
10268	40636	C	10329	186	401	
10269	40637	A	10330	194	482	
10270	40638	A	10331	224	495	
10271	40639	B	10332	138	1810	
10272	40640	A	10333	1	1351	MGGVGEPGPREGPAQPGAPLPT FCWEQIRAHDQPGDKWLVIER RVYDISRWAQRHPGGSRLIGHH GAEDATDAFRAFHQDLNFVRK FLQPLLIGELAPEEPSQDGPLNA QLVEDFRALHQAAEDMKLFDA SPTFFAFLLGHILAMEVLAWLLI YL\LGP\GWVPSALAAFILAISQ AQSWCLQHDLGHASIFKKSWW NHVAQKFVMGQLKGFSAHWW NFRHF\QHHAKPNIFHKDPDVT VAPVFLLGESSVEYGKKKRRYL PYNQQHLYFFLIGPPLLTLVNFE VENLAYMLVCMQWADLLWA ASFYARFLSLSYLPFYGVPGVL LFFVAVRVL\ES\HWFVWITQM NHIPKEIGHEKHRDWVSSQLAA TCNVEPS\LFTNWFSGHLNFQIE HHLFPRMPRHN\YSPVAPLV\KS LCAK\HGLSYE\VKPFL\TALVDI VRSLKK\SGDIVLDAYLHQ
10273	40641	A	10334	43	399	

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10274	40642	A	10335	1	2229	FLKVCPQNNAETFGCLGTG\EK GDRGNQTQKP\LHYKSWSLFHR SCPRDFYGSKVGDFQGKENGR G\GES\IYGGFFEDEGVSLVKDH\ KEFLLSMANRGKDTNGSQFFIT T\KPTPHLDGHHVVFGQVI\SGQ EVVREIENQKTDAASKPFAEVR ILSC\GELIPKSKVKKEEKKRHK SSSSSSSSSSDSDSSRYS\QSSSDS SDSESATEEKSKKRKKKHRKNS RKHKKEKKKRKKSKKSASSES EAEN/LLEAQPPVLLFRPEEIPLP IPENRFLMRK\SPPKADEKERKN RERERERECNPPNSQPASYQRR LLVTRSGRK\LKGRGPRRYRTPS RSRSRDLFRRS\ETP\PHWRQEM QRA\QRMRVSSGER\WIKGDKS ELNEIKENQRSPVRVKERKITD HRNVSESPNRKNEKEKKVKDH KSNSKERDIRRNSEKEDKYKNK VKKRAKSKSRSKSKEKSKSKER DSK\HN\RNEEKRMRFKELKGR DHENVKEKEKQSDSKGKDQER SRSKEKSKQLESKSNEHDHSKS KEKDRRAQSRSRECDITKGKHS YNSRTRE\RSRRRDSSSRVRSRP HDRDRSMSK\EYHRYRDQVYS RRVRSRSRERRTPPGRSRSRDR RRRRRDSRSSEREDSQSRNKDK YRNQESKSSHRKENSESEKRM YSKSRDHNSSNNSREKKADRD QSPFSKIKQSSQDDELKSSMLK
10275	40643	A	10336	3	3366	

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10276	40644	A	10337	3	2431	GCLQELSVLFARGEPRGPCHNL LHYMLALIGVPEVFWAFLFHCS LGLEEEKLAPLIKGEEKIVWLRS SFYFQHCLVDKSTLLPSSSVSLG IFHEEKNSGEFPIFAKAVRLALV PLRYVKLEDRDNWISVDSVTSE IKLAKLPDFESRYVQNGTYTVK IVAISEDYPRKTITGTVLINVEDI NDNCPTLIEPVQTICHDAEYVN VTAEDLDGHPNSGPFSFSVIDKP PGMAEKWKIARQESTSVLLQQ SEKKLGRSEIQFLISDNQGFSCP EKQVLTLTVCECLHGS\GCREA QHDSYVGLGPAAIALMILAFLL LLLVPLLLLMCHCGKGAKGFTP IPGTIEMLHPWNNEGAPPEDKV VPSFLP\VDQGGSLVGRNGVGG MAKEATMKRKVSSASIVKGQH EMSEMDGRWEEHRSLLSGRAT QFTGATGAI\MTTETTITARATG ASRDVAGAQAAAVALNEEFLK NYFTDKAASYTEEDENHTAKD CLLVYSQEETESLNASIGCCSFI EGELDDRFLDDLGLKFKTLAEV CLGQKIDINKEIEQRQKPATETS MNTASHSLCEQTMVNSENTYS SGSSFPVPKSLQEANAEKVTQEI VTERSVSSRQAQKVATPLPDPM ASRNVIATETSYVTGSTMPPTT VILGPSQPQSLIVTERVYAPAST LVDQPYANEGTVVVTERVIQPH GGGSNPLEGTQHLQDVPYVME
10277	40645	A	10338	5	354	RPRLTSQDIKKPDC/DGEDAIGR GFECDGLHLEKIVHFALHLEKN VNQSLLELHKLATDKNDPHLC DFIETHYLNEQVKAIKELGDHV TNMHEMGAPDSGVAEYLFDKH TLGDSDNES

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10278	40646	A	10339	1	2024	GEALMYHTHFSELLDEFSQNVL GQLLNDPFLSEKSVSMEVEPSP TSPAPLIQAEHSYSLCEEPRAQS PFTHITTSDSFNDDEVESEKWY LSTDFPSTSIKTEPITDEPPPGLV PSVTLTITAISTPLEKEEPPLEIEQ WGLIPRARPLFPKIKLEPHEVDQ FLNFSP\KEAKHLHIFPSWAACT CGSSGNSAIRIILAYSLALRVPT ETKKPRDLFGKTGREKGKEETS REKLYVAERERKAPVDHLHLPP TPPSSHGSDSEGSLSPNPRLHPF SLPQTHSPSRAAPRAPSALSSSP LLTAPHKLQGSGPLVLTEEEKR TLIAEGYPIPTKLPLSKSEEKAL KKIRRKIKNKISAQESRRKKKE YMDSLEKKVESCSTENLELRKK VEVLENTNRASHGELVIGVLGK GRRWDPLLTSPHAGDQCLGSV QGWAGECTPRQLDGSRTTLISE EDPGSPEMGGGEALGAIVSYA WRGREALHASRVGAVIQAPIA AGSDICLSDIRESATSSQTNISVT RTLLQQLQKLQTLVMGKVSRT CKLAGTQTGTCLMVVVLCFAV AFGSFFQGYGPYPSATKMALPS QHSLQEPYTASVVRSRNLLIYE EHSPPEESSSPGSAGELGGWDR GSSLLRVSGLESRPDVDLPHFIIS NETSLEKSVLLELQQHLVSAKL
10279	40647	A	10340	1	489	

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10280	40648	A	10341	1	2665	MESTLTLATEQPVKKNTLKKY KIACIVLLALLVIMSLGLGLGLG LRKLEKQGSCRKKCFDASFRGL ENCRCDVACKDRGDCCWDFED TCVESTRIWMCNKFRCGETRLE ASLCSCSDDCLQKKDCCADYK SVCQGETSWLEENCDTAQQSQ CPEGFDLPPVILFSMDGFRAEYL YTWDTLMPNINKLKTCGIHSKY MRAMYPTKTFPNHYTIVTGLYP ESHGIIDNNMYDVNLNKNFSLS SKEQNNPAWWHGQPMWLTA MYQGLKAATYFWPGSEVAING SFPSIYMPYNGSVPFEERISTLL KWLDLPKAERPRFYTMYFEEP DSSGHAGGPVSARVIKALQVV DHAFGMLMEGLKQRNLHNCV NIILLADHGMDQTYCNKMEYM TDYFPRINFFYMYEGPAPRIRA HNIPHDFFSFNSEEIVRNLSCRK PDQHFKPYLTPDLPKRLHYAKN VRIDKVHLFVDQQWLAVRSKS NTNCGGGNHGYNNEFRSMEAI FLAHGPSFKEKTEVEPFENIEVY NLMCDLLRIQPAPNNGTHGSLN HLLKVPFYEPSHAEEVSKFSVC GFANPLPTESLDCFCPHLQNST QLEQVNQMLNLTQEEITATVK VNLPFGRPRVLQKNVDHCLLY HREYVSGFGKAMRMPMWSSY TVPQLGDTSPLPPTVPDCLRAD VRVPPSESQKCSFYLADKNITH
10281	40649	A	10342	590	900	PLYSATVPSAFCSGQ/LVPHIKS FCRLNIFNR*LIELRHLVFFVLLL FRDLQHIMACNMRDAVRFFVC FLVIFFREGLSRSSCQKCSRKSQ NCGLFYNFFDVHVH
10282	40650	A	10343	1	804	
10283	40651	A	10344	207	299	
10284	40652	A	10345	738	1007	EDASCDEGSTARAVHSMEPAG ARNRQKPHPFQVRGAEPHPPW* RCSHPAVAVDPGIHALSGKPLC SWRLGSDLPTVWPLPTPDPPVS VS
10285	40653	A	10346	150	509	QLPAGSGEGPYHLEGQLSYCHR GGEKALAALLSSPTSKTRSPSEP DPEQDEQKLRFCKRHLYGQQP RSPVEIRLQHVAIAYQTHHAYD *FVQLYNQHVAQPVLEFPYPGA VVALLSRHL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10286	40654	A	10347	120	620	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSHRQFL*HQILFDRT PVSVDQSVEKKG*DHPVRPQ*A APGHVHYLTIPERSSQHYHPGA LQE*TSHPDHIQARGSILASVLS GSDRWRRTYRCL
10287	40655	A	10348	599	1185	MCQNLMTHSKSTEWKITKRFL TETEKHIRTFSSLSMKAIIHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSAKKR DAELANGALGIIELNNDYTSEK SNEAADHFKHVPQAKGNNVVI TSYMTNRGFFEDKKATFAPSFL MNIKGNKTSVVKNSILEQGQLT
10288	40656	B	10349	1	975	
10289	40657	A	10350	1	1080	
10290	40658	B	10351	58	1128	
10291	40659	B	10352	1	1029	
10292	40660	A	10353	10	108	
10293	40661	B	10354	208	2237	
10294	40662	A	10355	1	1153	
10295	40663	A	10356	1026	1274	LHIEKSNEAADHFKHVACHR*R *ACTCHCNNPWFPRPLPQPDCP TSATVEPPLYPIRSRGRTRKPAE GSRAPGCCCCQRPGK
10296	40664	A	10357	434	1128	MCQNLMTHSKSTEWKITKRFL TETEKHIRTFSSLSMKAIIHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSAKKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLFTDSRGSKMTIDGI NSNDIYMLGYVSNSLTGPYKPL NKTGLVLQMGLDPNDVTFTYS HFAVPQAKSNNVVNYGA
10297	40665	A	10358	300	491	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSHRQFL*HQPAQKY FQQIHSAIGLHNADHVHKHLLG DNRYPIWIMQPSAHHPARQPEH DNHFR
10298	40666	B	10359	1	1226	
10299	40667	A	10360	1369	1548	
10300	40668	A	10361	1	1365	

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10301	40669	A	10362	1560	2384	MCQILMTHSKSTEWIITKRFLTE TEKHIRTFSSLSMKAIIHPA/HNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWYLFTDSRGSKMTIDGINSN DIYMLGYVSNSLTGPYKPLNKT GLVLQMGLDPNDVTFTYSHFA VPQAKGNNVVITSYMTTRGFFE DKKATKAPSFLMNIKGNKASV VKNSILEQGQLAVN
10302	40670	B	10363	783	881	
10303	40671	A	10364	1	1359	
10304	40672	A	10365	1512	2010	ENFPHQPAQKYFQQIHSAIGLH NADHVHKHLLGDNRYPIWIMQ PSAHHPARQPEHDNHFR*VQQL YDGDSHRQFL*HQILFDRTPVS VDQSVEKKG*DHPVRPQ*AAP GHVHYLTIPERSSQHYHPGALQ E*TSHPDHIQAK*WHYR\GHYS YARN*RIHHRGSWCR
10305	40673	A	10366	62	368	TGARRVPWPRRGARLRGRARA RSDESGSAGDQPPSFPPWWGW RWVTTAASPANLWPSVARSTM VDRAINL/FFLKMKGDLALTED KREQAQNEQSAWKFTPGR
10306	40674	A	10367	2	305	CTINNPKSF/HGVGFKQHAPQA LTEIQKFAMKEMGTPDVRIDTR LIKAVWAKGIRNVPYRIRVRLS RKRNEDEDSPNKLYTLVTYVP VTTFKNLQTVNVDEN
10307	40675	A	10368	129	283	HLILLFLKHKYCFAREEEEK*R GVGGEEEEEEEEEEEGEEEEEEI FKSIVY
10308	40676	A	10369	777	1755	DIWDQTEHQSSGPWSYGTSTDP E\PTSDLAVIVFEKRGGGEEEEE KEEEEGRR\EEEEKEEEE\GRRR EEEKEEEEEEEE\GRRAQEEEEE KKEEEEEEEEEWCLGEEESQPG HAEEVPSPHKMGALTLRVEGV KEQEAKLLRSSDLMKGDFSSTS QHPPQCSKRTNSESNADAKSKK KERPIMTFRQRKTFRIRILPLPQ GRIAGSNKLSAKLCTDGRGAG DVGVLTNVMLKRLHFTIDHFLF KIIQMSPSASWNLWSLLDQDSL KCQICLEGYAQGGKPDVQLLPP RLTADWKGHRWGQMMGLDE KLTPSSVMVTSVALFWFEVSAQ

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10309	40677	A	10370	1	444	
10310	40678	A	10371	1	3799	MNRQLSKEDIQMANKHEKML NITNDQGNANQNHNAIQPYSC KNGHNRKIDVSMNMVNREHFY TAVHKASDLSFKPTSEKDLDTK LQANFPNLVKAPDKARICFCGK PYQPYVQGSPNSPVEIVENEPSQ LLHFLCVGSSKEEIDLGNPKGS QHTGLGHSMGKCNYFYLPILLV HGWKSHLHPCVASMKVAGTQ RTQDQDEAQEKEKRDKRKAEA LVAALQTYKTQNPQGAPANCY KCGKLGHFKKDCHSSKRKPL
10311	40679	A	10372	1	990	MTQKKNQTEQKEQKNEQKKQ HNERKEHKKKQTEYKTHETNR PRKTERAEHDEQKRENEGKRR RHKKRT/RERKKTNEETETRKG REKPEQARQARKEKQKRQRGE RQ\KEEKKRKNNRQENEEEEAN EQDRREQKEETRKRGPRKRRE HKEEEGRRERKKRKRKTKEKG RRAQQKERREEEQQQRRRRRR GKRKKNESEDEEDKASNKHRQ QERERQKRKGA\ERARRPAETG RRRRKRKRQRKA\AKQRQERQ GDGVLPCAPWTAHPRQPSQCW SARAPGGSAHRPRRYLLTGQA NGSLAMWDLTTAIGRPRPGPCR WPDGARADGTAGTL
10312	40680	A	10373	99	1365	KEAEGRALARLLGPSEERFAAH EGMRPMRAVFTRQGHIFTTGFT RMSQRELGLWDPNNFEEPVAL QEMDTSNGVLLPFYDPDSSIVY LCGKVLTAGQGEQGTGWRCG GPCPGAPLNRLILQGDSSIRYFEI TDEPPFVHYLNTFSSKEPQRG\M GFMPKRGLDVSKCEIARFYKLH ERKCEPIIMTV\PRKVRAWDRD LGRRSDAVPRIRQGPEPALEAD EWLSGQGRRNPCSFSLR\DGYC CPPTHRD\LRVTKRNILDVRPPS GPRRKPSRPATPPCRSSTPLETL LEEIKPLRERVQAQEQRITALEN MLCELVDGPHYPRAPGRASGL PTDPFGGAVRRACPVPPPLVPL ARAVRTLPLRYASSIAALVERM KAHMWAKGRATRDATAKRCS PMAQTTTQHLHVPCDREDESR WNYICCSS

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10313	40681	A	10374	1	361	MINPNPERSDDLVFWGLFRAG GMWSAIIAPVMILLVGILLPLGL FPGDALSYERVLAFAQSFIGRV FLFLMIVLPLWCGLHRMHHAM HDLKIHVPAGKWV\FYGLAAIL TVVTLIGVVTI
10314	40682	B	10375	70	256	
10315	40683	A	10376	224	414	LRWRSLPAFQSGNLSVPAALM NRANARGEAVCVLGRSSRFLA H*LAALGRSAAASGISSLKGG
10316	40684	A	10377	439	595	RAISCCPSHLVKRKTTLAPNTQ TASPRALADSLMQLARQVSRLE SGQ*AQRN
10317	40685	A	10378	1	391	FSSGTVPGDRPDREFIGDTLME RRNRRTGRTEKARIWETANTL AITMLMST\AMPAAAADGVTFS VPVTPHTFRHSYAMHMLYA\GI PLKGLQSLMGHKCIRSTGRLPQ RFLGLEWGLPGHPGGRLAMAE
10318	40686	A	10379	278	694	GHRSPLAIAGCPTIQNGAGPQC AAITRVRAARWCGYPPGSGIPTI PEDSFMLYPRALTTHQTGFSPA WGKPSVDRLLATLSGPGGEGQ YSCCPSHLVKKKTTLAPNTQTA SPRALADSLMQLARQVSRLESG Q*AQRN
10319	40687	A	10380	2	371	SVQVFIRDKLMERRNRRTGRTE KARIW\EVTDRTVRTCDCGGGL PAAAADGVTFFCSAPPNIRFR\H SYA\MHMLYAR*YPLKGLLSPI G\HKCIRSTGRLPQRFLGLEWG LPGHPGGRLAMAEV
10320	40688	A	10381	276	508	
10321	40689	A	10382	464	763	
10322	40690	A	10383	1	715	MQHLSHGSRRHILISENFRGCQ DQAVSQTLLTRPPLVSKEASFF LLPFDLHVLGLPPAFNLSHDQT LQFKSLTLVTSVRVPLEVARPG LSMLGLLRFMSSLLAVGDMGQ GDQVEFQDTKGNSEGRASSQPP MTPLTPTRVRRCPGGPTWGAK AEGVGRAEAATADPGSEGDVV LSRTGLLLAGLLHYFRGRHHLE EIMYNENTRRSQLLMLFDKFRS VLV\VTTHEDPVIAVFQALLP
10323	40691	B	10384	72	195	
10324	40692	A	10385	1	2331	

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10325	40693	A	10386	1	706	MTTSRSDTRSQDDPSAHLASPK LPQRLPKDLSEAQVERLLQAPLI DQPLELRDKAMLEVLYATG\LR VSELVGLTMSDISLRQGVVRVI GKGNKERLVPLGEEA\VHWLET YLEHGRPWLLNGVPINVLFPSQ RAQQITRQALWRRINHYDEL\A GIDSEKLSPHVVRHAFATYFAG SGGCIADFCGGSCAGSSAAESC LWFAGTGLYLHHAWVSGVWS RECSGAAWRDRRDVGGGE
10326	40694	A	10387	39	209	EPGTYVYNETDKSHSPCRPCVL LS**GIYLGSV*R*NGITYGALL AHIPNKFQVDY
10327	40695	A	10388	2	930	AWTHAGILLKHKYSFLVGCASI SDVIAQVVFVAILLH\SHLECRE PLLIPI\LSLYMGALVRCTTLCL GYYKNIHDIIPDRSGPELWGDA TIRKMLSFWWPLALILATQRIR RPIVNLFVSRHLGGSSAATEAV AI\LTATYPVVHMPYGWLTEIR AVYPAFDKNNPSNKLVSTSNTV TAAHIKKFTFVCMALSLTLCFV MFWDTQRV*GKSLIDIIGSGLW PLQELCVV\PLWIFSFFPVPVTV RAHLTGWLMTL\KKTFVLAPSS \VLRIIVLIASLV\VLP\YLGVHG ATLG\VGFLL\AGFCGENSTMG
10328	40696	A	10389	1	1389	GDATIRKMLSFWWPLALILATQ RISRPIVNLFVSRDLGGSSAATE AVAILTATYPVGHMPYGWLTEI RAVYPAFDKNNPSNKLVSTSNT VTAAHIKKFTFVCMALSLTLKD SVQKPDISLTGRLVQTLPTRMR HQRGESKDVAPLASWLSEPSTS SEASQTSSKLTINSQGEGKAKQ KLECGTLSIVLRSCEKNQERIKA AEKRNRSWTTLCGLGAWRPLL FELPVIVQTPDQTNRFQFRYPA KTQSGLCSFFHSFDLLTLEAFV KVWFPGCLLILIEYASSKNRKS KMLQNLKLLSADMTLKLCFVM FWTPNVSEKILIDII\GVDFAFAE LCVVPLRIFSFFPVPVTVRAHLT G\FLMTLNY\TFVLAPSSVLRIIV PHRPASWVLPY\LGVHGATLGV G\SLLAGFVGESTMVA\LATCY VYRKQKKKMENESATEGE\DS AMTDMPPTEEVTDIV\EMREEN

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10329	40697	A	10390	57	556	TGRCTCHDRHYWYSPVERIAY NVEAAR\VEQRTDLDKLVIEME TNGTIDPEEAIRRAATILAEQLE AFVDLRDVRQPEVKEEKPEFDP ILLRP\VDDLELTVRSANCLKAE AIHYIGDLVQRTEVELLKTPNL GKKSLTEIKDVLASRGLSLGMR LENWPPASIADE
10330	40698	A	10391	536	787	GRD*PDYAENAHVMPPVVIED ASDMLLAITQAGRMLMFPVSD LPQLSKGKGNKIINIPSAEAARG EDGLAQLYVLPPQSTLTIH
10331	40699	B	10392	868	900	
10332	40700	A	10393	1	278	MNPQEANYAYLRG/EVELVRLP DAEGRIAAE/GALPYPPGVLALE EGI/NLLPGFAPELQGVYIEE/HD GSGIIMLPTKLAEVGTI
10333	40701	A	10394	1	811	
10334	40702	A	10395	1	682	
10335	40703	A	10396	442	546	
10336	40704	C	10397	1	1776	
10337	40705	A	10398	2	1354	YFSPAAMKALDLLIKWTRSDQ NLGGCNTGLIRPISPIVLIYKLVI GEQMIDVLGPEKRRRRTTQEKI AIVQQSFEPGMTVSLVARQHG VAASQLFLWRKQYQEGSLTAV AAGEQVVPASELAAAMKQIKE LQRLLGKKTMENELLKEAVEY GRAKKWIAHAPLLPGDGDCTS FSDEPMTGWMAAAVVTLMIR MCFSVYTMLSESCQRMVIVGY GRR\PDRQNLMIQGSKP/SIFRQF C/PDFEHLQEPYE/LLWE/MYGN RGYLQLVSFMQKFIDQSIFANT QYDPSRFPSGKVPIQQLLKDLL TAYKFGVKTLYYQNTRDGAED AQDDLVPSIQDDGCESGACLIR RASVASGSGCRMQRERLILATA RICRPDKTRQRRIRHRMRRKMP YPALNSQQDTLMAYTTFSQTK NDQLKEPMFFGQPVNVARYDQ QKYDIFEKLIEKQLFFLLASGRS
10338	40706	C	10399	1	1269	

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10339	40707	A	10400	1	1909	MGFHHVAQAGFELLISSDLPAL ASQTARITAREARAPVEENKKA QLERDKQLSEQQKQAALAKEY KAQVKQLIEMNRITIANGDIGF NFTDGNLIKKIFVDKLTQAQLIN GRLAIARLLVDNNSEGEYAIIPA SVADKIAQRDASSIVLHSALSA EEQDEDDPYADFKVPDDLMWP TVYGRSVDRIRRSRRIRQSCAM PDATLCASYQAYGLRAKHPSFS SQGVPHCVPDVTLKIASEAPSPI VGGTLPVPMTSQLPSVTSMQLL LDLDTIPNEPLHYDWEALRESI KTHGLRNSTLSALMPSETSSQIS NATNGIEPPRGYVSIKASKDGIL RQVVPDYEHLHDAYELLWEMP GNDGYLQLVGIMQKFIDQSISA NTNYDPSRFPSGKVPMQQLLK DLLTAYKFGVKTLYYQNTRDG AEDAQDDLVPSIQ\DDG\CESGA CLIRRASVASGSGCRMQRERLI RPTARICRPDKTRQRRIRHRMR RVLPGRATRRDFPSLEAGYQW LPGRGLVIEPQAQVMYQGVQQ DDCTAASRARVSQSQGDDIQTR LGLHSEWRTAVHVIPTLDLNDY HDPHSTEIEEDGSTISDDAVKQR GEIKVGVTGNISQRVSLRGSVA WQKGSDDFAQTAGFLSMTVK
10340	40708	B	10401	1	1329	
10341	40709	A	10402	1419	1788	ALTSVLPRPSVHW*\SPKPRNVD WHIGRGVAIIMQKSGIPDIDQA NCMIKLESDGTFIVHSGGADIG TGLDTVVTKLAAEVLHCPPQD VHVISGDTDHALFDKGAYASS GTCFSGNAARLAAEN
10342	40710	A	10403	73	477	SMFPRIPFGY/WHI/GSRVAIICQ K/SGIPDIDQSNLHDQLESHGTFI VHSG/GFDYGTGLDTV/VLTKL AAEV/LHCPPQDVHVISGDTDH/ ALFDKGAYASSGTCFSG/NAAR LAAVNPRALAYSYGGGGGARV CIWGGWGRR

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10343	40711	A	10404	1	756	MSIAYQEIPQNERLRLSDSSITS VVEYLLAVVARSVYTSPDMAIF REHHSYMSLSMAACRKIRPCPQ ELPRSIPHMISAMWSQSAPDHV VQHEREQQSGFGDGTESHSTSD SNTEVRQNCSPPIGGVRNHRAL RGHQPAELEPENILKLLLMVAE RKAHKGWYYSGDLCRMDEAG YIKITGRKKDIIVRGGENISSREV EDILLQHPKIPNA\CMGAMSDD RLGERSCAYV\VLKAPHHSLSL EEVLCWRGC
10344	40712	A	10405	252	1245	GSRILPGASITRS\LEFIAGQAVK FNPLLPVSLVKRNTTLAPTTHT ASPRALADSLMQLARQVSRLD SGQRSVVFVRWSRRSIIVDSHA GLITTQRALGQSDMYRGSLPISE LRIIGPRHLRGVLRVVRLCPFSE PMLVECNPLLPSSLIIREPSLEPT LRFASRIALPDSTVLQIFSGVLP LSSGQAYIQFTYSETPRSTPREA NSAHILSVHQWKCGHIVMAAR VKVGYPQWTPISLSAGLSAVLY KPVERGGRCSHSCSTALSPQGF LSSLLRFISEGVFKSFTDKQMLR DFVTTRPALIVLLWQPLNVEGT SSTSHCIIMPTCNDHRD
10345	40713	A	10406	269	432	
10346	40714	A	10407	332	933	RVSRGRKVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFRLSE TKEITNPYAMRLYESLCQYRKP DGSGIVSLKIDWIIERYQLPQSY QRMPDFRRRFLQDFRLLGQ\TS VDRLL\QLSQGQAVKGNQLLPV SLVKRKTTL\APNTQTA\SPRAL ADSLMQLARQVSRLESGQ*AQ
10347	40715	A	10408	1	531	MRWKIDLARISKEIIDFYITQGV NRIGFIAGEDEPGKADIREVAFA EYGRLKQVVREEDIWRGGFSSS SGYELAK\QILARKDYPKPLFV ASDSIAIGVLRAIHERGLNIPQDI SLISVNDIPTARFSFPPLSTVRIH SEMMGSQGVNLVYEKAPDGR ALPLLVFVPSKLKLRGTTR
10348	40716	A	10409	1	1059	
10349	40717	A	10410	2187	2429	

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10350	40718	A	10411	1	835	MRPFGDYPDGGIDDLKISFSVP AAGVGPHFDQYDVFIIQGTERR RWRVGEKLQMKQHCPHPDLL QVDPFEAIIDEELEPGDILYIPPG FPHEGYALENAMNYSVGFRAP NTRELI\SGLPDYVLQRELGGNY YSDPDVPPRAHPADVLPQEMD KLREMML\ELSTHPDPFKQWLG EFISQSRHDLDIAPPDPPYQPDE FSDALNQGKVLGALGGLRVLR MGDAVYPNGEKMDSPPRPALD ALASTIALTAKNFGDALEDPSF LAMLAALVNSGYWFFEG
10351	40719	A	10412	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
10352	40720	A	10413	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL
10353	40721	A	10414	342	528	
10354	40722	B	10415	32	587	
10355	40723	A	10416	1	2141	
10356	40724	A	10417	1	748	
10357	40725	A	10418	321	411	RNRDRYKQWKQDFFHDSYNR QRCGCWRLYRRHHR*CRRYRR QQPHLCRLYES*KKSCFHCLYR SRF/RLRVKYPRDMYSCLGTFL RSPVAIRIPLSRNQVKR
10358	40726	A	10419	1	2235	

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10359	40727	A	10420	1	1884	MGKDFMTKTPKAMATKAKID KWDVIKLKSFCTAKETTIRVNR INKIDKPLARLIKKKREKNQIDT IKNDKGDITTDPTEIQTTIREYY KHLYTNKLENLQEMDKFLDTY TLPRLNQEEVETLNRPITGSEIV AIMNSLPTKKSPGPDGFTAEFY QRYKEEL\IILIPK/PGQDTTKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSINVIQHINRAKDKNH MTISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPTVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNKRQTESQ IMSELPFTIASKRIKYLGIQLPRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VTYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNVRPKTI
10360	40728	A	10421	1	822	
10361	40729	A	10422	2738	2949	
10362	40730	A	10423	1	1134	
10363	40731	A	10424	1	2118	
10364	40732	A	10425	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRSITGHVH HQ
10365	40733	A	10426	2	1624	
10366	40734	B	10427	1	3690	
10367	40735	A	10428	1	1056	
10368	40736	B	10429	1	2265	
10369	40737	A	10430	1	2037	
10370	40738	A	10431	1	2406	
10371	40739	B	10432	670	2568	
10372	40740	A	10433	3	4072	
10373	40741	A	10434	1	3171	
10374	40742	A	10435	1	1542	
10375	40743	A	10436	1	1008	
10376	40744	A	10437	1	2241	
10377	40745	B	10438	1	2682	

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10378	40746	A	10439	644	949	MRKPTLGRTYPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10379	40747	A	10440	1	1088	MARKDIQVLIIGTYEYYLVKGE KVLTILAIKLKVLKWSGYPGLC LPEYHLGEVEGEDDMEVTAMD GRCLEVKQGSERLQVADQECV GDGSGRLCPFDRCECEQRLQLV RPGLCNPRAIALTTKPQSPSPNI KRLVIGEQMIDVLGPEKRRRRT TQEKIAIVQQSFEPGMTVSLVA RQHGVAASQEGSLTAVDAGEQ VVPASELAAAMKQIKELQRLL GKKTMENELLKEAVEYGRAKK WIAHAPLLPGDGERTDDWMDG RRSRHTDDTDVL*SASWRQQV QRQEQPVLRRRQQ*DFLLGWL LHHVAGQRGRPSSPVQSSAEQL RSFPVWYAVCVSPALRHQSSVL
10380	40748	A	10441	1	2781	MGKKQNRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMNEMN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRDLD
10381	40749	A	10442	1	2445	
10382	40750	A	10443	1	1428	
10383	40751	A	10444	1	2478	

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10384	40752	A	10445	1	1746	METQKTLQKINESRSWFFEKIN KIDRPLARLIKKKREKNQIDTIK NDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEAESLNKPITGPEIEAII NSLPTKKIPGPDGFTAEFYQRY KEELQHIKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMIISIDAEKASDKIQQPFMLK TLNKLGIDGTYLKIIRAIYDKPT ANIILNGQKLEAFPLKTGTRQG CLLSPLLFNIVLEVLARAIRQEK EKKCIRLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQIE SQIMSELPFTIASKRIQYLGIQLT RDVKDLFKENYKPLLNEIKEDT NKWKNIPCSWIGRINIMKMAM LPKVIYRFDAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPDKNKQWG KDSLFNKWCWEIWLAIGRKRK LDPFLTPYTKINSRWIKDFNIRP KTIKTLEESLG\IQDISMGKKFTS
10385	40753	A	10446	2	541	
10386	40754	B	10447	1	1533	
10387	40755	A	10448	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10388	40756	A	10449	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR

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10389	40757	A	10450	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10390	40758	A	10451	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10391	40759	B	10452	1	2259	
10392	40760	B	10453	1	684	
10393	40761	A	10454	1	1419	
10394	40762	B	10455	1	462	
10395	40763	B	10456	1	915	
10396	40764	B	10457	1	1659	
10397	40765	A	10458	1	1659	
10398	40766	A	10459	1	1224	MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYPGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVERINIVKM AILPKTAKNGPVLPPLHSEEKIP FN\FH*LFR*TITATKA*QKRR* MCQNLMTH\QNQRSGRSQIYF* RRRKNISDRSAVYR*RQLYIRR QPYAERPS\HVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFCKESQKLQQSAKKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLFTDSRGSKMTIDGI LPISDPTIKQDFRLLGQTSVDRL LQLSQGQAVKGNQLLPVSLVK RKTTLAPNTQTASPRALADSLM QLARQVSRLESGQ

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10399	40767	A	10460	1	2241	MEDEMNEMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSMRQKVNKDTQE LNSALHQADLIDIYRTLHPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDAFKA/EIQTTIK EYYKHLYANKLENLEEMDKFL DT\YTLPRLNQEEVESLNRPITG AEIVAIINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKLFQSIEK QGILPNSFYEASTILIPKPGRDTT EKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGM QGWFNIHKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQRFML KTLNKLGIDGTYFKIIRAIYDKP TANIILNGQKLEAIPLKAGTRQG CPLSPLLFNIVLEVLARVIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVTAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIMKMAIL PKVIYRFNAIPIKLPMTFFTELE KTK\FIWNQKSAHITKGILSQKN
10400	40768	B	10461	1	1254	
10401	40769	A	10462	551	868	SIQHWSRISSRLVYRSKAVAAA LLPMNCSLWSTQAGFLPRFG*R *TRHLSTIEPEDYNLLFRRVSLK LSVWLPTWQSKSNGWSQKCL WMHLKFDSLNALLPPTGF
10402	40770	A	10463	1	2985	MEDEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFTTCICDDAEDLQSPSTA GPWFGVLYTKGGPYPQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPNQCH IGEVLLDGFTAEFYRRYKEELV PFLLKLFQSIEKEG
10403	40771	B	10464	1	2277	

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10404	40772	A	10465	1	1064	
10405	40773	B	10466	1	1827	
10406	40774	A	10467	1186	1208	ATKMVRLSVAALVQRMKEFCA AKFPAVITCWWSVWAQSA*WR *CWRKTKI
10407	40775	B	10468	1	1992	
10408	40776	A	10469	1488	1920	RVRVTAVITERDCVSRSRWTAV IVRHCTGRSLPAASTVKQYRTS CWERWN/CRFGNDLPSSPVEWL TDN/EFMLPG**NTPVRPDVGLE PT*TRAACQESRCN/RLTPGIVL EIIGVWMQRWSLECRLAIPCIFG WLPRVVGEESGA
10409	40777	A	10470	1	1659	
10410	40778	A	10471	1	987	
10411	40779	A	10472	1	1278	
10412	40780	B	10473	1	1556	
10413	40781	A	10474	1	1905	
10414	40782	A	10475	644	949	MRKPTLGRTYPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10415	40783	A	10476	1	1217	
10416	40784	A	10477	83	1134	
10417	40785	A	10478	2450	2607	

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10418	40786	A	10479	1	2604	MPLRAFNPVSSFRWARGMTIV AALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGEK QAIIAGMAADALGYVLLAFAT RGWMAFPIMILLASGGIGMPAL QAMLSRQVDDDHQGQLQGSL AALTSLTSIIGPLIVTAIYAASAS TWNGNRACSSSVTRIVSILSRFI GIITPMNRNPPYTEASVTKQEK TALNMARFIRSQTLTLLEKLNE LDADEQADICESLHDHADELYR SCLARFGDDGNSYDHDYAKLA CLQVEGRGGGTFAHELLAVEY AGWISPAFRLKVNQTFIDYRTG RLQPAIPQSLPEALRLAADLAE QKQRLEQKMLMDAPKVEFAER VATASGVLIGNYAKVLGLGQN YLFTWLRDNGILI/CNR*TQERP QTRIHISWVFH/LLKKP*SIQAM EAG/LSFTTRITGKGQQWLMKR LLDARNRDRYKQWKQDFFHDS YNRQSAGHILSQCANLAATTSE YFIHKPHRLIAAETGYSQSTVV RAFREAVNKGILSVEIVIGDHRE RRANLYRFTPSFLAFAQQAKNA LIESKLKISSAATKVKAVLAKTL ALFNFLSTPPCQNDTPSPCQDD VAIKNKKSQVKKTKRSVSGGA GTTSLKKLTSWIAKAKAKADN LRLSKKRTQKHEFKQKVEAAA RKYAYLKNKRSPDIGGISNFDN
10419	40787	A	10480	1	2559	

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10420	40788	A	10481	1	1676	MLNGEKLAVKQEALLAAISEK DANIALLELSSSKKKTQEEVAA LKREKDRLVQQLKQQVEGRGG GTFAHELLAVEYAGWISPAFRL KVNQTFIDYRTGRLQPAIPQSLP EALRLAADLAEQKQRLEQKML MDAPKVEFAERVATASGVLIG NYAKVLGLGQNYLFTWLRDN GILIATGERRNVPKQEYISRGYF TLKETVIDTSNGSRISFTTRITGK GQQWLMKRLLDADVVRTTSIV MLAKVTFLSCITMSDFTFSGYE LACFVTHSGLSRSAGHILSQCA NLAATTSEYFIHKPHRLIAAETG YSQSTVVRAFREAVNKGILSVE IVIGDHRERRANLYRFTPSFLAF AQQAKNALIESKLKISSAATKV KAVLAKTLALFNFLSTPPCQND TPSPCQDDVAIKNKKSQVKKTK RSVSGGAGTTSLKKLTSWIAKA KAKADNLRLSKKRTQKHEFKQ KVEAAARKYAYLKNKRSPDIG GISNFDNLPHCMTVNEALNAVL AKNKDNEQWGAVAGAYIADIT DGEDRARHFGLMSACFGVGM VAGPVAGGLLGAISLHAPFLAA AVLNGLNLLLGCFLMQESHKG ERRGELLKIVVLPGDHVGQEIT AEAIKVLKAISDVRSNVKFDFE NHLIGGAAIDLQGGGGKPRCVS KSLMLH/CWHSCRLEPRWR*QR VQRIRL*VHP*AFFAPAVAFALP
10421	40789	A	10482	1	3213	
10422	40790	A	10483	1089	1373	
10423	40791	A	10484	2720	2968	TTTLVRLPCRSPKRRIKALRSQL RRKSILKPLLS*SR*STTK*RNTP CSQVSSLSRLSTRYRRRMKHSV NLVWTWVPYSSAP
10424	40792	A	10485	2	2264	
10425	40793	A	10486	1693	1980	
10426	40794	A	10487	1776	2026	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRSSNRACSS SVTRIVSILSRFIGI
10427	40795	A	10488	1323	2064	
10428	40796	A	10489	53	243	WTVPLGAVPPVRMHEGLGCW CKLNGEVCMSGMCLLCWWDC D*RHDLKANLDRLMNVCQDGR KR
10429	40797	A	10490	1	3117	
10430	40798	A	10491	1	1227	

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10431	40799	B	10492	1	2119	
10432	40800	A	10493	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRSITGHVH HQ
10433	40801	A	10494	1	2822	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
10434	40802	A	10495	2	163	
10435	40803	A	10496	4051	4355	MRKPTLGRTYPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10436	40804	B	10497	1692	1781	
10437	40805	B	10498	1	3477	
10438	40806	A	10499	179	439	KKELVNLTTD*SLENR/WIDVL GPEKRRRRTTQEKIAIVQQSF/G TGDDGLPRCPATWCSSQPVISL A*AIPGRKSYCCRRRRTGCSCL
10439	40807	A	10500	1	7456	MYQANGKQKKAGVAILVSDKT DFKPTKIKRDKEGHYIMVKGSI QQEELTILNIYAPNTGAPTFIQQ VLSDLQRDLDSHTLIIGDFNTPL STSDRSTRQKVNKDTQELNSAL HQADLIDIYRTLHPKSTEYTFFS APHHTYSKIDHILGSKALLSKC KRTEIITNYLSDHSAIKLELMIK NLTQNHSTIWKLNNLLLNDYW VHKEMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRKQERSKIDT
10440	40808	A	10501	2476	2718	WPLRGRGGHRAAPGRHLHLQQ RLLLRLHLTACLLQDALDG/GP PRCWRGSCRWRCSAGPPRSWA RRPSATRSPSWPALECS

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10441	40809	A	10502	2	4517	HRLANWIKSQDPSVCYIPETHL TCRDTHRLKIKGWRKIYQANG KQKQAGVAIHISDKTDFKPTKI KRDKEGHYIMVKGSIQQEKLTI LNVYAPNTGAPRFIMQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR LTRQKVNKDTQELNSALHQVD LIDIYRTLQPKSTEYTLFSAPHH TYSKIDHILGSKALLSKCKRTEII TNYLSDHSAIKLELRIKKLTQIR STAWKLNNLLLNDYWVHNEM KAEIKMFFKNNEN
10442	40810	B	10503	88	501	
10443	40811	A	10504	1	971	MWALFMIRNVKKQRPVNLDLQ TIRFPITAIASILHRVSGVITFVA VGILLWLLEYRLSYLKGSSKLR DYGQLLTLEIPAALLPIHTGIVN QNINCTETLTASSDNLLRRAFC GDTHLHEVHLNTLFFNHFLCFA VIFDETRNKDICATSGQHAHFV DKKRKRELLSHMIGKGNWQQV LVFTRTKHGANHLAEQLNKDG IRSAAIHGNKSQGARTRALADF KSGDIRVLVATDIAA/RGLDIEE LPHVVNYELPNVPEDYVHRIGR TGRAAATGEALSLVRSFFDWC DDCAAAGGMGNRNAQLADGI YHLRCIELYLGDGMADFL

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10444	40812	A	10505	1	2201	MSFDSLGLSPDILRAVAEQGYR EPTPIQQQAIPAVLEGRDLMAS AQTGTGKTAGFTLPLLQHLITR QPHAKGRRPVRALILTPTRELA AQIGENVRDYSKYLNIRSLVVF GGVSINPQMMKL\RGGVDVLV ATPGRLLDLEHQNAVKLDQVEI LVLDEADRMLDMGFIHDIRRVL TKLPAKRQNLLFSATFSDDIKA LAEKLLHNPLEIEVARRNTASD QVTQHVHFVDKKRKRELLSHM IGKG\NWQQVLVFTRTKHGAN HLAEQLNKDGIRRAAKHGNKC KCAYSKFQKPSPHIFTMLIGVC GVNQSAITNVSNVSNMAKISGS GSHRLTKRVIKRDMRPIINHPV AYSDRRRLQTELLFWHARWLN HTRRQFRIKEGDNGGQCFLFLW TGRFNFNLPSFGRIQHQQRNNA VGFSLGAFVITFIAGRACMPSLF VISTVCLTVMVYVFPAYDGVT GRFYRASGSSLPVALQYTPNGA SRRYNQWRPSRMLSSLKKQKW RKGMSESLHLTRNGSILEITLDR PKANAIDAKTSFEMGEVFLNFR DDPQLRVAIITGAGEKFFSAGW DLKAAAEGEAPDADFGPGGFA GLTEIFNLDKPVIAAVNGYAFG GGFELALAADFIVCADNASFAL PEAKLGIVPDSGGVLRLPKILPP AIVNEMVMTGRRMGAEEALR WGIVNRVVSQAELMDNARELA
10445	40813	A	10506	1	168	MCEKNLAYAHKVKAALEKGA SPGDFPREDYETNWEG\RFTLA DLNIHGKRALGMDV
10446	40814	C	10507	1	3861	
10447	40815	A	10508	1	7407	
10448	40816	A	10509	290	661	QPLPEGRW/THLWHNDELDGS RWHK/QQHGFLSLPVYVRDNT LRALGNNDQRPDYVWHE/GTA FHLFN\LKAARTGNTITAIDASE ANNWTLCLRNGVKVNGLQDG SQAESEQGLVVKPQGNALTITL
10449	40817	A	10510	3	510	KFHFMSPFPAHSMVQALE*LYA LGGLDKDCRLTEPLGMRIAEFP LNPMFAKMLLESGNFGCSQEIL SIAAMMQIQNIFVVPPNHKSHAI RVHRKFAVEEGDHLTMLNIYE AFIKHNKDSKWCQEHFLNYKG LVRAATVREQLKKLLVKFQVP RKSSEGDPDLVLRCIVS

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10450	40818	A	10511	1	1920	MIWGRAWWLTPVIPALWAAK VAGRVAEERGAVLGHEVGYCI RFDDCTDQLATRIKRLTESFSLI LSVIMLDEAHERTLYTDIAIGLL KKIQKKRGDLRLIVASATLDAD EEVETVVSMLIEQARALARTG MKRHLRVLPMYAGLPSFEQMK VFERVSRSVRKVIVATNVAETSI TISGIVYVIDCGFVKLRAYNPRT AIECLVVVPVSQASANQRAGR GGRSRSGKCYRLYTEEAFDKLP QSTVPEMQRSNLAPVILQLKAL GIDNVLRFHFMSPPPAQSMVQA LELLYALG\SLDKDCRLTEPLG MRIAEFPLNPMFAKMLLESGNF GCSQEILSIAAMMQIQNIFVVPP NQKSHAIRVHRKFAVEEGDHL TMLNIYEAFIKVSTTTARSAAST HHPLEHNKDSKWCQEHFLNYK GLVRAATVREQLKKLLVKFQV PRKSSEGDPDLVLRCIVSGF\FA NAARFHSTGAYRTIRDDHELHI HPASVLYAEKPPRWVIYNE\LL QTSKYYMRDVTAIESAWAVGS WLHTFYSTRERTCSLESQKGPR SRDPLRREPTVYSCRDCWRPLL HAAAPGPRWGELAPAPVECLV ALKWAAACSLVLSSRCPQHLH PCWDPGGLCAWAGILLCCSGQ SGSWLTQHAH
10451	40819	A	10512	3	414	
10452	40820	B	10513	62	1408	

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10453	40821	A	10514	1	1388	MGTSSIFLCVLFLCGALGLTMS PARGRLRCYICGFTKPCHPVPTE CRDDEACGISIGTSGCRGIFQVP DGQRDSRSHFPADVTKITWAC GQSPPGFKPLFPSCSSPKTGQM DVLIDLDFGFELRNRGIWGEGA IRDTEEKSADNLEPCSSPPPLEE VICCEGNAGFYEVGCVSTPLEA GYSVLGWNHPGFAGSTGVPFP QNEANAMDVVVQFAIHRLFFH PQDIIIYA\LAIGGFTATWAAMS YPDVSAMILDASFDDLVPLALK VMPDSWRGLVTRTVRQHLNLN NAEQLCRYQGPVLLIRKTQDG NLTPTVP\KDICSNRANCLLVKA LQ\HRYPG\VMAEEGLLVARQW LEASSQLEEASIYSRW\EVEED WCL\SVLR\SY\QAEHGADFPW\ SVGEDMSA\DGR\RQL\ALFLAR KHLHNFEATHCTPLPAQNFPRC PWHPLGTQLGLIMEEWGERRH
10454	40822	A	10515	1	1519	MGFLPKLLLLASFFPAGQASWG VSSPQDVQGVKGSCLLIPCIFSF PADVEVPDGITAIWYYDYSGQR RVFMGNPEHRVCNLLLKDLQP EDSGSYNFRFEISEVNRWSDVK GTLVTVTARSLSPPGRHLETLH MAMSWQDHGRILRCQLSVAN HRAQSEIHLQVKYAPRGVKILL SPSGRNILPGELVTLTCQVNSSY PAVSSIKWLKDGVRLQTKTGV LHLPQAAWSDAGVYTCQAENG VGSLVSPPISLHIFMAEVQVSPA GPILENQTVTLVCNTPNEAPSD LRYSWYKNHVLLEDAHSHTLR LHLATRADTGFYFCEVQNVHG SERSGPVSVVVNHPPKTPTMM VFVEPEGGLRGILDCRVDSEPL ASLTLHLGSRLVASSQPQGAPA EPHIHVLASPNALRVDIEALRPS DQGEYICSASNVLGSASTSTYF GVRALHRL/LSVPAAALGPGTA/ VWASCSCCWAWGPATPGGTG YYLTGTYKSGGQTQMLSASLF
10455	40823	A	10516	3	615	
10456	40824	A	10517	373	631	SGGPDTDVVSIPYSCSRMHLCS *LCELLSFSWETLCRAVKENEL PKKE*RAPANQGPTGESSLSGL SDSPLQPGGDGVEERRALLF

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10457	40825	A	10518	1	5521	MANRFRSGEDSGGAIWQDCVE EGASELGFLESLLYTQGNDRKQ CSLTNQGRQVFALLMLRKGHL HVFVILFGPAGPAPPQPLPSVEQ VPLSLVPGPKGVAVSRTPPFFH QVHDCPFQDPKWEEQGSWDKI AALAIAELTLTSPVARDTSDPQ CAQQAAFLHGQASWGVSSPQD VQGVKGSCLLIPCIFSFPADVEV PDGITAIWYYDYSGQRQVVSHS ADPKLVEARFRGRTEFMGNPE HRVCNLLLKDLQPEDS
10458	40826	A	10519	1	1149	
10459	40827	A	10520	111	370	SHRRSLGEAARHPSFRPAGTAF E*VSQKVVHPRDLEDRSACVPV GCSLTRESFFRLNNQPHGTRFLP IPSNPESSRRAVPSAHLTV
10460	40828	A	10521	1	220	
10461	40829	A	10522	654	967	
10462	40830	A	10523	2	1415	
10463	40831	A	10524	2	293	CGKAFTQHSRLIQH/QRMHTGE KPYEYWEFGEKPRIYLQRKTFM KLDTTTGEGQSYQRNQMPECP YGEKPCKCKECGKSFRR/SSELT RHQRAHTGEKP
10464	40832	A	10525	51	378	GDFSPQKPPMAPHGCLTYLAFQ KVKEGKKEEKKEKKKRKKERK KERKKERKKERKKERKRKEKK E\EGKEGRKEGRKEGRKEGRKE KKEISKKEIVAPTSLNPLKCSVL
10465	40833	A	10526	1	235	
10466	40834	A	10527	545	793	NKEMHWPCTGLCSHQPWGFK DCSLLE*RLPGQQEQNSIERKK RKKEKKEKKEKRKKRKKGKKE ERKKERKYHFILLLGMPTS
10467	40835	A	10528	127	376	
10468	40836	A	10529	3	710	EPG/NPERLK/GFSYPEFEDLDA LFSTLGLNEESVDSFDDYLPRR GVDSFGDKYQD/RCNSDQYHD GCQDRFRDGSHQDMGQCGGR D*DDD*GSRDYDRGYDSATGS CRRAFGSGYLRDDDY\WESSET EQQPPTGSEGKVPPVQPSEERP AKKDENKVDGMN/APKVQSGN SGRGPGDGGNKDCWRESDRKD GKKDQVCRSAPESKKPEENPAS KFSSASKCAAVSVDGEDEKEG

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10469	40837	A	10530	1	548	MQRSENDILGMDLRPLICIKDE KEEVGEKEEGEKEEEECEEQEE EGGKEWEEPGNYHLGQSLSHD WQSSETEQQPPTGSEGKVPPVQ PSEERPAKKDENKVDGMN/APK VQSGNSGRGPGDGGNKDCWRE SDRKDGKKDQVCRSAPESKKP EENPASKFSSASKCAAVSVDGE DEKEGADYTK
10470	40838	C	10531	37	289	
10471	40839	A	10532	1	1062	
10472	40840	A	10533	1	1977	
10473	40841	A	10534	1	2050	LPLLHAGFNRRFMENSSIIACYN ELIQIEHGEVRSQFKLRACNSVF TALDHCHEAIEITSDDHVIQYV NPAFERMMGYHKGELLGKELA DLPKSDKNRADLLDTINTCIKK GKEWQGVYYARRKSGDSIQQH VKITPVIGQGGKIRHFVSLKKLC CTTDNNKQIHKIHRDSGDNSQT EPHSFRYKNRRKESIDVKSISSR GSDAPSLQNRRYPSMARIHSMT IEAPITKVINIINAAQENSPVTVA EALDRVLEILRTTELYSPQLGTK DEDPHTSDLVGGLMTDGLRRL SGNEYVFTKNVHQSHSHL\AMP INHSMDV\PPCISQLLDNEESWD FNIFELEAITHKRPLVYLGLKVF SRFGVCEFLNCSETTLRAWFQV IEANYHSSNAYHNSTHAADVL HATAFFLGKERVKGSLDQLDE VAALIAATVHDVDHPGRT\NSF L\CNAGSELAVLYNDT\AV\LES HHTALAFQ\LTVKDTK\CNIFKN ID/RGNHYRTLRQAIIDMVLATE MTKHFEHVNKFVNSINKPMAA EIEGSDCECNPAGKNFPENQILI KRMMIKCADVANPCRPLDLCIE WAGRISEEYFAQTDEEKRQGLP VVMPVFDRNTCSIPKSQISFIDY FITDMFDAWDAFAHLPALMQH LADNYKHWKTLDDLKCKSLRL PSDRLKPSHRGGLLTDKGHCES
10474	40842	A	10535	2	445	ERTFNCCYPGCHFKTVHGMKD LDRHLRIHTGDKPHKCEFCDKC FSRKDNLTMHMRCHTSVKPHK CHLCDYAAVDSSSLKKHLRIHS DERPYKCQLCPYASRNSSQLTV HLRSHTGPGP\ADLLEHSRLHQ ADHPEKCPECSYSCSSAA
10475	40843	A	10536	1	957	

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10476	40844	A	10537	1	1438	MSRRKQAKPQHLNSEEPRPARR ECAEVAPQVAGEPASELDDDV PKANCLSTESTDTPKAPVITLPS EAREQMATLGERTFNCCYPGC HFKTVHGMKDLDRHLRIHTVP FCFSKVYWNGFQLGMISPPKGT MSGDIFDCYNWRRKGSTGICIW TGGGGTPICPGYHLGQIFVAILT KKPLTLTPYVFEGDKPHKCEFC DKCFSRKDNLTMHMRC\HTSV KPHKCHLCDYAAVDSSSLKKH LRIHSDERPYKCQ\VCPYASRNS SQLTVHLRSHTA\GDTPFQCWL CSAKFKISSDLKRHMIVHSGEK PFKCEFCDVRCTMKANLKSHIR IKHTFKCLHCAFQGRDRADLLE HSRA/LHQADHT\EKCPECSYSC SSAAALRVHSRVHCKDRPFKC DFCSFDTKRPSSLAKHVDKVHR DEAKTENRAPLGKEGLREGSSQ HVAKIVTQRAFRCETCGASFVR DDSLRCHKKQHSDQSEKQNLT
10477	40845	A	10538	1	1427	MIAFDSMSHIQVMLMQEESTAP ATLEHILGHSQLCGSDGLAHAA VWVLAHLHYWFTGLSPGPMD VLPLHPAISSSFHLWRVAFISKA GKPRAAGHLLKRFLRCQFQRA ASSLLFTTVEAMLGTESGTEKV MRGAGTWYHIIIENWPSAECV WTEEYQQGRGQEDSAEDRKLF VGMLNKQQSEDDVRRLFEAFG NIEECTILRGPDGNSKGCAFVK YSSHAEAQAAINALHGSQTMP GASSSLVVKFADTDKERTMRR MQQMAGQMGMFNPMAIPFGA YGAYAQALMQQQAALMASVA QGGYLNPMAAFAAAQMQQMA ALNMNGLAAAPMTPTSGGSTP PGITAPAVPSIPSPIGVNGFTGLP PQANGQPAAEEI\FANGIHPYPA QSPTAADPLQQAYAGVQQYAG PAAYPAAYGQISQAFPQPPPMIP QQQREGFVSFDNPASAQTAIQA MNGFQIGMKRLKVQLKRPKDA NRPY

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10478	40846	A	10539	1	547	AAAPMTPTSGGSTPPGITAPAV PSIPSPIGVNGFTGLPPQANGQP AAEAVFANGIHPYPAQSPTAAD PL\QQAYAGVQQYAGPAAYPA AYGQISQ\AFPQPPPMIPQQQRE GPEG\CNLFIYHLPQEFGDS\EL MQ\MFLPFGFRE/RFDNPASAQT AIQAMNGF\QIGMKRLKVQLKR PKDANRPY
10479	40847	A	10540	96	1080	WFKCYGCNSS/RDWQRSTYLLS WEVR/G/RPVPDSGCKAVVALC SQPAHPSNICKGVGGCLTK\HLL LMGAMGIRVACLEVWRDGEER GGEEATFFTSLAERQVGTAHRH LHQPALYIQIRKVPAALHMCVV QKPSLFQADSRAPLEQGLRQQA SLATARPIVSGANAGPAGLKVP QAAQLQLSPYLHRGVGDEACR YGRSQPTRKAFALCICAAPALP CPALDGSWMVCGLGQETRTSL ANVQSFTQRPQQQPLTVWMLN RGRKPAQGTLTVICPIGPGHLLT STITESVCVPRRNKYHSRTLPA AQHCQWLVTAVPTALGLVIRA GSKKLC
10480	40848	A	10541	1	392	
10481	40849	A	10542	1	110	FFWSHS*VYYTCFLLQN*KHLK PGPSGSLSPSISGN
10482	40850	A	10543	1	978	MAAATRGCRPWGSLLGLLGLV SAAAAAWDLASLRCTLGAFCE CDFRPDLPGLECDLAQHLAGQ HLAKALVVKALKAFVRDPAPT KPLVLSLHGWTGTGKSYVSSLL AHYLFQGGLRSPRVHHFSPVLH FPHPSHIERYKN\DLKSWVQGN LTACGRSLFLF\DEMDK\MPPGL \MEVLRPFLGSSWVVYGTNYR KAIFIFISNTGGEQINQVALEAW RSRRDREEILLQELEPVISRAVL DKPAPLPSPNSGHHWKERLLD AVVPFLPLQRHHVRHCVLNEL AQLGPGAKGMRVVQAVLDSTT FFPEDEQLFSSNGCKTVASRIAF

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10483	40851	A	10544	1	560	ATSPHQSQQSTVDVGQLHDPQP YPQHAIQVQHIQVSEPTASAPSS AQGSSSTQGQG\LQQQQQQQQ NSSVQHTYLPSAWNSFRGYSSE IQMMTLPPGQFVITDSGVATPV TTGQVKAVTSGHYVLSESQSEL EEKQTSALSGGVQVEPPAHSDS LDPQTNKQQQTTQYIITTTTNG NGSSEVHITKP
10484	40852	A	10545	3	205	
10485	40853	A	10546	2	348	ADQARGKPTEWAVSATQFQLD FPIT*CYGLL*QRVSRRHIGALQ GKPVPLLHVLLYPITPREGGLG DRARLCLKQQQQQQQQQQQQ QLLLLLLLLLLLLLLQQCEGT EGRPFPD
10486	40854	A	10547	1	1146	MVTYKLVLIRCGESTWNLENH FSS\WQKRA/IRILWTVLDAIDQ MRLPVVRTWCLKEWHYGSLA GLNKAETSAKHGEAQSNISKGC RYADLTEDQLSSGESLKEIVPQI KEGKWVLTAAHGNSLRGIVKH LEGLSEEAIMELNLPTGIPIVYE LDKNLKPIKPMQFLGDEVTLCK AMEAVAAQSKAKKRRPAGML LSPGTPSLAIPSSAPAPCTCHTD HIWNSPVYSDLAILRANPFCVHI SKANYLVNELHTAVNVAGLYI GWRCPHYLWDCFRIGDESRCF CGHLLREHRIISDISVPCKVSQC RCFMFCFIPSRPEEVGCCCGCFE SNFLCAACDRRWEEHETFFDTQ KTRQRGGRPRGADYVPFAEMA VLREAILSNSDF
10487	40855	A	10548	2	516	GRLNERHYGGLTGLNIAETAA KHGEAQVKIWRRSYDVPPPPKE PDHPFYRNIRMDRRYADLTED QLPSCESLKDTIARALPFWNEEI GPQIKEGKRVLIATHGNSLRGIV KPWEGLSEEAIMELNLPTGIPIV YELDKNLKPIKPMQFLG\DEET VRKAMEAVAAQGKAKK
10488	40856	B	10549	123	237	

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10489	40857	A	10550	1	952	PAAPQVAGRLGLGCPLHLHVF AVVSAMLPLLRCVPRVLGSSV AGLRAAAPASPFRQLLQPAPRL CTRPFGLLSVRAGSERRPGLLRP RGPCACGCGCGSLHTDGDKAF VDFLSDEIKEERKIQKHKTLPK MSGGWELELNGTEAKLVRKVA GEKIPVPF\NINNSIPP\TFYGEKD PSQSQKV\EDREPELTSLPKF\VV EVIKNDDGRKA\LVLDCHYPED EVGQEDEAESDIFSI\REVSFQS\ TGESEWKDTNYTLNTDSLDWA LYDHLMDFLADRGVDNTFADE LVELSTALEHQEYITFLEDLQEV LSRAHRADRC
10490	40858	A	10551	1	879	AAGCRKENSLDLRSQFPRGRDS EDFNVKEEANAAAEEIRYTHIL NRVLPPDIRILAWAPVEPSFSAR FSCLERTYRYFFPRADLDIVTM DYAAQKYVGTHDFRNLCKMD VANGVINFQRTILSAQVQLVGQ SPGEGRWQEPFQLCQFEVTGQ AFLYHQVRCMMAILFLIGQGM EKPEIIDE\LLNIEKNPQKPQYSM AC\EFPLVL\YACKFENVKWIYD QE\LRSSNITHLQQLWANHAVK THMLYSMLQGLDTVPVPCGMG PKMDGMTEWGNVKPSVIKQTQ CLCRRSEDAHI
10491	40859	A	10552	231	358	
10492	40860	A	10553	2	319	
10493	40861	A	10554	573	1660	MAAPTPARPVLTHLLVALFGM GSWAAVNGIWVELPVVVKELP EGWSLPSYVSVLVALGNLGLL VVTLWRRLAPGKDEQVPIRVV QVLGMVGTALLASLWHHVAP VAGQLHSVAFLALAFVLALAC CASNVTFLPFLSHLPPRFLRSFF LG\QGLSALL\PCVLALVQGVG RLECPPAPINGTPGPPLDFLERF PASTFFWALTALLVASAAAFQG LLLLLPPPPSVPTGELGSGLQVG APGAEEEVEESSPLQEPPSQAA GTTPGPDPKAYQLLSARSACLL GLLAATNALTNGVLPAVQSFSC LPYGRLALPPGLWCWAVLPIP WACFLGHGCCCAGPWQGWGG LLSAGRVLWGLPDGRWQS

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10494	40862	A	10555	154	850	QFFRVITCLPFKGPDYRLYKSEP ELTTVAEVDESNGEEKSEPVSEI ETSVVKGSHFPVGVVPPRAKSP TPESSTIASYVTLRKTKKMMDL RTERPRSAVEQLCLAESTRPRM TVEEQMERIRRH\QQACLREKK KGLKCFSVLSDQSPLQSPSNLR DNPFRTTQTRRRDDKELDTAIR ENDVKPDHETPATEIVQLKETE PQNVDFS/IRGLLDCPSVSILPGR SIKRAKNQNS
10495	40863	C	10556	39	436	
10496	40864	A	10557	2	959	
10497	40865	A	10558	34	1044	QGCAVAGPLHPARLPCCVHGC PVRMHALSLCHVRCHFAVTFR LMYLDWLPTVIEPCGVGSNKV PVVQHPHHVHPLTPLITYSNEH FTPGNPPPHLPADVDPKT/GMC SCGTGRCAVARTCRIRSCVPCE ALSPCDARGAHSAGIPRPPHPPD ISPYYPLSPGT\QGQPVYPITTGG FRHPYPTALTVNASMSRKHQD SKKEEEKKKPHIKKPLNAFMLY MKEMRAKVVAECTLKESAAIN QILGRRLGYNARAFGLKRGWR LDKYRGFVWMEMAVWSLPPA FSFQGKKKKRKRDKQPGETND KPESSLGASSLMVVGNWTYRN QEKHIPTLELDHTVSV
10498	40866	A	10559	2	398	
10499	40867	A	10560	174	362	
10500	40868	A	10561	14	266	
10501	40869	B	10562	67	474	

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10502	40870	A	10563	1938	3291	ERRKRFGMLDATDGPGTEDAA LRMEVDRSPGLPMSDLKTHNV HVEIEQRWHQVETTPLREEKQV PIAPVHLSSEDGGDRLSTHELTS LLEKELEQSQKEASDLLEQNRL LQDQLRVALGREQSAREGYVL QATCERGFAAMEETHQKKIED LQRQHQRELEKLREEKDRLLAE ETAATISAIEAMKNAHREEMER ELEKSQRSQISSVNSDVEALRG QYLEELQSVHRELE\VLSEQYS AKCLENAHLAQALEAERQALR QCQRENQELNAHNQELNNRLA AEITRLRTLLTGDGGGEATGSP LAQGKDAH*LKGLM\RVKESEI QYLKQEISSLKDELQTALR\DK KYASDKYKDIYTELSIAKAKA\ DC\DISRLKEQLKAATEALGEKS PDSATVSGY\DI\MKSKSNP\DFL KKDRSCVTRQLRNIRSKSLKEG LTVQERLKLFESRDLKKD
10503	40871	B	10564	58	4405	
10504	40872	A	10565	3	156	NSSHHCHHHHHHHNHHHQHH QHNHC\HQHHHYNHHYDYHH DDNYYHHHHHHH
10505	40873	A	10566	10	445	HRSTITRQCPSGLETRIALLPPA VFPSGSRTLPPSTPGSSSPQPR/P PLTRGPGPPRTHALASGTRGPA RGEEKVADTPHHGEGGCPNSE KEPFLHPTAPPPRLPTPSPESGP VPHTLQQAPPLRRHLGGTPAGA PASPQSSEWGG
10506	40874	A	10567	1	288	
10507	40875	A	10568	50	542	TLSPERLSPELRLLPYMITLGDA VHNFADG\LAVGAAFAI\SWKT GLATSLAVFCHELPHELGGLRP LAAPGAVPCAKELLLNLASALT AFAGLYVALAVGVSEESEAWI\ LAVAT\ALFLYVAICDMLPAML KVRDPRPWLLFLLHNVGLLGG WTVPADAVPVRG
10508	40876	A	10569	1	690	
10509	40877	B	10570	34	465	
10510	40878	A	10571	1	624	
10511	40879	A	10572	3	933	

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10512	40880	A	10573	1	1481	RRFPPAGAVAVIERGVRGGSQR CRTMADQLYLENIDEFV\TDQN KIVTYKWLSYTLGVHVNQAKQ MLYDYVERKRKENSGAQLHVT YLVSGSLIQNGHSCHKVAVLRE DKLEAVKSKLAVTASIHVYSIQ\ KAMLKDSGPLFNTDYDILKSNL QNCSKFSAIQCA\AAVPRAPAES SSSSKKFEQSHLHMSSETQANN ELTTNGHGPPASKQVSQQPKGI MGMFASKAAAKTQETNKETKT EAKEVTNASAAGNKAPGKGN MMSNFFGKAAMNKFKVNLDS EQAVKEEKIVEQPTVSVTEPKL ATPAGLKKSSKKAEPVKVLQK EKK\RGKRVALSDDETKETENM RKKRRT\IKLPESDNSEYEVFPD SSGAYEAESPSPPPPSPPLEPVP KTEPEPPSVKSSSGENKRKRKR VLKSKTYLDGEGCIVTEKVYES ESCTDSEEELNMKTSSVHRPPA MTVKKEPREERKGPKKGTAAL GKANRQVSITGFFQRK
10513	40881	A	10574	1	100	

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10514	40882	A	10575	2	2271	PELLTEGVKEPIMDSQERDSGD PLVDESLKRQGFQENYDARLSR IDIANTLREQVQDLFNKKYGEA LGIKYPVQVPYKRIKSNPGSVII EGLPPGIPFRKPCTFGSQNLERIL AVADKIKFTAT\RPFQGLIPKPD EDDANRLGEK\VILREQ\IKELF\ NEKLR*GPWGLNRPVLVPYKL\ IRDSPDAVEVPGLPDDIPIRNPN TYDIHRLEKILKAREHVRMAIIS QLQLLQQQQHHISEGRPFAEIC NDAKVPGESEARKPPFCPVGTR LFLLKKREPEVSMNKDRYPQE APRNLQSLRTLLDILDDPRGGC VHLRQSQSRWRGADTRELPRG MLEGLRQLLSAIGCPRDPTCAP AQPGDQPLQRLAFTLANEPQTV LEKPPPRFRRRGAARSPEQLYTP RRGGVLPAEPERTQSASADAGS LACRALEVDSGCPTGPPCPKGS RRLTITSGVDCGLLKQMKELEQ EKVVLLQGLEMMAGSRLQRLQ PVQDRQCRLGQSRASADFGPA GSPHPLGRLLPKVQEVARCVGE LLAAAGASRALPTSSSGPLCPA LTFTSFPGWQQQTILMLKEQNR RLTQEVTEKSGRVMQLEQKSA LIMKQLFEAQALSQQDGEASGL HLHLARLGWAEPQGSSVTQPFE GGRPVSPNVSGWRPPAAQAVP EWAPSCPTCHPGFPGPPPAGPR TEPLTRFWLLVLTWAGALLSLH
10515	40883	A	10576	346	3136	ALRTKRLWPGGHCRAEAPQWP P/ASPLAPATALAAHSRHLSLCR SDKGSMSEDCGPGTSGELGGLR PIKIEPEVLDIIQVTVPDALPTSE EMTDSMPGHLPSEDSGYGMET LTDKKWTWDGAKAIGISEPIKV LYSKFLMHPEELFVVGLPEGISL RRPNCFGIAKLWKILEASNSIQF VIKSGEEIRWDRELFCRACSMP GGSLLQIAKSYTTGLESKSCDP AVESKASAGQDEMQPHARPKL LTEGVKEPIVD
10516	40884	A	10577	60	352	
10517	40885	B	10578	1	720	
10518	40886	B	10579	1	1478	
10519	40887	B	10580	1	1895	
10520	40888	A	10581	2	413	

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10521	40889	A	10582	2	969	WGSWAPQSRGCPYQPGAAQGR ALAPQHRGSCSPPWTGGGKE/Y LMRAHFGLPSVEAEDKEGKPPI SVKFEIPYFTTSGIQVRLAPGSL YGRKRSSLGKSHPSLLQVDGQ YSQQQGAGHPRGTKRGSQTPG ARQRVEPGKCWPVVCVPHVPC PPTSTALRKHLRPQRAIYTSRLA PGALGGHCSVCLLPGLAGLAC GAFPGPAWVTRCCHSARSVLT HQGAPPGPDITVPARLPEPEVE VSCRGRRPALLNAQQSPPSLPPP PPSAAAEASCSHHVRQRRLRAG PEGQGFYLFHDRNKHSILKLAK PREPFCVVTDSRIQFGPPH
10522	40890	A	10583	50	1083	NPRAIFKSVRTCPVPPTQPCRNV KARSCGVGAGTTSFTLSVWPH RYITQEGHKLETGAPRAPGTVT NAVCWRSEGIKYRKNEVFLDVI ESVNLLVSA\NGNVLRSEIVGSI KMRVFLSGMPELRLGLN\DKVL FDNTGRGK\SKSVE\LEDVKFHQ CVRLSRFENDR\TISFIPPDG\EFE \LMSYRLNTHVK\PLIWIESVIEK HSHSRIEYMIKAKSQFKR\RSTA NNVGDPHFPLPNDCRLNPSFK\T TVGERLSWVPENSEIVWSIKSFP GGKEYLMRAHFGLPSV\EAEDK EGKPPDSVFKF\EIPYF\LTSGIQ VRYLKIIEKSGYQALPWVRYIT QNGDYQLRTQ
10523	40891	C	10584	175	454	
10524	40892	A	10585	1	193	LLPRPGSGLDFLLSPVLPS/HSAS WACPLPRPSPMPSSCC*R*RKE MASGFSKGPTLGCCPTCPP
10525	40893	A	10586	2780	2965	SPSQGESIPT*WRPTGPSPPTSSP GPA*SSLSPRPSPSSASASPSMC VRPSMWAASLLKSL
10526	40894	A	10587	1	1502	
10527	40895	A	10588	1256	1990	RCAPMTTCAWASCCSPWPTPF GTGPPSTSVSTSWPWQPWGWG WL*VGAAPAGGRQHPSPPALPR RSSGRSKLSRPSLCQLVPGIL*T RLLSPPQKESLPWRGSWREFPL PQLNTLPATEADPGVSSLPSAQ RHLHSYKIKVLSRQESLAPAPA SGYPESTALPQNGRGPWAVGF GQIPFLCIHNVGRSLGAGPGSG KPLPCVFRSTFSSSHQYCRLGR KHNFHFTKGKLRCGCGPGDGR

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10528	40896	A	10589	375	678	RCCCCTTRPARKCRTTMGIRHS TWPAPTATRTTHSGSRSPGSTA ASPRGLCPRPALTDCPCGHLSG LPVASV*AGSCPHVPGDQTTRK SGTVFPTQCTRP
10529	40897	B	10590	1	2452	
10530	40898	B	10591	1	1140	
10531	40899	A	10592	1	1617	
10532	40900	A	10593	1	1448	RERSCLHLVCIRCSCDVVEMGS VLGLCSMASWIPCLCGSAPCLL CRCCPSGNNSTVTRLIYALFLL VGVCVACVMLIPGMEEQLNKIP GFCENEKGVVPCNILVGYKAV YRLCFGLAMFYLLLSLLMIKVK SSSDPRAAVHNGFWFFKFAAAI AIIIGAFFIPEGTFTTVWFYVGM AGAFCFILIQLVLLIDFAHSWNE SWVEKMEEGNSRCWYAALLS ATALNYLLSLVAIVLFFVYYTH PASCSENKAFISVNMLLCVGAS VMSILPKIQESQPRSGLLQSSVIT VYTMYLTRS\CMTNEPETNCNP SLLSIIGYNTTSTVPKEGQS\VQ WWHAQG\IIGLILFLLCVFYSSIR TSNNGQVNKLTLT\SGESTLIGR WVGAR\SDGITGRDGGTDVSPE AVRINGK/RDGCSLYSYSFFHF MLC\LASLYIM\M\TLTSWYRYE P\SAWMESQWTAVL/WVKISSS WIGIVLYVWTLVAPLVLTNRDF
10533	40901	A	10594	3	343	GVLLCRL*QGQNYW/NFLQTK VTGNMRDKRTTPMPEFLHASW PNTELRYWKENCPESQKGP*PM MALS*GCPLPWPAPNVTSSSKG WSPGQLWMYRFGRPLRISSETG WSLWLT

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10534	40902	A	10595	1	2500	MEDAWGIRKETGRVKEEAEKV TGWGNNWRNVEKSSMSRKVK AARPGFKKLPMTSDIPPKCTIKD LLPKEKSSTEAVFHTVVLERHE SPDIEDFSFKEPQKNVHDFECQ WRDDTGNYKGVLMAQKEGKR DQRDRRDIENKLMNNQLGVSF HSHLPELQLFQGEGKMYECNQ VEKSTNNGSSVSPLQQIPSSVQT HRSKKYHELNHFSLLTQRRKA NSCGKPYKCNECGKAFTQNSN LTSHRRIHSGEKPYKCSECGKT FTVRSNLTIHQVIHTGEKPYKC HECGKVFRHNSYLATHRRIHTG EKPYKCNECGKAFRGHSNLTT HQLIHTGEKPFKCNECGKLFTQ NSHLISHWRIHTGEKPYKCNEC GKAFSVRSSLAIHQTIHTGEKPY KCNECGKVFRYNSYLGRHRRV HTGEKPYKCNECGKAFSMHSN LATHQVIHTGTKPFKCNECS\Q VFTQNSQLANHRRIHTGEKPYK CNECGKAFSVRSSLTTHQAIHS GEKPYKCIECGKSFTQKSHLRS HRGIHSGEKPYKCNECGKVFA QTSQLARHWRVHTGEKPYKCN DCGRAFSDRSSLTFHQAIHTGE KPYKCHECGKVFRHNSYLATH RRIHTGEKPYKCNECGKAFSM HSNLTTHKVIHTGEKPYKCNQC GKVF\QNSHLANHQRTHTGEK PYRCNECGKAFSVRSSLTTHQA
10535	40903	A	10596	330	432	
10536	40904	A	10597	1	147	
10537	40905	A	10598	1	380	RTRGRGQRGKMELVQVLKRGL QQITGHGGLRGYLRVFFRTNDA KVGTLVGEDKYGNKYYEDNK Q/FFWHRWLHSMTDDPPTTKPL TARKFIWTNHKFNVTGTPEQY VPYSTTRKKIQEWIPPSTPYK
10538	40906	A	10599	9	536	VLKRGLQQITGHGG/LFRGYLR VFFRTNDAKVGTLVGEDKYGN KYYEDNKQFFGDERLQASGLA LTLCEQTEEGSCLWSQRSKLGK SQSMNFKNSKTRSFQRTVSAGK TKYYHPVVAGRQQQARATCD HVDPRTQEHGPGAAWPYWPRL GLKHALLTFTVALQYRAQPLFR LPNLPL
10539	40907	A	10600	239	263	
10540	40908	A	10601	1	600	

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10541	40909	A	10602	1	1178	
10542	40910	A	10603	1	1038	MHLEVNSSPEPLDENLDNTVTS ALSGHEQRIQTSLPVLLTTKTEI LARFSQLQFPEEQSSFAYPANC VKSKGMNTKLPLRPLKVCREL TIDSDRDILYRTLFMGDSGMGK VQFEFGEEVHIVIKSTGFGPFSS YATLEPFVAVQLWGGGQHYQ GQQPPMGMMGQVNQGNHMM GQRQIPPYRPPQQGPPQQYSGQ EDYYGDQYSHGGQGPPEGMN QQYYPDGHNDYGYQQPSDPEQ GYDRPYEDSSQHYYEGGNSQY GQQHDAYQGPPPQQGYPPQQQ QYPGQQGYP\KQQQGYGPSQG GPGPQYPNYPQGQGQQYGGYI PTQPGPPQPPQQRPYGYDQGQY
10543	40911	A	10604	130	213	LKVST*AMPLPR*TPSRRCQP*R TGTSP
10544	40912	A	10605	124	208	LKVST*AMPLPR*TPSRRCQP*R TGTSP
10545	40913	B	10606	140	589	
10546	40914	A	10607	1	302	
10547	40915	A	10608	2	98	
10548	40916	A	10609	2	190	
10549	40917	B	10610	1	856	
10550	40918	A	10611	123	1287	AFSLGK\MSEKKLFGPNGERMP FSKVKALCAGLQATVAAPKNA EENKAIQDVAKDTAFLGITDEA TEGQFMYLTGGRLTYSNWKKD EPNDHGSGEDCVILLNNGLWN GISCTSSFIAIFQWAHYQYRQAE NYPKGELHTLRVKLCGPSWPT NAIHFRSRLLMPLGPTVLLMTM AVFQLSQAVAMCSWCCGLVLP PAGCLQDKASKPRETQAQPGL CVRGNFRIPSRQDFAAALARAL SGLDLWASLWVPFADFLGSSLS VPWFSYLENDEEDLTRLSLRLN GERTFLESPGKKRIGAGTPPMS QEAVMLAVMERDPGQCRGEE GPTECRAMWPGWGGRHSLPGH PAMLCSFLGSDLEIRGSNGGWE PPFIPGLQPELARGIQGSGRGAE
10551	40919	A	10612	292	445	LSICLQSAVCTPGMD/PAAPCSL GILDWGTLPSTAEPGREGPADA WVDPGVR
10552	40920	A	10613	363	575	HLLPTQGALCPAEGWPAPWQG YTPTCDCAEDTTQLERAGQLPP VF*SCHRGGVSSQ*GSPGVPQL LHQPE

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10553	40921	A	10614	3	638	SSKLSGLTTNVVDIILAHHFGQE ELQANLDLIQTYRMHIAQDINQ DNLQLFLNSYNGRRDLEIERPIL GQNDNKSKTLKG\STLLVVGDN SPAVEAVVECNSRLNPINTTL\L KMADCGGLPPG*FSPGKLTEAF KYFLQGMGYIPLVLCYST\SGS MTSVARSR\THSTSSSLGSGESP FSRSVTSNQSDGT\QES\CESPDV LDRQQTMEVSC
10554	40922	A	10615	3	1152	KSCFNAFFNFEDMQEITQH\FAV CHVDAPGQQEGAP/SPFPTGYQ YPTMDELAEMLPPVLTHLSLKS IIGIGVGAGAYIL\SRFALNHPEL VERPLCSLMVDPC/ALKGWIDW AASKLSG\LTTNVV\EIILAHHFG QEELQANLD\LIQTYRMHIAQDI NQDNLQLFLNSYNGRRDLEIER PILGQNDNKSKTLKCSTLLVVG DNSPAVEAVMADCGGLPQVVQ PGKLTEAFKYFLQGMGYIPVCA AQSPEHRVST\SASMTRLARSRT HSTSSSLGSGESPFSRSVTSNQS DGTQESCESPDVLDRHQTMEIS LDDVLLSALLRNNGKSAQQKKI SAKPKLEFLCPRPGTCDHGSRE KQGHSRGPGQFPGRWPGRAVA ETRGAIDHRL
10555	40923	A	10616	169	270	GICPFLQLSFYHLLD*DTRYLQI LRLQLKPHSFH

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10556	40924	A	10617	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSSLGADAI AKQRKTSVSAAASVSATIPIRR VQGPTVVGSWARGVSAAASGP RGTGPKGKARSEKGCSLSHGPQ TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSHP LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAIIYMNMGNKL PIWCHLLEEGIYLEVWALEGQF GRAKNACPVQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAEWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPQGFR DSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSEASCQQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYLGLILARGTRTLGK ERIQPILAYPHPKTLKQLWGFL QIT/GFCQLWIPR*SKI
10557	40925	A	10618	1	1022	MKPSVWALIQLNLSPYEKGILG LTKRHQGRLCTDGRQGIQPLPP SQAHTGIPLLHPYSIQVDCAIDR GKLCFCCCIGECNYSDQQGPGT VAGSWARGISAAVSVSATILISR VQGPLHVLGQEVFLLLRRQTNL AGSERTENGAGQSPGGACYQC GLQGHFTKDCPMRNKLPPRPCP LYQGNHWKDGEPIEHDCQQIIV QTSAAREDLLEVPLANPDLNLY TDGSSFVENGEVAKAVIAQFPT TVGVSCLDGRLRVLEVLARAIR /LGEGNKGYSIRKRGSQIVPVCR *HDCISRKPHHLSPKSP*ADKQL QQSLRIQNQCAKITSILIHQ*QT
10558	40926	A	10619	1	2091	
10559	40927	B	10620	1	2269	
10560	40928	A	10621	1	1776	

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10561	40929	A	10622	112	1465	LLKGARCLIQRPSFA/LQQETHR AHTLLLEWEPQAETAFTTLKQA LLQAAALTLPTRQNFSLYVTDR AEIALGVLIQTCGTTPQPVAYLT IEKGKERGEQQHKQLAEAAER KERKRQEVREREKEKETERQSK KEREEETKMESERKRETEKEVS TLAALEEPFSPPQPSLGLAEAGA GSLFSWGGVEGEVRGGGRAAH SAHRLVQVPGGQVRVQVFENP LLKAIKSDLPRSSLWSGRKTSV SAAALKEIRKEISKGTQIPLGYR LCPLQAVGGGEFGPTKIHVPFS LSDLKQIKADLGKFSDDPDRYI DVLQGLGKTFDLTWRDVMLLL DQTLAFNEKNAALAAASEFGGI WYLSQVNDRMTAEERDQFPTG QQAIPSMDPHWDLDSDHGDWS HKHLLTCVLEGLRGIRKKPMN YSMMSTIIQGKEENPSAFLQQL WKSLRKYTPPSSKSL
10562	40930	C	10623	52	690	
10563	40931	C	10624	199	285	
10564	40932	A	10625	59	411	SWPSDKQTLVVQRGQKMEQA NHPDPTDHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLALLNFLANQGYK/LSRSK AQLCLQQVKYLCL
10565	40933	A	10626	280	571	DIYVPIRII*KLPQAYAD/PAVPP CTSGRIWL*IHAGAWSSFWLVS Y*LLPQFQILLLVYSEIQILPGLV LGECMCQGICPFLLDFLVYLRR GVCSIL
10566	40934	A	10627	60	148	WGRGEPLCLAQGL*THQSAPC QNRPLGSL
10567	40935	B	10628	1	397	
10568	40936	A	10629	55	219	LGNKHLLGSIDPRGSWVTGEYI FLRPPIAA*GRQ*DFLPFPELWW TSLNNSWAFS
10569	40937	A	10630	3	494	
10570	40938	A	10631	2	689	
10571	40939	A	10632	157	277	DV*SNNSMTSLQVRCRTSMYLS GSSENFPRSTWICDAVAETPLA QEPATVPGP
10572	40940	A	10633	230	543	PSDRQTLVVQRGQKIEQANHL VGLVTSVVWKDTLKKIVHGMA FSMLISC/PRQLSSRSITIQGILGR AVTRYFSHLLSCNWETLLQIDQ GHQATDGLTNGTPNELN
10573	40941	B	10634	1	669	

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10574	40942	A	10635	119	409	GDICHHLGLTPVGSHSLLSCSR*QVA*VGAVTAATIGTGILLQQLAFLVCNWLLLSGSSENFPRSALICFKSEREKGTCIQVGPNSPPPTACKGHN
10575	40943	A	10636	3	482	LSSYSGGDLEKLYV*LRDCKYTNQHSVSSSRFVNIPISTLCLTQGL*MHPMDTLYLATLGGDLENLCVHTLYLANLVGMWRTFVSSSGIVNAPISTLSKQTT*LSVKWTNQQDVGGARQENKSRLPEPAVTTPLGSPPTPWKLCSFALCNKSCYCPKKKK
10576	40944	A	10637	1	2331	
10577	40945	A	10638	879	1353	SNNRTEGARGKRQLMSSP/STEPRVRLTIEGQETDFLLDTGAAFSVLISCLGRLSSRSVTIR*ILGQPVTRYFS/QPLSCNWETLLFSHAFLIMPESSTPLLGRDILAKAGAIIYINMGNKLPICCP\LLVEGINPEVWALEGQFGRAKNARPLQIRLK
10578	40946	A	10639	345	1996	
10579	40947	B	10640	97	1110	
10580	40948	A	10641	728	5171	
10581	40949	C	10642	1	2049	

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10582	40950	A	10643	1	2019	MNAHPEFRMAMKDGELVIWD SVHPCYTVFHEQTETFSSLWSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGFIENMFFVSANPWV SFTSFDLNVANMDNFFAPVFTM GKYYTQGDKVLMPLAIQVHHA VCDGFHVGRMLNELQQYCDE WQGGAQYPLRPEAHKGIQDIV KYLKAQGLGRKCSSPCNTPILG VQKLNGQWRLVQDLRLIN/EGF F*SSKLQAMQAMFAENSMSSV YSPTQEAEYWLPHGILQPADCF FEAASTSRSMWPRE/DWLSTT/S LTTWNMDFADFGTTIKQDFRLL GQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGH LDHGSHSYRRSDNSLDPRSHSC CRSDIGLGPRSHLYCRSDYQRE TTIPSMPVKGNQAPCMKSNNA LIVILGTVTLDAVGIGLVMPVLP GLLRDIVHSDSIASHYGVLLAL YALMQFLCAPVLGALSDRFGR RPVLLASLLGATIDYEIMATTPS WEDEEPIEHDSQQIIVQTYATR DDLLEVPLANPDLNLYADGSSF VENGIRRAGYAIVSDVTVLENS LAAVTLQNRQGLDLLTAEKGG LCTFSGKECCFYTNQSGISSPLE DTTTAGPFLHPIQQEVARAIIGQ FPTAFGVSCLEGRLRGEASWTS
10583	40951	A	10644	803	1171	
10584	40952	A	10645	1	2148	
10585	40953	A	10646	1094	3886	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKD
10586	40954	A	10647	762	1298	

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10587	40955	A	10648	893	2165	GPRGTGPKGKARSEKGRSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIIYMNMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAEWFP VLDLKDAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGLILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIARPLYT
10588	40956	A	10649	2	403	
10589	40957	B	10650	51	1038	
10590	40958	A	10651	581	1128	SPCRAQRHSCMWGLWQQSPCS PGSWQDSSPAQSGPPPR*PFSVP SSPWCLPSTWPLSPSPLPASWR RKTSAPSLLSLATAGPP*AGVC E/AKTPKKKYSDDDEEEESEEN SRDSESDFSDDFSDDFVETRRR RSRRNQKRQINYKEDSESDGSQ KSLRRGKEIRRVHKRRLSSSESE GYFFIKS
10591	40959	B	10652	1	4296	
10592	40960	A	10653	2	447	KEKKRNKKKKTIGSPKRIQSPL NNKLLNSPAKTLPG/AC/GSPQK LIDGFLKHEGPPAEKPLEELSAS TSGVPGLSSLQSDPAGCVRPP\V VKYCTDLIEEKDLEKLDLVIKY MKRLMQQSVESVWNMAFDFIL DNVQVVLQQTYGSTLKVT
10593	40961	C	10654	286	336	
10594	40962	A	10655	421	638	

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10595	40963	A	10657	1	888	MMNEKNLEKGLGVDSVDKDA MNAAIQQAIKAQPSMSPKKAPP APAKEARNVVAVGTGGRGTHD RDPSEKPPRLQWFEQQAKKLA KQQEEDSEEEEEDLDGDVLEIG KSKIKVLAESVSDWEDIDSDEE LECEDTEAMDDVVEQDAEEEE AEEGPPLGAIPITDCLFCSHHSSS LMKNVAHMTKDHSFFIPDIEYL SDIKGLIKYLGTHSSSSNVCKGL WDLEKRPSIDLK/CRT*YSTKRH /CTRTLSASSHFILCQWFSVLS/P VHASTDQEIQEMHDDQSNPQN AVVREHCVGWGWGV
10596	40964	A	10658	1	1545	MATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAP VTAEGFQERVRA\HGPSRRRRA RARP/LYCTVCSKKFASFNAYE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDAMNAAIQQAIKAQPSMSPK KAPPAPAKEARNVVAVGTGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQQEEDSEEEEEDLDGD VLEIGKSKIKVLAESVSDWEDI DSDEELECEDTEAMDDVVEQD AEEEEAEEGPPLGAIPITDCLFC SHHSSSLMKNVAHMTKDHSFFI PDIEYLSDIKGLIKYLGEKVGVG KICLWCNEKGKSFYSTEAVQA HMNDKSHCKLFTDGDAALEFA DFYDFSWRLAVGGHDWVERLT ASHYFYGYYPGARVGHRSLMR YYKQRFGLSRAVAVAKNRKAV GRVLQQYRALGWTGSTGAAL MRERDMQYVQRMKSKWMLK TGMKNNATKQMHFRVQGSQK EIQIFHSSEIDGIATAVEDDFASP TPTKDAKN
10597	40965	A	10659	3	943	

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10598	40966	A	10660	1	2427	MATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAP VTAEGFQERVRA\HGPSRRRRA RARP/LYCTVCSKKFASFNAYE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDAMNAAIQQAIKAQPSMSPK KAPPAPAKEARNVVAVGTGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQQEEDSEEEEEDLDGD DWEDIDSDEELECEDTEAMDD VVEQDAEEEEAEEGPPLGAIPIT DCLFCSHHSSSLMKNVAHMTK DHSFFIPDIEYLSDIKGLIKYLGE KVGVGKICLWCNEKGKSFYST EAVQAHMNDKSHCKLFTDGD AALEFADFYDFSWRLAVGGHD WVEVEGRIRGCGSREDNECLL VCNFSVIGVAIQITRKGRTPIRA EELPSEKNLEYDDETMELILPSG ARVGHRSLMRYYKQRFGLSRA VAVAKNRKAVGRVLQQYRAL GWTGSTGAALMRERDMQYVQ RMKSKWMLKTGMKNNATKQ MHFRVQMDCRGIAVLVFKAPS FYLIMAPKHKSGDAGDSNMPK GSRKVLPLSEKVKVLKEKKLY AEVAKIHGVKLQTFGVSVTAH KGSVDPKSEQQQDLLQRVKEQ SFHSVEADPAAEGAGSGLSQLR KGLPQCSSRLNGSSSATKVGAQ AEEAPRASEGCEGCQHAVTSQ
10599	40967	A	10661	3	658	GTKGWAFPITDCLFCSHHSSSL MKNVAHMTKDHSFFIPDIEYLS DIKGLIKYLGEKVGVGKICLWC NEKGKSFYSTEAVQAHMNDKS HCKLL\QDGDAALEFADFYDFR SSYPDHKEGEDPNKAEELPSEK NLEYDDETMELILPSGARVGH\ RSLMRYYKQAIWLVKNLWQLP KIRKAVGRVLQQYRSPGIGLGS TGAALMRERDMQYVQRMKSK MGC
10600	40968	A	10662	1	221	MNPLANSTLTDVHPHFIFKQMA ELDRDMDEAGNHHSQQTNTRT ENQTPHVLTHKWELNNENTRT QQGREHHTSEEFIAIQPEYYQKE KSNSDINLEGTSYWTENHCSGI YKVINCLESEIHSEEN*CQN*IFL SDNIQVELR*IPLMCDVPCPVSV CSHCSTPTYE

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10601	40969	A	10663	1	1815	MHEAGNHHCQQSNTRKENQTP DVLTHKWEGFDQLRLEGLLCD VTLMPGDTDDAFPVHRVMMA SASDYFKAMFTGGMKEQDLM CIKLHGVSKVGLRKIIDFIYTAK LSLNMDNLQDTLEAASFLQILP VLDFCKVFLISGVTLDNCVEVG RIANTYNLTEVDKYVNSFVLKN FPALLSTGEFLKLPFERLAFVLS SNSLKHCTELELFKATCRWLRL EEPRMDFAAKLMKNIRFPLMTP QELINYVQTVDFMRTDNTCVN LLLEASNYQMMPYMQPVMQS DRTAIRSDTTHLVTLGGVLRQQ LVVSKELRMYDEKAHEWKSLA PMDAPRYQHGIAVIGNFLYVV GGQSNYDTKGKTAVDTVFRFD PRYNKWMQVASLNEKRTFFHL SALKGYLYAVGGRNAAGELPT VECYNPRTNEWTYVAKMSEPH YGHAGTVYGGVMYISGGITHD TFQKELMCFDPDTDKWIQKAP MTTVRGLHCMCTVGERLYVIG GNHFRGTSDYDDVLSCEYYSPI\ LDQWTPIAAMLRRQSDVGVAV FENKIYVVGGYSWNNRCMVEI VQKYDPDKDEWHKVFDLPESL GGIRACTLTVFPPEETTPSPSRES
10602	40970	A	10664	1	1226	MNEIEFRLERTPVDESDDEIQH DEIPTGKCIAPIFDKRLKHFRVT EGSPVTFTCKIVGIPVPKVYWF KDGKQISKRNEHCKMRREGDG TCSLHIESTTSDDDGNYTIMAA NPQGRISCSGHLMVQSLPIRSRL TSAGQSHRGRSRVQERDKEPLQ ERFFRPHFLQAPGDMVAHEGR LCRLDCKVSGLPPP\DMTWLLN GQPVLPDASHKMLVRETGVHS LLIDPLTQRDAGTYKCIATNKT GQNSFSLELSVVAKEVKKAPVI LEKLQNCGVPEGHPVRLECRVI GMPPPVFYWKKDNETIPCTRER ISMHQDTTGYACLLIQPAKKSD AGWYTLSAKNEAGIVSCTARL DIYAQWHHQIPPPMSVRPSGSR YGSLTSKGLDIFSAFSSMESTM VYSCSSRSVVESDEL
10603	40971	C	10665	166	229	
10604	40972	B	10666	251	371	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10605	40973	A	10667	79	1391	PWEGSAPATSPLGEDSAWGSA DGSESWSCRELLQPGDVLGESC GLTPPALPAHCIQEGCLPPLTQE LRCCQPPRMGRWALDVAFLW KAELTLGLELLYY\CFFIGINFY NKWLTKSF/HIFPLFMTMLHLA VIFLFSALSRALVQCSSHRARV VLSWADYLRRVAPTAALREVA SLFRKPSAEEMLCPPARQRGEA RELSQNPIIRAGEGRLQGHRQV ATVICAPAPFSVMGLSPELQQCI VGNFASRYTMTKSSAVLFILIFS LIFKLEELRAALVLVVLLIAGGL FMFTYKSTQFNVEGFA\WCWG PRSSVAFAGPSPRCSCRRLNSAS RIPSTPCSTCSHSCS/WGLFPLFA VFEG\TGLLLRVLGSLFLGGILA FGLGFSEFLL/VSSRTSSLTLSIA GIFKEVCTLLLAAHLLGDQISLL NWLGFA\SASREYPSTLPS
10606	40974	A	10668	1	1129	MGRWALDVAFLWKAVLTLGL VLLYYCFSIGITFYNKWLTKSF HFPLFMTMLHLAVIFLFSALSR ALVQCSSHRARVVLSWADYLR RVAPTALATALDVGLSNWSFL YVTVSLYTMTKSSAVLFILIFSLI FKLEELRAALVLVVLLIAGGLF MFTYKSTQFNVEGFA\WCWGP RSSVAFAGPSPRCSCRRLNSASR IPSTPCSTCSHSCSWGLFPLFAV FEGLHLSTSEKIFRFQ\DTGLLR RVLG\SLFLGGILAFGLGFSEFLL VSRTSSLTLSIAGIFKEVCTLLL AAHLLGDQISLLNW\LGFA\SAS REYPSTLPSKPCIPEVTQSPFQK PLVSVLLPVTLSDSDAGSVPGG SAAVTPLGRCGGHLQSGWVGP
10607	40975	A	10669	566	1026	PVMPKLIYVIRTGKQLKISLGH VDFQTVPSFLQQLNV/WQTIKA SEHPDRNDCVAVLRQKRSLGS VENTSGKRKCWGGQSGFTTSE LEETEEDSDLSDYGDDVDGRK DALAEPCFMLIGEIFELRGKPQY QLEIWQVPTGTPDHLEEEANEK

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10608	40976	A	10670	1717	2340	GIDVQGKKNSFSLSSFLERLPRD FFSHQEEETEEDSDLSDYGDDV DGRKDALAEPCFMLIGEIFELR GMFKWVRRTLIALVQVTFGRTI NKQIRDTVSWIFSEQMLVYYINI FRDAFWPNGKLAPPTTIRSKEQ SQETKQRAQQKLLENIPDMLQS LVGQQNARHGII/NKYSNALQE TRANKHLLYALMELLLIELCPE LRVHLDQL
10609	40977	A	10671	181	399	NRYIVPISQIMKRKRRKVSIVLN VTGY*/RGM/RKPGLLNLASGFL LSTSPTSENSNRCRGLWQIDPW EEGETYV
10610	40978	A	10672	66	535	CWWQDPLQRTRQKSVTATSTK ID\ISNVKIPKHPADAYFKKQQL WKPRNRKLAGKLSTPAARDAP RARPPHEAPPPPPPPELRYRVPP RPAPSSWRHPSGKGRRGPPGIG GRIVGERQLRTEYGNDRPGREG DPAPGCCGGARTLSLYGEIKLR VKF
10611	40979	A	10673	67	585	SAAKSEMAGEKVEKPDTKEKK PEAKKVDAGGKVKKGNLKAK KPKKGKPHCSRNPVLVRGIGRY SRSAMYSRKAMYK\RKYSAAK SKVEKKKKEKVLATVTKPVGG DKVGGTRG\VKLRK\MPRI\YPT EDVPRKLLSHGKKPFSQHVRKL RASITPGTILIILTGRHRGKRVVF
10612	40980	A	10674	2	282	CIALYCHLLNICSKVKAEMQNL GREFIVPGMDSATSLIWATK/DL MNAVIEAPEKKPLLKREKQDES QSEIKWASQKKHLNPVQALSEF KAMDSI
10613	40981	A	10675	2	2798	
10614	40982	A	10676	14	2858	PDWRETKQRPSASGLWNLALA QLAAEMTAVHAGNINFKWDPK SLEIRTLAVERLLEPLVTQVTTL VNTNSKGPSNKKRGRSKKAHV LAASVEQATENFLEKGDKIAKE SQF\L*E*LLAAVEYVRKQGDL MKTAAGEFADDPCSSVEQGNM VQAA*TLLSAVTCLLILA\DMG NVYTLLIQLKVVEDDILKLRNA GNEQDLGI*YKALKPEVNKVNI MAVKRQQELKDVGHRDQMAA ARGILQKNVLIFYTASRA
10615	40983	A	10677	1	4545	

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10616	40984	A	10678	1	1921	MAGLGMGEEGIPGGERWEHKR RAHIVSNHRITRTGTHPYTHSPY PHKDNVHTARREHKTQDLGTI RSVGHSSEHTQHTTPDTVPPLV VIVCRVCYRPPHGETRAEYTRH RGQNRRTKFWVGIKEEKNLAQ QERTEEQLANIARGGYVLKDC AGQPELIFIATGSEVELAVAAYE KLTAEGVKARVVSMPSTDAFD KQDAAYRESVLPKAVTARVAV EAGIADYWYKYVGLNGAIVGM TTFGESAPAELLFEEFGFTVDNP LASRAVRLRLPFNNDQVEAAV GWKLAVERHNGPTALILSRQN LAQVERTPDQVKEIARGGYVL KDSGGKPDIILIATGSEMEITLQ AAEKLAGEGRNVRVVSLPSTDI FDAQDEEYRESVLPSNVAARV AVEAGIADYWYKYVGLKGAIV GMTGYGESAPADKLFPFFGFTA ENIVAKAHKVLGVKAGSHIPRK KYDVPGKKSFSPVKYSTIGSPSP ERPVSITTIPNSFVIITANRVLHC NADTPEEMHHWITLLQRSKGD TRVEGQEFIVVEKLIRGLAMED SRNMFAL/S*IQRPRRQSH*KSN RRS*CLSQV*KRASW*AFTNI* WPDRHGLRKYSF/WSPGNIHHL RHCRML*VVRLLLRLLNAVYE
10617	40985	A	10679	1	2940	
10618	40986	A	10680	2	404	
10619	40987	A	10681	2	546	WCPHRWRPHTLTPTAAPAVTK SPEATHLYGQVSWNSQNLHLE GQLQSASLQGSFMLK**GDPLD F/VMSPPRPLFERLKARISQSTK TFTPCERLEKRRTSFLEGTLRRS FRTGSVVRQKVEEEQMLDMWI KEEVSSARASIIDKWRKFQGMN QEQAMAKYMALIKEWPGYGST LFDVEGTDT
10620	40988	A	10682	1	555	
10621	40989	A	10683	1	627	

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10622	40990	A	10684	1	7232	MPEPPTHSMGSCAAGASLTSTA PCSTAPSPIDHLRAKECERTAQ DWQAAPPAALVRDPLAALVRT WRTFMSSSRIVNTPIGTLCLAQ GFQWFSVLSQVHASTDQEIQE MHDEQANPQNAVGTLDVGLID SVCASDSPDRPNSFVIITANRVL HCNADTPEEMHHWITLLQRSK GDTRVEGQEFIVRGWLHKEVK NSPKMSSLKLKKRWFVLTHIPG LLQEFREDALNWGPDEKIFKET ELVNDMDKINGRIERAE
10623	40991	A	10685	1	2146	IDSVCASDSPDRPNSFVIITANR VLHCNADTPEEMHHWITLLQR SKGDTRVEGQEFIVRGWLHKE VKNSPKMSSLKLKKRWFVLTH NSLDYYKSSEKNALKLGTLVL NSLCSVVPPDEKIFKETGYWNV TVYGRKHCYRLYTKLLNEATR WSSAIQNVTDTKAPIDTPTQQLI QDIKENCLNSDVVEQIYKRNPIL RYTHHPLHSPLLPLPYGD\INLN LLKDKGYTTLQDEAIKIFNSLQ QLESMSDPIPIIQGILQTGHDLRP LRDELYCQLIKQTNKVPHPGSV GNLYSWQILTCLSCTFLPSRGIL KYLKFHLKRIREQFPGTEMEKY ALFTYESLKKTKCREFVLSRDEI EALIHRQDMTSTVYCHGGGSC KITINSHTT\AGEVVEKLIRGLA MEDSRNMFALFEYNGHVDKAI ESRTVVADVLAKFEKLAATSEV GDLPWKFYFKLYCFLDTDNVP KDSVEFAFMFEQAHEAVIHGH HPAPEENLQVLAAHATSSIMQG DYT\LHA\AIPP\LEEVYSLQRLK ARISQSTKTFTPCERLEKRRTSF LEGTLRRSF\RTGSVVRQKVEEE QMLDMWIKEEVSSARASIIDK WRKFQGMNQEQAMAKYMALI KEWPGYGSTLFDVEVRTGCHV LGWAGCWHLRTWITAKFMWR EDKMEHFALSTSFFRAPKIVPLT PPFSSQFLFSCVVNASVILGMN

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10624	40992	A	10686	28	561	MDIVQDATFVYATLQTAHYHR DAGLPVYLYEFEHHARGIIVKP RTDGADHGDEMYFLFGGPFAT GAKVPPDTPTGCPVSHLWMQT HPSIGWPQGAHQFLICYALPNE SLLLRKQQKQQE*GGRNPNDG NLPCWPRYNKDEKYLQLDFTT RVGMKLKEKKMAFWMSLYQS QRPEKQRQF
10625	40993	A	10687	148	444	
10626	40994	A	10688	1	1531	PLPGARRCLHEFWGQLASMYV STRERYKWLRFNEDCLYLNVY APARAPGDPQLPVMVWFPGGA FIVGAASSYEGSDLAAREKEGL VFLQHRLGIFSFLSTDDSHARG NWGLLDQM\AALRWVQENIAA FRGRPREILTLFGQSAGAMSISG LMMSPLASGLFHRAISQSGTAL FRLFITRNPLKVAKKVAHLAGC NHNSTQILVNCLRALIR\AKVM RVSNKMRFLQLNFQRDPEEIIW SMSPVVDGVVIPDDPLVLLTQG KVSSVPYLLGVNNLEFNWLLP YIMKFPLNRQAMRKETITKML WSTRTLLAKNSWGAEHGSKSL VGPPLAQLAPRPQNITKEQVPL VVEEYLDNVNEHDWKMLRNR MMDIVQDATFVYATLQTAHYH RDAGLPVYLYEFEHHARGIIVK PRTDGADHGDEMYFLFGGPFA TGLSMGKEKALSLQMMKYWA NFARTGNPNDGNLPCWPRYNK DEKYLQLDFTTRVGMKLKEKK MAFWMSLYQSQRPEKQRQF

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10627	40995	A	10689	138	1898	ICKYIMNDQWARQNCLHSPTY GPSENVLSSAESKPEIQLSPSCPL IFSSQQALSQHVWLSHLSQLFSS LWAG\NPLHLGKHYPEDQKQQ QDPFCFSGKAEWIQEGEDSRLL FGRVSKNGTSKALSSPPEEQQP AQSKEDNTVVDIGSSPERRADL EETDKVLHGLEVSGFGEIKYEE FGPGFIKESNLLSLQKTQTGETP YMYTEWGDSFGSMSVLIKNPR THSGGKPYVCRECGRGFTWKS NLITHQRTHSGEKPYVCKDCGR GFTWKSNLFTHQRTHSGLKPY VCKECGQSFSLKSNLITHQRAH TGEKPYVCRECGRGFRQHSHL VRHKRTHSGEKPYICRECEQGF SQKSHLIRHLRTHTGEKPYVCT ECGRHFSWKSNLKTHQRTHSG VKPYVCLECGQCFSLKSNLNK HQ\RSHTGEKPFVCTECGRGFT RKSTLITHQRTHSGEKPFVCAE CGRGFNDKSTLISHQRTHSGEK PFMCRECGRRFRQKPNLFRHKR AHSGAFVCRECGQGFCAKLTLI KHQRAHAGGKPHVCRECGQGF SRQSHLIRHQRTHSGEKPYICRK CGRGFSRKSNLIRHQRTHSG
10628	40996	C	10690	160	294	
10629	40997	A	10691	3	82	SWACAIHPTGYLIEQAGG*WVT ARRD

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10630	40998	A	10692	1	1399	MLRRYRPDITSCHGSTAESKGG VVLDVSGRARPLRRTRNSPSPT SLTSSKMSGLDGGNKLPLAQTG GLAAPDHASGDPDRDQCQGLR EETEATQVMANTGGGSLETVA EGGASQDPVDCGPALRVPVAG SRGGAATKAGQEDAPPSTKGL EAASAAEAADSSQKNGCQLGE PRGPAGQKALEACGAGGLGSQ MIPGKKAKEVTTKKRAISAAVE KEGEAGAAMEEKKVVQKEKK VAGGVKEETRPRAPKINNCMD SLEAIDQELSNVNAQADRAFLQ LER\KFGRMRRLHMQRISFIIQNI PGFWVTAFRNHPQLSPMISGQD EDMLRYMINLEVEELKHPRAG CKFKFIFQGNPYFRNEGLVKEY ERRSSGRVVPFSTPI\RWH\RGQ\ DPQAHIHRNREGNTIPSFFNWFS DHSLLEFDRIAEIIKGELWPNPL QYYLMGEGPRRGIRGPPRQPVE SARSFRFQSG
10631	40999	A	10693	3	441	
10632	41000	A	10694	190	2716	
10633	41001	A	10695	1	793	MARQKKMGQSVLRAVFFLVLG LLGHSHGGFPNTISIGKRKRASR RSRLSLTRDHCPGKAFPAVFRA ERSTGGEQEAGMLQGGEESRLF GSLLWTLPWRACSSWKLSQGD ADCLAAPGRITRARGAQSVVSG CRETGW\GLFMRNTVQEHSAFR FAVQLYNTNQNTTEKPFHLNY HETSPIPLKSPPVSFCCALVVHS TLHRPSLCSVSSLAHRSHIPSPH CHCKNCCCTPLQPTNVLVDYA LFARSREKANVTLKLPLTEVIPF
10634	41002	A	10696	2	2744	
10635	41003	A	10697	2	2740	
10636	41004	B	10698	47	7237	

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10637	41005	A	10699	426	2118	GFGHTVHAAEGGDFGGSWQG DSVLLCSTVDPGSWAASRGKG SPCRGPLCGCCPGRSS\QPSKVE VAVSCSCGALLGMCMPPVVLA LEGCPRGVAAKGKGSPQAQTV RRSPSADQSLEDSPSKVPKSWS FGDRSRARQAFRIKGAASRQNS EEASLPGEDIVDDKSCPCEFVTE DLTPGLKVSIRAVCVMRFLVSK RKFKESLRPYDVMDVIEQYSAG HLDMLSRIKSLQSRQEPRLPVQ QGTRTGIDMIVGPPPPSTPRHKK YPTKGPTAPPRESPQYSPRVDQI VGRGPAITDKDRTKGPAEAELP EDPSMMGRLGKVEKQVLSMEK KLDFLVNIYMQRMGIPPTETEA YFGAKEPEPAPPYHSPEDSREH VDRHGCIVKIVRSSSSTGQKNFS APPAAPPVQCPPSTSWQPQSHP RQGHGTSPVGDHGSLVRIPPPP AHERSLSAYGGGNRASMEFLR QEDTPGCRPPEGTLRDSDTSISIP SVDHEELERSFSGFSISQSKENL DALNSCYAAVAPCAKVRPYIA EGESDTDSDLCTPCGPPPRSAT GEGPFGDVGWAGPRK
10638	41006	A	10700	1	774	
10639	41007	A	10701	124	815	HPGTAMDALNSMQNFLRGRPK TFKSLENAIEWSVKSGQIRNLES ARVSMVGQVKQCEGITSPEGSK SIVEGIIEEEEEDEEGSESISKRK KEDDMETKKDHPYTWRIELAK TEKYWDGWFRGLSNLFLSCPIP KLLLLAGVDRLDKDLTIGQMQ GKFQMQVLPQCGHAVHE\DAP DKVAEAVATFLIRHRFAEPI\GG FQCVFPGLLVTCCPPLLQHRAL LVNTFAPEAHC
10640	41008	A	10702	69	370	
10641	41009	A	10703	1	224	MCNTPAYCDLGKAAKDVFNK GYGFGMVKIDLKTKSCSGVEFS TSGHAYTDTGKASGNLETKYK VCNYGLTFTQK*NTPAYCDLG KAAKDVFNKGYGFGMVKIDLK TKSCSGVEFSTSGHAYTDTGKA SGNLETKYKVCNYGLTFTQK
10642	41010	A	10704	2	171	

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10643	41011	A	10705	1	740	MCNTPTYCDLGKAAEDVFNKG YGFGMGKIDLKTKSCSAVEFST SGHAYTDTGKASGNLEPECKV CNYGLTFTQKRNTDNTLGTEIS LENKLAKGLKLSLDTILVPNTG KKSGELKASYKWDCFSVGSNV DLDFSGPTIYGWAVLVFEGWL AGYQMSFDTAKSKLSQNNFAL GYEAADFQLHTHVTDGTEFGG SIYQKVNGIEMSINLAWTA/GSN NTHFGIATKYKLDCRTSLSAKA VVLGTRVGSC
10644	41012	B	10706	1	318	
10645	41013	A	10707	2	100	
10646	41014	A	10708	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KARLTWGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
10647	41015	A	10709	284	969	RVSRGRKWFFIALKRMPAMKK AMNLFLGLSNVRTVHPEGFTV YISTHISFPSLSGYRTGLRSFGLV KQKKSPIRMPCVYTNPCVSIHP LWLRLRSPSARWLRCGSPSLG WTRTEPAPSPPRGGRTEKARIW EVTDRTVRTWIGEAV/AAHAA DGVTFSVPVTPHTFRHSYAMH MLYAGIPLKVLQSLMGHKSISS TEVYTKVFALDVAARHRVQFA MPESDAVAMLKQLS

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10648	41016	A	10710	2817	3297	AGCVRHRLSENRLDHRALPAA SKLPAYA*LPPPLPAGRL*RIPH RQFL*HQI/RL/PTERRCLLTRRT EKARIWEVTDRTVRTWIGEAV ARLAADGVTFSVPVTPHTFRHS YAMHMLYAGIPLKVLQSLMGH KSISSTEVYTKVFALDVAARHR VQ\FAMPES
10649	41017	B	10711	1	963	
10650	41018	A	10712	1	1296	
10651	41019	A	10713	1	1167	
10652	41020	A	10714	349	3195	
10653	41021	A	10715	163	864	
10654	41022	A	10716	576	754	
10655	41023	A	10717	1	1449	
10656	41024	A	10718	1422	1600	
10657	41025	A	10719	489	726	ISCCSFFSPRPPH\TFRHSYAMH MLYAGIPLKVLQSLMGHKSISS TEVYTKVFALDVAARHRVQFA MPESDAVAMLKQLS
10658	41026	A	10720	1	1596	
10659	41027	A	10721	1	1572	
10660	41028	A	10722	2	100	
10661	41029	A	10723	561	804	TLRQTKPDNSADPPHT\FRHSY AMHMLYAGIPLKVLQSLMGHK SISSTEVYTKVFALDVAARHRV QFAMPESDAVAMLKQLS
10662	41030	A	10724	1	867	
10663	41031	B	10725	1	825	
10664	41032	A	10726	1	942	
10665	41033	A	10727	2	100	
10666	41034	A	10728	39	359	RILGKGAGQTRAESLVWGRGV PARCC*PGGPFLVPGPPP*VR/H LSYARPM\L*PGIPLKVLQSLMG HKSISSPEVYRKVFALNVAARH RVQFAMPEFDAVAMLKQLS
10667	41035	B	10729	41	724	
10668	41036	A	10730	1	1023	
10669	41037	A	10731	1	1314	
10670	41038	A	10732	1	1128	
10671	41039	A	10733	892	1611	
10672	41040	B	10734	78	1099	
10673	41041	A	10735	1	936	
10674	41042	A	10736	766	1056	
10675	41043	A	10737	1	1422	
10676	41044	A	10738	1214	1721	

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10677	41045	A	10739	2592	3233	RWGRWRTGGSSRSEPTMELRA PAWPRGRPGQGGARPAGSELR GNATAPSPACLCRNILCRMEES PNTDGKRPETGSNKRGKAGDK WWKIKTGI\IRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSVPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKVISSTDFYTKVFALDVA ARHRVQFAMPESDAVAMLKQL
10678	41046	A	10740	6323	7130	
10679	41047	A	10741	319	522	RNTRYWVINSISVIPPSSALISKR SPRLMAKKTAHFLGISRTSVAE FTFTRSGISRDHCVKGAGAADR RPNAPPRAEFQSGWFLIMECFA R*VGDPQL/TA/HFDAV/RRE/IM PL/PREG/KTL/QTEVREMPRKC AVFLAINLGDRFDIKADEGGIT DIEFITQYLVLRYAHEKPKLTR WSDNVRILELLAQNDIMEEQEA MALTRAYTTLRDELHHLALQE LPGHVSEDCFTAERELVRASW QKWLVEE
10680	41048	A	10742	2	640	
10681	41049	C	10743	1	2358	
10682	41050	A	10744	1264	1894	RGDKPQHIVTVHRADVVKAQL FKQRARHYHAFNMFFGAFEQL FNWRHARENFFPAGKQLCQMV VERADIFGNRHFIVVENHQHIR TDIARVIHRFKRHACGNRAIAN DTDGAAIFAFTAILYGIQFSCAS FYLFVVYEHGSLKTVGCPLQEV /WRTALESCKPAHIQLSGVLAI/S SIVMQSVNAMPSWSGYSSSQA ASAARWLLARSGLIC

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10683	41051	A	10745	872	3111	VLKPNHLTERKGC/GFACGRYG KLGAWELDYSPDLDIIFLNDCP MNAMTAGERKIDGRQFYLRLA QRIMHLFSTRTSSGILYEVDARL RPSGAAGMLVTSAEAFADYQK NEAWTWEHQALVRARVVYGD PQLTAHFDAVRREIMTLPREGK TLQTEVREMREKMRAHLGNKH RDRFDIKADEGGITNIEFITQYL VLRYAHEKPKLTGWSDNVRIL ELLAQNDIMEEQEAMALTRAY TTLREPRFSRFSLFWGCSPLGLF DYLADLFKIDNSHGGRFKTVLL TFLPPALLYLIFPNGFIYGIGGA GLCATIWAVIIPAVLAIKARKKF PNQMFTVWGGNLIPAIVILFVLP WFYFIPPGLICTSLVYRASPPIS MPAKAVAYCVLRISGGDGSCD VICRGKVADRSKFWNPNWSKT HTEPTQQSQTATSNRTSATTAE QRSDEKEGNNRTRHEEQRSQN ATQHKRRERATTTQKTCSETVT PTTMNMCNEPELRRHARVLPP VLYIVQRRYDESHLRISISACNV CRTERHAVHTDETIHSTVVADC KERVAVMRLRLPLCAACRHIG DVIVYSAYVCEHRCMRLLATR RHYVVTLTTHLRRRLFLTEVNA RYVCIYDDEHSRSSTVTHAHPI DHQSAHYDTYVYDIGTVSYMR LNTSVRLIRRRAHTCTSRALMD SHSKDGRPMDYASAVVVTHPL
10684	41052	A	10746	1577	1668	TINPPELAFVKTVH*SPRICLGFI HIFLLN
10685	41053	A	10747	486	674	HWWKNWRRCWIPVIWH*RRSR TIWRCCKKWITASTLLSRSSPSK LPPCMSGFQPVVAGRKRR
10686	41054	A	10748	254	396	ADDQIPHSKTHLKLSLEVEENQ Q*EI*RPLLQ*GGMSVPRCVHG RSG
10687	41055	A	10749	3	674	ISAELNRPFAIRGDLG/VVWERQ KQETGWRSWVP/WPHVHAEDII LGNPPDI/PEVTMVHLPRVEATL /APLALLTKTVWLPWIKLESPRI RFQFSHHVRRAVLCEDAYYKL TLAQVEKLKNGGKVIASDELM TKFRIPNTLEFCAPVMADAPAI ALLRLSLACLDLAQAMMPAFH KPISSSFVNDYAGTSFACAASD MDERRMLNAPLSLRLTLVEKL RRCWIPVIRH

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10688	41056	A	10750	1	1755	
10689	41057	A	10751	1	1662	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQAL SKPDKYADVKKRISEIYHENRG RYGYRRVTLSLHREGKQINHK AVQRLMGTLSLKAAIKVKRYR SYRGEISSTTKLFLTAFRMIVVA IILIATFDWNRLKPTINQKVSAE LNRPFAIRGDLGVVWERQKQE TGWRSWVPWPHVHAEDIILGN PPDIPEVTMVHLPRVEATLAPL ALLTKTVWLPWIKLEKPDARLI RLSEKNNNWTFNLANDD/NKD ANA\NRRHGRFGWIIFFSIKGGS PLMTNDIHGSLVYTTGKPRPKL EGDVESRQLRLADLGPLIGVDS GKGAEKSKRSEQKKGEKSVQP AGKVLPYDRFETDKWDVMDA DVRFKGRRIEHGSSLPISDLSTHI ILKNADLRLQPLKFGMAGGSIA ANIHLEGDKKPMQGRADIQAR RLKLKELMPDVN
10690	41058	A	10752	1	477	SELGHAGLNGDILVWNPVLED AFELSSMGIRV\D\ADTLKHQLA \GDEDRLELEWHQALLRGEMP QTIGGGIGQSRLTMLLLQLAHI GQVQCGVWAAAVRESVPSLPL QLFHFTRHVVRQPLSDKIRNHQ RIGIKPFPALQAFHNGAKTTGKI GADTKLLA
10691	41059	A	10753	414	794	RPSPLPTGLGDTGLGFLPRFIEM EKLPF\DVAEAEQELQEGPLPEY SGPGLALAKWG\LG\LKQVVM ASLFVALFLPFGR\AQELSLACL LTSLVVTLLKNINSMTAGILVC LVTVVSPGLIKVLIYDQ
10692	41060	A	10754	88	227	
10693	41061	A	10755	26	261	
10694	41062	A	10756	164	361	
10695	41063	A	10757	1347	1656	RVGRPGHRASAQSGGNPQNHR RLGEPVSARHPAYLSTGSGDAA AARYRRSA*SLRR*SRASSHPPE RAGTPVAPGTIDIFRWRTAARQ HRPRLYRRLPHSAA

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10696	41064	A	10758	2096	2248	RLIGLHGQNSRSVPQLPMESAS VA*RCTAALDGGVSSTSTRWLF ASCTRL
10697	41065	A	10759	1	2240	
10698	41066	A	10760	1	1082	MEHERYVGISNLMLKPELYLA VGISGQIQHMVGANASQTIFAI NKDKNAPIFQYADYGIVGDAG ALMSEDIFDAIIVGAGLAGSVA ALVLAREGAQVLVIERGNSAG AKNVTGGRLYAHSLEHIIPGFA DSAPVERLITHEKLAFMTEKSA MTMDYCNGDETSPSQRSYSVL RSKFDAWLMEQAEEAGAQLIT GIRVDNLVQRDGKVVGVEADG NRVMKKILTTPIKAEDLQDIRV GDVIYL*RHRSLSVG*RAESGG* RSGRIVKRTG
10699	41067	A	10761	987	1191	
10700	41068	B	10762	1	1506	
10701	41069	A	10763	204	527	GPDRCQIGPLAE*NTGNSHKAA LRQQRAEGRWWQKPHGEWRA ATADGRTYAAISAQATAPQSPA GQSTMPRPPRWLSTPALPVMPA VTVDRQITPASVSTTKQAISA
10702	41070	A	10764	1041	3024	
10703	41071	B	10765	1	763	
10704	41072	A	10766	729	989	HLTRQGIPTDLQLRVLSVRRKT NKQKGHPHRKRICTSPSSKTKS R*NHKDGEKTEQKNWKL*NAE HLSSSKGTQFLTSNGPKLDGE

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10705	41073	A	10767	89	1755	LSEGKLTNRKDIHTKTPSVRHH HQRPKCWKFWPGHSGRRRK*R /CIQVGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMTELPFTTASKRIKYLGIQLTR DVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFIELEKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYNYLIFDKPEKNKQWGKDS LFNIWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRSKTIK TLEENLGNTIQDIGMGKDFMSK TPKAMATKAKIDKWDLIKLKSF CTAKETTISVNRQPTEWEKIFAI YSSDKGLISRIYNELKQIYKKKT NNPIKKWVKDTNRHFSKEDIYA AKRHMTKCSSSLAVREMQIKT TMRYHLTPVEEVRAGEMAKTR RCQNVKGASEEGIRALALFLIN LTVHMEGNHIDGDIEIQTNRSPL QAPGEICESFTALMAMQLLSKL FWS
10706	41074	A	10768	533	760	
10707	41075	A	10769	1067	1225	
10708	41076	A	10770	1080	1250	SSGLHSWDARLVQYTQINKYN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10709	41077	C	10771	55	1842	
10710	41078	A	10772	1575	1745	SSGLHPWDARLVQYTQINKCN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10711	41079	A	10773	2798	2871	
10712	41080	A	10774	601	876	
10713	41081	A	10775	1194	1421	

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10714	41082	A	10776	587	1683	GWKFWPGQSGRRRK*R/CIQLG KEKVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVGRISIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI WNQKRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKTAWCWY QNRDIDQWNGTEPSEIMPHIYN YLIFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTIKTLE ENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLKSFCT AKETTVRVNRQPTTW
10715	41083	A	10777	1260	2176	SSGLHPWDARLVQYMQINQCN PAYKQNQRQKPHDYLNRCRKG L*QNSTTLHAKNS/AIN*CWKF WPGQLGRRRK*R/CIQLGKEEV KLSLFADDMIVYLENPIISAQNL LKLISNFSKVSGYKINVQKSQA FLYTNNRQTESQIMSELPFTIAS KRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWKNIPCSWI GRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR ARITKSILSQKNKAGGITLPDLK LYYKAIVTQNSMVLLPKQRYR PMEQNRALRNNAAYLQLSDL
10716	41084	A	10778	3813	3983	SSGLHPWDARLVQYTQINKCN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10717	41085	A	10779	1312	3348	
10718	41086	A	10780	1636	1815	
10719	41087	A	10781	67	403	KFLCRPPIIRPPKTFNTLIVLARR CIQCFRFFDIACFNRVGKGFGV GHQLRGFRHDIRGFAQWTHLP DGCAFRDRCYAAGAQCENVPA LTACGDNNQR\GACWYPQQEV
10720	41088	A	10782	506	915	WASVKSPVPCWNCWISHRRRV TCRHVRFAPGFNLAKAV/QGAA LVITGKGRIDSQTAGGKAPLGV ASVANQFNVPVIGIAGVLGDGV EVVPQYGIDAVFSILPRLAPLAE VLASGETNLFNSARNIACAIKIG QGIKN
10721	41089	A	10783	1	906	

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10722	41090	A	10784	2	597	SILKVACDVDNPLVGARGAAA VFGPQKGATPEMVEELEQGLQ NYARVLHQQPEINVCQMAG\A GAAGGMGIAAP\VFFNGDIKPGI EIVLNAVNLAQAVQGAALVITG EGRIDSQTAGGKAPLGVASVA KQFNVPCDLGLLAYVGDGVEV VHQYGIDAGFNILP\FLAPLAEV LASGETNLFNSARNIACAIKIGQ
10723	41091	A	10785	1	1140	
10724	41092	A	10786	13	628	LLIPARPPGINPYYWKVSEANLI RYFQQVGDSVTLPVMLYNFPA LTGQDLTPALVKTLADSRSNIIG IKDTIDSVAHLRSMIHTVKGAH PHFTVLCGYHDHLFNTLLLGGD GAISASGNFAPQVSVNLLKAW RDGDVAKAAGYHQTLLQIPQM YQLDTP\FVNVIKEAIVLCGRPV STHVLPPASPLDEPRKAQLKTL LQQLKLW
10725	41093	A	10787	3	1185	EQSGRGARDGGARDGVREGG\ SWTQQHGLPLTKVELATVAEY PVCLWQRLTL\SPQYGSIP/RGD QSDGWKVDYNGPFSLWKGQH FVINGIDTCSGCKFAIPVCSASA KLLPMSSQNVYHRDILHRIDSE QGTHFRVKEVQQWALGRGFY WSYYISHHPEAAGLVEQCNGIL KTPSQFQMGRNTLQGWGKVLP SLEGCAFSSSKSNLCSVVLKVF VPKEGMVPPGDTTMIILNCKLR LPP\MPLNLLASKEVTVLD/YQG EIGQLLHNRGKEECVWNTGDC LTYLLILPSSVIKVKEKPQPHPG RTINGPDPSGMKTWVTPPAGA VFLIGSWLRYDYGQYTWRAAS SQMLDRKGMNLASNLFHIGILG IFVGHFFGMLTPHWMYEAMTY GSCDTDNANV
10726	41094	A	10788	396	504	WKRLERRAIQGDSPVHKNARA GELDE*AATRAIPG
10727	41095	A	10789	24	611	EILPVPGPVVIAW/AIFRRIAGES WSAIVISGLSIARHAQQKRIITFT ASLAARLEIALKIVRNADGTES ASEQLYQVVGAGCKMPWQSE AMKDVLICDKRRLMRRTGGTE TSKYPEEKKSTEIPPVAASERGG AQSLNQCATEAVVLTRVDSHL KVGDSLSHTTSFLKKFAARFGG QLEKALGLGSMQAFSDIRGL
10728	41096	A	10790	212	578	

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10729	41097	A	10791	1	1707	
10730	41098	A	10792	3	313	NAE/TVKMFTTSSKEDATFGL/G WRVNGNATMTPTFGT/LASPQT YGHTGSPPLPPICPVRPPGYLRR LSPRFPRLFGISLPQRPPGILERS LQRRRNPSGWRRRNQ
10731	41099	A	10793	1	1992	MDVQSAADDTGLPMLVVRGPF NVVWQRLPAALEKVGMKVTD STRSQGNMAVTYKPLSDSDWQ ELGASDPGLASGDYKLQVGDL DNRSSLQFIDPKGHTLTQSQND ALENAILAVIRHEICLSDVVRIR ASRRFDKTSGTPDRQKILKLGY LLPAGWLADVDPRLVGVMNV WTLLVPAALFFFGAGMLFPLAT SGAMEPFPFLAGTAGALVGGL QNIGSGVLASLSAMLPQTGQPG VVDDLNGIVDRAVLAAAGDAD VASGAARLSARHRSIVISSMGE RCCFIRSRITRICGFLAAGVGLD QLAPDFATPVIRELLALLLCLFS GGLAMYGYLRWLRNEKAMRL KEDLPYTNSLLIISLILMVVAVI VMGLWIPPTCIVDDRMAKYIPG LADSPNDTIKGKNTLRISDLLH HSGGFPADPQYPNKAVAGALY SQDKGQTLEMIKRTPLEYQPGS KHIYSDVDYMLLGFIVESVTGQ PLDRYVEESIYRPLGLTHTVFNP LLKGFKPQQIAATELNGNTRDG VIHFPNIRTSTLWGQVHDEKAF YSMGGVSGHAGLFSNTGDIALF NAETVKMFTTSSKEDATFGLG WRVNGNATMTPTFGTLASPQT\ YGHTGWTGTVTVIDPVNHMTI VMLSNKPHSPVADPQKNPTMF
10732	41100	A	10794	2	137	NCLSPVSAN*WPAKTGRPILPS ATVTASTRNVLSKHWRIWVST VC
10733	41101	A	10795	271	553	ATQRQDLHFVRSPGDAVYTQIT PEAADAVVARNPDTAQHLHC/ VYP/HTSNAALAQKYLHIAASP EVMVPLSAFHAASYSMFFMEF NLIAMWANFS

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10734	41102	A	10796	1	747	MLLGLHSLAAFLQRESFSGKQS WGCQLAALLQRRITKMTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQRAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGTRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQRAVDLIS NVAGDRVTYRITKGEDLREQG YMGLHTVGRGSERSPVLLALD YNPTGDKEAPVYACLLGDIITY RNGKKVEVMNTDAEGRLVL
10735	41103	A	10797	444	548	
10736	41104	A	10798	951	1648	TTGRFPPSVQDSFVNESSRMGL PDEFTLQREFERARQQGALAQ W/IAAFEGGFTGIVATLDTGRPG PVMAFRVDMDALDLSEEQDVS HRPYRDGFASCNAGMMHACG HDGHTAIGLGLAHTLKQFESGL HGVIKLIFQPAEEGTRGARAMV DAGVVDDVDYFTAVHIGTGVP AGTVVCGSDNFMATTKFDAHF TGTAAHAGAKPEDGHNALLAA /AQATLALHAIAPHSEGASRV
10737	41105	A	10799	1495	2282	FDRHVGEFFLNQLETTNSLAKL HALIGVARRIFKGAHRRTVVGE GYQETFMVELFFDAVKAVTFPT EHVFLVQFHVVKGDFTAAIHTQ TELFKFGHFDARFAHINKPFGV DRFVRRSPVARHHHDVRGVGA AGNKTLTTIKINLTISTGISRFQA THVGARARFGDR*VRTDSTTTV GHRDCIITGGHR/HKSFQPGHEA PQAVPLPGRFHHH*PSHDHCR* LVSLAGAAYRSPQDPVPYMPIS PGLDWVRQIVCCVMASDAD
10738	41106	B	10800	1	3618	
10739	41107	A	10801	3	490	TGIVATLDT/GRPGPVMAFRVD MDALD/LSEEQDVSHRPYRDGF /ASCNAGMMHACGHDGHT/AIG LGLAHTLKQFESGL/HGVIKLIF QLHRYAAHAGAKPEDGHNALL /AAAQATLALHAIAPHSE/GASR VNVGVMQAGSGR/NVVPASAL L\RQPTRSALNTTQQLNAR

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10740	41108	A	10802	1	513	MGIESLQAFLRSAGALGVWVY TFLERILIPTGLHHFIYGQFISGP AAVEGGIQMYWAQHLQEFSLS AEPLKSLFPEGGFALHGNSKIFG AVGIYLAMYFAAAPENRVKVA RLLIPTPLAAMLVVIPEPL\EFTF LFISPILYAVHAVLTASMSPVM YLPGVVGNMGEGKID
10741	41109	A	10803	1	4941	
10742	41110	A	10804	1	1083	
10743	41111	A	10805	1	1363	MPVRKNMIMNEGNITTPTNGC RIRASCGVPMICINQLKDGNKK PSPLTAARMKQKAIILFLIRTVR TDTHVVEDTGRKGSRKANSRE RFPDAFPEFHGFADFRVLRQAM IQIWLVSMVQHVHNVCTTDAC RIVQTRIVVTAGFQLSNASLVA MRRWVYRVRRIQYRRTTQTAV FHSTHGNYREGQPVGTLIDDRY KANENVELVHYAQPLLNEADS LAKVMPSDIPLKQRRWLGLQM LEGDIYSRAYAGEASQHLDAAL ARLRNEMDDPALHIADARYQCI AAICDVVSNTLTAEPSRFTTAV DKIVLNRFLGLPIFLFVMYLMF LLAINIGGALQPLFDVGSVALF VHGIQWIGYTLHFPDWLTIFLA QGLGGGINTVLPLVPQIGMMY\ CFSSFLKTPALACREIFVPLMRL RVNLRWYPPVL*RISWWTNSRI PTTFSTRGSACWRATPAK
10744	41112	A	10806	199	1083	RLFEHPRLGVAAVENGALGKR SAVVLPGFDAVNHKTRFIEFVK SAIEGNRLTVRAIGPQFFTQTPV IVFNQGVSGAQNIAGRAVVLLQ TNSFGTGEIIKETLNILHLRPAPA VD*LVVITDDHHFAGVARQQA DPRVLNVVGILEFVHQDIGKTF AVVLQDMRLVKPQLVSAQQQL GEVHQARAVTRFLIRLIHLLPGL LHRITVALNMMRTQAFIFLAVD VPHCLPRRPLLLVEVHGFDQTQ KVAAWRGHRFALFVIKAVEQV RNVHWHRRVKIGWAEKRNAL RQKAGNFQMRQ
10745	41113	A	10807	49	273	DFLGRGAFNVINIGAWASRPVQ GSTVDLSHGLHLVLHLKNNL*F YGFDSHFLKSFFYKGTSISIQVE VGISQGNL
10746	41114	B	10808	91	2183	

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10747	41115	A	10809	8	219	FSLWPL/KKFSNRFLKKKPMEF GSWTTREILIASFAGVRGAITLA GVLSIPLLLPDGNVFPARYELVF LAAV
10748	41116	A	10810	84	509	
10749	41117	A	10811	3	163	ENTTWLYAD*NAGRDADFGHA KRKWTLWLAILAAVATAMAN RQPGAGLFALFT
10750	41118	A	10812	1	707	MGWRMGIWLRVFTVAKHLQR AESDQIGFRLKEHCWKRYAVR HPVKDVSGFSPVLTVNMRAPQ SN/PARRTVGWLRMFRRLRKR/ RKPRPLPLSPLHMDV/HAGNLV HSASGLKLIDW/EYAGDGDIAL E\LAAVW/VENTEQHRQLVNDY ATR/AKIQPAQLWRQVRRWLP/ WLLMLKAGWFEYRWRQ/TGD RQFIRLADDSWRQLHRSNKESS RELVARLRVFAQSSGGAVDQE GGRVQCFREGL
10751	41119	A	10813	1	227	SFINVERYRAEPQTADAAPLKR GAFGSWLPEPDHYAED/DHQQ YLHKNPYGYCGIGGIGVCQAY KIVQIQYIARTA
10752	41120	A	10814	1	283	
10753	41121	A	10815	315	569	
10754	41122	A	10816	65	580	SDRS*IPVRPTHRDSGNRHDGSS GYCRCYG*HG*HRGIRYRCWPE KSQTRSGLLP\LTVNYQERTYA AGRIPGSFFRREGRPSEGETLIA RLIDRPIRPLFPEGFVNEVQVIA TVVSVNPQVNPDIVAMIGASAA LSLSGIPFNGPIGAARVGYINDQ YVLNPTQDELKESK
10755	41123	A	10817	235	1236	TDHDGRNDTQRIGSGERNRPFS NANTAHHQCRFAGFALFCGEIF TTNQRRQPHPQRRDTNTHGSD GHHGINTLSNANQHEGIGHFVN RTAHIERQHQTHDHRQHNNAA NSGTEVSQ*AR*HAAV*RYVAE REIHSGDRCGKRNSAHKIMPG WWCALPDTAPSLSKVVFFKGC PHLCPWCANPESISGKIQTVRRE AKCLHCAKCLRDADECPSGAF ERIGRDISLDALEREVMKDDIFF RTSGGGVTLYRGEDPAEDARY AHTNQPRQNKAVVDDEATDV GGAGTVKLNRCQIARISRQDVI TVASRCEHGFCHPCDTVHRHD GDHTGTEDFVF
10756	41124	A	10818	1	400	

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10757	41125	A	10819	783	1116	SVLHLYYEQNTE\HDTRGYRPI KTLDIVPAFEASHLLWQSYENS WEQIFSASVGASWQKHYGTDV LTQLGYGQRIIWNDIIDAGATL RWEKRPYDGDREHNLYVEFD MTFRF
10758	41126	A	10820	3	474	TCGE/AASIVDRIRGFFEPSSILV STLVLTLRPTGLLPLVTDSLPM RLLPTEIMAGSPIRS/RDISLGDD PGINGQRAQGTWERWTVRADE PQAFHIEGVMFQIRNVNGAMPF PEDRGWKDTVWVDGQVELLV YFGQPSWAHFQFYFNSQTHKV GPRAVA
10759	41127	B	10821	93	786	
10760	41128	A	10822	191	748	GPATPRQPFKVLASLGRLVQHG GRWDAQHLHNAVHLVDLIGAT EEGLSGVHLHKDAAQGPHVNG QVVGCAQEHLR*AVEAALDIL VDPLAKLAGAAEVHNLDGAAL GVAQQDVFGLEVAVNDAEAQ AWPERAVPCRAAAPASGSGSA RRRGSGCCAGGRTGCRTAAQIP STSGFRNMKCRFRCTI
10761	41129	B	10823	1	2724	
10762	41130	B	10824	116	2458	
10763	41131	A	10825	1	1317	

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10764	41132	A	10826	99	2052	NPADGRTGFTLCATGEALSSAT IAAAERRQALQEGCDDILS/HG DADMVSMAR/PFLADAELLSK AQSGRA/DEINTCIGCNQACLD Q/IFVGKVTSCLVNPRACH/ETK MPILPAVQKKNLA/VVGAGPAG LAFA\FNIAKQIPGKEEFYD/TL/ RYYRRMIEVTGVTLKL/NHTVT ADQLQAFDETILAVG/IVPRTPPI DGIDHP/KVLSYPDVLRDKAPV/ SN/KVAIIGCGGIGFDTAM/YLS QPGESTSQNIAGFC/NEWGIDSS LQQADCDAPAKASKPGQGLGK TTGWI/HRTTL/LSRGVKMIPGV S/YQKIDDDGLHVVINGANQGS DMLRLQGELDSASRIGRRSAAP KLGSLNDGRCFINCHILDRLPY KGLVPACSWNGGSLDPLEGRP DEPHVEVLGIPPAAMLDQAPRL ASTLNGCLGVAGPYEDERTQE GLPGPRDTAAEEVLGVQTGGA GSRGRVRGPQPADLPSASGPGA ACWSMSPPPDQPPCVLAHGFFR RTPTSTQQRPAEQCFHSPAPLEL PLSSTSSILSFAEYGNAMAWLY RGKILPSGTPDDLKAQSANDGN PDPTMEKAFIQLIHDGIRSIAMS NPILSCRRYGRYQEWCLTIPAV FISAPYVRRYVRFHEHQEGGGV RQEATVREIPLAIAVIPNSRTPC
10765	41133	A	10827	1	525	DAMVSSWNRAAPNTIPTAAKA GGNYLSSLLVGSEARRHGYQE GIALDVNGYISEGAGENLFEVK DGVLFTP/PGFTSSALPGITRDAI IKL\AKE\LGIEVREQVLSR/EKS LYLADEVF\MSGT\AGEITPR\RS GNGYSGLAKGRCGPVTKRIQH ALQGVYSWVTPGYFESVRCTA
10766	41134	A	10828	8	573	REPAGENGPPVCDGAMLDLKA/ WGSECHQQLTGRDNQQIKRSIY LLPERAKLAELRLLVIPGQVDY LQHIEELAAFIKGLGDVPVRLN AFHAHGVYGEAQSWASATPED VEPLADALKVRGTCRPDKTRQ ASHQALCANCRMRRERLIRPTV RHKPVGMIRRDKRRIRHYAPTA GCGVNALSGLRFGTDL

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10767	41135	A	10829	1	479	SNATNGIEPPRGYVSIKASKDGI LRQVVPDYEHLHDAYELLGEM PGNDGYLQLVGIMQKFIDQSIS ANTNYDPSRFPSGKVPMQQLL KDLLTAYKFGVKTLYYQNTR/G RR*RRTRRSGAVNPGTMGCESG ACKNPGYLRMPGCRRKTPLIPA LPGFGFW
10768	41136	A	10830	1	443	MDSLMDMLAST\QGRRMDDQR VTVSSLPGFQPVGSKAYKPSRR PDKAFTPHPASQYQILHAPLVA AIVSGLTAARVVFVRLQQPSLG VLSNTSGCDATNVVGRLQDNA SVSPGIVHTDSVIWRSCQVRRS AVHTLWRQKTRLFDAVDA
10769	41137	A	10831	1	323	MDLVTGSRKVIIAMEHCAKDG SAKIL\RRCTMPLTAQHAGHML VTELAVVRSFDGKMWLTEIAD GPTSQAQPAATYRIPLSNSRVR RRYRHRYYRYNLSIRKKRHRPL
10770	41138	A	10832	526	975	TPYPAYVQHVTPGRIRRGKRRI RQCLPVLESRFHNTQKSRGETE GASGFSLQHHLGDSSRAAPGPY RVSTAAADSGGRAGSSAPSALV PRGC*GPSLAPAGRSQR*HRGG GQLSPAAPRTANKAAGLGPPA RLNFFIRAQCDSRINDITR
10771	41139	A	10833	1906	2049	PLSIIEADFRIWANAG*RMVAGI KPSIARVPLVLQVSALEVPEQC YRH
10772	41140	A	10834	1	808	MPKPNTRWSAWGLRRLKRKW SVARGSNLNRSVQYEFTGRGD RIGWVKGIDDNWHLTLFIENGR ILDYPARPLKTGLLEIAKIHKGD FRIT\ANQNLIIAGVPESEKAKIE KIAKESGLMNAVSPQRENSMA CVSFPTCPLAMAEAERFLPSFID NIDNLMAKHGVSDEHIVMRVT GCPNGCGRAMLAEVGLVGKAP GRYNLHLGGNRIGTRIPQITRRI EHRANDARTHRKVAEAFTRFA LFRPAPYQFIKRRQDFRLVMFSI YMPVPS

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10773	41141	A	10835	248	830	HHYRKMNIQQSKWLIVTVCDG KLNWLLSGSKVCCTWMLCVQ/ SEPELAKAWIFANLLAAFLIDDI IQPSLDFPPRRAEITIAADGTISA LNPGDPANTVAPVGRLKLVKA TGSEVQRGDDGIFRLSAETQAT RGPVLQADPTLRVMSGVLEGS NVNAVAAMSDMIASARRFEMQ MKVISSVDDNAGRANQLLSMS
10774	41142	B	10836	328	481	
10775	41143	A	10837	14	675	FRKLQVCWLPRPHLRPWWTCK PRWFGSCLRVFL/LERVI/GDV/ WGLRLWSALGVAFFG/WAFITS LQAKRGWMRIVPIILLAAALVS VRPLQDWAFGATHTAQTQTHL NFTQIQTVDELNQALVEAQGKP VMLDLYADWCVACKEFEKYTF SDPQVQKALADTVLLQANVTA NDAQDVALLKHLNVLGLPTILF FDGQGQEHPQARVTGFMDAET FSAHLRDRQP
10776	41144	A	10838	1	1413	GMALTYTALGLVVAAAGLQFQ AALQHPYVLIG\LAIVFTLLAMS MFGLFTLQLPSSLQTRLTLMSN RQQGGSPG/GAILLYIAQSGNM WLGGGTLYLYALGMGLPLMLI TVFGNRLLPKSGPWMEQVKTA FGFVILALPVNIAPGSLDKALNQ YAAHSGFTLSVDASLTRGKQSN GLHGDYDVESGLQQLLDGSGL QVKPLGNNSWTLEPAPAPKED ALTVVGDWLGDARENDVFEH AGARDVIRREDFAKTGATTMR EVLNRIPGVSAPENNGTGSHDL AMNFGIRGLNPRLASRSTVLMD GIPRPLRPLRSAAAFTGSRFARQ HGCHCTWYAVVVRCVTDTQS VGGVVNFVTRAIPQDFGIEAGIL MSDLKHGSLVGACLGRLGPGA VLYLAVAVLGVRVRRGVVLVC PLGGTGLGYSCQGGAFQFAAS CFLGRYGVVQGVIHVCFGPRSV FLDDCLRFDLPCLVWLSCPR

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10777	41145	A	10839	1	908	LLKPFHVIAIATGRSLAVFCMG RLRTICSHATPPASAI/LLYI/AQS GTWGGGGTLYLYALGMGLPL MLITVFGTRLLPKSGPWMEQV KTAFGYVILALPVFLLERVIGD VWGLRLWSALGVAFFGWAFIT SLQAKRGWMRIVQIILLAAALV SVRPLQDWAFGATHTGQTQTH LNFTQIKTVDELNQALVEAKGK PVMLDLYADWCVACKEFEKYT FSDPQVQKALADTVLLQANVT ANDAQDVPTSAPFISPPNALVAI IVQLRFGDFYNRVSKGSRPTVF GRTLKARRITLSEKSILKAKIH
10778	41146	A	10840	3	808	SSGGHGRRAAGRLQHPLLRVH VPVVDTSCVPSCSRLQWHHLPL CPGQLQHGHFHGPWCFPPSG*G *GQGGRLPGSAVQERGCARYP GPHEVVCHVPLLPPAALLPLQR L*QLCRGL*PPLPLGQ/PTASGV ETIATSSCSCCHSVHTWWASWP SAWSTC*TTLRGWEPRTPPSRIL GSCGPHCRGDVDRGHVHPGE* AFQSLVPCQGTPKGPMAPP*VG RGVSP/PGTRVEAALSCESPPHA RQSMCFNLHTHSIDPKQSRRPY SDNVGKE
10779	41147	A	10841	2	646	CSWQPAVPTQPQPAGPSAPRQG LPGHSRGAQPALVSPHKGLTPV PGTPA\PASTPPAPAGGEGLPSP AAGAPPAHCPG/HPPAPATAAP VPGLCGPCPSLPACPQTR/PPTH VNTKKRV/PG/VRPAARRPWPP GCTWRGARTVTFLHQLNPGVN CQMLTVGRSGIRPTCTIASCSV NKLHPQMHPATQPHHRMALSP SHSEGPSHCWGLSLGDISPIPR
10780	41148	A	10842	3	550	

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10781	41149	A	10843	2	1132	LCLVMILYTRRRWCKRRRVPQ PQKSASAEAANEIHYIPSVLIGG HGRESLRNARVQGHNSSGTLSI RETPILDGYEYDITDLRHHLQR ECMNGGEDFASQVTRTLDSLQ GCNEKSGMDLTPGGDGRKARL MNKYKDNIIATSPVDSNHQQAT LLSHTSSSQRKRINNKARGMHV *H*GEGDSGTEAENDPQLTFYT DPSRSRRRSRGRNDRGGRNKTT LTLISITSCVIGLVCSSHVNCPLV VKITLHVPEHLIADGEPVLLRM GSQLDASDWLNPAQVVLFSQQ NSSGPWAMDLCARRLLDPCEH QCDPETGRREHRAAGNCQRDH ARAHSVWLGSPPYHDTSLRWS PMYTTMESAPHAFPPSVTADAE
10782	41150	A	10844	3	3935	HASGPGLKMALAGLCALLACC WGPAAVLATAAGDVDPSKELE CKLKSITVSALPFLRENDLSIMH SPSASEPKLLFSVRNDFPGEMV VVDDLENTELPYFVLEISGNTE DIPLVRWRQQWLENGTLLFHIH HQDGAPSLPGQDPTEEPQHESA EEELRILHISVMGGMIALLLSIL CLVMILYTRRRWCKRRRVPQP QKSASAEAANEIHYIPSVLIGGH GRESLRNARVQGHNSSGTLSIR ETPILDGYEYDIT
10783	41151	A	10845	184	357	ALQGWSKNLH\PEDIQLGKTPP P*QVAQEGGWSRRVGSDTWIL EEQPGSTTRRVSVGM
10784	41152	A	10846	226	609	VILSSFDLIKHGILLEISDSIQFRG CKRSRIPELGGLEELW*PGDCR QPRP\WRA\GRHLQPGSLGSLVS KHQLRGSRKTL/YSAFRKCHLL SVWEGKPLKI*RGDQVADSSQK KQLAADAHTPYRGGDI

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10785	41153	A	10847	20	1317	SSHQKQMLAPCFLGSLQNWQH HTAGKGK/WVLGTCAFGEQLA ASGHMKETRADRSKKLFRHYT VGSYDSFDTSRGGRVRKPYAGF FPDLQDICDEQPRPLHSTLRPAC GGIQPGKQQPMPFAKTDTCASD KHVEKKLERLIHQAVSDAPEPS RVVKGIFIGGLPCARLWVVPYL MGHVQEVTMAEGYERASQATF REQMQEVPCCLQRSTGSSMKT GNKIRRVTDNVLTRSGPLINDIL SVAVDSSVSVLIWMHLFSSHPL GIVRYWGCMGISCKLLLLTRVC YLITPLDLERFPFPNTEQVTFPE RRVSVFLLPLSWCLDTRLPREP GCRSRRDSFTHRVFYSVTPTSG DVPGSHPFCDKPVRRGDDPYIR NDRGTLYSTLQFISTCVQVVGV YGHLPGFKSDAAQAVPRLLSQ KRDQNHKEEEITDGDERPK
10786	41154	A	10848	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
10787	41155	A	10849	1	3654	
10788	41156	A	10850	1	5127	
10789	41157	A	10851	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
10790	41158	A	10852	1	3663	

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10791	41159	A	10853	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
10792	41160	A	10854	1	3354	
10793	41161	A	10855	1	5073	
10794	41162	A	10856	1	3235	
10795	41163	B	10857	1	3300	
10796	41164	A	10858	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
10797	41165	B	10859	1	3420	
10798	41166	B	10860	1	4019	

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10799	41167	A	10861	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKL\GIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGQ
10800	41168	A	10862	1	4449	
10801	41169	A	10863	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
10802	41170	A	10864	1	3297	
10803	41171	A	10865	1	4791	
10804	41172	A	10866	3	3316	
10805	41173	B	10867	1	3415	
10806	41174	B	10868	1	4753	
10807	41175	B	10869	1	3384	
10808	41176	A	10870	1	3345	
10809	41177	B	10871	1	3772	
10810	41178	A	10872	1	3720	
10811	41179	A	10873	1	3894	

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10812	41180	A	10874	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
10813	41181	A	10875	1	3780	
10814	41182	A	10876	1	3852	
10815	41183	A	10877	1	3345	
10816	41184	A	10878	965	4362	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFFSAPHHTYSKI DHIVGSKALLSKCERTEIITNYL SDHSAMKLELRIKNLTQNCSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTNQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREKNQIDT
10817	41185	A	10879	1	3921	
10818	41186	A	10880	1	3988	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNL
10819	41187	A	10881	2	462	YFTDRLRARLAGTPL/IMFGTIA RSGVRIVSREPLNRRAILIIALSL AVGLGVSQQPLILQFAPEWLKN LLSSGIAAGGITAIVFSLAGHPA LATNAQPMEAFLLHQTTFFQNL IRVKEAICSDQFNTTMFRGLQG NSACTKCNPRCLNELTPTE
10820	41188	B	10882	16	163	

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10821	41189	A	10883	2	1509	RDEVNGCIRLVYDMYSTFGFEK IVVKLSTRPEKRIGSDEMWDRA EADLAVALEENNIPFEYQLGEG AFYGPKIEFTLYDCLDRAWQC GTVQLDFSLPSRLSASYVGEDN ERKVPVMIHRAILGSMERFI\GIL SEEFAGFFPTWLAPVQVVIMNI TDSQSEYVNELTQKLSNAGIRV KADLRNEKIGFKNRSGELSHLP PINQSKPRNFPSAALPQVPQPTH LSQRPRASPKPPPPDPERVELSL EEHREMLEGFYEEISKGRKPTLI LRTQLSVRVNAILASLESVKPL YTMALGLLVKYPDSALGQLRIE STVDGSRLYITGNGVLFQHVKF HAFLLYLGYTPQAAREVRIMQF CHTLREFALEYRTCRERVLQQQ QKQATYRERNKTRGRMITETE KFSGVAGEAPSNPSVPVAVSSG PGRGDADSHASMKSLLTSRPED TTHNRRSRDRHGPRGCQVCSA QPSLLRAVPVADMRALMTGKD CPPCPGKRLRGAELGPL
10822	41190	A	10884	296	757	ISRFRRRALSPKAESSLSSILPRE KRSPSRTWILTPRRLFSLAISSKS AGNTLSSRIFK*KA*ACK*RGR VSTRCRIFLALFIVTIKHRLMMR STASNRQYSISIWTILPCWSARC FSIKIAGIPAEPPRYLLISPGILTG LKINFFTTVSFW
10823	41191	A	10885	1	519	MGLPWQVGMGAIFWGAIGLLL LTIFRVRYWMIANIPVSLRVGIT SGIGLFIGMMGLKNAGVIVANP ETLVSIGNLTSHSVLLGILGFFII AILASRNIHAAVLVSIVVTTLLG WMLGDVHYNGIVSAPPSVMTV VGHVDLAGPIGNSLV/GCPYFAI LRRFSDGSGGLGRNQI
10824	41192	B	10886	1	3489	
10825	41193	A	10887	817	1528	WGSRDNRDEIRNTLVLDTLRLQ RVCAQRAFLVLFVLGKVTFEEL NFTFILVIQNVRGDTVEEPTVVR DNHRTARELQQGVFQRAQGFD IQVVGWFVEQQHVAANLSRCR LVNTPTQQVRFSTATFRVIWRV TPTAGKLSGGFLFKMYGLPAA AIAI\GTLLNQKTARKWAVL*SP PALTSFLTGITEPIEFSFMFVAPI LYIIHAILAALFMWKFVPETKR KTLEELEALSNRIAAE
10826	41194	C	10888	1	573	

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10827	41195	A	10889	2321	2554	WRKRCVKVRNLSPLCLPDRKL TLPCCSIAIRNCIAKLPVS*LWV ALWGWVTGRLRLNLIFTLTRK RQKLSSSQGSRW
10828	41196	A	10890	1	4350	
10829	41197	A	10891	137	686	KLLELRSKREAGMLERSSSRMV TCSQWAATRNPVVALPIYGFIE RCLVPFGLLHIWNVPFQMQIGE YTNAAGQVFHGDIPRYMAGDP TAGKLSGGFLFKMYGLPASAIA IWHFVKPETRAKVGGIMIFAAL TSFLTGITEPIEFSFMFVAPILYII HAILAG\WHSQSVFFWGCVTVR RSRTV
10830	41198	A	10892	3	3831	SIGMMGLKNAGVIVANPETLVS IGNLTSHSVLLGILGFFIIAIL/AS RNIHAAVLVSIVVTTLLGWML GDVHYNGIVF\APPSVMTVVGH VDLAGSFNLGLAGVIFSFMLVN LFDSSGTLIGVTDKAG\LADEK GKFPRMKQALYVDSISSVTGSFI GTFSVTAYIESSSGVSVGGRTG LTAVVVGLLFLLVIFLSPLAGM VPGYAAAGALIYVGVLMTSSL ARVNWQDLTESVPAFITAVMM PFSFSITEGIAL
10831	41199	A	10893	6	146	
10832	41200	C	10894	1	1197	
10833	41201	A	10895	1	763	MCSEKVAMCCDDDDDDDDDD DDDDDDDDDYSCSHGFWDFSY TWNTSIPQGHLGMGSPIKGLVE IRDKLGDRTQRVYIQRITGNGL EFENPCKQFRGLTRMYIRRLTR LSVQWYMVALERPVLQKYRY RGSKAHETSHSMSTVTSSNEKQ DNTRIDTQGATNR/VATLRHRE TVLANEVAPYAATDNVLAAST DVGDVSWKLPVAQCFSPCFAV GTPLHTWQ/SGLLQECQQEHQQ VTDTQPYHCPIPKNVTPSPLK
10834	41202	A	10896	2	412	LFEFTLDVKVRESPIL\FRDESM RTACSPDGLCSNGFGLELKCPF TSRDFMKFRLGGFEAIKSAYMA QVQYSMWVTGKDAWFFANYD PRMKREGIHHVVVERDPQYMS DFNEMVPEFIEKMDEALAEIGL TVRELGI

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10835	41203	A	10897	3	663	ARGKKPPRRGKEDFWDLSIATR VSVNPIKFPVEA*PFLKP\LQQV S\GPLGGRLPLPIPGNLLLQVAD GTLSLTGTDLEMEMVARVALV QPHEPGATTVPARKFFDICRGL PEGAEIAVQLEGERMLVRSGRS RFSLSTLPAADFPNLDDWQSEV EFTLPQATMKRLIEATQFSMAH QDVRYYLNGMLFETEGEELRT VATDGHRLAVCSMPIGQSLPSH
10836	41204	A	10898	377	1077	WRGQRCLASVFPRHPGAEGRG RPVFRAETIFL**SRRGLAR/TGR RKLPVKLKAADFPNLDDWQSE VEFTLPQATMKRLIEATQFSMA HQDVRYYLNGMLFETEGEELR TVATDGHRLAVCSMPIGQSLPS HSVIVPRKGVIELMRMLDGGD NPLRVQIGSNNIRAHVGDFIFTS KLVDGRFPDYRRVLPKNPDKH LEAGCDLLKQAFARAAILSNEK FRGVRLYVSESQLKSRQ
10837	41205	A	10899	591	871	VRGFPSGAEQLYG*SVSLLILLP NLSNSG/RTGFPVAPLPYSKSPS DFMSLLISTVPGSQL*QPIQRAE LVCTTCSPIVSAPTGQAPTQGAF SH
10838	41206	B	10900	1	1765	
10839	41207	A	10901	1	1177	MKSLIIVNPADCIGCRTCEVAC VVAHPSEQELNADVFLPRLKV QRLDSIKRFWEQMMRIVTAAV MASTLAVSSLSHAAEVGSGDN WHPGEELTQRSTQSHMFDGISL TEHQRQQMRDLMQQARHEQPP VNVSELETMHFPGMLFETEGEE LRTVATDGHRLAVCSMPIGQSL PSHSVIVPRKGVIELMRMLDGG DNPLRVQIGSNNIRAHVGDFIFT SKLVDGRFPDYRRVLPKNPDK HLEAGCDLLKQAFARAA\ILSN EKFRGVRLYVSENQLKITANNP DQEEAEEILDVPYSGAEMEIGF NVSYVMDVLNALKCENVRMM LTDSVSSVQIEDAASQS\AAYV GMPMRLEGSPPLGNPEFQKISSP CALYIALCSKARHHTGRYLGLC
10840	41208	A	10902	527	925	

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10841	41209	A	10903	1	1514	MAFGLFWLIWILMSTITRGIDG MSLALFTEMTPPPNTEGGGLAN ALAGSGLLILWATVFGTPLGIM AGIYLAEYGRKSWLAEVIRFIN DILLSAPSIVVGLFVYTIVVAQM EHFSGWAGVIALALLQVPIVIRT TENMLKLVPYSLREAAYALGT PKWKMISAITLKSAVVGNMTRI L\LRMAPIVVKTAPLLFTALSNQ FWSTDMMQPIANLPVTIFKFAM SPFAEWQQLAWAGVRNLNFYY GKFHALKNINLDIAKNQVCVC YNQCTESLVNGLYANAAHLVS VGQRSTGNSSVIKARQGSSIRP MIVKYSALCLCRMRSERFIRRT KHRKFDRLQCTCRPDKRSASG NLAFVISLRPVPLVAVVFALFA AFPMFSDVSIQLRHFIFANFLPA TGDVIQRYIEQFVANSNKMTAV GACGLIVTALLLMYSIDSALNTI WRSKRARPKIYSFAVYWMILTL GPLLAGASLAISSYLLSKQWAI DIDSVNRLGAIILTALITGDT
10842	41210	A	10904	900	1250	WYACDQCQTCLPDHAPECAVA *AKTCCTAIETGTYRQSGRERK QSAMVL*RVRVLL**RRETACH VRAGLL*S*GTALGGHYRRLQQ *NSTGRHAGSGGTPLRQRSSVV SSGVADG
10843	41211	A	10905	626	850	LRFCLVFNILSRYSLISTVQKFSP AMLNGTLPLENILH*LRNITAIM NLVIFHGLSA*SVCYIPGRGSV MSDRV
10844	41212	A	10906	307	858	
10845	41213	A	10907	698	1115	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHSGTRGRRAR FSVRATYAAGRLATIPGYRGGP LGLMCGQPNRKPTDGANERLT MIRAATAMSE
10846	41214	B	10908	1	721	
10847	41215	A	10909	1	2615	
10848	41216	B	10910	1	1164	
10849	41217	B	10911	1	1930	
10850	41218	A	10912	689	1033	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPH\DGPEHSVFM PSR*APMTR*KIYSSPPYRSSQR AHRHA

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10851	41219	A	10913	393	686	NPSQLWEAAPPQWKWIQGAGK VSCQLSRAADQLGRQHHISDPC FSIVPLIL*FAAYFPINPAVLKLA PVALYADAIRYNARTPLQGSLL PLTRLVWA
10852	41220	A	10914	1313	2370	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHRANPDANVV SEDVLRESVGKSVVNLIHGVRD MAAIRQLKATHTDSVSSEQVD NVRRMLLAMVDDFRCVVIKLA ERIAHLREVKDAPEDERVLAAK ECTNIYAPLANRLGIGQLKWEL EDYCFRYLHPTEYKRIAKLLHE RRLDREHYIEEFVGHLRAEMK AEGVKAEVYGRPKHIYSIWRK MQKKNLAFDELFDVRAVRIVA ERLQDCYAALGIVHTHYRHLP DEFDDYVANPKPNGYQSIHTV VLGPGGKTVEIQIRTKQMHEDA ELGVAAHWEI
10853	41221	B	10915	1	1556	
10854	41222	A	10916	1566	1947	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPH/ECAGLSLAT GISAAAGL*WARRSFIQRDSRD PRYRAPIRIHPLPGANHLRQ
10855	41223	B	10917	1	1571	
10856	41224	A	10918	2024	2589	QDMQNLLVLRETSVKPEYPGL KVPEAFR/RIQGRKGEPGEGAY VYRSAFSVFQKPRFSCALGGAI AASWAGGGAPSPCGRRAELPW GPGPVGVAQTVCPERPRRERRL RGEREEEAADKVMARRWRKSR RRKRKEMEERMSPEETEGTNF DFAGEAVGQAERKGPAFSAAE ESFHEEEKRRRKEQSDLTF
10857	41225	B	10919	690	2724	
10858	41226	A	10920	3892	4338	

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10859	41227	A	10921	2573	3473	ANGARLALPPLGTFQGRQLRRR RPRWRRRRPGEASGPVMRLRG PRPGASAQPWDGGSQVAR*WC PFPSPQGWDGGSQGGQGDGAR FRTHRAKVQQDGDGR*DEADG VHRHAPLQGRLVLVQVGVADE REDDAGNEGLQHLQQPGYGGH IASDLAGPGPGPGHFGGVSHTR DAGEEGGGDGVVPRTAVGQEL DIGGGVDDGGREAEEGRIAGEG DGEVAPRQGEAGLEPAQLHDE DDQGHGEAEAPGEHGPVAHGP RPGAHASHQREGHAGRHQLQQ AKETQGLCQGPRGPHDHGGPQ
10860	41228	A	10922	819	1274	NPLPRLQLRRQLHLPSVRNCCQ TRRCGR*HRQRLRQ*ARRKLVR SVYFGSCLRQLLREEWK*Y*RV *VLGWYSAVSTSSLPFDYCFLP NSDGYRRVVDPGSLSGHPFLYQ RYGWQHDDVHQPDLGLGPPGS LHPDPACFRCVLRNCGNLLA
10861	41229	A	10923	720	3546	RDGRKPLQPDAARNCGGSQSQ RSGSRKRRGDRRI/TLMSLKTRK ANRWA*SFRRKMAAISTP/RTDI ACAKYRYETLHADRVLYYIDS RQHQHLMQAWAIVRKAGYVP ESVPLEHHMFGMMLGKDGKPF KTRAGGTVKLADLLDEALERA RRLVAERTRYSAKSWKTVFRL VIGEQMIDVLGPEKRRRRTTQE KIAIVQQSFEPGMTVSLVARQH GVAASQLFLWRKQYQEGSLTA VAAGEQVVPASELAAAMKQ
10862	41230	A	10924	764	1227	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHNPTLEWFLS HCHIHKYPSKSTLIHQGEKAET LYYIGKGSVAVLIKDEEGKEMI LSYLNQGDTIGDLGLFEEGQER SAW
10863	41231	A	10925	2467	2653	WLPFGLSHHNSPHPTSWGAN\G GFCQLLSMSVLIMHSGTLGAH WDFSPVIGLEANRGVGDGS

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10864	41232	A	10926	1	860	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEPFY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RLFARLSLDSALPDRTTIMNFR HLLEQHQLARQLFKTINRWLAL GVMMTQGTLFDATIIEAPSSTK NKEQQRDPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNQLGNLLHGEKQF VSAMPATKEPQREELAEVDVD LLIAERPGKVKTLK/TESAQ/GT KRPSTSNT*KPASVPGWSTRFA SSSGSSAS
10865	41233	B	10927	754	910	
10866	41234	A	10928	2395	3454	
10867	41235	A	10929	1	1377	MSCMTPASDGTFISIDDEEAKQ FRESVVEWLMTNHPHDCPVCE EGGNCHLQDMTVMTGHSFRRY RFTKRTHRNQDLGPFISHEMNR CIACYRCVRYYKDYADGTDLG VYGAHDNVYFGRPEDGTLESE FSGNLVEICPTGVFTDKTHSER YNRKWDMQFAPSICQQCSIGCN ISPGERYGELRRIENRYNGTVN HYFLCDRGRFGYGYVNLKDRP RQPVQRRGDDFITLNAEQAMQ GAADILRQSKKVIGIGSPRASVE SNFALRELVGEENFYTGIAHGE QERLQLALKVLREGGIYTPALR EIESYDAVLVLGEDVTQTGARV ALAVRQAVKGKAREMAAAQK VADWQIAAILNIGQ\HPLFVT/N VDDTRLDDIAAWTYRAPVEDQ ARLGFAIAHALDNSAPAVDGIE PELQSKIDVIVQALAVFRLVIGE QMIDVLGPEKRRRRTTQEKIAN
10868	41236	A	10930	19	586	IAALLKDKHPAMLLLAATKRG KALAARLSVQLNAALVNDATA VDIVDGHICAEHRMYGGFAQE KINSPLAIITLAPGVQEPCTSDTS HQCPTETVPYV/APRHEILCRER RA\KAASSVDLSKAKRVVGVG RGLAAQDDLKMVHELAAVLN AEVGCSRPI\AEGENWMERHAQ HKSWNPLSWAPLGSQAHP

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10869	41237	A	10931	1	1364	MLRILCLALCSLLTGTRADPGA LLRLGMDIMNREVQSAMDESH ILEKMAAEAGKKQPGMKPIKGI TNLKVKDVQLPVITLNFVPGVG IFQCVSTGMTVTGKSFMGGNM EIIVALNITATNRLLRDEETGLP VFKSEGCEVILVNVKTNLPSNM LPKMVNKFLDSTLHKVLPGLM CPAIDAVLVYVNRKWTNLSDP MPVGQMGTVKYVLMSAPATT ASYIQLDFSPVVQQQKGKTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVNI QDTMIGELPPQTTKTLARFIPEV AVAYPKSKPLTTQIKIKKPPKV AMKTGKSLLHLHSTLEMFAAR WRRKAPMSLFLLEEHFNLKGQ HSLHENQLQMATSLDRLLSLSR KSSSIGNFNERELTGFITSYLEE AYIPVVNDVLQVGLPLPDFLAM NYNLAELDIVELGGIMEPADI
10870	41238	A	10932	111	415	VSALSLLLHRAPRCRRPSLPPLQ DAGLHGWEHGVQRGRGPAAH RDPV*EGWHHSGHLAQGHSEG *PCGDSETPAGREGKTAGHRTG RCGCRQEQTEGAQQD
10871	41239	A	10933	2	219	FLGGEGVIFPRGWWGAAMRFV STGSRHTTP*GSEKSAGPHTQW HQNSK*ATSETRLHSCASEGIVP AGCRPY

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10872	41240	A	10934	1	2358	VPMVVVPPVGAKGNTPATGTT QGKKAEGTQNQSKKAEGAPNQ GRKAEGTPNQGKKTEGTPNQG KKAEGTPNQGKKA\EGTPNQG KKAEGAHNQGKKVDTTPNQG KKVEGAPTQGRKAEGAQNQA KKVEGAQNQGKKAEGAQNQG KKAEGAQNQGKKAEGAQNQG KKAEGGQNQGKKTEEAQKQG KKAEGAQIQGKKNEGAQTQGK KAEGAQNQGKKNEGAQTQGK KAEGAQTQGKKADGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKADGAQNQGK KAEGAQNQGKKAEGAQNQGT KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KVEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGQ KGEGAQNQGKKTEGAQGKKA ERSPNQGKK\GEGAPIQGKKAD SVANQGTKVEGITNQGKKAEG SPSEGKKAEGSPNQGKKADAA ANQGKKTESAFVQGKNTDVAQ SPEAPKQEAPAKKKSGSKKKGE PGPPDADGPLYLPYKTLVSTVG SMVFNEGEAQRLIEILSEKAGII QDTWHKATQKGDPVAILKRQL
10873	41241	A	10935	967	1574	SLKCLIISLSPVHSYPGKRPEVSF SPINSGQPPNYEMLKEEHEVAV LGVAYNPAPPTSTVIHIRNETSV PDHV/VLVPVQHSLHEP\CCLGF IAFAYSVKSRHRKMVGDLTGA Q/ALCLHRQVPEHLGPDFGHPH DHSAHHHPSVDLPSLPSSFLLLF LFLFLPALQLLFLSFSLVFFFFS FFPLFQRLELWGWGEWDHHST
10874	41242	A	10936	3	370	RVATIVDIWEKSISGKKNSQNL FVNPCCLGFIAFAYSVKSRDRK MVGDLTGAQA/LCLHRQVPEH LSPDCGHPHDHSAHHHPGVDL PSLSIDQEASSRPGARALQDGA WASVFPSVQWEQQGW

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10875	41243	A	10937	76	614	PDRRWSSLDTMNHTGQTFFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHIRSETSVPD HV/VLVPVQHPLHEP\CCLGFIA FAYSVKSRDRKMVGDVTGAQ/ ALCLHRQVPEHLGPDSGHPHD HSAHRHPSADLPGLWIDQEASL RPGALPMTCIPRTPTSIPRPAPR GQELCP
10876	41244	B	10938	695	1011	
10877	41245	A	10939	410	5501	EAKTHKSVVMTDPLLDSQPASS TGEMDGLCPELLLIPPPLSNRGI LGPVQSPCPSRDPAPIPTEPGCL LVEATATEEGPGNMEIIVETVA GTLTPGAPGETPAPKLPPGEREP SQEAGTPLPGQETAEEENVEKE EKSDTQKDSQKAVDKGQGAQR LEGDVVSGTESLFKTHMCPECK RCFKKRTHLVEHLHLHFPDPSL QCPNCQKFFTSKSKLKTHLLRE LGEKAHHCPLCHYSAVERNAL NRHMASMHEDIS
10878	41246	A	10940	446	1704	GGPDMDARAPAVGGSCHQHGP SGAPGP/CIGRMES/EVGVRDHA IPEGARCNRFRKETTEGPLHCSR CGLLCPSPASLRGHTRKQHPRL ECGACQEAFPSRLALDEHRRQQ HFSHRCQLCDFAARERVGLVK HYLEQHEETSAAVAASDGDGD AGQPPLHCPFCDFTCRHQLVLD HHVKGHGGTRLYKCTDCAYST KNRQKITWHSRIHTGEKPYHCH LCPYACADPSRLKYHMRIHKEE RKYLCPECGYKCKWVNQLKY HMTKHTGLKPYQCPECEYCTN P\ADALRVHQETRHREARAFMC EQCGKAFKTRFLLRTHLRKHSE AKPYVCNVCHRAFRWAAGLR HHALTHTDRHPFFCRLCNYKA KQKFQVVKHVRRHHPDQADPN QGVGKDPTTPTVHLHDVQLED PSPPAPAAPHTGPEG

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10879	41247	A	10941	1	944	MSILLTSIARQSRDKRTRLGHK QRILAGLGSNHPIRRNLQGLRR FALVDRQLVVQNVVTRWCRM VYQSAANVFIQHRPISHDERVQ QRGTAITMMVQQAQWAERGK SGLSGVAIGPAVDTSALQAQLR ETLPPHMVPVVLLQLPQLPLSA NGKLDRKALPLPELKAQAPGR APKAGSETIIAAAFSSLLGCDVQ DADADFFALGGHSLLAMKLAA QLSRQVARQVTPGQVMVASTV AKLATIIDAEEDSTRRM/WIRNH SAVA*R*WPDAVLFPSCVRFCL AVQRALALSRSTMVDYRHSVT APQWPHADGGKPG
10880	41248	A	10942	1	939	MRTILTIDIQLRYPRRPGAFGTH TFLKCAFSNKQRRFTVKRFAFL AARYPASQEMPPVRHGHAVAA AIPCGNVPANGNTPARYKGQC GLCSSTLQDALRDFIQVAHTCEI PLMPACFGLADDKLWRWLNE KLPCSLMLLPTLPPSVLGIRLQN QLQRKIVLFGGVWMPGDEVKK VTCKNGVVNEIWTRNHADIPLR PRFAVLASGSFFSGGLVAERNG IREPILGLDVLQTATRGEWYKG DFFAPQPWQQFGVTTDETLRPS QAGQTIENLFAIC\SMLGGFDPI AQGCGGGVCAVSALHAAQQIA QRAGGQQ
10881	41249	A	10943	25	479	
10882	41250	A	10944	2	453	APSRTSGSSVGLQGSYVLDVDG REFGCERVKG*FLVHRAGHL/L TLWLFSSQINKMEWWSRLVSS DPEINTKKINPENSKVSPGWLG ELQQEGEGPRCFQSFTDSCHCL PS\LSDLDSETRSMVEKMMYDQ RQKSMGLPTSDEQKKQEILKK

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10883	41251	A	10945	3	1110	RDPQERRERGTRVQSSGTWIGA GAMGGEQEEERFDGMLLAMA HQHEGGVQELVNTFFSFLRRKT DFFIGGEEGMAEKLITQTFSHH NQLAQKTRREKIARQEAERREK AERAARLAKEAKSETSGPQIKE LTDEKAEKLQLEIDQKKDAENP EAQLKNGSLDSPGKQDTEEDEE EDEKDKGKLKPNLGNGADLAQ *RLNPDPCRELDLAVPF\CVNFR LKGKDMVVDIQ/RRQHLGVGL KGQPAIIDGELYNEVKVEES\SW LIEDG\KVVTVHLEKINKMEW WSRLVS\SDPEINTKK\INPENSK LSDLDSETR\SMVEKMM\YDQ\ RQKSMGLPTSDEQKK\QEILK\K FM\DQHPEMGFFPKAKFPTNPC
10884	41252	A	10946	50	426	
10885	41253	A	10947	1	942	QVWKQNCFKHYSNETDNSTTQ LVGLQTLQVVVPSLILCEHCMN FSSPHVWCCLVQAVPGGQGQTI MQVPVSGTQGLQQVSNI*KY*A VYQRRGFKE*IITTYQTQQIIQQ PQTAVTAGQTQVIPLALSHRSK TDLEESDN*VRYFPVNADGTIL QQGKCTHKLP*DFLGQLFCPLD N*HLSSSGQGTVTVTLPVAGNV VNSGGMVMVRKCIFQLCL*NF LEHAT*CLLKFEPLYVNAKQYH RILKRRQARAKLEAEGKIPKER RVCITLGRI*ERRIAGFYF*NYLL YPKEKDSPHMQVGRHIHFILLFI TLY
10886	41254	A	10948	24	378	
10887	41255	A	10949	15	658	QRPNAAQTQPSRGCQLSAPARA GRFHPQSCRPSRVGCKGHVCIP GDRSLALWPPRLGCGE*TSSAL DSQGILVSNFPHEGS/PTPQQSG LKTGRILLNHGRRRLKVSQSEG RFLEVGWKQRGPTAHRTHSNR TRRRHALSTGGDTGRARNARS GGGRSPRSSLPAASSTPGVCWS PRMSQARQPPSCRRGVPRRPEM LRSLSPSCQICVCVRFRH

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10888	41256	A	10950	1171	1639	PMALWADGRARHKVGTECEC GMHPGLKCSGRTLGSQTMLAT TPCDSPT*I/SNKNGLRSV/SYR* CLINALWLFSISPHILVRCGTESS *LLPSLVPSWLP*LVRVR\PLPT GWC*IPSCLKP\PPTWSSHHSPQ RLP*NPATLVCLQNGTARSHSS TPV
10889	41257	A	10951	2	357	HERLLNPGRETDWATCYSETAS CSVA*ATVQ*HDHGSL*PQTPG LKWFSHFSLPSSWDYRHVPPCP ETGPCPVTQDGVQWSYHGSL*P QTPRLKQSYHVSLPSSWDYRW EHPVAGKQA
10890	41258	A	10952	15	578	IQTTPKGRRTKPCHRQKRTIVTP RQSTPRSNRGKDTRSKQRDETT E*TTRAQDTNKEGATQDRTETA RRTQSNMEKEKPNQHNRKRKD RDSRKDKGHERETKNTERNRT KRREKRKDNKHNEAKSQRQTR KKKETKETATRKREEPSNSCSM HPFQISWLHSVGDNGRRDQLLC QGFHLYYLMCFPQ
10891	41259	A	10953	2	369	DIDPTGLQSQGSPKGQDPPLMF SEDYQKSLLEQYHLGLDQKLR KYVVGELIWNFADFMTNQCQP KTTPSVILFLPSCEEPQANKATL VCLMNN/FYPGILMVTWKADG TLITQSVEKTTPSKQS
10892	41260	A	10954	1	417	FGTGPSASPRTSFRHQCGH*PH WTAVTVDSQGAGQPKTTPSVIL FLPSCEEPQANKATLVCLMNNF IPGILMVTWKADGTLITQSVEK TT/PSKQSNNKYVASSYLSLTPE \SWRSRRSYSCQVMQEGSTVEK SVAPAECS
10893	41261	A	10955	113	767	GPMRPGTGQGGLEAPGEPGPN LRQRWPLLLLGLAVVTHGLLR PTAASQSRALGPGAPGGSSRSS LRSRWGRFLLQRGSWTGPRCW PRGFQSKHNSVTHVFGSGTQLT VLSQPQ/ALTPSVILFLPSCEEP\ QANKA\TLVCLMNDFYPGILTV TWKADGTPITH\GVEKTTPSKQ SNNKYVASS/YTLSLTPEQWRS RRSYSCQVMQEGSTVEKS\VAP

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10894	41262	A	10956	1	344	GSAAGQVQQQQQRRHQQGKV TVKYDRKELRKRLVLEEWIVE QLGQLYGCEEEEMPEVEIDIDD LLDADSDEERASKLQEALVDC YKPTEEFIKELLSRIRGMREN*A PPPKKSV
10895	41263	A	10957	3	349	TMNNMRGQILLLFLLIWLWNR YGQLVGSSEKHKIASQLELIQS QFHYCVTLDKLLNFSEPVHVK QEQLLSVCSEKEVTEVKVLALV NHVGSKCCFLIFCSGPS*PKFSV SQVFSD
10896	41264	A	10958	998	1383	
10897	41265	A	10959	39	402	TDHIMREYKLVVLGSGGVGKS ALTVQFVQGIFVEKYDPTIEDS YRKQVEVDCQQCMLEILDTAG TEQFTAMRDLYMKNGQGFALV YSITGQSTFNDLQDLREQILRG* RTREDV\PMILVGN
10898	41266	A	10960	25	739	YKKNFDISLLSVKCETCTHMLT SSSL*C*NLICRSLFLIDFNL*AG FVI*VGFTAQSTFNDLQDLREQI LRVKDTEDVSIFSLCKMLCHLS VAK*KSACFQNLARQWCNCAF LESSAKSKINVNEVTYNCWAA QTSAFLVCFKLTARLLALSITNV SSCTGWGVQRSHQDQGNSKHA ASSVWKVGFGIVRLGTGTCLSS LERGYMCMEKEMFDPYTPSRV LKPRSEALELFGPLKSLT
10899	41267	A	10961	946	1424	YFRFLCVIFCSFLLRCLVSRVLL YPMLIAEIPRVQGRGGPSWPGL GGRLLKELSRLLTFLKVRKLSIL SGWREVPLGQPSLTEPP/PPAPP HPGPGSWLASASAPHLSQPPAA GPAGQPPSPGSPVPGGCSLALP VTSVLCLEPPALKPAAASAPVV AVH
10900	41268	A	10962	1	148	TALQEFGTRSGIPALGCPPPDP* PPPGSCPPPEPQLLSVGEPSRCS CSP
10901	41269	A	10963	10	233	LGAARRAQLLESWPRA\PPPAR LHACHLQP/LPRTPKVHTS*PTQ QQGGFSLCLKKKNVPVSVEMIC SSARLKLTE
10902	41270	A	10964	1	331	RPLLLSTLCWELRAALSYWRA GRAPPPPARLHAGPASGFWVLT PSGGEEGEPRTHLWGGGGRRG GGRKKKD*GGQGRGAGGFATF SPPANAPRLHTSLTNSSARWIFL CV

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10903	41271	A	10965	4	1023	FPRAGEKPYTCEESGRAFNQS* TLTTHMTIHAG*KPYKCEECGK AFYRFSYLTKHMIIHTGETFYK CEECGRGFNWSSTLTKHNRIHT GEKPYKCEQCGKALNESSNLT AHKIIHTGEKPYKCEECGKAFN RSPKLTAHKVIHSGEKPYKCEE CGKAFSQSSILTTHKRIHTGEKP YKCEECGKAFNRSSNLTKHKII HTGEKSYKCEECGICRTPKMAV FSQCHQVLKITNIHYPSSIATIVH GDRAQSHVDICTLGDKASGAII GTAFYTTQCEQRAYNETAVSR YTISRPPSHHGGDSETTEFSPAI GRCNGVHKSWGSNRCSDRWRS
10904	41272	A	10966	1	290	
10905	41273	A	10967	1	1508	MSWAARPPFLPQRHAAGQCGP VGVRKEMHCGVASRWRRRRP WLDPAAAAAAAVAGGEQQTP EPEPGEAGRDGMGDSGRGECP SRRAGEPVTALSATPPPPPFPVIS SSMGSPGLPPPAPPGFSGPVSSP QVRGCDQLTAWPLSFSCFPCNP VLGVRGLHCPPPPGGPGAGKRL CAICGDRSSGMWLRG*TERESL GHVSSPVG*DLTYSCRDNKDCT VDKRQRNRCQYCRYQKCLATG MKREGKDPPCPGVLDHMPFSLI PLRPPEEMPVDRILEAELAVEQ KSDQGVEGPGGTGGSGSSVSV GVNPLSFVMGVGGGSLGLWAK RIPHFSSLPLDDQVILLRAGQ*P WIPLTS*HLTPL*LPDLFLATGL HVHRNSAHSAGVGAIFDRSVA LG*AGM*IEGVGL*AGPCLRAII LFNPGKRRITFVSQGQGNLGAS SSPMETYCKQKYPEQQGR*DG AGGH*GSLGGGECYEDVFLFFF KLIGDTPIDTFLMEMLEAPHQL
10906	41274	A	10968	945	1131	MICTVAISYVLFVDVYISLLSAT CSPKPQGSAVFQHD*VSPGI*NG SERCCSRDRHRQFLW
10907	41275	A	10969	37	332	AEGIRTIQGTENIFCKVVWGRQ VSLSQTNTLEGQSNDHGCQLR KRTFISTFTAHYSRFFLQRF/VFP YTGFEKCQSTAW*KPRYLLSHS VKGKRNLHPA
10908	41276	A	10970	137	283	
10909	41277	B	10971	1	624	

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10910	41278	A	10972	3	618	KTQDPAKAPNTPDILEIEFKKG VPVKVTNVKDGTTHQTSLELF MYLNEVA\AQHGVGRIDLGDN R\FIGMKGRGIYYTPTGTILYHA HLHIEAFTMDREVRTIIQGLGLK FAELVYTGFWHSPECELCRHCI AKSQERVEGKVQVSVLKGQVY ILGRESPLSLYNEELVSMNVQG DYEPTDATGFININSLRLKEYHR LQSKVTAK
10911	41279	B	10973	1	1102	
10912	41280	A	10974	748	1396	LYLQRPFFQIRSSLQVLGHRQIF PQSPRCLHLAPPPLMRHSHRSPT WY*FSPRRTQQSRPVSAQPLGS CGGIQPAPPPVTQPSQLSPPRGS R*LGSDGAGTQPRHVQNPCPLT CVHM*SPPPPCLNLQARCPQSL RAKVVPAVEQRARVGHVESPG SHCWLEREPEVGSGPQQGQRPL PAGAAD*CLGAFWQTHLDLGD SLISCSHDLQGWQLSQA
10913	41281	A	10975	1	846	
10914	41282	A	10976	2	851	WNSAELGRGGPGAGGAGVIGM MRTQCLLGLRTFVAFAAKLWS FFIYLLRRQIRTVIQYQTVRYDI LPLSPVSRNRLAQVKRKILVLD LDETLIHSHHDGVLRPTVRPGT PPDFILKVVIDKHPVRFF\VHKR PHVDFFLEVVSQWYELVVFTAS MEIYG\SAVAD\KLDNSRSILKR RYYRQHCTLELG\SYIKD/LSLV VHSDLS\GIVIL\DNSPGA\YRSH PGYGGR\DNAIPIKSWVSVTPS\ DTALLNLLPMLDALRFTADVRS \VLSRNLHQHRLWVTACFPLPP
10915	41283	A	10977	25	153	
10916	41284	A	10978	1	741	MMSFDSMSHIQVMLLQEVPSS YPASKKNEA/PQTSGGGPGTPR KGLGE/PAVVPMSPAVGT/PALT QCHGPHAEDDLEEPILTTDPVA RDCPLDLLMDGKTGAIISSLLHS NCLPAPFCQCSHAVKWQLKTV HSCCPLGEVQPQRRCVIATAKE KGIGVKHHCNIHSDNVNSIITAT VAAHQQQQLPQNGNNSGIKNN QNSSENTVTNNSKNISNHIICRN SSKNSKSSSSSSSNNNKNSSNTI NSNNKAR

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10917	41285	A	10979	1	669	MMSFDSMSHIQVMLLQEVPSS YPASKKNEA/PQTSGGGPGTPR KGLGE/PAVVPMSPAVGT/PALT QCHGPHDEDDLEEPILTTDPVA RDLTMPTAASQHLQKQCLEHH HYFHSYNINSDITVSRNNISSIIT TPVHHCNIHSDNVNSIITATVAA HQQQQLPQNGNNSGIKNNQNS SENTVTNNSKNISNHIICRNSSK NSKSSSSSSSNNNKNSSNTINSN NKAR
10918	41286	A	10980	3	980	IESPGPFPPGLQRPVPHRGEFCL RCTSSEALPCFYSWTVTFSPWT VAAAQGQPRPGPASRTLLLATQ SEIAAAELGPGSWGGPSSCPSE QSSHGPPASS*AAPLQTGRRLRS RAS*RSGAPSVAALPAPLSRPQE RHPSVSASRSGHPPGPCPSPPPP AARPVQPSPCRAPPGSAAGRAR APHA*AAPGSWLSSAGAAARR WPFQTAKGSGS*DRPGRPGPDA PAAPPGWHRAPPSGSSSGAGTG RHPQPFGRPRRRTPAPYAAPCA FVATLVFS*LLIFGGAFSFPALS HCPTSA*LKRLLSEPAPIAFPFG LHPGTLLSRASE
10919	41287	A	10981	1	5229	
10920	41288	A	10982	1	7044	
10921	41289	A	10983	1	3228	
10922	41290	A	10984	10	209	TLSGGEPQRLEAERRARLQDEE RRRQQQLE*MRKREAEDRARQ EEERRRQEEERTKRDAEEKVM
10923	41291	A	10985	293	363	
10924	41292	A	10986	3	434	
10925	41293	A	10987	3	1536	
10926	41294	A	10988	315	993	VPVAPIFHFSHFSPAPTVFTQSR QDSMQCILRQHCHLILISRSSSL VPAGLRGAMAFALAIRDTASY ARQMMFTTTLLICPELLALLLS LSHSRSLLLHGYHGPS*YALFFS LSFSLVTWVGAKPGRYQSLIFV VVVGCTFQNQEPLREEDSDFIL TEGDLTLTYGDSTVTANGSSSS HTASTSLEGSRRTKSSSEEVLER DLGMGDQKVSSRGTRLVFPLE
10927	41295	A	10989	3	320	

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10928	41296	A	10990	3	582	GPPTPRRPRPLPSSLPSRRSRDPP RIPLCA*FPQTRKQIARSEPD*T WASQSSTSIPRIWRFVHA*KFST APLTATPPPGKMCSAGCRETVK TT*PPLRGGPAPFLLPSRAVARG TRPGFRSALSFRRPGNRSRGVN LIKLGLRSPPPPYPGFGGSYTPE NSQPLPSLLLHPLEKCALRDAE RQLKPPDHHLMVAWLIPDVWN GEGEPSPSHTRHSLRASSSNYV LRAPEGNLLARRLPRETAINLQ PKACYKTLSHPESFSHFYNQFC PRRHQWLPAQPPGHFFLG
10929	41297	A	10991	3	338	NSPSRPRSSQRGVAGRRSEAGP VAVP*GGPKKGRGC*GNGRWG QRPRWMLRASGSGESTTPACSA ENRHAS*RKKRKRPGQVSWEE TEETRSGHSQPRGHAEPLLHRP QRR
10930	41298	A	10992	3	226	TILSS*SSSSSSSPSPSPSPSPSP SPSPSPSPSPSPSPSPSSSFFLRWS PALFPRSLSFSLFPGTGTPFSCP
10931	41299	A	10993	24	489	KEYLVRTK*QKGKGENPLVKIT FRPPPGLRTYPSAPWSARSTYG RAAAVWRPHSPSAPRRGTHPW PAGHRGQRASGEGVGTHTHAH MSSVCACSTHTCWSRNCKDPR EDRGRGLTVLLEAAVCNSCLLL VLKTPRNPQLPILYTDSDTKSST GNP
10932	41300	A	10994	1	1491	
10933	41301	A	10995	140	308	RNVIKLKGWSRPSKQQDNPTLR PGPPSPAGGFQQLLMRMRRPLA GGGKSWGIAHFYKPLQRERRA GAECGLARQVRAEVTKWIGVN RRPRKRKRMEKEEVFEKLLPD QLGLLLEHLLEQKTLSPRTLQS LQRTYHLQDQDAEVRHRWCEL IVKHKFTKAYKSVERFLQEDQA MGVYLYGELMVSEDARQQQL ARRCFERTKEQMDRSSAQVVA EMLF*RGQDRFSLKKCDKVKG MVKTQQATGQPDSPPRPALTG RRVPATADADEKAFGGWRKIL GYRTFL

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10934	41302	A	10996	219	688	RRMHAYVSLDPLERPPFFFFFLF FFFFFFFLRRSFALVAQAGVHW RDLGSPQPPPPRFK*FSCLSLPSS WNYRHAPPRPANFVFLVETGL QLPTSGDLPASASQSVGITGVS HCAWPGNWLLKETRCGSSVGR QITGPITPDAWVDPGIPDRYLQ
10935	41303	A	10997	3	298	FFFFFLRQSFALVAQAGVQWRD LCSPQPPPPRFK*FSCLSLPSSW NYRHGPPHPANF*FLVEMEFH HVGQACLKLLPSGDPPALASQS AGITGVSHRA
10936	41304	A	10998	2	438	APSVRSGNERDLARDEEAQETQ VRGCHASGG\CTPAATAGASPP AWAGRRGTGQRLRSQPRQTGR QPPRVQPLAPPPGAPAPLPNPQ NCRRKTRSHPRFWAGTLAPGPC PGLWCLPGLVQVDVLAAGRCD HLSCLPPLCPQAFLL
10937	41305	A	10999	2856	3044	GAATGEGGCCRLPGHPALAST A*AIPCRGPRVQETSPPPVLGW DPGSRAMSRALVFAWVGAG
10938	41306	A	11000	1	908	GLGDPGVPVLRSGGLGPPADLK GDQAVAE*LHEASGVTEHHPS AQPGPGGEAAEPAHLIV*EPEG GSPGHPGGGPGHPG*SEGPAGG KPGPAGGGSAQGCRRSSEPSGT *SGRSPR*GPHGHPDCRTHPAR EGAQVHSRSPLPGGAPVRRGCS QGPEQRLQQEDFLRVQQLSAA GPLRPQLYPQVWLCPDEHQLLE QYPRSYFSERIDVFKPCGVQQG CPVLDRASSKISPEDAAGSVVR LRSLWAASGLQQGASGLATFL QLLTCGVLWPDEELVHLLLDE VVASAALRCPDPVPMEPTCG

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10939	41307	A	11001	218	990	VLQLLKAMRLELFLPPGGFMV LLASGVKLQTFATQVPSWLHP VDPSPGLEVELPASPVQCAHTP QPLGGRWDWVPWSRGQRSSG RLGPHGSPWRRWEAQAWQPA GPKPCPVGS*GPVRNRGQRRW AGTAGDPVHPPQPLAQVLSPSL PGADRAGQLLRVQGPPSPCPPG TPAGPQGRCAAPVPTGVSPSTP PCKLREQAPALASPERGSHSAA VG*RAPQVLPKW*PELMFRWV RSFFLLVGSWLTSGVKLHPFVV SVTALKGDASGVIPSSRWVHGL AGLRCEAADLRDSGAQLASPS GSLTRTGGGAACQSRAVCPHSS AFGWSMGLGAMEQGAALIGEA RASREPMEEVGGSGMAACRSQ ALPRGQLRPSEKSRAAPVGWH CWGPSTPSAATGPGAKPLIARG RQGRPAAQSAGPAKPMPTRNSS WPARAVRSPGSHWRLSLHTSL QAERAGSGLGQPRKGLPQCSSG LKGSSSAAKVVAQAEEAQRAS EGCEDYLARCHLSIRKMRRRN
10940	41308	A	11002	3	644	EPPGPTGPPSPQSPWHPGLPGR WSSTHVVFTHLHLAGPGWSCD HRWMGKQLPVSLSASGVQGVP RFRSQDMYQSSRNKFPSGAAH VPQEWAVPWKNQGNTHQSSRP SESGCCAQAEGSNQCHQRQEA AGPSRLSLPDGGRRLETPRHPN GPWYWNNSPQRLN*WRRGDPS WPEPQGKPHTGGARVPACQRR EICLSPFRGPRRRQKENIYEYL
10941	41309	A	11003	202	438	FHGHPAPGEMRGWPRVTKRSP AQSGKT\HFPPGSPGPPDTSTESI FRRAWKAPGFPGRGRTADPET ARCGAWDEIVEPV
10942	41310	A	11004	520	1094	GPLSQCPPLPRLLPPLGVYSKGR APHADTHSPGHRRTHAHAQPA AAAATATR*QRRRRLPPRRTPF RRPAARPDRRVPAHSSAVLPRP GKPGAFQALRKMDSVDVSGGP GEPGGKLGFARLRRAPPDRLPG CPSSHSFQTQSLSFMAHNVDEP LESATSLLGLLRRSWFCFTWQK QTVYWSTGRIRHSGEK
10943	41311	A	11005	1	138	SISLMNIDVKILNKILANQIQQHI RKLIHHD*VGFIPCLRILVIYI

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10944	41312	A	11006	65	297	NQRLPQPFLPTTPPPPATRAT*D EEKSPYPGPGSDKKCPTLQLPSP PTPSAGGFPPLGESGSPGGLVK AQIMEGISM
10945	41313	B	11007	322	6900	
10946	41314	A	11008	3	215	
10947	41315	A	11009	1	234	
10948	41316	A	11010	149	300	
10949	41317	B	11011	28	162	
10950	41318	A	11012	700	861	RRKCIPGRRNSKHKGPDGAGRP *VCREQQEGQCAWTGYPGAQG PDPYCGKGPYS
10951	41319	A	11013	291	744	LKRTKCDQLLKTSFLDLGRGPI LKWLCTSKWGHQQIIIRA*GTE YKTTSFFFFFETASRLCHPGWE CSGAISAHS*FLLPGSCHSPASA S*VAVTTDTREHAQLIFF*HFSR DGFHVVARWLDLLTCDLPLSL QVLGYRNYIIIVRQLPSR
10952	41320	A	11014	139	414	SFKTAPPGFFFSF*LHLILMLKFT PGAIKLVFL\QFLLGISFFFLGKP PSSWFRNESCSVFRKESSQSWQ GRAHVWG*SDPWSSGRSRRAH L
10953	41321	A	11015	5	565	VHTTEATCTTTGAKPCPWPSKL ATRQDHSVLSTSNPRGPTPHKS GSPETAGALSSGDAGSRGEGPR TVSSERSSPGKGGSTLLGTTA*G PGPAHFASAVLGPSSKSLQAAS *EVDSFPSSLLKTAVSVLASTVR LSVSFMPPFITVSVTSSVISASSS PSELASMATLPGASG*AARAVN FELDEE
10954	41322	A	11016	188	515	SQTVSIVGELPIPRKRCEIGIWD AQKR/CPRLTGPWATISVPTISK KATGN/PQHPNHPRARYQINAE *WKVHF*TNTDRPSHECPCTLV VHRTLDQLRHKSSTSGGKTHG
10955	41323	A	11017	80	397	SVQRSVDHL*DHP*TSVDWELY LDGSSFANPCKVTLKTTTSPAS VTPEADWSMHSQSMRNSLRDS FSLKFGLIIIHDFLTPTFNPLENP CGFLTRFCCVPNQISS
10956	41324	A	11018	104	392	PSQFHLKLLHLMLALLYPVGTC QVKDSSLLQKSTSVPPDSPQTG H\SKLGPFNPGRFR*RPQCQPGV LPPDVELSCHSWSNVLWTTAA KTPIFCSY

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10957	41325	A	11019	125	1404	NLALGMAMWN\RPCQRLPQQP LVAEPTAEGEPHLPTGRELTEA NRFAYAALCGISLSQLFPEPEHS SFCTEFMAGLVKWLELSEAVLP TMTAFASGLGGEGTDVSVQTL LKDPILKDDPTVITQDLLSFSLK DGHYDARARVLVCHMTSLLQV PLEELDVLEEMFLESLKEIKEEE SEMAEASRKKKENRRKWKRYL LIGLATVGGGTVIGVTGGLAAP LVAAGAATIIGSAGAAALGSAA GIAIMTSLFGAAGAGLTGYKM KKRVGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYRTFSAPWA ALAHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGIVAALTWPASLLSVAN VIDNPWGVCLHRSAEVGKHLA HILLSRQQGRRPVTLIGFSLGAR VIYFCLQEMAQEK
10958	41326	A	11020	3	1693	CQRLPQQPLVAEPTAEGEPHLP TGRELTEANRFAYAALCGISLS QLFPEPEHR*VLLSCPLGTPVGL HSDAHYGQRLAVAVHVEGTLP FTSSTFAAASVFQKARPWQHPG EQMAFSGKPFLVAAVTSAGGS GAPSVGCTELISTSVLGYHTAL EMAGLVQWLELSEAVLPTMTA FASGLGGEGADVFVQILLKDPI LKDDPTVITQVHPTPGVKDGKL IF*ARVLVCHMTSLLQVPLEEL DVLEEMFLESLKEIKEEESE*ES PATKTEGGGEDKDRKHPLMGD KMTESKTDLWIYEMGNAGVLL FRRYLWLQPKKKENRRKWKR YLLIGLATVGGGTVIGESS*RCA PLVAAGAATIIGSAGAAALGSA AGIAIMTSLFGAAGAGLTGKVQ KE*VGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYREDQEDQA ALAHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGKCPHLPWPASLLSVAN VIDNPWGVCLHRSAEVGKHLA HILLSRQQVPGNGCVIGFSLGA RVIYFCLQEMAQEKGEHGLL
10959	41327	A	11021	208	324	VSLLKAADNWLVNSYPFCNSV SSEFFFR*IRDFFLFWIH
10960	41328	A	11022	1265	1459	
10961	41329	C	11023	188	730	

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10962	41330	A	11024	64	228	QHLLRRWGRSGLLLNDR*VSN EIKMEINKFIELNNNSDTIYQTL WDTANTVLKFM
10963	41331	A	11025	1	648	
10964	41332	A	11026	26	613	VGAGGRGWRFAAAVRRAAGG GLRPGPAPGPRAGGGGPRGAH LALLRRAGALRAGKEYGKADA RWVYFDPTIVSVEILAVALDVS LALFLIYAIVKEKYYRHFLQITL CVCELYGCWMTFLPEWAHPEA PNLQQPATGWLYWLGFTLFFF* RCVGFLIPRNWLLWAVHGPRTS RKWHQKGNQFQWKEVFSGTF
10965	41333	A	11027	2	252	ARGRAGVAGGPR*AAELPGLP RDPFPASRPLRRSDCLGGLIRHK PPDPGAGARVEGEALPSWSPGG ALEEGVT*PGTRGPPWE
10966	41334	A	11028	3	637	RDQVRRGQGGEPARIQCPRRRL GEGPGAPNRLGPPARDPRCSPW PRADSPRDPNRLSSPQLPRPAYL GPACFP*PSWGVSRSLPSLAPW RPHRLPDSQRFPNGGSRSRATS GSWTWKSKECREWRPSGSRGT RGSSGSGAGSSGSSAGVGRRAG HGRWHLR*GPLFPAAPASATCP LWHGWKGASLDLGLQPWATF YPRVTGARGGRTLGP
10967	41335	A	11029	158	462	
10968	41336	A	11030	339	866	QICHSPPGNKAHSHLLPYQTPV PSSQYPPSPSRTLQLPFPTPWNP CQWPSRGSCGPSAVGTGPPFPT GIPSVP*APSARG*HHSSACGCH PGCAGPQPARSPHGPAPASGCH TVSGCCHALLQSCLAPGRPSPA GTWPHPPPGGLPSAPGTEPCTA FEGFQPPCWLSQHPLSPCL
10969	41337	A	11031	621	944	TPQGGTAPSGGRHPWASASPHR LPPL*CSARPGCH/SSRMRSPGT RPSGPL\QDCHPPPRPQTPHAGS HHTSAPQAPAGTF**RQRVAPG SSCWHLPQSWSCSAWLGGC
10970	41338	A	11032	3	257	AGRASKGG*NPSKAVQGSVPG AEGSPPEGGCGQGPAGLGLPGA RQDCSRA*QHPPGPGGGQEVY LDISLAPGSTGIQGLEAKHL
10971	41339	A	11033	94	227	SSYVFKSILTAFGMTWMRLETII LSEVTQG*KTKHQMFSLICGS

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10972	41340	A	11034	404	894	FVYFFRGELCKISSTLGFKGTGQ GLQPSKVS**VPSRPAGNGRPA YPETSQPPPGPSGG*HWLAGW Q*GGPEPGWTCIWP*GS*GTEIG SPSQPGPEPAGVPSPRDAGSAA TGCHTGLAGVVWPPRLCHRRV TDGRKSMKRCLSRSYCTSSVRA SGGGAGRIT
10973	41341	A	11035	1	408	
10974	41342	A	11036	68	204	SFLWHPLGLHFHTHH***NYKS SSK*MVRIRVTFSKFIFVRNNYC
10975	41343	A	11037	5	188	PQCRLHLRQGLALSPKLECSSAI TAHCSLELPGSSNPPSASRF*GS RSVAQAGVQQCYHSSLQPRTP GVKQSSLSFPFLRLQPKVSSATL PVRLQE
10976	41344	A	11038	1	263	
10977	41345	A	11039	2	283	
10978	41346	A	11040	1	1965	MAAENEASQESALGAYSPVDY MSITSFPRLPEDEPAPAAPLRGR KDEDAFLGDPDTGEAR*PRPCP ALGSPRSSFFCVKHPGSPLRETR KDPFSAAAAECSCRQDGLTVIV TACLTFATGVTVALVMQIYFG DPQVRGTNGEGEETGEWGVG* CLRNCGKGSSVDAAVAAALCL GIVAPHSSGLGG*GAVEVGVPQ AYFLPPGL*ASCAARALREETL QRSWETKVGTLVRRESSGESLF IALLLTQALIC*VLAQDGFNVT HDLGQWGLGIWERHEVDGEG* NL*DLEPPPLPGSLLHRPDLAEV LDVLGTSGPAAFYAGGNLTLE MVAEVSARVVRVGACPKVPIA GHPRPHFFGVYRGDLSPGSQGP PSGEASQSMATSFWPFNLTSLV SREQALHWVAEVRLTRLPFPGF KDIRSGEIGYCHRADDMLRWV LGRTWGLQRQRWVWGKGQEK SSYELDGAPTAAQVLIMGPDDF IVAMVRYASSDSEPGTRDPLNQ EGVGAG*RFSWPNRTANHSAPS LVGFASLLSWGP*GL*VGGAM AWLPLCGTYLALGANGAARGL SGLTQVRFTPWLAFFSREPSCG LDCRCLS*QSNLLQVDSECRAE TSWGGHRDR*RKDSSQGCPWV HGSRRTNNFIIAVKDPRSPDAA

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10979	41347	A	11041	1	363	SSMTTVHATTATQKTVGETLA* LLQNIIPVSTSVAEAMGKVIPEP DKRLTGMAFCVPTHNMLVVAL ICHLQKAAKYDGMRRCFNATT GITFNGHFVRLLSWDEFGSSNR VVDLMVHTASKE
10980	41348	A	11042	162	303	CLLLKSCSQEAAAALALPALGL VFDVFL*IYFVRTKYLRVGFRN FF
10981	41349	C	11043	56	118	
10982	41350	C	11044	345	410	
10983	41351	C	11045	7	439	
10984	41352	A	11046	2	80	
10985	41353	B	11047	205	5326	
10986	41354	A	11048	1	813	
10987	41355	A	11049	1	1454	
10988	41356	A	11050	2	1624	
10989	41357	A	11051	1	1185	
10990	41358	A	11052	1	2149	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTRPVLK ELLKEALNMERNNWYQPLQKH AKNMPNSIILIPKPGRDTTKKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGMQGWF NIHKSINVIQHINRTIDKNHMIIS IDAEKAFDKIQQLFMLKTLNKL GIDGTYLKIRIKYLGIQLTREVK DLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAISNKLPMTFFTELEKTTL NFIWNQKRARIAKSILSQKNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWGKDSLF NKWCWENWLAVCRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPSLAIREMQIKT TMRYHLTPVRMAIIKKSGNNR QTESQIMSELPITIASKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVK\M AILPKPTNVHVTNLAAQDTTAL EAAQISLEGHPQEKEISVTAMPL
10991	41359	A	11053	1	2031	

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10992	41360	A	11054	1	1188	
10993	41361	C	11055	1	353	
10994	41362	B	11056	151	1608	
10995	41363	A	11057	1	373	
10996	41364	B	11058	1	488	
10997	41365	A	11059	1	1257	
10998	41366	A	11060	2	3527	
10999	41367	A	11061	1	2373	
11000	41368	A	11062	1	1755	
11001	41369	A	11063	1	1599	
11002	41370	B	11064	220	1286	
11003	41371	A	11065	1	1826	
11004	41372	A	11066	1	1645	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRIN\ILKMAILPKNW KKTTLKFIWNHKRACIAKSILS QRNKAGGITLPDFELYYKATVT KTAWYWYQNRDIDQWNRTEP SEITPHIYNHMIFDKPDKNKKW GNDSLFDKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEESLGNTIQDIGIGK DFMSKTSKAMTTKAKIDKWDL IKLKSFCTAKETTIRVNRQPTE WENIFAIYSSDKGLISRIYKELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKKHMKKCSSSLAI REMQIKTTMRYHLTPVRMAIIK KSGNNRTRENYFKIHMESKKSQ NSQGNRKEKEQSWRHHATRLQ TIVQGYTVAKTACYWYKNRPT DQSNRTENQEIRLHTYNHLIFD KPDKSNGETTPYSINGARITG
11005	41373	A	11067	1961	2588	KLAQDRDALSPPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSGYKINVQKSQAFL YTNNRQTESQTMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIK\EDTNKWKNIPCSWV GRINIVKMA\ILPKVN\YRFNAIP IKLPMTVFTELEKNYFKVHMGT KKEPASPSQS
11006	41374	A	11068	2	278	
11007	41375	A	11069	3	274	

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11008	41376	A	11070	261	1382	LELSFPPAGQRGVLSGDPQNLC TCPSGSWHVPRCWAVERQRPN LPRTVTQLVAEDGSRVYVVGT AHFSDDSKRDVVKVSAATRHIP DTGWCKLLPGSRDGLVRFPTY RVSMLKMDESTLLREAQELSLE KLQQAVRQVRSRGQGSGSGSG SKPPHITEQLGMAPGGEFREAF KEVGTG*GRGWPQGCGSQAVT FKRAIAALSFWQKVRLAWGLC FLSDPIR*GCPRDPGRPAGWSV GMAEMIGEFPDLHRTIVSERDV YLTYMLRQAARRLELPRASDG DGRPQAWDPL*G*GPRGHVPGI EKNWSTDLNIQEIMT*VPAPPC KPHPTSPQVAAFFGLLGYSLYW MGRRTASLVLSLPAAQYCLQR
11009	41377	A	11071	3	506	KDCQF*VGPEQKKALYKVHAPI QAALQLGPYE*ADQKRTCVRF GRHTCETAAFTFWKSLGLDKV TKPRSSSSQLLALAIRSSPGSTT DACLLDSFSGKSRISSWFGS
11010	41378	A	11072	2	374	IRRESTHLQQALGTTPQDRLTC TGHSAQPPACSASPLPPGPP*SS AWPLPPSTRLARQKQAAATAQ P*PLTTQTLGPWSSASTWTSAH KQPGAAAQEWTSTAGSRQLLA GASGSSPSSCSVWTN
11011	41379	A	11073	3	553	
11012	41380	A	11074	239	547	GHHFQMNVVCRCSVWMLSLEP HPVGQIHSC**ERAKLCGKEFN RMHNLMGHMHLHSDSKPFKCL YCPSKFTLKGNLTRHMKVKHG VMERGLHSQVSRPSLEA
11013	41381	A	11075	1	267	MAISMVTTRSTTIRTTAAGCHY ENDMAHNHSDRGGLPLKVVLT TPFLTPPGKGGGAAGALERRTE EGDRDAGGAAQEGGLTPTSVP PSS*HTLWLRTVDPEASTSPSTP RHPYPNRGGGGRALEPHPRR*V *AGCHYENDMAHNHSDRGGLP LKVVLTTPFLTPPGKGGGAAGA LERRTEEGDRDAGGAAQEGGL TPTSVPPSS
11014	41382	A	11076	1	1707	
11015	41383	A	11077	1	1407	

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11016	41384	A	11078	1	1275	MVKGSIQQEELTILKIYAPNTG APRFIKQVLSDLQRDLDSHTIM TGDFNTPLSTSDRSTRQKVNKD IQELNSALHQADLIDIYRTLHPK STEYTFFSAPHRTYSIIDLIGGSK ALLSKCKRIEITTNCLSDHSAIK LELRIKKLTQNRSTTWQLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTIQKISESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDQGDITTLERVVLEEPD TLHLLNYTPRKVLYRWNRQSS TSVIETNKTSVELSLPFDEDYIIE IKPFSDGGDGSSSEQIRIPKIS/NK KTK*PNPWRQK*G**LAVADA YARGSGASTSNACTLSAISTI
11017	41385	A	11079	1	426	MLHTKQHLSMGTEDMDDKLH FSDCSAASLVSLSTTTGGHVLT NMSADIARYLPVLYRWNRQSS TSVIETNKTSVELSLPFDEDYIIE IKPFSDGGDGSSSEQIRIPKISNA *ARGSGASTPNACALSAISRIMI SLTARSSL
11018	41386	A	11080	3	620	DRTLAEAPHTAPARSGHRGWC PRPHRRRRNRGRQLLAPGRGA DPGAGEAATVQWRLLRGQPAA ALHVQQGAGDAANAGLQRGA HADSHDRAVPAGHAPGPVAAA GRGHDGQVPAALG*AGGPVGL RRPEPPLQTRGKGRLAPATQQV GQARRLPTGRGQLLLRRPQPAA HHGPRPRLGGRGRGGSHKSPPH GIWPRLAGWRATLE
11019	41387	A	11081	335	640	PLGVLWSLWKSLVHSDAGAGE L*EVITGSTWPNP*QCCLVPNV DDEEEGEEQDDDDDEEEEGL*D IDEEGDEDEGEEEEDDDDVEEG EEDEGEDDWKFAKE
11020	41388	A	11082	2	204	

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11021	41389	A	11083	3	1471	SKDTKRDVDSKSPGMPLFEAEE GVLSRTQIFPTTIKVIDPEFLEEP PALAFLYKDLYEEAVGEKKKE EETASEGDSVNSEASFPSRNSDT DDGTGIYFEKYILKDDILHDTSL TQKDQGQGLEEKRVGKDDSYQ PIAAEGEIWGKFGTICREKSLEE PKGVYGEGRISRPCGDRW*RSD AEESSHHRGRQSGYPENKLCGF LLKTPHHVLERADEAGSHGNE VGNASPEVNLNVPVQVSFPEEE FASGATHVQETSLEEPKILVPPE PSEERLRNSPVQDEYEFTESLH NEVVPQDILSEELSSESTPEDVL SQGKESFEHISENEFASEAEQST PAEQKELGSERKEEDQLSSEVV TEKAQKELKKSQIDTYCYTCKC PISATDKVFGTHKDHEVSTLDT AISAVKTVIRDSDKTKSGEGAY GREMKSPHKFPEGKIHNDKEH DRIVQEFLAETGPKVTRFNEQC RFRPRIYVYENNQTQIMVEEPQ
11022	41390	B	11084	148	235	
11023	41391	A	11085	30	420	VSGTRGPSPCLGTSWASGAWR PPLGGLPPSAGANGPGRVRSAA GCSLVAGCKVLGSWVSGFAGR SHVACAGSSGESVRARCPGTA* AAGGPGPQAFQAAY*QGSRMH RAPPRPNRQVQTWWEEGAGTG
11024	41392	A	11086	2	73	ERLRMPGVAKGRPR*GNPRRG RG
11025	41393	B	11087	1	1412	
11026	41394	A	11088	39	427	PPYWGHFHSSAAASAALKGKD GGSSRSLVPPAQ*HSHSPSKTHC VHTPSRSCAQGLTHTLTQSPPSL KIAQSPSFDARAHARLRIWQIPS APRVPPLSASLSPTRTAGSVRFE SQSTKTSRSHRFLPRT
11027	41395	B	11089	1	813	
11028	41396	A	11090	3	365	RTPSSKGCGRPPRGMGAQGSA GCGRRRSPRRSRQARRWSHPC* PPSSPPWPRPARSPPGCSHRAAL SSPSPPSSFLARHSARPRLALAL GPPPWCSSGCASSAPFDLQHPE QSQNQDARG
11029	41397	C	11091	295	412	
11030	41398	A	11092	21	164	GAVTENDFYDLVRTIGGDLVE KVDLIDKFVHPK*VKSFLILPLTI SV

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11031	41399	A	11093	1	1373	GISTMVGSALRRGAHAYVYLV SKASHISRGHQHQAWGSRPPAA ECATQRAPGSVVELLGKSYPQD DHSNLTRKVLTRVGRNLHNQQ HHPLWLIKERVKEHFYKQYVG RFGTPLFSVYDNLSPVVTTWQN FDSLLIPADHPSRKKGDNYYLN RTHMLRAHTSAHQWDLLHAG LDAFLVVGDVYRRDQIDSQHY PIFHQLEAVRLFSKHELFAGIKD GESLQLFEQSSRSAHKQETHTM EAVKLVEFDLKQTLTRLMAHL FGDELEIRWVDCYFPFTHPSFE MEINFHGE\WLEVLGCGVMEQ QLVNSAGAQDRIGWAFGLGLE RLAMILYDIPDIRLFWCED\ERF LKQFCVSNINQKVKFQPLSKYP AVINDISFWLPSENYAE\NDF*Y LVRTIGSDLVERVDLIDKFVLPK THKTSHSYRIMYR\HMEPTLSQ\ REVRHI/HIQALQEAAVQLLGV
11032	41400	A	11094	8	119	
11033	41401	A	11095	2	475	QAGPSGGIPEGIAITGDDSSMHA IAPEDLPVGQDVEAEDSDTGDL DPVLTVFRRGVEREFFSNWYKT AWSFSKLAQKGLLSS*PSSLSSS SSSSDKAVTAGTELFASSLSSSS DPRRSISSSSLLFVAPLPVVSSTL AGPYLPTAFFTPGRLAFSFS
11034	41402	B	11096	677	696	
11035	41403	A	11097	1	357	STMIEAHVDVRTTDGYFFLLFC VGFTKKHNNLIPKTSYA*HQQY ICLPHQDDRVTHQNPSLPDGSIA RVLSIYYLYISRREMNSIISQGL QKVHIHIVIPGSLMNQELLDDLI TVFFKA
11036	41404	B	11098	1	541	
11037	41405	A	11099	14	671	PAPWRLGKNKRLTKGGKKGA\ KKKGVNPFSKKEWY\D\VKAPA MFNIRNIGKTLVT\RTQGTKIAS DGLK/GVRVFEVSLADLQNDEV AFRK\FKLIT\EDVQGKNCLTN\F HGMDLY/TRDKMCSMVKK\WQ TMIEAHVDVKTTDGYLLRLFC VGFTKKRNNQIRKTSYA\QHQQ \VRQIREGRWM\EIMDPRRWQD QMDLEEVGHELIAGSIWKRHR KGLPIYLSSP

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11038	41406	A	11100	1	217	RQGLTLSFRLECPGVISAHCSLN LPGSSKPPASAPQVAGTTGVYH HAS*FFIFFVEMGFHHVAQPGL CNFVF
11039	41407	A	11101	2	442	LDVQIQEAQRTPGKFIAKRYSP RHFVIRLSKLKTKERILRAVRQ KHQVTYKGKPIRLAADFSTETL QARRDRGPIFSLLKQNNYQPRI LYPEKLSIIYEGKIQSFSDKQML REFAIRKPPLQELLKGSLNLETN PGNT*KQNFFKA
11040	41408	A	11102	2	545	EPRPGEKTAHVYGPDCLCGSCV QLSFSGAFFSTRWVSYEQANCK GEQFVFEKGEYAHWDWWTSS QRT/DLSSLRPIKVDSQEHKIILY ENPNFTGKKMEIIDDD\VPSFHA \HGYQEKVSSVWLRSGTWVGY *YPGYRGLQYLLEKGDYKDSS DFGARHPQVQSVRCIHDMQGH QCGAFHPSK
11041	41409	A	11103	2	389	EIIDDDVPSFHAHGYQEKVSSV WVRSGM*VHCQPWLTLPQELR LWGPRSGETLALTSAPVSKTCD FGARHPQVQSVRCIHDMQGHQ CGAFHPLGTQEEEEAGQKEQM EQVPFWLARGDICELSGKKSV
11042	41410	A	11104	1	446	MEEEELEFVEELEAVLQLTPEV QLAIEQVFPSQDPLDRADFNAV EYINTLFPTEQLPMPSAHGGVSS CGNAGGPVSFATRENARCGIW GSGGVCDGVFGA/GAAGWGGV *GGGALGWMLSGRRIVLRSAIF TSPVSRAGSPERGWSCDC
11043	41411	A	11105	1	210	SSDGRHLAFDQGSPG*VLGHVG KQRAVDVQPSVAVRVRQPLLL LSTIMGSGLLGWEQGIDILNSIEI CSI
11044	41412	A	11106	2	287	AAESPGRSTRTDGAGLTRSLPR GSRCAGAWVAAGGLSWARGG GRQEAGWRNDG*GGTGARGG AGSRAAAHARGAAGHRASVSK PGPSRSSRFQCC
11045	41413	A	11107	150	389	GEEIAWLGAARPGKPTPSRIPL* PSLFPWRPHKFPERSVFAGSQP ASQSPPLRPPPPSHPEGSCLGSR LPPPGYLLPLR
11046	41414	C	11108	43	213	
11047	41415	A	11109	3	246	SSFPAPAREGALAPCRCLAGISV TLQGNP*GRCHHHHHHHHHHH HRCYDSQESGKLPRPGPKAELE GPPAWLLVGPGAHP

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11048	41416	A	11113	1	726	
11049	41417	A	11114	2	251	LSCGRSLHQGSVTSCKTINALT LTVDTWRGCAW*GCACTFHCR SATNMIRAYVYFSTISVLSLQEI RLSLRAILADLRLSICF
11050	41418	A	11115	1	1041	
11051	41419	A	11116	1	398	MGPNSTLENLLKGATSVFYNR DQEEAQKKERKLRGRTKALAA ALQ/SWQSPGAPRCIH*LLSVW QARVF*RGMPRQQDEATSTLSI QWQKPVETELSPDMEVTGFRA SLTDERVHLPEVLPQEYTEQRR QGHL
11052	41420	A	11117	5	137	
11053	41421	A	11118	5	272	
11054	41422	A	11119	2	211	WNQPRCPSTVNWIMKIWYIYT MEHYAAIKRNMIMSFAATWME LEAIFLSKMPQ*QKNKYCVFLH ACLES
11055	41423	B	11120	1	1560	
11056	41424	A	11121	1	588	
11057	41425	A	11122	80	574	EPAAQGNVLVDLLC*MKNRNR WLPNELSQVLHVTQSQFSKTG MSAKHTAFAMRMSPAQMTDIV VGLSTGQSPFMVLMQQGGHSA MQETRIASLPVTAIPAGMKIPCV TAGSACMVGPSVRVNEWFSAY GMAGMAYSRVSTFVRGLSPRY LTTREAPGCGSSAGH
11058	41426	A	11123	48	131	
11059	41427	A	11124	1	1195	
11060	41428	A	11125	2	1028	
11061	41429	A	11126	1	1008	NMMEQVLDIPSL*VISKDNANV TIDAVCFIQVIDAPRAAYEVSNL ELAIINLTMTNIRTVLGSMELDE MLSQRDSINSRLLRIVDEATNPL ALKIAARMIEDGELDKRIAQRY SGWNSELGQQILKGQMSLADL AKYAQEHHLSPVHHQVAEWM RARNGQLFRLRSNHLTLLVEQN NFYARGAKIYPDIHIDRSLKKCP SDLFAANARCGICQQSDERCLR YQPRRERGLYRIDITYPGKSYTT TALPSRFVWFVTGKAQSTQAS ALSYIDSLLYHHLDLYGQRLGH LDDGTDSWNHVPTLNGQCTLV LIHEYVDTRGPEIKTILVISWWN ILVFH

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11062	41430	A	11127	3	333	DIGIGEENRKRWLRTGKCSFLP KEREWMDRLMSWGLVDTFRH ANPQTADRFSWFDYRSKGFDD NRGLRIDLLLASQPLAECCV*T GIDYEIRSMEKPSDHAPVWATF RR
11063	41431	A	11128	2	136	YCKLACLQVDSRGSQVFALDV AARHR*QFAMPESDAVAMLKH LS
11064	41432	A	11129	3	431	GVFGRVSEKQRPAAPAAGERPL PRPRPLPCGAAARTGPFAAQAA *RAAAAPRSERRRHHGAEEGH QRCIYRHAADRALGEAARRTG YALRPAGEPELAAAARRR*RAP DPGPRVPRHLGLLATRACPPGG AHCSPERGAISW
11065	41433	A	11130	64	2436	RRQGLEGWWAIGLEGLTGKAL AWLFTVPGVRGLQWSPRFFLTR LRTLLCKVLGVLFSVAGGKKG PTCILQILKGQRRQEA*CISGWA ERVWASGQA*WEVWLHWAKS RNWFLFWKQHVHALRVRLDTT LFSLEEGSSFWNQGLTWKVVR RTFSESINHTPRITLGVPYSVHSF QLPGLLNFGEFKVCFVLSPRIFN LTHENFLSSEGPEIGGLLGATFN CLNKRLAKYRMRNVHPKPKLV RYLHSRLPPEPAAAP*AWCGPR HLSCRQMSSSSQIGNDSFQLQV TPVHLLPLSHTTRKNPEMYDLP LLFFNPQESAILQLFHQDGECLH CSPIVGDWCHLGHSQACPSFSV PSGLFVPSLLCGAAFGRLVANV LKRYSVCVRVCAHVHVCARVR VYACVWVRMTISLTVILIESTN EITYGLPIMVTLMVSTLPPGPCQ AQGHVRPTGPIFRSLLEWETEV EMDK*GHDFAHVLVSECISSEA *GMLLFCGGPDRSLFSTFRAVW SLSRLLDSVIAAGKQ*A*RT*SV GYSLLCPDLKGDPSAVSILRTT VHHAFPVVTENRGNEKEFMKG NQLISNNIKFKVKKTA*EERQV RDKRSRLTRLSALELRNMCDE HIASEEPAEKEDLLQQMLERR* EPGGAPTARRATQRWGEPLAQ MFPLTFHGLILRSQLVTLLVRG VCYSESQSVSLSEAEISQARPDE
11066	41434	A	11133	3	80	

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11067	41435	A	11134	2	958	LKCELS\DQGLAPAIQTVRLTHE SLTALEIPNALLQTIQDLILDLR VRCVMATLQHTAEEIKRLAEK EDWIVDNEGLTSLPCQFEQCIV CSLQSLKGVLECKPGEASVFQQ PKTQEEVCQLSINITQVFIYCLE QLSTKPDADIDTTHLSGDVSSP DLFGSIHEDFSLTSEQRLLIVLS NCCYLERHTFLNIAEHFEKHNF QGIE*ITQVSMASLKELDQRLFE NYIELKADPIVGSLEP*IYAGYF DCKDCLPPTGVRNYLKEALVNI IAVHAEVFTISKELVPRVLSKGI EAVSERAQSTDAVCFILQQKWS
11068	41436	A	11135	52	1053	MDEEERVYRACYILCISLLSSPG NPGLHSPMLDLDNDTRPSVLG HLSLFLIQKYNHSILFFSPLAWR YKTPHRVAFVEKLTKLVLSQLP YF*IISNMFYFVFLIFKTAEKSNP INHI*TRLCLFLVF*KMIQEVMH SLVKLTRGALLPLSIRDGEAKQ YGGWEVALRSHSAHFCLDVFV RRLTHESLTALEIPNDLLQTIQD LIFRPGSQL*PVSRIFIFSAGTFRF KNHLHDFTGFHTCLTGAPRGPV GGCASDDGQAAADTSQWLS*I* VLYL*LFLLASMFSLSVDVFSL AP*R*FSKHLFCF*EQRLLIVLSN CCYLERHTFLNISHGSP
11069	41437	A	11136	50	426	
11070	41438	A	11137	2	949	QQVWKQNCFKHYSNETDNSTT QLVGVQTLQVVVPSLILCEHCM NFSSPHVWCCMVQAVPGGQGQ TIMQVPVSGTQGLQQVSNI*KY *AVYQRRGFKE*IITTGQTQQIII QQPQTAVTAGQTQVIPLALSHR SKTDLEESDN*VRYQPVNADGT ILQQGKCTHKLP*DFLGQLFCPL DN*HTTSSGQGTVTVTLPVAGN VVNSGGMVMVRKCIFQLCL*N FLEHAT*CLLKEEPLYVNAKQY HRILKRRQARAKLEAEGKIPKE RRVCITLGRI*ERRIAGFYF*NY LFSPKEKDSPHMQVGRHIHFILL FITLY
11071	41439	B	11138	26	80	

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11072	41440	A	11139	203	797	HRHIARHLFPRTTPTP*LSWQGS *TPRWKGVRAVVTQPRKERRA ESEQFQATKPRSQL*LQPPTPSL VSSCQLKTTAASRPLT*PSKSVY PSAPFHPWLPC/SKPERSVSPES NDSISEELNHFKPIVCSPCTPPK RLPDGRVLSPLIIKSTP/PQPKQK PAEADFL*GQSTDPQKVGTDLS GAADQKDPFKSHSYLSGS
11073	41441	A	11140	33	379	EATSNFKQPPSLPFWCLKSRTSL KPRQSKVCSSSFPVI*GKTGNEL ALQIP*FKSSCGPRFPD***PAGR /SAPSLGPPPSQSCAHQ*EHWVQ VCIKHGITNAEPPAEHLKVLVR E
11074	41442	A	11141	248	622	SESSGRFWLCGLGPGTSPLLSL KFPHLLPASRGRSPPSPRPRVPR GKATQVVWAWGYRCVDEDPA RCLGTPGRTD/PHCGQGLLCPL GKSCSTSQPLSQGDGRGTSWDR SHACSPGGHPHRCIGCM
11075	41443	C	11142	1	1311	
11076	41444	A	11143	452	1286	
11077	41445	A	11144	2	299	GLPLAHGLLGRFGMDRIYEGQ VEMTGD*CDVESIDGQPGAFTC YLDVGLARTITGNKVFGALKG AVDKGCSVPHSTR*FPACDSAE FALGIPYFVQPNI
11078	41446	B	11145	49	832	
11079	41447	A	11146	1	1074	
11080	41448	A	11147	1	360	
11081	41449	A	11148	1	1155	
11082	41450	A	11149	75	266	
11083	41451	A	11150	2	222	
11084	41452	A	11151	1	549	
11085	41453	C	11152	453	665	
11086	41454	A	11153	1	1962	
11087	41455	A	11154	1	295	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN
11088	41456	A	11155	1	363	
11089	41457	B	11156	1	375	
11090	41458	A	11157	1	197	
11091	41459	C	11158	1	270	
11092	41460	C	11159	1	146	
11093	41461	C	11160	1	268	
11094	41462	C	11161	1	301	
11095	41463	A	11162	1	289	
11096	41464	B	11163	19	240	

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11097	41465	A	11164	2	253	
11098	41466	B	11165	1	978	
11099	41467	B	11166	1	316	
11100	41468	A	11167	191	319	
11101	41469	A	11168	608	763	
11102	41470	A	11169	274	437	
11103	41471	A	11170	1	417	
11104	41472	C	11171	1	792	
11105	41473	A	11172	3	449	IYLTKELKDLYKEKCKTLLKEIT DDTNKWKHIPSSWMGRINIVK MTTLPKAIYKFNAIPFRIPPSFFT ALEDTILKFIWNQKR/CPHSQCK IKQKEQIWRHHTT*FQAIL*GHS HQNS/IGTWMKLENIILSKLLQG QKTKHCMFSLIGGN
11106	41474	A	11173	1	441	
11107	41475	B	11174	1	597	
11108	41476	A	11175	5	265	
11109	41477	A	11176	3	280	SIYPNTCTRMFIVALLTIAKTWN QAICPTMIDWIKKMWHIYSME YYAAIKNDEFMSFVGTWMKLE TIIFSKLSQGQK\TKHRMFSLIGG ELEQ
11110	41478	A	11177	590	747	KAYQPEKAQDQVDSQPNSTRG TWMKLETIILSKLTQEQK\TKHC IFSLISGS
11111	41479	A	11178	3	274	FYYKDTCTHMFIVALFTIAKTW NQPKCPSVIDW/IMKNMWHIYT MEYYAAIKNDEFMSFSGTWMK LETIILSKLTQE\QKTKHCMFSLI SGS
11112	41480	A	11179	1940	2061	
11113	41481	A	11180	493	743	KATRSVNC/WWDHL*RPFWGS PH
11114	41482	B	11181	1	1248	
11115	41483	B	11182	50	8445	
11116	41484	A	11183	40	125	
11117	41485	B	11184	1	1896	
11118	41486	A	11185	1	624	
11119	41487	A	11186	1	357	
11120	41488	A	11187	1	304	
11121	41489	A	11188	681	834	
11122	41490	A	11189	3	2128	
11123	41491	A	11190	175	402	

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11124	41492	A	11191	46	790	NPGAVKMPAYHSSIMDPDTKLI GNM/AHLLPIRSQFKGPAPRET\ KDT\DIVDEAIFLPSGPNVFF\KN YEIKNE\ADRTLIYITLYISECLK KLQK\CQFPKAQGGGKEMFYA GESTNFSHFLGEPGF\PTLTAILC PNPANK\QEDE\VMRALFTNQP KGKRLGLRLCEKSFSDP\QNG*T PAKWVDLAFVKRQF\MNKSLS GPWTVEGSPGQPTVSRGPGAAF FQQDVTQSFCLYLVKFYRDERR ACLYLKNS
11125	41493	A	11192	1	828	
11126	41494	A	11193	1	525	
11127	41495	A	11194	43	1826	THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLLPLPAAGRVVVRRL AVVRSGSRSLSTADMTKGLVL GIYSKEKEDDVP\QFTSAGENFD KSLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDPCG DAQAAAEGAVLGLYEYDDLK QKKKMAVSAKLYGSGDQEAW QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICSAIVS AAKLNLPINIIGLAPLCENMPSG KANKPGDVVRAKNGKTIQVDN TDA\EGRLILADALCYAHTFNP KVILNAATLTGAMDVALGSGA TGVFTNSSWLWNKLFEASIETG DRVWRMPLFEHYTRQVVDCQL AD\VNNIGKYRSAGACTAAAFL KEFVTHPKWAHLDIAGVMTNK DEVPQSTGKA*LGRPTRTLI\EF L\LRFSQDNCLVQILKNVFHSVL NWTVELKKVFE
11128	41496	A	11195	1	273	

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11129	41497	A	11196	2996	8256	LPTRRSWAVFFKGGESGAHTLR RKARKKRKKQVKGGSPKKGEE AKKVEAPRLPKLAAPGGGAGA KGGAGGTSDMRLWSWVLHLG LLSAALGCGLAERPRRARRDPR AGRPPRPAAGPATCATRGPRPP RLAAAAAAAGRAWEAVRVPR RRQQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAF TLQVWLRAEGGQRSPAVITGL YDKCSYISRDRGWVVGIHTISD QDNKDPRYFFSLKTDRARQV
11130	41498	A	11197	75	266	
11131	41499	B	11198	1	363	
11132	41500	A	11199	1	649	PRIRHEVIEEVIRMMLEIINSCLT NSLHHNPNLVYALLYKRDLFE Q\FRTHPSFQDIMQNIDLVISFFS SRLLQAGAELSVERVLEII\SQG\ ALRCPKDRLKEISQKLKFKYVE EEQPRGVF*SPYVWSLVLQLQQ SALYWEFHRTFQLFHPWDSRLR GRDASSPPGTPSSQGRPFQSSFIS GVTEVGQTGYLVYLLLKEDCT SVFSSHTLIWRIGC
11133	41501	A	11200	108	210	
11134	41502	A	11201	53	259	
11135	41503	A	11202	1	2679	
11136	41504	A	11203	1	675	
11137	41505	A	11204	834	1077	KGLWTVPPSFGDTVSGPPVPTG GSAGHTVPPPPR*CRRQPPPSPP WRRLFLPQLRSRSSQPPAGPAR HLPPPAARPECFCA
11138	41506	A	11205	1	681	
11139	41507	A	11206	1777	1940	VPILPQPLLLHPIILLS*VPILPQP/ PAPPPYNPFITSPPHTWSGLQFH SVTSPPPPAQQFTLKRVAEAKGI VK
11140	41508	A	11207	3	547	
11141	41509	A	11208	1	578	
11142	41510	A	11209	194	379	
11143	41511	A	11210	1	927	
11144	41512	B	11211	1	916	
11145	41513	A	11212	1	441	RRKLQKQALGPEQNLETLLNL ATSVFYNRDQEEQVQKEKRDQ RKAAALVMALRQTNLGGSERT EHEAGQSPGKACYQCGLLGHF KKDCPMRNKLPPR/RVSTMLRQ SLEGALPQRMKVPWVRSPQPD DPTTGLRVPGASASSCHHPH
11146	41514	A	11213	164	359	
11147	41515	C	11214	157	189	

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11148	41516	A	11215	13	399	VEAFPTGSEKATAVISSLLSDIIP QSRLPTSIPSDNRRAFISQISQAV FQALSIP*NLYIPYGPPSSRKH/T LTKLSHQLKKDWTILLPLSLLRI QACPRNATGYSPFKVLYRHSFL LRPSLIPDTRPT
11149	41517	A	11216	2	152	WYGEIMGDVSQGCFER*WAMF LRAASSGIRGGVGT*SGRH*AE GRFYGDFRGNRAASVFSR
11150	41518	A	11217	1	1143	
11151	41519	A	11218	28	453	
11152	41520	A	11219	275	1128	DISTPSLATDHMPITIPLNLIT/TY PTQRQYPIPPHALKGLKPVITDL LQHRLLKPINSPYNSPILPVQKP DKSYRLVQDLRLTNQIVLPIHP VVPNLYTLLSSIPSSTTHYSVLH LKDAFFTIPLHPSSQPLFAVTWT DPDTQQSQQLTWAVLPQGFRD SPHYFSQALSHDLLSFHPSASHL IQYIDDLLLCSPSFESSQQDTLL LLQHLFSKGYQSDDRPAFTSQI TQAVSQALGIQWNLHIPYHPQS SGKVEWTNGLLKLLLLLLTANI DDTSYLQIPHKGLQ
11153	41521	A	11220	1	606	
11154	41522	A	11221	713	835	LSQWRSDNGPAFISQITQAVSQ APGIQ*NLYIPYHPQSSGK
11155	41523	A	11222	1	1133	AEALPVQFYFHLSDIRGMLLHE PDLQKGIKAVSQEDPQWSYQA DSPGIARRDYMVSRLVEGLKK AAYKAVNYDKLKKTTQVTIVP GPDFNLASHIIPDTTPDPHDCYL SDTPGIHSISHISFFAIPHPDHTW FIDGSSTTPNRHTPAKAGYAIVP STSIIEAAALPPSATSRQAKLIAL TRTLTLAKELCVNIYTDSKYAF HILHHHAVIWAERGFLTKQGW SNINASLIKTLLKATLLPKEAGV IHCKGHQKASDPIAQGNTYAD KIAKEAASGPTSVPHGQFFSFSL VTPTYSPTKTSTYPSLLTQGKW FLDQGKYLLPASKAHSILPSFH NLFHVGYKPLAHLLEYLISFLS WKSILKEITSQ*SICYSTTPQG
11156	41524	B	11223	1	1156	
11157	41525	A	11224	1	4991	
11158	41526	A	11225	3	590	
11159	41527	A	11226	203	1772	
11160	41528	A	11227	1	1669	
11161	41529	A	11228	1473	1604	
11162	41530	A	11229	82	159	

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11163	41531	A	11230	1	1323	
11164	41532	A	11231	377	631	LLKGKLTNRKDIHTKTPSVRHH HRRPKPGRDTTKKIILNQYPW* TSMQKSSIKYWQTESSSTSKSLS TMIKLASSLGCKNWKKL
11165	41533	C	11232	1	1677	
11166	41534	A	11233	753	966	FVFLWSLMMVTYRWGFGVDV LSVC*FSFQQS\EPQLQVCWSLL EVHS*PCLPGYQQRRNSCWPRG SCDVVIT
11167	41535	A	11234	1253	1459	LSDSPKLK*RKKC*GQPERKVG LPTKGSPSD*QQISWQKLCKPE ESGGQYSTFLKKRIFNPEFHIQQ
11168	41536	B	11235	1	924	
11169	41537	A	11236	299	436	
11170	41538	A	11237	259	536	FQKEWYQLLLVPLV/EIWL*IHL VLDFF*LVNY*LLPQFQSMLLV SSEIQLLPGLVLGECMCQGIYPF LLDFLWSLMMVTYRWGFGVD VLCVC
11171	41539	B	11238	79	1587	
11172	41540	A	11239	1608	1763	
11173	41541	A	11240	1	2001	
11174	41542	B	11241	1	741	
11175	41543	B	11242	1	1368	
11176	41544	C	11243	1	3924	
11177	41545	A	11244	470	619	KVTRGWGSPHQDAG*SPCQSH QDQTP*GILKEHQEKARRK*RQ LCVLQL
11178	41546	B	11245	1	3546	
11179	41547	A	11246	363	476	
11180	41548	A	11247	1	759	
11181	41549	C	11248	376	986	
11182	41550	A	11249	556	821	MSIRSTWRRAEFNSWVSFLTFR LVDLSLVFDDGDVQVGFWCGC PSCLLVFLL/ISQDPQLQVCWSL QEVHSRPCSPGYQQQRLQYSEY
11183	41551	A	11250	119	340	
11184	41552	B	11251	1	942	
11185	41553	A	11252	436	732	LHIWPFLLPCKAQNQVHCSKFC PLGRFPFMAVLQGCPRKGL*CC SCPLLGGIWISCRIICAFRTYLRP IMYIPLPFADGMLLCTAHSMAR CFGYCSLVV
11186	41554	C	11253	1	1878	
11187	41555	A	11254	720	1535	ILPEVQGGAGTI*LSLFLIE*PLF LSPA*LPWPELPTLC*IGVVRDG TPVLCQFSKGMLPVFAHSV

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11188	41556	A	11255	2	1059	WLLAASPLWLCRIRP/LILAAFM GWQSRSALGTQSQESGKGSPD QVLVPQDCGPWLGSVELVSVP GSQAGEEPILSENKGRVTQMKI PEERSGSNICCSAIFAVLQPPLLI PRQTRSGVDLQQNPTDLQLRVL TVRRKTNKEKGHPHQNPTCTSP ASKTKGALRFIKQVLRDLERAL DSHTIMGDFNTPLSTLDRSTRQ KVNKDIQELNSALHQVDLIDIY RTLHPKSTEYTVFSAPHHTYSKI DHTVGSKALLSKCKRIEILTNCL SDHSAIKLELRIKKLTQNHSTTL KLNNLLLNDYWVHKETKAEIK MVFEIDENKDTIYQNLWDTFK AVCRGKFIALKAHKRKQERVT
11189	41557	A	11256	82	159	
11190	41558	A	11257	820	1358	HTDGFLVWMPFLFVSFPSNSQD RQLQVCWRLLEVHSRPCFPGY QQRWLQNNRY/SVNRKCCCLIV PLEVLSQRSTHQHVGEWLCLL GRKFPAGMEACTAMLCSSSVL EAATLSFSVQHRACTGGS*KPQ QGRVYPSEGREHNGAAAFGPF CSSECPASCPDPGTQPCAPGTYI PFFSCQT
11191	41559	A	11258	2435	3261	QVRGYRCRFVTWVNCMSLRFG VQRIPSPSLTGTQPPVGAD*HLT RPGTPLR*NFQRNDQAVTFAVH \HIH\FVQPLLLIPMQTGSGVDLR QTPTDLQLRVLTVRRKTNKQK GHPHRNPICMSPSSKTKARQAN IQIQEIQRTPQRYSSRRATPRHII VRFTKVEMKEKKLRAAREKGR VTHKGKPIRLTVDLLAETLQAR REWGPIFNILKEKNFQPRISYPA KLNFISEEEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNQ YQPLQNHAKL

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11192	41560	A	11260	1439	2544	VSSTTKEKALSVPPRWCILQKK NPPNHQPVSLPEVFLPQILKFSG PPHWRRIEDEYKVMRLNIGDM KTKKKMLEKYEQLEIRHQQKS RT*KAVCCIT*LSRHIILLGQAPL VQQSM*QPESHHQVNPPETSYG IHQTPKLS*IGIK*RPWIM/MSEV KGYKVGNFFFAKAPNRAPPLL KPRQTGSGVDLQQTPADLQLR VLTVRRNTNKQKGHPHQNPICT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPVME DQMNEMKQEEKFREKRMKRN EQSLQEIRDYVKRPNLRLIGVPE SDGENGTKLENTLQDIIQENFPS LARQANIQIQEIQRMPQR
11193	41561	A	11261	2772	3111	QSGPSAAGLLEFAGGPLQTLFA WVSAAEVGKCKGSGSSLS*PK KGVMDGTWKIGSLPPEYCAFPT G*KNGAP/LRLYPTPGSEGPTPT ESP*/FASTAVGDQTARQQRGW GRGARH
11194	41562	A	11262	248	597	DRCPAAWDRHPAGIQSSRREPS KATWTLRSKLSVQDGRRDSSL RLNCKVAARLGAGHPPMLRLG LRC*YPGKQGLEWTSSKLQQTC H*GS*LLKGKLTNRKDIHSKTPS VRHYHQR
11195	41563	B	11263	1	2250	
11196	41564	A	11264	1298	1681	GVSVPLLWGASQLGYLGVMDP LAEAVCPFSDLQLHSGRTSTVF KAALGQSGAHCPERCVSAQS* AD*RALREHKQ*FGSTLCGPVM VVAMELGSSTMVELVSSPANS VKVFLFLHIFSSTCCFLTFS
11197	41565	A	11265	1272	1497	SGLLPIKVAFTKPQFLFILLRIWL *RGYVFCSWKVTTPREQPQCIT DGYQIFIFMQKTLSCLSILGKRT MSLMQ
11198	41566	A	11266	1	1071	
11199	41567	A	11267	788	1286	
11200	41568	A	11268	3	455	
11201	41569	A	11269	1	711	
11202	41570	A	11270	225	525	GGGENFSYPWYLLVGCGWFSS SPIVPDVPPFSLLLPAQKKKPAP PK\PEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK

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11203	41571	A	11271	914	1261	TAKPKTNWCCRAPTSRLASTFA TMPFKKAECVGDAHPATVKDE PQRISARLS\AKPAPPKPEPKPK KAPAKKGEKVPKGKKGKAD\A GKEG\NNPAEN\GDAKTDQAQK A\EGA\GDAK
11204	41572	A	11272	3	359	
11205	41573	A	11273	440	642	WKAEREEIEPR/PKKAPAKKGE KVPKGKKGKAEAGQDGDNPTE NGDAKTDQGQKAEGAGDAKR TVSHQN
11206	41574	A	11274	499	723	
11207	41575	A	11275	147	459	STYVPLPSPPSSMPKRKAEGHA MGDKAKVKDEPQRRFARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK
11208	41576	B	11276	179	400	
11209	41577	A	11277	24	601	
11210	41578	A	11278	266	441	
11211	41579	A	11279	17	570	HQPKKDLTGFVKWPRYIRLQR QRAILYKRLKVHLAINQFTQAL ARQTATQLLKLAHKYRPETKQ EKKQRLLARAEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVGPIELVVFLPA LCRKMGVPYCQ\IKGKARLG\R LVHRK\TCTTCRFTQ\VNS\EDK GALAK\LVEAIRTNYNDRYDEI R\RHWGGNVLGPKSVARIAKL\ EKAKAKELAH*TGGSYQDQLQ
11212	41580	A	11280	175	289	RPCVKESGKPHLKSSTMWTTL KLLRI*PRRTTCSPRLS
11213	41581	A	11281	205	361	
11214	41582	A	11282	144	396	CLEVLHKILFFEMESHSVTQAG VQWRDLGSLQPLPPG\SSNSPTS ASQVAGIRSMRQKGRANFFVFL VEMGFHHVGQADLELLTL
11215	41583	A	11283	241	550	
11216	41584	A	11284	2	106	
11217	41585	A	11285	2	447	PPLSRLLCPRHPHSGWPEGYSPE HLRCGLRSGTLRSRQALHCQVS SNP*PPSLWF*GCGNVL*ELCLF VLPVSVNLYQVLLSEIWEFHRT

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11218	41586	A	11286	1	2172	PAGRCRTAWAVAAQQLMLSA ALRTLKHVLYYSRQCLMVSRN LGSVGYDPNEKTFDKILVANRG EIACRVIRTCKKMGIKTVAIHSD VDASSVHVKMADEAVCVGPAP TSKSYLNMDAIMEAIKKTRAQ AVHPGYGFLSENKEFARCLAAE DVVFIGPDTHAIQAMGDKIESK LLAKKAEVNTIPGFDGVVKDA EEAVRIAREIGYPVMIKASAGG GGKGMRIAWDDEETRDGFRLS SQEAASSFGDDRLLIEKFIDNPR HIEIQVLGDKHGNALWLNEREC SIQRRNQKVVEEAPSIFLDAETR RAMGEQAVALARAVKYSSAGT VEFLVDSKKNFYFLEMNTRLQ VEHPVTECITGLDLVQEMIRVA KGYPLRHKQADIRINGWAVEC RVYAEDPYKSFGLPSIGRLSQY QEPLHLPGVRVDSGIQPGSDISI YYDPMISKLITYGSDRTEALKR MADALDNYVIRGVTHNIALLR EVIIN\SRFGKRNLNT*FL\SKGF PEAFKGHLLTKS\EKTQFLAIAS\ SLFV\AFQLRAQHFQENSRMPVI KPDIANWELSVKLHDKVHTVV ASNNGSVFSVEVDGSKLNVTST W\NL\ASPLLSVSVDEHSEGLFQ CLSREAGGNMSIQFLGTVYKV NILTRLAAELNKFMLEKVTEDT SSVLRSPMPGVVVAVSVKPGD AVAEGQEICVIEAMKMQNSMT
11219	41587	A	11287	62	2600	
11220	41588	C	11288	277	508	
11221	41589	B	11289	94	1440	
11222	41590	A	11290	57	237	FLHAENKAHRPGISLCGLRAQP RQPASRHAW*SMRSEQRPWLT ASGRSSGQTRSSRSLG

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11223	41591	A	11291	3	1968	EFDYSEDKSSWDNQQENPPPTK KIGKKPVAKMPLRRPKMKKTP EKLDNTPASPPRSPAEPNDIPIA KGTYTFDIDKWDDPNFNPFSST SKMQESPKLPQQSYNFDPDTCD ESVDPFKTSSKTPSSPSKSPASFE IPASAMEANGVDGDGLNKPAK KKKTPLKTDTFRVKKSPKRSPL SDPPSQDPTPAATPETPPVISAV VHATDEEKLAVTNQKWTCMT VDLEADKQDYPQPSDLSTFVNE TKFSSPTEELDYRNSYEIEYME KIGSSLPQDDDAPKKQALYLMF DTSQESPVKSSPVRMSESPTPCS GS\SFEETEALVNTAAKNQHPV PRGLAPNQESHLQVPEKSSQKE LEAMGLGTPSEAIEITAPEGSFA SADALLSRLAHPVSLCG\ALDY LEPDLAEKNPPLFAQKLQREA\ VHPTDVSI\SKTALYSRIRTTEVE KPAGLLFQQPDL\DSALQIARAE II\TKEREVSEWKDKYEESR\RE VMEMRKIVAEYEKTIAQMIEDE QREKSVSHQTVQQLVLEKEQA LADLNSVEKSLADLFRRYEKM KEVLEGFRKNEEVLKRCAQEY LSRVKKEEQRYQALKVHAEEK LDRANAEIAQVRGKAQQEQAA HQASLRKEQLRVDALERTLEQ KNKEIEELTKICDELIAKMGKS
11224	41592	A	11292	63	2203	
11225	41593	A	11293	27	586	
11226	41594	A	11294	89	288	
11227	41595	A	11295	1	522	HERFETTYFKKFP\GYYVTGDG CQRDQDGYYWITGRIDDMLNV SGHLLSTAEVESALVEH*RLLQ EA\AVVGHPHPCEGVNASYCFV TLCDGHTFSPKLTEELKKA\VM RKRLAPFATPDYIQNAPGLPKT\ RSGKIMRRVLRKI\AQNDHDLG DMSTVADPS\VISHLFSHRCLTI
11228	41596	A	11296	2	569	
11229	41597	B	11297	1	990	
11230	41598	A	11298	1	252	
11231	41599	A	11299	39	174	RHIYSSNEVH*KEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEEEIPLSSL

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11232	41600	A	11300	16	379	ILDTSPMRWTQKNFSMILAQPE QQCKTLSQNKNKDRRIKKKEE KKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKKKEKE EEKKK/QEEEEEEEEEEEEEEEE EEEEEEEEEEERRRR
11233	41601	A	11301	1	249	
11234	41602	A	11302	1	353	
11235	41603	A	11303	1	847	
11236	41604	A	11304	3	224	QEKKRRKEKKK\KEEEEEEEEE EEEEEEEEEEKKKKKKKKKK KKKKKKKKKKKKKKKKKKK KKKKKKKKKGRKTDLAVDPV
11237	41605	A	11305	1	417	
11238	41606	A	11306	1	1314	
11239	41607	B	11307	1	133	
11240	41608	A	11308	45	266	
11241	41609	A	11309	35	313	FLQMEDTYIVTKLLLLLRFAWL YLDLVFVLI*YRKKRRKKKRKK KEKEKEKEKKKKKKKKKKK KKKKKKKKKKKRKKEMALQS CSLWYLYA
11242	41610	C	11310	240	391	
11243	41611	A	11311	1	579	
11244	41612	A	11312	141	410	PEPILTMESKGMWQLFELTL/H NSKVNTLSKELHSEFSEVMNEI WASDQIRSAVLISSKPGCFIAGA DINMLAACKDPSRSNTAITRKH RE
11245	41613	A	11313	1	358	KWFTPMEFEIKGGYA*SKNWR LSVRCGGWPLRRLMEEGSLPNP SRIYYRNKLRILKSQNNSSVDPC MRNLDECEVCRDGWELFCCDT CSRVFHDDCHIPPVESEKMKES AGSQQCCQES
11246	41614	A	11314	1	921	
11247	41615	A	11315	108	2765	

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11248	41616	A	11316	98	2418	AKLMAQQGQQGQMASGDSNL NFRMVAEIQNVEGQNLQEQVC PEPIFRFFRENKVEIASAITRPFP FLMGLRDRSFISEQMYEHFQEA FRNLVPVTRVMYCVLSELEKTF GWSHLEALFSRINLMAYPDLNE IYRSFQNVCYEHSPLQMNNVN DLEDRPRLLPYGKQENSNACHE MDDIAVPQEALSSSARCEPGFS SESCEQLALPKAGGGDAEDAPS LLPVSCKLAIQIDEGESEEMPKL LPYDTEETFDLKTPQVTNEGEP EKGLCLLPGEGEEGSDDCSEMC DGEERQEASSSLARRGSVSSEL ENHPMNEEGESEELASSLLYDN VPGAEQSAYENEKCSCVMCFS EEVPGSPEARTESDQACGTMDT VDIANNSTLGKPKRKRRKKRG HGWSRMRMRRQKNSQQNDNS KADGQVVSSEKKANVNLKDLS KIRGRKRGKPGTRFTQSDRAAQ KRVRSRASRKHKDETVDFKAP LLPVTCGGVKGILHKKKLQQGI LVKCIQTEDGKWFTPTEFEIKG GHARSKNWRLSVRCGGWPLR WLMENGFLPDPPRIRYRKKKRI LKSQNNSSVDPCMRNLDECEV CRDGGELFCCDTCSRVFHEDCH IPPVEAERTPWNCIFCRMKESPG SQQCCQESEVLERQMCPEEQLK CEFLLLKVYCCSESSFFAKIPYY YYIREACQGLKEPMWLDKIKK
11249	41617	A	11317	1	1210	
11250	41618	A	11318	1	743	MRYKKEQPLFLPKYDLGADAA ILQPQEEDCGSTQVRGGHHRTK TEETGLLVTSLNQGIKPHDSVT KLLSPQRSSVLFLLLITSGVHTD SSKAVLESRRSLGYEASFLEYF QSFYKLFPVDRLYAWHCSDHR NTTVTAINTDRPGLLTLSLTVTI GQGSKKAPSGFSHISPAPTVKQ QPILCDDRDFSPSSFPSTNTPSQF ATNEVLTTGPPPGAG/CCQYSTI TRKTGPNCQAGGCPGGARPAK
11251	41619	A	11319	314	486	
11252	41620	A	11320	3	122	
11253	41621	A	11321	1	289	
11254	41622	A	11322	1	399	
11255	41623	A	11323	3	259	

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11256	41624	A	11324	1	369	MPATWEAEARESHKREFETHL/VQHSETPSEKEEE\EEEE

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11270	41638	A	11338	1	503	MKHQHFALLVPEKFLIAQSTAS RVDRRQIWRDVSSERGEISQCL KVGTSLNSTDVSAVEAVRATV LGSGTLTPTVLRSNAGPYTRIST VPACLLGQEEEEEEEEEEEEEEE EEEEEEE\EEEEEEEK/EEEE/EEE EEEEEEEEEEEEEEEEEEEEE EEGEEEERRKS
11271	41639	A	11339	1	651	
11272	41640	A	11340	1	2184	MNIDANIPNKILENRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTKDKNCMIISIDAEK AFDKIQQCFMLETLNKLGIGGT YLKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGVQLGKE EVKLSLFADDMIVYLENPIVSA QHLLKLISNFSKVSGYKINVQK SQAFLYTNNRQTENQIMSELPF TIASKRIKYRGIQLTRDLKDLFK ENDKPLLKEIKED/DKEMEEHS MLMGRKNQYRENSHAAQELE KNYFKVHMEPKKSPHYQVNPK PKEQSGRHHVT*LQTILQGYSN QNSMVLVPKQTYRSMEQNRSL RNNATYLQLSDL*QTQEKQAM GKGFPI**MVLGKLASHM*KPE TGSLPYTLYKNQFKVD*RLKR* T*NHKNQRRKPRHYHSGHRHG QGLHV*NTKINGNKNQN*QMG SN*TKELLHSKRNYRQSDQATY KMGENFHNLLIRQRANIQNVQ* TQTNLQEKNKQPHQKVGEGHE QTLLKRRHLCSQKTHEK\NSPSL AIREMQIKTTMRYHLTPVRMAI IKKSGNSRKHIQKKEEEEEEEEA EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEE EEEKCSLKHTEAPCVKGIETIFW NKFSLCDITKSYLSGVQKLEER AHKVKLALKFKKEIKMALHGG
11273	41641	A	11341	1	870	
11274	41642	A	11342	2	259	GSTISCARCAELRGSASRFRPLP AAAMKWMFKEDHSLEHRCVE SAKIRAKYPDRVP\LTMGQLYE KEKDEDGFLCVAYSGENTFGF

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11275	41643	A	11343	1	461	GCRCRCRRRCCCARCAELRGS ASRFRPLPAAAMKWMFKEDR W\LEHRCVESAK\IRAKYPDRVP VIVEK/VSQGSQIVDIDKRKY\L VPSDITV\AQFMWIIRKRIQLPSE KA\IFLFVDKTVPQSSLTMGQLY EKEK\DEDGFLYVA\YSGRGTLF
11276	41644	A	11344	1	966	
11277	41645	A	11345	1	1037	RPPFPVPGVQKCPLPTRGGLHIG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSPVASGREM VVLSVPAEVT\VILLDI\EGTTT\P IAFVKG/DILFPYIERKMLK\EYL QTHW\EEEEFQ\QDVSLFEGNK A\EEDAHLDG\AVPIPGKHLGIG V\DD\LQQMI\QAVVDNVCWQM SLDRKTTALK\QLQGH\MWRAA FTAGRMK\AEFFADVVPA\VR\K WREAG\MKVYIYSSGSVEAQKL LFGHSTEGDILELV\DGHF\DTKI GHKRRRVKVTRK\IADSI\GCST\ NKHFVFWTDVTSRRASAGLRE AGCCTLAVV\VRPG\NAGINR*L RKTYYSLITSFQWNYYLPSST
11278	41646	A	11346	346	858	
11279	41647	A	11347	1	234	
11280	41648	A	11348	1	1696	
11281	41649	A	11349	1	234	
11282	41650	A	11350	1	1696	
11283	41651	A	11351	1	211	
11284	41652	A	11352	1	417	
11285	41653	A	11353	1	1458	
11286	41654	A	11354	219	329	
11287	41655	A	11355	132	451	
11288	41656	A	11356	1	996	
11289	41657	A	11357	1	867	MARLWGALSLWPLWAAVPWG GAAAVGVRACSSTAAPDGVEG PALRRSYWRHLRRLVLGPPEPP FSHVCQVGDPVLRGVAAPVER AQLGGPELQRLTQRLVQVMRR RRCVGLSAPQLGVPRQVLALEL PEALCRECPPRQRALRQMEPFP LRVFVNPSLRVLDSRLVTFPEG CESVAGFLACVPRFQAVQISGL DPNGEQVVWQASGWAARIIQH EMDHLQGCLFIDKMDSRTFTN VYWMKVND*SFATGAEDSGY QDANTFTLSWANLTWHQLGW LAYDRKLDCQGMAD
11290	41658	A	11358	3	226	
11291	41659	A	11359	1	756	

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11292	41660	A	11360	35	142	
11293	41661	C	11361	151	484	
11294	41662	A	11362	1	1245	
11295	41663	A	11363	2	1464	CQAKFIMNRLKK/NERQKVQDI KEVKQNIHLIRASFAGKGKQLE EKMQPLEPEAIMLSELMQEQKT KCRMFSLISGKHGVHMDSKTG ATDSGAYLRVEEIQTTIREYYK HLYANKLENLEEMDKFLDKYT LPRLNQEEVESLNRPITGAEILAI ISSLPTKKSPGPDGFTAEFYLRY KEELVPFLLKLSQSIEREGILPNS FYEASIILIPKPGRDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNL RKSINVIQHINRAKDKNHMIISI HEEKAFDKIQQPFMLKTLNKLG IDGTYLKIIRAIYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLARAIRQEKEIKGIHL GKEEVTLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASRRIKYLGIQLTRDMKD LFKENYKPLLSEIVTVF
11296	41664	A	11364	41	559	
11297	41665	C	11365	63	370	
11298	41666	A	11366	3	211	
11299	41667	A	11367	47	358	PDMGLEDEQKMLTESGDPEEE EEEEEELVIGLRLSVHTGNLGRP GM*NFPLLLSIQN*MGDPHSAIS GGQCGSASWPSARIPLQQVREQ CRASWKKCVK\ARERLEL\CDE R*SSRSHTEEDCT\EELFDF\LH A\RDHC\VAHKLL*QLAFCTDPP TTSERAMPSQLEEMCKRPGSG
11300	41668	A	11368	1	2082	

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11301	41669	A	11369	1	2013	MKHLKRWWSAGGGLLHLTLL LSLAGLRVDLDLYLLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRALGVPFVPRTSV DAWLVHSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGGCASEE NGVLREKHEAVDHSSQHEENE ERVSAQKENSLQQNDDDENKI AEKPDWEAEKTTESRNEGISLG DIPLPGSISDGMNSSAHYHVNFS QAISQDVNLHEAILLCPNNTFR RDPTARTSQSQEPFLQLNSHTT NPEQTLPGTNLTGFLSPVDNHM RNLTSQDLLYDLDINIFDEINLM SLATEDNFD\PIDVSHLFDEPDS DSGLTLDSSHNNTSDIKSNSSHS VCDEGAIGYCTDHE\SSSHHDL EGAVGGYYPEPSKLCHLDQSDS DFHGDLTFQHVFHNHTYHLQP TAP\ESTS\EPFPW\PGGRSQEGL RE*DTLKDTDRNLSRDEQRAK ALHIPF\SVDEIVGMPVDSFNSM LSRYYLTDLQVSLIRDIRRRGK NKVAAQNCRKRKLDIILNLEDD VCNLQAKKETLKREQAQCNKA INIMKQKLHDLYHDIFSRLRDD QGRPVNPNHYALQCTHDGSILI VPKELVASGHKKETQKGKRK
11302	41670	A	11370	3	255	
11303	41671	A	11371	1	1611	
11304	41672	A	11372	109	207	MLCLQRFYMIFVDFQSRPQF*L KSCQHIISCHQ
11305	41673	A	11373	1	666	
11306	41674	A	11374	1	1254	

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11307	41675	A	11375	33	1458	KLPLKAKMGKEKTHINIVVIGH VDSGKSTTTGHLIYKCGGIDKR TIEKFEKEAAEMGKGSFKYAW VLDKLKAERERGITIDISLWKFE TSKYYVTIIDAPGHRDFIKNMIT GTSQADCAVLIVAAGVGEFEA GISKNGQTREHALLAYTLGVK QLIVGVNKMDSTEPPYSQKRYE EIVKEVSTYIKKIGYNPDTVAFV PISGWNGDNMLEPSANMPWFK GWKVTRKDGNASGTTLLEALD CILPPTRPTDKPLRLPLQDVYKI GGIGTVPVGRVETGVLKPGM\V VT\FAPDNVTTEV*SVEMHHEA LSEALPGDN/VGAFNVKNVSVK DVRRGNVAGDSKNDPPMEAA GFTAQVIILNHPGQISAGYAP\V LDCHT\AHIACKF\AELKKKI\DR RF\GKKLED\GPK\FWKSGDAAI VDMVP\GKP\MCVESFSDYPPL GPFAVHDMRQT\VAGGAHQKQ VDKK\AAGA\GKVTK\SAQKAQ
11308	41676	A	11376	1	880	
11309	41677	A	11377	1304	2340	KETEAQRKRLRRNEPEEQEIRT RKTRSPQTPDQQTYKKGRNER LCGISQPTKEPTRGGFCRFRNPP SNRIFACWGKPAWTACCNSLR ARRMLMERNARAAGSRKRMG RMDCWARVLDI\NLAAEAKSEP EKKAGVKRICKRRCTGSSFDL\ DY*LFNGDYYDRMYSYP\ARVP PPPPIARAVVP\SKRQRVSGNTS RRGKSGFNSKSGQRGSSKSGKL KGDD\LQAIKE\ELT\QIKRKSGF LFLGKTWEKIEKEQSKQAVEM KK**SQKEEQSSQLR*KKDET*C *RLEVLKGGA\EDSA\EEGDLLD DDDNEDRGDDQLELIKDDEKE\ AEEEEDDRD\SANGR\DDSLST

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11310	41678	A	11378	80	1141	ETQNRISSPSPSCEIFLIFSYIFRL CEKPYHQTRSASNVTNKTDPRS MNS\RVFIGNLNTLVVKKSDVE AIFSKYGKI\VGCSVHKGFALSF SMLMKRNARAAVAG\EDGRMI AGQVLDINLAAEPKVNRGKAG VKRSAAEMYG/SQ*QNTLLRPL YFSSSFDLDYDFQRDYYDRMY SYPARVPPPPPIARAVVPSKRQR VSGNTSRRGK\SGFNSKEWNSG VSSKFWKR*KGDDLQ\AIKEEL T\QIKQKVDSL\LENLEKIEKEQS KQAVEMKNDKSEEE\QSSSS\LK KDET\NLKMESEGGCRLTLPEE GDP\LD**YDE**RSGGNDPAGS *SKDDEK\EAEE\GEDDRD\SAN G\EDDS
11311	41679	A	11379	1	1134	
11312	41680	A	11380	1	642	
11313	41681	A	11381	397	898	
11314	41682	A	11382	1	663	
11315	41683	A	11383	44	398	ATMLGLNIISRKWFYKSSEKSL GLRGGLGRPLAFTLYSLLQAAL LCVNAIAVLHE/ERRISSKNICA GGTRTIGIGWIWEKEPGIKSQL MNLIRSVRTEMRVPLIIVNSIAI VLLLLFG
11316	41684	A	11384	3	754	GLYYRKCQLISKEDVTHDTRLF CLMLPPSTHLQVPI/GEHVYLKL PITGTEIVKPYTPVSGSLLSEFKE PVLPNNKYIYFLIKIYPTGLFTPE LDRLQIGDFVSVSSPEGNFKISK FQELEDLFLLAAGTGFTPMVKI LNYALTDIPSLRKVKLMFFNKT EDDIIWRSQLEKLAFKDKRLDV EFVLSAPISEWNGKQGHISPALL SEFWKRNLDKSKVLVCICGPVP FTEQGVRLLHDLNFSKNEIHSFT
11317	41685	A	11385	1	1785	
11318	41686	A	11386	95	369	
11319	41687	A	11387	511	728	
11320	41688	A	11388	1	100	
11321	41689	A	11389	1	777	

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11322	41690	A	11390	2	707	PNPKCR*VFPVFLFYRPI*PFPSS PA/SLIARPS*VPILPQPPLL/TPY NPPTTSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVNAHVP FSLSDLSQISQHLGSFSSDPTKYI QEFRYLTLSYNLTWSDLNVILT STLSPDERERVFPVSQSH/V**P/ SGFMSQTSRKALEQFPERIPQW NYQANSPGKNFKN*NLALKPH NRN*STLPSTCTIIERKQPDGNA FLSYNYLPP
11323	41691	A	11391	2	339	LLLFRSLPAKLNQAPILPWPL/PP PPYNPSITSPVHTWFSLQFHSET SPPPPAQQFPLRAVAGTEGIVR MNGKEFFLQPNLTLITAGFKSQ TSRKALEQFPERIPNGTIRQIPQ
11324	41692	A	11392	1	993	
11325	41693	A	11393	3	1127	TKETRFIHGPKTPAPVTDWEGS LPLVFNHCRDASLIIHSRFKGVR PHRDTCLGPSPLAASPAFLGKG QAAHCQAELSPNSSSASTPPPY NPSITSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVRVHVP FSLSDLSQISQCLGSFSSDPTKY TQEFQCLTLSYNLTWSDLNVIL TSTLSPDEWERVSSLAQSHADN \PGFTSQTSRKALEQFPE/TDPQ WNHQANSPGIARRDYMVSCLV EGLKKAAYKAVNYDKLKETTQ GEDENPAQVVARLAATLRRFT ALDPEGPEGRLILNMHFITQSAP DITKKLQKLESGPQTPQQELINL TFKVHNNGEETDAARSPWKPP GPSRTPSFRACFPCPHNFCGY
11326	41694	A	11394	1	312	
11327	41695	A	11395	1	244	MFADR*LFSTTHQS\IVPLYL\LF GA*AGVLATA\LSLLIRAELGQP GNLLGNDHIYNVIVTAHAFVIIF FIVIPIIIGGFGN*LVPLIIGAPDM AFPRINNISF*LLPPSLLLLLAS\A IVE\AGAGTRLNKSYPP\LAGNY SHPWKPPVDLTIFSLHLAGVSSI LGAINFITTIINIKPPAITQYQTPL FV*STTHQSHRTTIPIYSAHELA SSPQPLSLLIRAELGQPGNLLGN DHIYNVIVTAHAFVIIFFIVIPIIIG GFGN
11328	41696	A	11396	1	1287	
11329	41697	A	11397	3	583	

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11330	41698	A	11398	3	419	ILSISKLRTSLAGEGSVDTPKAS GVTRHIKGPGVAAEMSAFILPL PG*VSPGWEWAASAVLNGLRT TLALRRGVCLIRSRPGTLGLED GASPRTESLHTGTACKGAVDGS SEVDEKLKRIALDFLGLHGGDD PRSSWH
11331	41699	B	11399	1	1242	
11332	41700	C	11400	504	755	
11333	41701	A	11401	155	710	ETETTGEREGSLSNHPSNPTAA GLSLDTMKSHCPNHSSLLSTAA SPPKLWRCFKEEH\ELAVLGAP PKPLLPPTSHRDPTSASVYLRAP THVVWSLFKHPLS*TPCCMGF\I AFA\YSVKSRDRKIGCERDPGPI AYASTAK\CLN\IWALILGLLHD HSGSSSSPVLIVPGLWDRSGGIT GGQELCP
11334	41702	A	11402	1	1158	
11335	41703	A	11403	80	996	LKGKFLSMSG\ALDVLQMKEE DVLKFLAA\GTH\LGGTNLD\FH MEQYIYKRKSDGIYIIYLMRTW EKLL\LAARAIVAIENPADVSAI SSRNTGQRAVLKFAAATGATPI AGRFTPGTFTNHIQAAFRE\PR\L LVVTDPRADHQPLTEASYVNLP TIALCNTDSPLRYVDIAIPCNNK GAHSVGLMWWMLAREVLRM RGTISREHPWEVMPDLYFYRDP EEIEKEEQAAAEKAVTKEEFQG EWTAPAPEFTATQPEVADWSE GVQVPSVPIQQFPTEDWSAQPA TEDWSAAPTAQATEWVGATTD WS
11336	41704	A	11404	1	819	
11337	41705	A	11405	1	1032	
11338	41706	B	11406	63	344	
11339	41707	A	11407	49	281	FFKSTVCSFQKQFQTLPVPIGGS IMY*DISDHRGQR**NVGPCGH
11340	41708	A	11408	985	1213	TQCVTINY*GMKWGSFGYIVFH KDGCALIDKRFHTFCVSFKGSQ IQSSAAFLIPDVQVHQRLQKDF QGLMVPIVGS
11341	41709	A	11409	1	774	
11342	41710	A	11410	3	249	
11343	41711	A	11411	3	619	
11344	41712	A	11412	3	493	

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11345	41713	A	11413	3	292	DALPRWPSGSGDGGAVREAGQ QGTRLERPAAVLIRAADPGRRT QALA/GLPRG*PHPRMDPPESFQ ATGGTQQMTSTAPSWLTM*LR SVSGW*ELKD
11346	41714	B	11414	190	315	
11347	41715	A	11415	227	545	
11348	41716	A	11416	1	1896	
11349	41717	B	11417	52	1822	
11350	41718	A	11418	1	458	
11351	41719	C	11419	196	327	
11352	41720	A	11420	258	375	TRALSKFGSSRVEQS*AGYSGP GTP*EGGSGILGETVC
11353	41721	A	11421	3	854	
11354	41722	A	11422	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDKEKACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
11355	41723	A	11423	1	642	
11356	41724	A	11424	260	534	
11357	41725	A	11425	1	438	
11358	41726	C	11426	391	750	
11359	41727	A	11427	786	926	AQGQRQETIQGGRSLSRTLYL* GRSGTSLSQKLAQLSSLTGDST
11360	41728	A	11428	488	649	VLQLLKVAHPELFIPPGGFVFSL TSGVKLHT*ALQLLKVAHPELL IPPGSWSH
11361	41729	A	11429	1	2028	
11362	41730	A	11430	1022	1417	SLMGTSTSSALGMHVPRAITRD VLSAPVIVSGNTAKFCTMLGHF LKKTRTERRDIQAP*SFISLPPKS TWEKLSSAAMVSTLR*GASDQ K/C*LLGGNDRVSLIVIQVEG\PL QDPGTLGRLLQSLTVKRISV
11363	41731	A	11431	1	535	
11364	41732	A	11432	3	1186	
11365	41733	A	11433	201	458	QVDGCIPELKV*F*KKRGRRGR RGRRRRRRGRRREEGGGGGGG SFWRTHHTKPKDQHKKDTMG HFRSCAFQEGFVVHVPLLSSEK
11366	41734	A	11434	1392	1532	AQGQRQETIQGGRSLSRTLYL* GRSGTSLSQKLAQLSSLTGDST
11367	41735	A	11435	1253	2820	
11368	41736	A	11436	1504	1718	VIGIWALALGILARPQRGFHVV HLQDVGGAAA*AAKGLLRNVV R**VDQVQVSGAQGIAGVVVT VGGEEDF
11369	41737	B	11437	1	1383	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11370	41738	A	11438	3	310	VHGRASSLGVG/TPIPKGHGQIK P/DRLKPPVYGACKLLDMELEM AFFVGPGNRLGEP/IPISKAHEPI FGMVLMNAWSARHIQKWEYV PLGPFLGKSFGTPVKSS
11371	41739	A	11439	1	1337	MSFIPVAEDSDFPIHNLPYGVFS TRGDPRPRIGVAIGDQILDLSIIK HLFTGPVLSKHQDVFNQPTLNS FMGLGQAAWKEARVFLQNLLS VSQARLRDDTELRKCAFISQAS ATMHLPATIGDYTDFYSSRQHA TNVGIMFRDKENALMPNWLHL PVGYHGRASSVVVSGTPIRRPM GQMKPDDSKPPVYGACKLLDM ELEMAFFVGPGNRLGEPIPISKA HEHIFGMVLMNDWSARDIQKW EYVPLGPFLGEEFWGHCLLPW VVPMDALMPFAVPNPKQGPRG PCRYLCHDEPYTFDINLSVN\LK G\EGMSQAAT\ICKVQILKYMY WT\MLQQAHSPTLSNGC\NL\RP GDLLGFLGPI\SGPGAQKNFGS\ MLELSWKGTKP\ID\LGNGQT\R KFLLD\GDEVIITAMATRDFKW YS\QGDGY\RIGFGQ\CAGKVLP ALLPIMRFFLLF
11372	41740	B	11440	100	383	
11373	41741	A	11441	1	263	MEYYAAIKKDEFMSFVRIWMK LETIILSKLSQGQKTKHRRFSLI DG/IHHRSFTRTENSSQRTGRKC WN**PTCGLARSWFGKTWSGN
11374	41742	A	11442	2	160	
11375	41743	A	11443	150	308	CLHR*GRGSPRPGPGGGSTGGA GPGAGPSLAPPLPAQNAEGLGG RRRGNKYL
11376	41744	A	11444	1	372	
11377	41745	A	11445	49	177	SQQGLYAKPTSSQAL*GDGQAS AEMGRILSYE*EHAVFGFSSL
11378	41746	B	11446	1	420	
11379	41747	C	11447	1	334	
11380	41748	C	11448	1	268	
11381	41749	C	11449	1	564	
11382	41750	A	11450	1	264	
11383	41751	A	11451	33	194	
11384	41752	C	11452	1	309	
11385	41753	A	11453	1	738	
11386	41754	A	11454	1	2028	

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11387	41755	A	11455	3	1008	LKDAVFSIRISPESQKLFAFQWE DPESGVTTQYTWTQLTQGFENS PTIFGEALARDLQKFPAKDLGCI LLLYMDDLLLGHSTAVRCAKG MDALLQHLEDCGYKVSKKKA QICRQQVTKWGDWERFEWEPL QQQAFCKLKEKFMSAPALGLP DLTKPFTLYVSEREKTAVGVLI QTVGPWPTPVAYLSKQLDGVS KGWPPCLRALAATALLAQEAD KLTLVQNLNIKAPHAVGTSAQ KPELIALTRALELSEGTWMKLE TIILSKLSQGQK/DQTLHVLTGIS RST*ACSCLASLQVGLETGSQL SLENPLRVGIQRRRCFTCAVDG EGFLLGVPMA
11388	41756	A	11456	677	879	KRRNHQILEIRSHLQSVEDNLK SGLGSTASL*MSWTQPRNGAE VGFLLILGYIKETPRNAETPSMV
11389	41757	A	11457	1	624	
11390	41758	A	11458	3	130	VEEEQGHSFRNAR*IISW*RNEN GLDRMDCSCRNGERDKGHG
11391	41759	A	11459	1	1477	MADPPWSSVQVNKYDSGLLSS VSAEPLASSASSHPGMSDNAPA SLESGSSSTPTNCSTSSAIPQPGA ATKPWRSKSLSVKHSATVSML SVKPPGPEAPRPTPEAMKPAPN NQKSMLEKLKLFNSKGGSKAG EGPGSRDTSCERLETLPSFEESE ELEAASRMLTTVGPASSSPKIAL KGIAQRTFSRALTNKKSSLKGN EKEKEKQQREKDKEKSKDLAK RASVTERLDLKEEPKEDPSGAA VPEMPKKSSKIASFIPKGGKLNS AKKEPMAPSHSGIPKPGMKSMP GKSPSAPAPSKEGERSRSGKLSS GLPQQKPQLDGRHSSSSSSLASS EGKGPGGTTLNHSISSQTVSGS VGTTQTTGSNTVSVQLPQPQQQ YNHPNTATVAPF*EGFHLP*HA *VITF*TANYASSDNDLNVGYT H*LTASEFFQSRLSSLGEVAGLH AHTC*A*LGSNIPFSVRLRPVPA ASAEDLRGHQGLIKDRAQVS
11392	41760	A	11460	1	327	LLLMGLKHNVLKLPRGPMVTL RESVWETLNFLK*SFV*LNMLIF KKSS*RLQ*VRFHFLCPRVLIVQ LPFMSENMRCLVFCSCVSLLRM MVSSFIHVPFFKVLSFFALG
11393	41761	B	11461	119	203	
11394	41762	B	11462	1	677	

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11395	41763	A	11463	2	74	
11396	41764	A	11464	1	1256	MSASQDSRSRDNGPDGMEPEC VIESNWNEIVDSFDDMNLSESL LRDIYAYGFEKPSAIQQQAILPC IRGYNVIAQARSGTGKMATFAI SILQQIELDLKATQALVLAPTRE LAQQIQKVVMALVDYMGASC HACVRGTNMRAEVQKLQMEA PHIIVGTPSRVFDMLYR\RYLAP\ KSIRMLVLNEADEMLSRGFKG QIY\DISKRLNSTTK\VVLLSAT MPFD\VLEVTKKFMRGPH/IRIL VKKEELPLEGIRHFYINVEPEE\F NLDTLC\DWYEP*PIT\QAVIFHQ PPGGKVDW/LSPEKMHARDST VPPMHGDMTKKE\RD\VIMREF RSGS*PEF*ITPLTLPGQRPLMC QPGFL*SFKLMTLPPPTRGKLLI HRNRSRVDRFGRKGVA\INMVT EED\KRTL\RDIETFY\NTSIEEMP
11397	41765	A	11465	1	402	KSRGRGLPYTMDAFMLGMGM LKYPNFVAT*ARGYPGFAPSYG YQFPGFPAAAYGPVAAAAVAA ARGSGSNPARPGGFPGANSPGP VADLYGPASQDSGVGNYISAAS PQPGSGFR/HTGIAGPLIATAFT NGYH
11398	41766	A	11466	226	486	
11399	41767	A	11467	2	432	
11400	41768	A	11468	1	834	
11401	41769	A	11469	205	570	
11402	41770	B	11470	61	939	
11403	41771	A	11471	96	269	
11404	41772	A	11472	123	593	VAVLEARLLSPVRASKMTKKR RNNGRAKKGRG\HVQPIRCTNC ARCVPKDKA\IKKFVIRNIVEAA A\VRDISEASVF\DAYVLPKL\YV KLHYCVSCAIHSNVVMESISVK ARKD\RTPPPRFRPGGCWPHVP PPKPNVRELEFFKDLKDRLISS WEEK
11405	41773	A	11473	1	228	
11406	41774	C	11474	187	423	
11407	41775	A	11475	1	546	
11408	41776	A	11476	1	1254	
11409	41777	A	11477	1	1386	

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11410	41778	A	11478	1	1445	HLKAKMGKEKTHINIVVIGHVD SGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVL DKLKAERERGITIDISLWKFETS KYYVTIIDAPGHRDFIKNMITGT SQADCAVLIVAAGVGEFEAGIS KNGQTREHALLAYTLGVKQLI VGVNKMDSTEPPYSQKRYEEIV KEVSTYIKKIGYNPDTVAFVPIS GWNGDNMLEPSANMPWFKGW KVTRKDGNASGTTLLEALDCIL PPTRPTDKPL\ALPLQGVH\KLG GIGTVSSAPMET\GFSNPGMVV TFAPSPR*QRKVKSVE\MH\HEA L\NEALSGEQCGLSMSKKVSVK ECFVRGN\VAG*PAKNDPTQWE ASWLSLLQVIILEPSQAQISAGL CPLYWDC\HTGSHLHAKFAELK EKIDRR\SGKKV\EDGPKIL/RSL GDAAIVDMV\PG\RPMCVESFS DYPPLGRFAVRDMRQTVAVGV IKAVDKKAAGAGKV\TKSAQK
11411	41779	A	11479	1	996	

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11412	41780	A	11480	1	1875	MPSDLAKKKAAKKKEAAKAR QRPRKGHEENGDVVTEPQVAE KNEANGRETTEVDLLTKELEDF EMKKAAARAVTGVLASHPNST DVHIINLSLTFHGQELLSDTKLE LNSGRRYGLIGLNGIGKSMLLS AIGKREVPIPEHIDIYHLTREMP PSDKTPLHCVMEVDTERAMLE KEAERLAHEDAECEKLMELYE RLEELDADKAEMRASRILHGLG FTPAMQRKKLKDFSGGWRMR VALARALFIRPFMLLLDEPTNH LDLDACVWLEEELKTFKRILVL VSHSQDFLNGVCTNIIHMHNKK LKYYTGNYDQYVKTRLELEEN QMKRFHWEQDQIAHMKNYIAR FGHGSAKLARQAQSKEKTLQK MMASGLTERVVSDKTLSFYFPP CGKIPPPVIMVQNVSFKYTKDG PCIYNNLEFGIDLDTRVALVGP NGAGKSTLLKLLTGELLPTDG MIRKHSHVKIGRYHQHLQEQL DLDLSPLEYMMKCYPEIKEKEE MRKIIGRYGLTGKQQVSPIRNL SDGQKCRVCLAWLAWQNPHM LFLDEPTNHLDIETIDALADAIN EFEGGMMLVSHDFRLIQQVAQ EIWVCEKQTITKWPG\DIL\AYK EHLKSKLVD\EEPQLTKELPTTC
11413	41781	A	11481	194	418	YGLASVSPTQISSSSCNPWMFE GGTLVGGDWIGSHDSEGVLTR SGCLISVWHFSCAVSPATL*RRC LLLLRLPP
11414	41782	A	11482	1	675	
11415	41783	A	11483	1	1125	
11416	41784	A	11484	1	711	
11417	41785	A	11485	673	796	
11418	41786	A	11486	3	570	RLQEFGTRNRHLPVNSPKLTNT KGKRRGTR\YMF\SRPFRKHGV VPLATYMRIYKKGDIVDIKGM GTVQKGMPHKCYHGKTGRVY N\VTQHA/VMGIVVYKQA*GQR FLPKRI*CCVIEHI\KHS\KSRDSF \LK\RVKENDQKKKEAKE\KGT W\VQL\NRQLAPPREAHFVRT\N G\KEPGACWNPIPYEFHGHNR
11419	41787	A	11487	1	2091	
11420	41788	A	11488	1	2208	
11421	41789	A	11489	430	1032	

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11422	41790	A	11490	3	1158	EDQIDRLDFIRNQMNLLTLDVK KKIKEVTEEVANKVSCAMTDEI CRLSVLVDEFCSEFHPNPDVLKI YKSELNKHIEDGMGRNLADRC TDEVNALVLQTQQEIIENLKPLL PAGIQDKLHTLIPCKKFDLSYNL NYHKLCSDFQEDIVFRFSLGWS SLVHRFLGPRNAQRVLLGLSEPI FQLPRSLASTPTAPTTPATPDNA SQEELMITLVTGLASVTSRT\SM GIIIVGGVIWKTIGWKLLSVSLT MYGALYLYERLSWTTHAKERA FKQQFVNYATEKLRMIVSSTSA NCSHQVKQQIATTFARLCQQV DITQKQLEEEIARLPKEIDQLEKI QNNSKLLRNKAVQLENELENF TKQFLPSSNEGSVTIEIALVTLIG GNRNL
11423	41791	A	11491	132	381	SKAESVFPPTLPRQRPAAAAGP HWGAG*GQDEAGLHPGPEDRG FLRETPADPGLQAGLGQVHPPR SRADPPAPYQVPPRMGT
11424	41792	B	11492	129	470	

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11425	41793	A	11493	1	1955	FVSCQAPWSHPPAQLSPVGADA MTLTLSVLICLGLSVGPRTCVQ AGTLPKPTLWAEPASVIARGKP VTLWCQGPLETEEYRLDKEGLP WARKRQNPLEPGAKAKFHIPST VYDSAGRYRCYYETPAGWSEP SDPLELVATGFYAEPTLLALPSP VVASGGNVTLQCDTLDGLLTF VLVEEEQKLPRTLYSQKLPKGP SQALFPVGPVTPSCRWRFRCYY YYRKNPQVWSNPSDLLEILVPG VSRKPSLLIPQGSVVARGGSLTL QCRSDVGYDIFVLYKEGEHDL VQGSGQQPQAGLSQANFTLGP VSRSHGGQYRCYGAHNLSPRW SAPSDPLDILIAGLIPDIPALSVQ PGPKVASGENVTLLCQSWHQID TFFLTKEGAAHPPLCLKSKYQS YRHQAEFSMSPVTSAQGGTYR CYSAIRSYPYLLSSPSYPQELVV SGPSGDPSLSPTGSTPTPGPEDQ PLTPTGLDPQSGLGRHLGVVTG VSVAFVLLLFLLLFLLLRHRHQ SKHRTSAHFYRPAGAAGPEPKD QGLQKRASPVADIQEEILNAAV KDTQPKDGVEMDARAAASEAP \QDVTYAQLHSLTLRREATEPPP S\QEREPPAEPSIYAPLAIHLAHG GPRSHTQQKETQRLQKARELPP VDTNEPQPAWDP

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11426	41794	A	11494	22	1991	GLIPLQSAGSPEGDAMTPALTA LLCLGLSLGPRTRVQAGPFPKP TLWAEPGSVISWGSPVTIWCQG SLEAQEYQLDKEGSPEPLDRNN PLEPKNKARFSIPSMTQHHAGR YRCHYYSSAGWSEPSDPLELV MTGAYSKPTLSALPSPVVASGG NMTLRCGSQKRYHHFVLMKEG EHQLPRTLDSQQLHSGGFQALF PVGPVNPSHRWRFTCYYYYMN TPRVWSHPSDPLEILPSGVSRKP SLLTLQGPVLAPGQSLTLQCGS DVGYDRFVLYKEGERDFLQRP GQQPQAGLSQANFTLGPVSPSN GGQYRCYGAHNLSSEWSAPSD PLNILMAGQIYDTVSLSAQPGP TVASGENVTLLCQSWWQFDTF LLTKEGAAHPPLRLRSMYGAH KYQAEFPMSPVTSAHAGTYRC YGSRSSNPYLLSHPSEPLELVVS GHSGGSSLPPTGPPSTPGLGRYL EVLIGVSVAFVLLLFLLLFLLLR RQRHSKHRTSGLRLCPSSPRPE K\ADFQRPAGAAETEPKDRGLL RRSSPAADVQEENLYAAVKDT QSEDGVEIYTRQSPHDEDPQAV TYAEVKHSRPRREMASPPSPLS GEFLDTKDRQAEEDRQMDTEA AASEAPQDVTYAQLHSLTLRRE ATEPPPSQEGPSPAVPSIYATLAI
11427	41795	A	11495	1	1818	
11428	41796	A	11496	3	574	IRCSSVDPRVRPRVRGASGAAA YCCRHVSIPRDHTTHNQSRKW HRNGIKKPRSQRYESLKGVDPK FLRNMRFAKKHNTKGLKKMQ ANN\AKAMSARAEAIKALVKP KEVKPKIPKGGQPINLIRLAYIA HP\KLGKRARARI\AKGLKLCRP K\AKAKAKAKAKDQTKAQAA APASVPAQAPKRTQAPTKASE
11429	41797	B	11497	45	331	
11430	41798	A	11498	1	1779	
11431	41799	A	11499	1	837	

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11432	41800	A	11500	3	557	ERGYSFTTTAERDIVRDIKEKLC YVA\LDFEQEMATAASSSSLEES YE\LPDGQVITIGNE\RFRCPEAL FQPSFLGMESCGIHETTF\NSIM K\CDVDIRKDLYANTVLSGGTT M\YPGFADRMQKEITALAPSTM KIKIIAPPERKYSVWIGGSIL\AS LSTF\QQMWISKQEYD\ESGPSI\ VHRKCF
11433	41801	A	11501	1	1188	
11434	41802	A	11502	1	684	
11435	41803	A	11503	1	1398	
11436	41804	A	11504	22	1239	
11437	41805	A	11505	837	971	
11438	41806	C	11506	1	3018	
11439	41807	A	11507	23	368	
11440	41808	A	11508	1	816	
11441	41809	A	11509	1	441	
11442	41810	A	11510	195	293	IKVSPSGRDPVRDN*ITW*FLPY CSSTTGSLH
11443	41811	A	11511	56	372	MELPASPALFARTPQPLGGRW DWAPWSRGWRSSRRLGPHRSP RRGSEAQAWRAAGPEPCPAGR QLRPVNIEWLFALILTHTFGTFQ VLA*TSQALI*NPRVLYPD
11444	41812	B	11512	108	326	
11445	41813	A	11513	3	326	GSKKKFH*HSRILERSRSWRTS YQGRPQEPSWLHPVDPHRGCR WSCLPVPCRAPSTPQPLGGRWD WAPWSRGRRLSGRLGPHRSPR NRGRLRHGGLQVPSRASQEGS
11446	41814	A	11514	3	619	VRDIHGSPTHHRPGGLRGKNGF VGEARDPRYRSGHCFRECRTQ ALVAFT*C*SCGFTEVKN*GLSC LPAGQGSGPAARHV*ASHPLHG LPCGPSLP/NRAPPPTPRRPVPST TQGLRNASARRGTGRQLHLQP WCGIH*VKPAGLLSLLHGQAC GDPATPSRERLSQPAVPTALGS RRRLLLGPAGSPGSSLPPSRQPP GGRRRPP
11447	41815	B	11515	1	1524	
11448	41816	A	11516	1	1365	
11449	41817	B	11517	1	654	
11450	41818	B	11518	1	795	

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11451	41819	A	11519	486	929	QKQEESWPEDTYPRALAAFPR GRARDLQPAMPEPPTLSMGSC APEPPRGAPPPAPRRRIPSTTQG LRSSGAGRRTCRQLHLQPRCRI HWVKPAGLLSLWLFQMHSASC WWNYHSGAWRMVALFSWLH* ECPSGESGAPILHFPFALP
11452	41820	A	11520	35	473	VLQLLRRHVWSCSFPPGVVVSL ALAVKLQTFVTQEPSWLHPVD PAPGLQVELPASPLQCTRTSQPL GGRWDWAPWSRGRRSSGRLGP HRSPWRG*EAQAWRAAGPEP/ WPRGKA/C*GPARNRAKRRFPH CTF*EEVTVCSPQKRGGD
11453	41821	A	11521	23	229	RSWNPQTLFVGMYNATAAWK PI*QFLKKLNMKLP*DPGREPLN QTG*KGKRGGQEAFLEKGISSR MSQ
11454	41822	B	11522	152	901	
11455	41823	A	11523	1	3063	
11456	41824	A	11524	242	263	VLQLIKAVWTQRTQEPSWLHP VDPALGLQVELPASPAPCACTP QPLG\PLLPGLPLWRHLRSPSVH HCTVGAPFWAGQGRSPLPQRR CALFLAGP
11457	41825	A	11525	1584	2082	QRAGSPHSPRSLSVPPLPGLPLW RHLRSPSAHRCTMGAPFWAGQ GHSRLPQLAGRRGGRGASGNR CCVQRLQASWSSRWAWAWRA PHSEQPAGPAGPGQ*GTWHPG QRLQRMYWVLQQCRLTGAVL DFSPGLSCLPAGQGSGPAARHA *AFHPLHGLLCGRSLPD
11458	41826	A	11526	1293	1558	CIQHCHHCCCYRCRASAAGAA SLQGSTHVRIQH\CTP\CPVLLTP SVRLRDVCTRSIWPLVVTGLPS AMNVSSWCSTSSPAFGVLVLWI
11459	41827	B	11527	179	1031	
11460	41828	A	11529	1	342	
11461	41829	A	11530	1	3081	
11462	41830	A	11531	1	371	
11463	41831	A	11532	1	501	
11464	41832	A	11533	1	836	
11465	41833	A	11534	88	573	
11466	41834	A	11535	1	675	
11467	41835	A	11536	1239	1556	FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFFLRWSFAVVAQAV\ VQWHNLSSLPFGFKQFSCLSLP SSWDYRCPPPRPANFCIFTRDG VSPCCPGWSRTSDLR

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11468	41836	A	11537	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTLDPVEKALRDA KLDKSQIHDIVLVGGSTRIPKIQ KLLQDFYEAVAYGAAVQAAIL SGDKS\ENV\QDLLSL\DVT\PFP LGIETAGG\VMTVPH
11469	41837	A	11538	2	295	NRMGNHFIAEFKRKHKKDISEN KRAVRRLRTACERAKRTL/SSST QASIEIDSLYEGIDFYTSITRAPF EELNAWGISWWWSLPPPVGAS SGPTIEEVD
11470	41838	A	11539	1	1659	
11471	41839	A	11540	1	810	AGKPHCGGEFCTPNVHHFFR*F *ANPKRTII/ENKEALTPPPTV/C* RAKPTLSSAPRAVI/EIDSS*E/GI GLYTSITPPRFEELNADLFLAPL TPVEKALRNA\KLDKSQIHDIVL V\GGSTRIPKIQSFLQDFF\NGKE LNKSINPDEAVAYGAAVQAAIL SGDKSENVQDLLLLDVTPLSLG IETAGGVMTVLIKRNTTIPTKQT QTFTTYSD\NQPGVLIQVYEGER AMTKDNNLLGKFELTGMPGG MPGGFPGGGAPPSGGASSGPTI EEVD
11472	41840	B	11541	848	2399	
11473	41841	A	11542	1	876	
11474	41842	A	11543	16	1203	SIPHEPWPVSLLLFQEQVPGKK ELRKGLALLEAIISICGSLDKVL KEKRKLFIHSMGEGTINGLLDE LLQTRVLNQEEMEKVKRENAT VMDKTRALIDSVIPKGAQACQI CITYICEEDSYLAETLGLSADQT SGNYLNMQDSQGVLSSFPAPQ AVQDNPAMPTSSGSEGNVKLC SLEEAQRIW\EQKSAEIYPIMDK SS\RT\RVALIICNEEFDSIPRRTG AEVDITGMTMLLQNLGYSVDV KKNLTASDMTTELEAFAHRPE HKTSDSTFLVFMSHGIREGICG KKHSEQVPDILQLNAIFNMLNT KNCPSLKDKPKVIIIQACRGDSP GVVWFKDSVGVSGNLSLPTTE EFEDDAIKKAHIEKDFIAFCSST PDNVSWRHPTMGSVFIGRLIEH
11475	41843	A	11544	2	654	
11476	41844	A	11545	3	291	LIPPLLRPLVQSGGIPEMGKFMK PGKVVLVLAGRYSGRKAVIV\R YSVDIPLDKTVVNKDVFRDPAL KRKARREAKVKFEERYKTGKN KWFFQKLRF

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11477	41845	A	11546	157	386	
11478	41846	A	11547	2	531	FWQESASGHLWLSGFLSGPFSL LSAEMGKFMKPGKVVLVLAGR YSGRKAVIVKNIDDGTSDRPYS HALVAGIDRYPRKVTAAMGKK KIAKRSKIKSFVKVYNYNHLMP T\RYSVDIPL\DKTVVNKDGFTD P\ALKRNARMEA\KVKFEERYK TGKNKWFF\QKLRVLDAFVLII KNYKE
11479	41847	A	11548	1	414	LGGLKGTWGETKPAMAAAEEE DGGPEGPNRERGGAGATKTLL YTGNHLFSPQWLETRPERQECP VCKAGISREKVVGEKSLLTFSL HFLRLKTPQICRLPV*LFLPP*GF QPFGDTGGFHFSFGVGAFPFGF FNSPSY
11480	41848	A	11549	1	654	
11481	41849	A	11550	3	663	RGQEVVSGLLGRVYVYLGGLK GTWGETKPAMASAEEE\SGAPN VPNRERGGAGRPKTPFECNICL ETAREAVVSVCGHLYCWPCLH QWLETR\PERQECP\VCKAGISR EKVVP\LYGRGS/QRSPQDPRIK NSPRPPGGRGPAPE\SRGGSQP\F GDTGGFHF\SFGVGAFPFGFFTT VF\NAHEPFRRGTGVDLG\QGH PSLQLGKEFPLPGFSAIFFLFWL
11482	41850	A	11551	3	369	
11483	41851	A	11552	375	851	
11484	41852	A	11553	1	927	
11485	41853	A	11554	104	845	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11486	41854	A	11555	200	1496	ETIQAVVFMSLHFLYYCSEPTL DVKIAFCQGFDKQVDVSYIAKH YNMSKSKVDNQFYSVEVGDST FTVLKRYQNLKPIGSGAQGIVC AAYDAVLDRNVAIKKLSRPFQ NQTHAKRAYRELVLMKCVNH KNIISLLNVFTPQKTLEEFQDVY LVMELMDANLCQVIQMELDHE RMSYLLYQMLCGIKHLHSAGII HRDLKPSNIVVKSDCTLKILDF GLARTAGTSFMMTPYVVTRYY RAPEVILGMGYKENVDIWSVG CIMGEMVRHKILFPGRDYIDQW NKVIEQLGTPCPEFMKKLQPTV RNYVENRPKYAGLTFPKLFPDS LFPADSEHNKLKASQARDLLSK MLVIDPAKRISVDDALQHPYIN VWYDPAEVEAPPPQIYDKQLD EREHTIEEWKELIYKEVMDS\EE KT*KWC*LKGQPSP\SAQVQQ
11487	41855	B	11556	56	1564	
11488	41856	A	11557	1	970	
11489	41857	A	11558	1	903	
11490	41858	A	11559	237	479	PVGTNTECEIPFQPMETGHSSR VDASGYK*PCLLCSVYSRGKTA GECTLF*VHHFLSSLCPVNLGA NNQLHYIPWFSTDG
11491	41859	A	11560	1	477	
11492	41860	A	11561	125	1133	
11493	41861	A	11562	1	837	
11494	41862	A	11563	2	708	CQHYKFRYHQQGEGQEEPPLN PHGAARAEVYLRKCTFDMFNF LASQHRVLPEGATCDEEEDEVQ LRSTRRATSLELPMAMRFRHLK KTSKEAVGVYRSAIHGRGLFCK RNIDAGEMVIEYSGIVIRSVLTD MRKKFYDGKGIG\CYMFSMDD FDVVDATMHGNAARFINHSCE PNCFSGVIPGGGPENKIVIFGLR RILGGEEVNLRTKKFPIE\DAK\N KLPC\NCGAKRCRRFLN
11495	41863	A	11564	2	136	
11496	41864	A	11565	1	551	AILYAKRASVFVKLQKPNAAIR DCDRAIEINPDSAQPYKWRGKA H/RAQKIAEHRRKYERKREEREI KERIERVKKAREEHERAQREEE ARRQSGAQYGSFPGGFPGGMP GNFPGGIPGMGGGMPGMAGM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPANMSKYQSNPK VMNLISKLSAKK

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11497	41865	A	11566	1	804	
11498	41866	A	11567	64	1215	PPSFAHHLPTMDPRKVNELRAF VKMCKQDPSVLYTEEMRFLRE WVESIGGKVPPATQKAISEENT KEEKPDSKKVEEDLKADEPSSE ESDLEIDKEGVIEPDTDAPQEM GDENAEITEEMMDQANDKKVA AIEALNDGELQKAIDLFTDAIKL NPRLAILYAKRASVFVKLQKPN AAIRDCDRAIEINPDSAQPYKW RGKAHRL\LGHWEEAAHDLAL ACKLDYDEDASAMLKEVQPRA QKIAEHRRKYERKREEREIKERI ERVKKAREEHERAQRE\EEARR QSG\AQYGSF\PGGFLGG\MPGN FP\GG\MPGMGGG\MPGMG\GM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPA\NMSKYQSNP K\VMNLISKLSAKFGGQA
11499	41867	A	11568	1	265	VKAKIQDKEGIPPDQQRLIFAG KQLEDGRTLSDYNIQKESTLHL VLRLRGGIIEPSLRQLAQKYNC DKMICR/KKCGHTNNLRPKKK
11500	41868	A	11569	3	318	
11501	41869	A	11570	7	57	RFFNFLGGIP/P*SGPKGMTL/DQ TQGSKSKQIQWPALTFKPLVER NIPSSVTAVEFLVDKQLDFLTE DSAFQPYQVRNFRLLFKIKG*L NFIDIQTFFKQYSLNIISSNF*LC EKPNECSQLILLIG*TVY*FFNFL GGIPLNLGQKE
11502	41870	A	11571	1	2109	
11503	41871	A	11572	50	251	
11504	41872	A	11573	1	1922	
11505	41873	A	11574	2	479	
11506	41874	A	11575	1	909	LILTSVLLFQRHGYCTLGEAFN RLDFSSAIQDIRTFNYVVKLLQL IAKSQLTSLSGVAQKNYFNILD KIVQKVLDDHHNPRLIKDLLQD LSSTLCILIRGVGKSVLVGNINI WICRLETILAWQQQLQDLQMT KQVNNGLTLSDLPLHMLTNILY RFSDGWDIIT\LGQVTP\TLYML SEDRQLWKKLCQYHFAEKQFC RHLILSEKGHIEWEVGCNFATF RKHYPAKEQYGRQHCIFCRHCS ILFWKDSGHP\CTAADPDSCFTP \VSSQQFIALFQVLRAAPCHPY WRFVNPAVCAGLIVSVL
11507	41875	A	11576	1	1035	

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11508	41876	A	11577	63	606	FAKNERTQRGKRRG\TRYMFSR PF\RK\HGVVPLGPHICRI\YRKG DIVDTQGNGVLFKKGMPHKCY PWPKLEGVLQLLPQHA\VAIVV NQPVLGQSFFPRE*IVRIEHI\KH SKSPR*ASLK/RVLKENDSEKER SPNEKGTWGSNLKRHLAPPQK KHTL*RTNGKEPEL\LEPIPYEFH GHNRC
11509	41877	A	11578	1	490	
11510	41878	A	11579	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLRA L*G*DLTHHIIILFPFFFL**PAPP REAHFVRTNGKEPELL
11511	41879	A	11580	336	476	GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV LCG
11512	41880	A	11581	1	626	WAFRPEPPSSSKFAQNDGPQRG KRRGT\RYMF\SRPF*ENHGVVP LAHIFMR\IYK\KGDIVRHPRGM GYCSKKGMPPTSCYPWQKLGR V\YNVTPAMLFGIVCKQTKLKG NDSLPRG/ILMWRI*AHLRHF*G ARD/RASLKTCGRENGSRKKER KPKGGKVTWGFQLKRRHLGFP PQEEATFLLKEPIGGREP*ACLE PYFPYWISWGINRC
11513	41881	A	11582	499	723	
11514	41882	A	11583	96	411	PAPTSRCRRRRAPLPKKKAEGD AKGNKAKVKDEPQRRSARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK
11515	41883	A	11584	3	493	
11516	41884	A	11585	588	759	GEGCGWAEVGRCRPGPPDPAG PAGAAGP\GAARGGLFRGVLSP SSRCGGGSSSSRSGR
11517	41885	A	11586	213	626	
11518	41886	A	11587	1	645	
11519	41887	A	11588	1	739	
11520	41888	A	11589	327	676	NPNPSWNLAHVWDMDRK*EQ RGIQ/V**SNINKS*KEKMSMQC LEMPRNPDH*GRIDVSFQNLMR LTR*SQMGYLPWDLKQELETFS KLS*KQVMLSVVVTFVRNMLQ LRFLTSFSG
11521	41889	A	11590	11	328	

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11522	41890	A	11591	1	378	LFIVTVCPAFLRFSSAICDSFLIC PQVGGCVRRVLLVTVGVLLSIS LDMAATGVSLGSSWSLFLGIW LMIRFQVS*WYPNWLLILSWRN ISITSTPSYYFTYFPTFCYQISPPN QLFCFCLCSWFL
11523	41891	A	11592	1	780	
11524	41892	A	11593	1	1461	MVTLMGHAALCLHYVMQLGT TGGAWYFPRASSQAREMPQCP TLESQEGENSEEKGDSSKEDPK ETVALAFVRENPGAQNGLQNA QQQGKKKRKKKRIIIISGKVLED FLALAMHFADEETGQKRCSLN QTIQLLITPDTGSIWHQAFLSSIV RRAAQQYGFREGGEDDDWTL YWTDYSVSLERVMEMKSYQKI NHFPGMSEICRKDLLARNMSR MLKMFPKDFRFFPRTWCLPADP AQLDLWSQTFWPRPRTAPDGT GADGLGLRLGSLGK/VSFWFPA CHGLG*PEASYTAS/MACGSLP/ WKLSTFSAYLEDHSYNVEQIW RDIEDVIIKTLISAHPIIRHNYHT CFPNHTLNSACFEILGFDILLDH KLKPWLLETEKMQTAGALFISP ALPSYSNFPLQVARREFQTSVV SRDIDTAAKFIGAGAATVGVAG SRAGIGTVFGSLIIGYARNPSLK QQLFSYAILGFALSEAMGLFCL MVAFLILFAM
11525	41893	A	11594	1	2301	
11526	41894	A	11595	3	381	
11527	41895	A	11596	1	729	
11528	41896	A	11597	1	1006	MVKVKARVNEFGYTGCLVTRA AFNSGKVDIVAINDPFIDLNYLA YMLQYDSTHGKFHGTIKAENG KLVINGNPITIFQE*DPTKIKWG DAGTEYVVESTSIFTAMEKVGA HLQRGAKRVMIFAPSTEAIMFM MKVNYEKYDNSLKIISNASCTT NCLAPLAKVIHDNSGIVERLMI TVHVITTTQKTVDGPCRKLRPD GHRALQNIIPASTSTAKAMVKV IPELNKKLTGMASHVPTAKVLV VDPTCHL/EKPAKYYDIKKMM KQASEDPIKGILGYTEHQIVSSD FNSDTQSSTFDAGAGITLNDHF VKLISWYDNEFGYSNRVVDLM AHMASKE
11529	41897	A	11598	3	508	
11530	41898	B	11599	1	5068	

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11531	41899	A	11600	58	659	PVATTCECIFIHLGEADVWIGN AA/WELYYLEQSIQHDSPMPSD KTTG*GDN*FYASS\GAGKFVS RAVFINLEPIVTDEVCTGTYHQ LFHPEQLITDKEDAAHNYAWG HHDIGKIIGCYSTNKTKCTIQFV DWCFTSLKVGINCQLPTVVPAG NLANIKRAACMLSNTIAIAEAW VCLGHKSDLSYANCSFVHQFFN KSIH
11532	41900	A	11601	511	1173	
11533	41901	A	11602	3	497	WCDGPQNRYALICQQC/YSHNG MALKEEFEYIAFRCAYCFFLNP ARKTRPQAPRLPEFSFEKRQVV EGSSSVGPLPSGSVLSSDNQFNE ESLEHDVLDDNTEQTDDKIPAT EQTNQVIEKASDSEEPEEKQET ENEEASVIETNSTVPGADSIPDP ELSGESLTAE
11534	41902	A	11603	2	764	
11535	41903	A	11604	1	444	
11536	41904	B	11605	44	1748	
11537	41905	B	11606	1	1134	
11538	41906	A	11607	1	549	
11539	41907	A	11608	212	548	
11540	41908	A	11609	1	905	ESVAAAARAFPFTAPKELERQQ RRRFRFHHLFLFPSLRTPCRVSV SLQPWLWKATEVMAMFEQMR ANVGKLLKGIDRYNPENLATLE R\YVETQ\AKENAYDLEPNLAV LKLYQFNPAFFQTTVTAQILLK ALTNLPHTDFTLCKCMIDQATI QERNGPIPDQIFVPSGTLLEDPA HFPGPFWQTPGNGRACQKAWD ENHWTLFGKVLT\GF*RLLVRK FIC\HVVGYHLPSHIDR\WLLAE MLGDL\SDKPAKRCWMSKIRLR EDDRRGQIF\ICS\QE*EHLNPRN\ IVEKIDFDSVSSIMASSQ
11541	41909	A	11610	186	209	QLWPN*LLSRNKEATLRYSQLP TCHSICY*MPAF*HTISDLSFNK NINCKSYHLRVFYKYV*IVCHF *VPKVYWTKYYQTSCRT*WR* SGVE*PPIISSSSSACCLLRRLPT EGTCPEIFWNPRLGISAECRDSC GPTSF
11542	41910	A	11611	2	2948	
11543	41911	B	11612	1	999	
11544	41912	A	11613	1	657	
11545	41913	A	11614	1	707	
11546	41914	A	11615	1	297	

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11547	41915	A	11616	1	1287	
11548	41916	A	11617	242	540	LTNEKKVQDQMDSQPNSTRGT RRSLYPFLLKLFQLIEKEGILPNS FYEASIILIPKPGRDTTTTKKEF* TNIPDEHRCKNPQ*NTSKPNPA AHPKAYPP
11549	41917	A	11618	193	916	
11550	41918	A	11619	1	2169	
11551	41919	A	11620	1	615	
11552	41920	A	11621	39	568	NSAWARRPLVLPLMSLVSPWK SSQHIF\RVLNPPNLDGRRKNSP LPITCHLRVWARRYAHVV\LRK AD\IDLTK\RAGEL\TEDEVERVI TILQ\NPRQYKIPD\WFLNRQKD VKDGKYSQVLANGLDNKLRED L\ERLKEDSAPIEGLRH\FWGLR\ VRGQHTQDQLGRRGRHRGASA GARR
11553	41921	A	11622	1	378	
11554	41922	A	11623	1	222	
11555	41923	A	11624	2	367	
11556	41924	A	11625	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
11557	41925	A	11626	1	633	
11558	41926	A	11627	164	714	IGVNRHLIQESPSWNLAGAPLE QIFQRKEQAAIFAILQPLLVISRQ TGSGVDPQQTPADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTIINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
11559	41927	A	11628	504	936	TESSSININKKDDHAKTP\PKDH NSSPAREQNKTENEFDELTEIGC RRWVITNSSELKEHVVTQCKEA KNLEKMLQELLTRITSLEKNIN DLMELKNTAQELREAYTIINSQ TDQAEERISEIEDQLNEIKGEDN IREKTVKRIE

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11560	41928	A	11629	1949	3232	PGKQDLEWTSSKLQQTCRRGT LLVEGKLTNRKE*HQHQQKLR PHGNLIQRDHNCSPARE\QNWM ENEFDKLTEVGFRRWTITNSSK LKERVLTQCKEATNLAKRLEK LLTRITSLEKNKNDLMELKNTA QELREAYTSISGRINQAEQRTSE IEDQLNEIKRRGVSVCPQPSEDT PRSTARVPKGMVPFRPRVPLVT PPREKKEAPWLACLRTRALRILI DPPSQVWDIVSCDAENETKLEN TLQDIIQENFPNLARQAN\VQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEK\MLRAAREK\GQVT HKAKPIRLTADLSAENLQAR/R TEWGPIFNILKEKNF\QPRISYPA K\LSFISEGEIKYFTDKQMLRDF\ VTTRPALK\ELLKEALN\MERD N\RYQP\LQNHAKFVKTIEAREE TCINLMCQITS
11561	41929	A	11630	1	421	
11562	41930	A	11631	2	415	
11563	41931	A	11632	59	492	GHIGVRPSLHPVTSTTSGNVSPT LARAMASISELACVYLALILHD DEVIIMEVNINTLIKAASVNVE/ PFWPGLFGKALANVNIGSLICN VGAGGPALAAGAAPAGGPAPSI AAASAEEKKMEAKKEESEESD DDMGFGLFTKPVL
11564	41932	A	11633	100	527	PPRTGQRQPLHSARRHGPSVS\E LACI\YSALISARTDEVTVT\EDK INALIKSSPL*MLSPFWPWLCLQ RPLA\NVNIGSL\ICNVRGPVEPA ASQPGA\GPARKVLAPST\AAAP S*RRRKLEAKKRKNPKEVLNDE HGLLVFLN
11565	41933	A	11634	1	675	
11566	41934	A	11635	1	1032	

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11567	41935	A	11636	3	976	HEAKHQMADDAGGS/AGGPEG PGGPWDGKTPLLSGEVFGIVIR GRGSRP/RGRGRGR\GRGARGG KGPRIK/WIGMPVHQVGAALVK DH*RSKFPWKEIYLFSLP\IKGIK DS*FSFLAGPLSKDEGFEGLCPV QKQTRAGQAQQVSRPFVAIGG LQMAHVGSGVLSAPKE\VATG HPVGAIILAKLSIRPRAQKGIWG TKYWQSPNTVP\CKV\TGRCGF VVVRLIP\APRGSGIVSAPVA\K KLLMMAGIDDCYT\SAPGCTAT LG\NFAKGHPLIAIFK\TYKLP*P PDLWK\ETVFTKV\PYQ\EFT\DH LVKDPHPESSVQRDLRLQLVAT
11568	41936	C	11637	279	322	
11569	41937	A	11638	1	107	
11570	41938	C	11639	69	134	
11571	41939	B	11640	223	950	
11572	41940	B	11641	1	684	
11573	41941	A	11642	1	564	EFGTRDNRVLLPLVNPTVFFDI AVD/GVYPLGRVSFELFADKVP KTAENFRALSTGEKGFG\YKGS\ CFHRLFP\GFM\CQGW*L*SHHN GT\GGKSHLWGRNLKDENFI\L KHTGPGILS\MANAG\PNTNGSP VFLTSCTA\KTE\WLDGKH\AGL GKVKEGMNIVEAMER\FGSRN GKTSKKIISIA\DCGTTSN
11574	41942	A	11643	1	877	MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHSVGLMW WMLAREVLRMRGTISRGHPWE VMPDLYFYRDPEEIEKEEQAAA EKAVTKEEFQGEWTAPAPEFTA TQPEVADLSEGVQVPSVPIQQF PTDDWSTQPATENWSAAPTAQ ATEWVGATTDWS
11575	41943	A	11644	1	1674	

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11576	41944	A	11645	1	1121	MLEAVLEESPREEAAFSWVMK GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQMKEEDVL KFLAA\GTH\LGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWEKLL \LAA\RAIVAIENPADVSVISSRN TGPEGLCLKF\AA\ATGATPIAG\ RFTPG\TFT\NQIQ\AAFREATGF LVVTWTPGLD\HQPLTEA\SYV YLPTIA\LCNTDS\PL\RYVDIAIP CNNKGAHSVGLMW\WML\ARE VLRMRG\TISREHPWE\VMPDL YFYRDPEEIEKEEQAAAEKAVT KEEFQGEWTAPAPEFTATQPEV ADWSEGVQVPSVPIQQFPTED WSAQPATEDWSAAPTAQATE WVGATTDWS
11577	41945	A	11648	1	396	
11578	41946	A	11649	1	567	
11579	41947	A	11650	1	226	
11580	41948	A	11651	3	377	
11581	41949	A	11652	19	450	PDRRWSSLDTMNHTGQTFFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHIRSETSVPD HVVWSLFNTLFMNPCCLGFIAF AYSVKSRDRKMVGDVTGAQA YASTAK\ALNIWALILGILMTIL LIVIPGLIFQAYG
11582	41950	A	11653	210	2206	
11583	41951	A	11654	450	644	SLRLWVTERTAVTNLPSSSRGV GDKPPVGSPHLFLSLVVAFNPL QSTRNPASASQPQ\PCSAEQPAR RG*AEPALRTVLPIHAEMWLPR LHEFEEHRLVHRCFTLTFVDET DHCAVLPRGAGSGQGGGFERIL SQSPGSLWESC*PGLWLNILSNP PPCPLPAPLGRTAQ
11584	41952	A	11655	66	157	RGTWSIIA*KSQGISWDRFEEVT LCREPFT
11585	41953	A	11656	1	2538	
11586	41954	B	11657	68	1602	
11587	41955	B	11658	1	1464	
11588	41956	A	11659	587	1081	ILSWLTLWSILRLYIVTLTGKIC SLTSEASEATSPPRGTNNSRSVA LAVVTLVWRVCSFIFDSKAFIL AFAFFFSHWFSILPFPPQHGATL WYFWGDFECSRGPRNIHTDDR ARLVPMTERGGPPQGGEPART RSPRQGGRGGMEGGE*YPCPPH LGGQERKPG

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11589	41957	A	11660	180	583	YTEVLKGPDGAENHGTRTT** MHKPH*PIRSTGRKADKQLQQS LR\NKINVQKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQL TMDVKDLFKENYKPLLKEIRG YKQMGEHSMLMGRKNQYSEN GHTAQ
11590	41958	A	11661	82	159	
11591	41959	A	11662	2	1008	NAAPLQQRNKAGCR/YDLDEL REEGFRRSNFFKLKAEVRTQCK ETKNLEKTLDKWLTRKTSVEK SLNDLMELKTMVQGLRDKCTN FSNGFDQLEERVSVIEEQMNEM KQEKKYREKKDRSMTQKVNK DIQELDSALHQEELIDIYRTVHP KSTEYTFFSAPHRTYFKIDHIVG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYENLWDTFKAVCR GKFRALNVHKRKQERSKIDTLI SQLKELERQELTHSKASRMQEI TKIRAEQKEKETEKNIQKNQRI QELFLLKDQQN
11592	41960	B	11663	1	1529	
11593	41961	B	11664	111	1350	
11594	41962	C	11665	1	2127	
11595	41963	B	11666	1	1350	
11596	41964	A	11667	1	1506	

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11597	41965	A	11668	1	1855	MIIIVPLYSSLGDRVKSCEKKRE RERERRKKERKKERKKERKKE RKKASSKEREEGRKKERRKKL RKKEEKERKKRKKKRREGRKE RKKEKERKEGKKEERKNIPGKR RESTDPLKEMDHRCLLPEMLK GTWWTTPARASGPAVPLLCEF RQWTVDTTSVVPESTHMPGQM TQPIPAPDSHNMDEAGGHYPK QTNTRPENQILHVFTDKWELNT EYKDPKKRTTDTRAYLRVEAT LAADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQTEGRSSFVLATL AADWMVPTQIEGRGRMTPHM AGYSSETKLPEERSGSSICGSPIS AVLQPPLLIPRQTGSGVDLQQT PTDLQLRVLMERSSSPATEQSW MENDFDEMRDEGFRRSNYSEL KEEVQTYCKEVCRGKFKALNA HKRKQETSKIDTLTSQLKELEK QEETHSKASRRQEITKIRAELKE IETQKTLQKINESRSWFFEKINK IHRPLARLIKKKTEKNQINAIKN DKWDITNNLTEIQATIREYYKH LYANKLENLEEMDKFLDTYTL PRL*N/CRQSLIAYQQIKVQDQ MDSQSNSTRGTRRSWYHSF
11598	41966	A	11669	2678	2897	PDGAKKHGKRT\RDERTSFSSEF NQLEERVSVIENQMNEMKREE KFREKRVKRNEQSLQEIWD\M* KDQMRSTS
11599	41967	A	11670	843	2004	NNQCREVLKGVDGAESQGSRT\ REERRSLRSRCDQLEERVSVIED QMNEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DGENGTKLENTLQDIIQENFPN LTRQANIQIQEIQRTPQRYSSRR ATPRHIVVRFTKVEMKEKMLR AAREKGRVTHKGKPIRLTADLS AGTLQARREWGPIFNILKEKNF PPRISYPAKLSFISEGEIKYFTDK QMLTIVHLKTLDIIYMYNIRRPK GGEKKADQEVNSEPRNNIVLET KGDRGPQAPASPGGPPPRRVRR SASGSRAGITFHPVHYLTRRPFA HRFHYQSHGYGVGSVQSAELR HKTNSAARAALRDGGVDCRGR ERGSACQKRSDDEAGGLVLSD LPRVMSGSWEVRR
11600	41968	B	11671	1	3221	

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11601	41969	A	11672	82	160	
11602	41970	A	11673	1	551	AAAMADSGTAGGAALAAPAP GPGSGGPGPRVYFQSPPGAAGE GPGGADDEGPVRRQGKVT\VS YDRKELRKRL\NL\EDWIL*QLN GAFYDCQ\EEEIPELEIDVDELL D\MESD\DARAA\RVKELLVDC YKPTEAFISGLLDKIRGMQKLS TPPEEVRVPDPGRTVAPTGQSL PPDLVATAITGGT
11603	41971	A	11674	362	650	
11604	41972	A	11675	1	651	
11605	41973	A	11676	1	3101	
11606	41974	B	11677	1	2838	
11607	41975	A	11678	1326	1980	TSEASRQSERVDSAALSALSLLS RSSKCRPWGTARVARAGGCLT PLLSRRFLETRPFTGPWDPGLG VTCWCCPPKRRLKSTPRPKFSV CVLGDQQHCDEAKAVDATFEV CLGDQVLSNANGFLSLSAKKY DAFLASESLIKQIPRILGPGLNK AGKFPSLLREEGQAICYSSTNLT *SSLPSSQVLCLAVAVGHVKMT DDELVYNIHLAVNFLVSLLK
11608	41976	A	11679	11	720	EAMSSKVSRDTLYEAVREVLH GTQRKRRKFL\ETVELQISLKNY DPQ\KDKRF\SGT\VRLKSHSPAL SFSVCVLGD\RQH\CD\EAKA\V DIPPHGPSEAAEKTSTKNKKLV QKSWPKKV*MPFLA\SESSDQA RFPRIPRAPGLNKAGK\FP\SLLT HNGKHGGPKVDEVKVPQSRFQ MKKVLCLAVAVGHVKMTD\DE LVFNIHLA\VNFL\VSLLK\KNW QKCSGALYYQEAPMGQSPKRL
11609	41977	A	11680	34	507	
11610	41978	A	11681	407	806	LRVGMLQRSKANGPDDDHLLG ASCTCGPSTGSPSPRLPSLPQRP QKGLLHQ/RATRMKPGNIAKGL WKRLSKGTVMKLWLLTAVPRL SGLLVCPLVHQLLLAFKFLKRF PIFCLWFRAANRHARFSILFKLS RP
11611	41979	A	11682	1	1551	

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11612	41980	A	11683	1	751	MAGYSSETKLPEERSDSSIRGSR KSTVLQTLLLIPRQTGIKKLTQN RSTTWKLNNLLLNDYWVHNE MKAEIKMFFETNENKDTTYQN LWD/YIQSSV*REIYSTKCPQEK AGKIQN\DTLTSQLKELEKQEQ THSKASRRQEITKIRAEPKEIQT QKTLQKINESRSLFFKRINKIDR PLARLIKKKREKNQIDAIKN\EK GISPPIPQNYKLPSENTTNTSMQ IN*KI*KKWINSWTHTPSQE*TR KKLNL
11613	41981	A	11684	49	551	VRATYFHHAPANCTEFVPRQL VSRAENLPQATSLPTEKASRAF RVLLIPRQTRSGVDLQQTPTDL QLRVLIVRRKTNKQKGHPHQN PICTSPLRRSNFFELKEEVRTHG KDAKNLEKRLDKWLTRISSVE KSLNDLMELRTMA*ELCDECTS FSS*FNQLEERVSVI
11614	41982	A	11685	1	1566	MNSLLTGQIPESQQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRSGS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRRKS NKQKGHPHQKPICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTCSKIDHIVGSKALL/EQM*KN RNYQKLSLRPQCNQ\LELRIKKL TQNHSTTWKLNNLLLNDYWM QKRPLKIQQCFMLKTLNKLGID GTYLKIIRAIYDKPTANIILNGQ KLEAFLLKTGTRQGCPLSPLLL NVVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLPKLISNFSKVSGYKIN VQKSQTFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRACIAKSILSQKNKAG GITLPEFRLYTRLQ
11615	41983	A	11686	1	4962	
11616	41984	B	11687	101	3772	
11617	41985	B	11688	1	1047	
11618	41986	A	11689	21	287	

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11619	41987	A	11690	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSAMEDEINEMKRE EKFREKRVKRNEQSLQEIWDYL KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSLRRATPRHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL
11620	41988	A	11691	1	1257	
11621	41989	A	11692	1	759	
11622	41990	B	11693	107	511	
11623	41991	A	11694	170	726	LLEGKLTNRKDIHTETPSVCHH HQRPKDIIQENFPNLARQANIQI QEIQRTPQRYSSRRATPRHIIVR FTK/VEMKEKMLRAAREKGRV THKVKPIRLTADLLAETLQARR EWGLIFNILKEKNFQPRISYPAK LSFISEGEIKYFTDKQMLRDFVT TRPALKELLKETLNVERNNRYQ PLQKHAKL
11624	41992	A	11695	1	569	MAGYSSETKLPEERSGSNICCSP ISAVLQPPLLIPRQTGSGVDLW QTPTDLQLRVLTVRRKINKQKG HPHQNPICTSPSSKTKGQIRAEL KEIETQKALQKINESRNWVFEK INKIDRPPARLIKKKREKNQIDA IKNDRGDITIDPTEIQTTIREYYK HLYANKLENLEERDKFLNTYTL PRLNQEEVESLNRPITGSEIEAII NSLPTKKSPGPDGFTDAFYQRY KEDLVPFLLKLFQSIEKDRILSN SFYEASIFLIPKLGRDTTKKEN* QTERTSTPKPHLYITIIEDQRPD QSRTEGNRDTKSPSKNQ*IQEL/ WFLKRSTKLI\ATSKTNKEEKRE ESNRCNKK**RGYHHRSHRNT NYHQRIL*TPLCK*TRKSGRKG* IPQHIHSPKTKPGRS
11625	41993	A	11696	3	1039	
11626	41994	C	11697	1	1251	
11627	41995	A	11698	1	807	

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11628	41996	A	11699	1	713	MNSLLTGQIPESQQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRSGS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRRKS NKQKGHPHQKPICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTCSKIDHIVGSKALL/KQM*K NRNYQKLSLRPQCNQTRTQD*E THSKPLNYMETEQPAPE
11629	41997	A	11700	1	1768	MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQQEELTILNIYAPNTEAPR FIKQVLSDLQRDLDSHIIIMGDF NTPISTLDRSMRQKVNKDIQEL KSALQQADLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHIVGSKAL LSKCKRMEIITNCLSDHSAIKLE LRIKKLTQNRSTTWKLNNVLLN DYWVHNKMKAEIKMFFETNG NKDTTYQNLWD/YIQRSV*REI YSTKCPQEKAGRI*N*HPNI\QL KELEKQEQTHSKVSRRQEITKIR AELKEIETQKTLQKINESRSWFF EKFNKIDRRLARLIKKKREKNQ IDAIKNDK\GISPLIPQKYKLPSE NTINTSTQIN*KI*KKWINSSTHT
11630	41998	A	11701	535	666	KGRNIQLNGLVIGTLSN*LKCL KMFFTMPLGYINGGISSDFFLH
11631	41999	A	11702	20	262	
11632	42000	B	11703	1	1254	
11633	42001	A	11704	1	1032	
11634	42002	A	11705	481	1491	
11635	42003	A	11706	2	717	

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11636	42004	A	11707	348	1976	SRVRPVVHLRRAPMVCQGHTT PPVCGSLAGPGDCVHYSVPAG YSSETKLPEERSGSNICCSPISAV LQPQLLIPRRTGSGVDLQQTPT DLQLRVLTVRRKTNKQKGHPH QKPICMSPSSKTKGSNSHITILTL NVNGLNAPIKRHRLANWIKSQ DPSVCCIQETHLTCRDTHRIKIK GWREIYQANGKQKKAGVAILV SDKTDFKPTKIKRDKEGHYMM VKGSIQQEELTTLNIYAPNTGAP RFIKQVLRDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDIQ DLNSALHQVDLIDIYRTLHPKS TEYTFFSALHHIYSKIDHIVGSK ALLSKYKTTEIITNCLSDHSAIK LELRIKKLTQNRSTTWKLNNLL LNDYWVHNKMKAEINTLFETN ENKDTTYQNLWD/YIQSSV*REI HSTKCPQEKAGKI*N*HPNI\QL KELEKQEQTHSKASRRQEITKIR AKLKEIETQKILQKINESRSWFF EKINKIDRPLARPIKKKREKNQI DAIKN\EKGISPLIPQKYKLPSEN TINTSMQIN*KI*KKWINSSTHT PSQD*TRKKLNL*INTSMQIN
11637	42005	A	11708	1124	1717	LLEGKLTNRKDIHTKNPSVRHH HQRPKVDKTTKMGRKQSRKTG NSKNQSASPPPKERSSSPATEQN WTENDFDELREEGFRRSNYSEL KEEVRTNAKEVKNFEKKLDEW ITRITNAEKSLKDLMELKTTAR ELRDECTSPSSQCNQLEERISAM EDKMNEMKREEKFREKRIKRK E\QSLQEIWDYVKRPNLCLIGVP
11638	42006	A	11709	1	3549	
11639	42007	B	11710	209	403	
11640	42008	A	11711	3	248	
11641	42009	A	11712	61	594	IQPLVSVLDEKPSNGVLVHMVK LLIKTFLDGIFDDLMENNVLNT DEIHLIGKCLKFVVSNAENLVD DITETAQTAGKIFREHLWNSKK QLSSVHGSEHEDKALTCHWVG HPGFPEKLKERKKFCGIMVVGL FGFTTDSGKAGADIHGRFLQGN FCNDAVTKAHVEKDF\IAFKSST

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11642	42010	A	11713	1	430	FSAVREDGGCYLWQIYPIKERM DRIRLVLIICNKEFDHLPPRNGA DFAIMEMKKLLEDLGYSVDVE ENLTAR/HNVSQGETGTKGLPIF ITQLIACFQRYSWRCHL\EEVFW KVQQAFESPEATVQMPTIERVS MTRYFYLFPGN
11643	42011	A	11714	3	1195	
11644	42012	A	11715	35	1288	
11645	42013	A	11716	1	1641	
11646	42014	A	11717	1	2933	MVCSAAPLLLLATTLPLLGSPV AQASQPLWPMAKGQTMWAQT STLTLTEEELGQSQAGGESGSG QLLDQENGAGESALVSVYVHL DFPDKTWPPELSRTLTLPAASA SSSPRPLLTGLRLTTECNVNHK GNFYCACLSGYQWNTSICLHYP PCQSLHNHQPCGCLVFSHPEPG YCQLLPPVPGILNLNSQLQMPG DTLSLTLHLSQEATNLSWFLRH PGSPSPILLQPGTQVSVTSSHGQ AALSVSNMSHHWAGE
11647	42015	A	11718	1	357	
11648	42016	A	11719	73	1494	KSSHCIKMGPQIFHKTSELFLPA TSCPSCPDQNEEDVSQTQYKEC CGGGWCSHSIFAVWHFI*RPDA T*FG*SSAYGFVASDQCP*GSS* LYHLWYSYSGSENKQCG*R\AA LGAGFSDKTPAHTVTMACISAN QAMTTGVGLIASGQCDVIVAG GVELMSDVPIRHSRKMRKLML DLNKAKSMGQRLSLISKFRFNF LAPELPAVSEFSTSETMGHSAD RLAAAFAVSRLEQDEYALRSHS LAKKAQDEGLLSDVVPFKVPG KDTVTKDNGIRPSSLEQMAKLK PAFIKPYGTVTAANSSF/LLTDG ASAMLIMAEEKALAMGYKPKA YL/RRDFMYVSQDPKD\HLLLG PTYATPKVLEKAGL\TMNDIDA FEFHEAFSG\QILANFKAMDSD WFAE\NYMG*KKPRFGLPPLWR RFNNWG\GSLSLGHPFGATGCR LVMT\AANRLREEGRASMA*V A\ACAAGGQGHA\MIV\EAYPK
11649	42017	A	11720	1	642	

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11650	42018	A	11721	17	960	KSGARSLQPQFLRAPEDGGPLS LPNAAMARGPKKHLI\RVAA\P KHWMLDKLTGGCA\PRHSPVP HKL\RECLPLIIF\LRNRLKYALT GDEVKKICMQRFIKI\DGKV\RT *YNPTPAGFHGMSSAFDKTGEE NFPS*SIDTKGSAFA\VHPYLTTL EEGQSTSLVPKVKKRSFVGHKK GIPSSWVTS*WPATIR*PRSPSSK VN*YHFRLDLETWQRLLDF\IKF \DTGNL\CMGDWGGA\NLGRN WVLITN\RERHPGSFDPWFHV\K DANGN\SFATRLSNIFVIGKGNK PWISLPRGKGIRLTIAEERDKRL AAKQSSG
11651	42019	A	11722	1	460	
11652	42020	A	11723	1	243	
11653	42021	A	11724	94	311	
11654	42022	A	11725	400	792	
11655	42023	B	11726	473	596	
11656	42024	A	11727	1	1707	
11657	42025	A	11728	3	484	
11658	42026	A	11729	122	253	
11659	42027	A	11730	1	803	RGGRGGAGAAGAELAGPLPSP APFESPGFTPPGPWGSICPAAFA HALHSGTVPARSGRTMARGAA LALLLFGLLGVLVAAPDGGFDL SDALPDNENKKPTAIPKKPSAG DDFDLGDAVVDGENDDPRPPN PPKPMPNPNPNHPSSSGSFS\DA DLADGVSGGEGKGGSDGGGSH RKEGEE\ADAPGVIPGIVGAVV VAVAGAISSFIAYQKK\KLCFK\ EN\AEQGEVDMES\HRNAQRQK PAVQ\RTLLEKIEDCPEKQPQAF GSRVRTAA
11660	42028	A	11731	335	476	
11661	42029	A	11732	2	169	
11662	42030	A	11733	49	289	VPVVQVPAAPGPLPGPATGSCS ASAAPRPPDPPPGHPEGHHGHS P/GVLGFEVGIFSYCQEQPQKCV TIKIFESPPIRRRL
11663	42031	A	11734	22	412	ARVGFLLGQEGKAGARASGPA DDVC\GKGASAIRSHMRASRSP PSPRRCHHHHEATGTASGSAAG GPGAGCVWLCRLALTPSAQDG RNSTFQTYKKEVCLPRHSHPCW MHAAGTTAGGSAVMSACCPSS SR

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11664	42032	A	11735	250	571	KGPRVTQGATVPKRQAPSAGL D/GSPISQFPWSY/DV*AIAILCG QGVT*PLPVSPPGGPAPPESVAL AEWVCSGSRRPLSNSGIARRPIG VIQPLDFLQNWPKPVLRC
11665	42033	B	11736	1	1593	
11666	42034	A	11737	2	1175	
11667	42035	B	11738	206	354	
11668	42036	B	11739	850	1461	
11669	42037	A	11740	2	663	VLLDERSAALDGAKRDGTLAL AAGALCREARAAQVFFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFPV SIPDHSTNSALSYLQSLITTSSHC
11670	42038	A	11741	1	474	
11671	42039	A	11742	3	1354	WAVCATRVGGAVGGTAKKPR SPEPRVTLLSQSKSGFWFGAER PGGLAFPRKAPPCPWPREQTKS TAGPITLGALRPAMVMEVGTL DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIAGSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAALD GAKRDGTLALAAGALCREARA AQVFFLKGGYEAFSASCPELCS KQSTPMGLSLPLSTSVPDSAES GCSSCSTPLYDQGGPVEILPFLY LGSAYHASRKDMLDALGITALI NVSANCPNHFEGHYQYKSIPVE DNHKADISSWFNEAIDFIDSIKN AGGRVFVHCQ\AGISRSATICLA YLMRTNRVKLDEAFEFVKQRR SIISPNFSFMGQLLQF*VPQD/VL VPHCSAEGWEAPDMAVL\DRG T\STTTVFNFPVFIPV\HST\NSAL SLPFRGPINGPFPAG
11672	42040	A	11743	196	1260	
11673	42041	A	11744	5	447	
11674	42042	A	11745	1	328	
11675	42043	A	11746	3	364	
11676	42044	A	11747	1	816	
11677	42045	A	11748	1	1377	

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11678	42046	A	11749	1	989	EGRTVLGGGLGSAAAMASRLL LNNGAKMPILGLGTWKSPPGQ VTEAVKVAIDVGYRHIDCAHV YQNENEVGVAIQEKLREQVVK REELFIVSKLWCTYHEKGLVKG ACQKTLSDLKLDYLDLYLIHWP TGFKPGKEFFPLDESGNVVPSD TNILDTWAAMEELVDEGLVKA IGISNFNHLQVEMILNKPGLKY KPAVNQIECHPYLTQEKLIQYC QSKGIVVTAYSPLGSPDRPWAK PEDPSLLEDPRIKAIAAKHNK\T TAQVLIRFPMQRNLVVIPKSVT PERIAENFKVFDFELSSQD\MTT LLSY\NRNWRVCALLSCTSHKD
11679	42047	A	11750	1	855	
11680	42048	A	11751	2	367	
11681	42049	A	11752	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
11682	42050	A	11753	1	1536	
11683	42051	A	11754	1	2541	
11684	42052	A	11755	1	1788	
11685	42053	B	11756	1	1014	
11686	42054	A	11757	1	777	
11687	42055	A	11758	1	1029	
11688	42056	A	11759	1	2052	
11689	42057	A	11760	1	1392	
11690	42058	A	11761	1	993	
11691	42059	A	11762	1	1240	PTDPAAEGPCLLDAKTNKRKGP STPILPFCPSPFIRGPKVDSTHGA WGQKQHR*TGIF*RSRAPSPP\P\ KEHGSSPATEQSWMENDFDEL REEGFRRI\NYSELKEEARTHGK EVINLEKK\LDEWITRITNAEKC LK\ELMELE\TKA\RELREECRS\ LRSRRNQLEERVSAMEDEMNE MK\QEEKFREKKNKKK*TKAL KELWDYVKRP\NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QAN\VQIRGNYRERPQRLPPRG RATPRTH/IIVRFTKVGNGREKM FKGQPGGKGR\VTLKGKPITLTT ADLSAETSTSQKTEWGPIFNILE GKEFSNPEISYLSQT*AFISGREE LNSFYRTSQMLRDFCHHQASRL P*KSTRPALKELLKEEALKHGK GNNPVPSHLQKFIA

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11692	42060	A	11763	1	1917	
11693	42061	A	11764	268	307	AHHTHLCLLTESPPEGR*VCWG CGLGWGVVLSLVCPP
11694	42062	A	11765	2	349	
11695	42063	B	11766	1	1734	
11696	42064	A	11767	1	603	
11697	42065	A	11768	1	420	
11698	42066	A	11769	115	796	EWSSVRRSLVEKRALRRPHPQC LCFRMKTILSNQT\VDIPENVD\I TLKGRTVIVKGP/REGTLRRDFQ SPSMENFTFLERKKKRLRVDK WWGNRKE\LATVRTICSHVQN MIKGVTLGFRYKMRSV\YAHFP HQPLLSRGNGSLV\EI\RNFFG*K NISARVRMRP\GVA\CSV\SQAQ KGEF/ISLEGNDI\ELVSNSA\ALI QQATT\VKNKDIRKFLDGIYVFE KGTVQQADE
11699	42067	A	11770	1	295	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN
11700	42068	A	11771	3	342	
11701	42069	A	11772	1	182	
11702	42070	A	11773	1	439	
11703	42071	A	11774	1	325	
11704	42072	A	11775	2	91	
11705	42073	A	11776	167	861	IWAILADPRMAQGKLRMEIGTK LRCLIWTVHKGVHWVTFWWV ERSQTGNLEVRRLWLGLLTHL HSGVNSLFTRARIWNPSMIDW/I KKMWHIYTMEYYAAIKKNQF MSFAGTWMKLSAPAAPTVLFL ASFTNHYNLRASLLVESCLAPS YTSVEPRFSIPQSLTPARGSSDG HTCFSHQSHDSLLICADSTHFW LSAHIWIQANAPPVPRAPSELSL KTRLKCSPQLNLRRPP
11706	42074	A	11777	1	660	
11707	42075	B	11778	1	2633	
11708	42076	A	11779	1	2985	
11709	42077	A	11780	398	605	
11710	42078	A	11781	204	585	VTMCDRKAVIKNADMSEEMH QDSVECATQALEKYNIEKDIAA HIKKEFDKKYNPTW\HCI\VGEG TFGSLC*HIETKHFHLTSYLGAK WAISFCFKFWFKRHGTVATHPV IPFQKQGIAALNFQLPED
11711	42079	A	11782	1	810	
11712	42080	A	11783	188	534	

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11713	42081	A	11784	1	1188	
11714	42082	A	11785	1	1137	
11715	42083	A	11786	19	428	ERRNSGNMALRVERSVRAVLC SLHVVLAPAAPCLSRPWQLGM GAVW\YCNLPEVGTKLNKQDE FGALERVKAASELYSPLSGEVT EINEALAENPGLVNKSRYEDG WLIKMTLSNPS*LDELMSEEAY EKYIKSIEE
11716	42084	A	11787	66	631	RRDPRTPANMALRVVRSVRAL LCTLRAVPLPA\APCPPRPWQLG VGAVRTLRTGP\ALLSVRKFTE KHEWVTTENGIGTVGI\SNFAQ\ EALGDVVYCSLPEVGTKI*TKP SWSLVLLE\SVKAASELYSPLSG \EVTEIN\EAL\AENPGTCKTNFC Y\EDGWLIKMTLSNPSE\LDELM SEEAYEKYIKSIEE
11717	42085	B	11788	46	743	
11718	42086	A	11789	209	401	MKPPVRSLSTPPRSIIMGSSATEI EELENTTFKYLTGEQTEKMWQ RLKGMEIKKLN*G
11719	42087	A	11790	135	313	
11720	42088	A	11791	1	624	
11721	42089	C	11792	81	299	
11722	42090	A	11793	5	166	SPVMMSFFLFVCLLTT*RSPSSS SSSSSSSSSSSSSSSSSPSPSSSFS GSVV
11723	42091	A	11794	3	173	
11724	42092	A	11795	169	291	SCNSSILSFLSLSLVADPQIATYR /S*CSRLGHKGTLLPGS
11725	42093	C	11796	1	429	
11726	42094	A	11797	1	279	
11727	42095	A	11798	3	376	
11728	42096	B	11799	1	736	
11729	42097	A	11800	753	2455	
11730	42098	A	11801	1	312	
11731	42099	A	11802	48	397	
11732	42100	A	11803	51	286	
11733	42101	A	11804	1	420	
11734	42102	A	11805	11	537	PDRPTRPCRQCARSFRRKLKAA VGVEGPSLSSGELGTRVPAAPS PTTRPRAMAFCLPSFACI\YSALI LHDDE\VT\VTEDKI\NALIKSSR V*MLSPFWPGLFAKAL\ANVN\ MGSLICNVGAGGPCCPASWVL QPAGRSLPPPLLAASSLREKKV\ EAKKEGFRGSFD*LTWGFGSF
11735	42103	A	11806	114	399	

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11736	42104	A	11807	3	599	AIRRLRISAREEERENQPRLLPL SLGAGGGVGGFVQQWPRFKAR DLRGKKKEEL\LKQL\DDLKVE LVPSARRQKRQGGAAS\KLSKI R\VVRKSIAPCSPRLFTQTQKEN LRKFYKGKKYKPL\DLRPKKTR AMRRRLNKHEENL\RTKKQQR KERLYPLRKYAVKALGGALSIK HKENLKTKKQQRKERLYPLRK YAVKA
11737	42105	A	11808	226	370	AGSP*FPQFSEA*RRGALGSGA DQDLSHPRITIETLTSCRSLQTSS PR
11738	42106	A	11809	3	7964	RGSGSSKFEPRSRSASVLAPSAL GPPNTSPRQLVAHCALPATRMP VTEKDLAEDAPWKKIQQNTFT RWCNEHLKCVNKRIGNLQTDL SDGLRLIALLEVLSQKRMYRKY HQRPTFRQMQLENVSVALEFL DRESIKLVSIDSKAIVDGNLKLI LGLVWTLILHYSISMPVWEDEG DDDAKKQTPKQRLLGWIQNKI PYLPITNFNQNWQDGKALGAL VDSCAPGLCPDWESWDPQKPV DNAREAMQQADDWLGVP
11739	42107	A	11810	1	636	
11740	42108	A	11811	3	261	QKKPLKQPKKQA*EMDEVRAG AEALAGAGALGDRPELNTLCLS P\EDKAFKQKQKEEQKKLEELK AKA\AGKGPLAT\GGIKKSGKK
11741	42109	A	11812	1	621	
11742	42110	A	11813	1	1024	
11743	42111	A	11814	174	332	SHCLANAPGDVKVRNDPESPRE L*HL*R*RINYTRWKRSI*EEWC QGHSWRG
11744	42112	A	11815	1	1323	
11745	42113	A	11816	1	2322	
11746	42114	A	11817	1	336	
11747	42115	A	11818	22	391	PPPPAAKTRRKKVLATKVLGTV KWFNVRNGYGFINRNDTKEDV FVHQTAIKKNNPRK\YLRSVG\D GETVEFDV\VEGEKGAEAANVT GPDGVPV/EKGSRYAA\DRRR\Y RRCY\YDR\RRGPPPEYW
11748	42116	A	11819	433	866	PPPPAAIDAEKKVLATKVLGTV KWFNVRNGYGFINRNDTKEDV FVHQTAIKKNNPRKYL\RSVGD GETVEFDVVEGEKGAEA\ANVT GPDGVPVE\GSRYAADRRRYRR \GYYGKARWPFPANYAGGGRR RKGAAQVEGFLPPLPLD

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11749	42117	A	11820	63	484	
11750	42118	A	11821	1	819	
11751	42119	A	11822	150	463	
11752	42120	A	11823	63	594	FAKLPNPKGKGGEATRYMFSR PF*ENHGVVPLGHNN*RF\YKK GDIVDIQGEWGTLFQKGNCPH KVVTHGQNLEGVLPMVTPAML VGHLL*TNQF*GKVFS\KRINVR IEPIK\HSKSR\DSFLK\RVKEND QKKKEAKEKGTWVQLKRQPA\ PPREAHFVRTNGKEPELLEPIPY
11753	42121	A	11824	2	1376	
11754	42122	C	11825	132	341	
11755	42123	A	11826	155	245	
11756	42124	A	11827	3	293	
11757	42125	A	11828	204	467	LRAPHVACSRCNQGPCMENCL NTDQTHTQTQRQG*EEKSSSSK/ PISSLMEYYKRSQCSVKSKARS VF*LKLRAQAQLLQETKKPVFR L
11758	42126	A	11829	1	768	
11759	42127	A	11830	348	568	REISYKERIGM*MPPSVILNSYV KSMLETYPHPLLRGVVAPGPLK KGFLTESLLALPDPSFSGRMTSF KITPV
11760	42128	A	11831	1	840	
11761	42129	A	11832	2	216	
11762	42130	A	11833	1	726	
11763	42131	A	11834	3	3231	PGGWLRRALPGRERLQSPVHA VPPQHGTSHSRLLVTWPGAGR DQDFSSPPLLLLGETDHLHLDL PLSPLPTSDELFLPGICDPYVKL SLYVADENRELALVQTKTIKKT LNPKWNEEFYFRVNPSNHRLLF EVFDENRLTRDDFLGQVDVPLS HLPTEDPTMERPYTFKDFLLRP RSHKSRVKGFLRLKMAYMPKN GGQDEENSDQRDDMEHGWEV VDSNDSASQHQEELPPPPLPPG WEEKVDNLGRTYYVNHN
11764	42132	A	11835	1	624	
11765	42133	A	11836	2	361	
11766	42134	A	11837	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
11767	42135	A	11838	1	684	

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11768	42136	A	11839	9	247	AVTSDEPKGKKAKAKKVAPAP AVVKNQEAKKVVDPLFEKRHK N\FGIGQDIQPKRASPRLCELPR\ YIRLQRQRAILYK\RLKGPFCDY PGFTRALDRQTV*SSLLKL\AHK YRP\ETKQEKK\QRLFARAREEG VLAKGDVPNERDPPV\LRARSL TPFHHPWVEKQEKLQLVVNWH TDV\DPI\ELVVLLALPLCREKW GVP\YCNYRREKARLWDRLVP QERPCTTCPPFTQGELRKTKGG FWLKLGWKLIRTQFTIDQILMR SRRH\WG\GNVLG\PKSVGS*SP KLEK\AKAKELAH*TG
11769	42137	A	11840	1	273	
11770	42138	A	11841	1	218	
11771	42139	A	11842	1	1522	
11772	42140	A	11843	136	441	
11773	42141	A	11844	24	274	SRQAWHEAASASARRRGTRSP ALSPARAPAGPIWTNARRSARA NSVSPAAAPPPRRPVSLS\DPGE SCTRDPRAPDPCGPFRCC
11774	42142	A	11845	194	365	
11775	42143	A	11846	1	782	LLVVGTTVVVYFPNGRFKEFM SRHVHLMCYRICVRALTAIITY HDRENRPRNGGICVANHTSPID VIILASDGYYAMVGQVHGGLM GVIQRAMVKACPHVWFERSEV KDRHLVVK\RLTEHVQDKSKLP ILIFPEGTCINNTSVMMFKKGSF EIGATVYPVAIKYDPQFGDAFW NSSKYGMVTYLLRMMTSWAIV CSVWYLPPID*ERQIEDAVQFA NRVKSAIARQGGLVDLLWDGG LKREKVKDTFKEEQQKLYSKM
11776	42144	A	11847	3	916	
11777	42145	A	11848	13	473	DPPTDSLSPDGGSIELEFYLAPE PFSMPSLLGAPPYSGLGGVGDP YAPLMVLMCRVCLEDKPIKPLP CCKKAVCEECLKVYLSAQIQCP TCQFVWC*CAGCAWKTSPSSPC LAARRPCARSASKST/SSAQIQC PTCQFVWCFKCHSPWHEGVNC KEYKKGDKLLRHWASEIEHGQ RNAQKCPKCKIHIQRTEGCDH MT
11778	42146	A	11849	92	1103	
11779	42147	A	11850	1	516	
11780	42148	A	11851	1	642	
11781	42149	B	11852	200	608	

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11782	42150	A	11853	1	1856	MEETGMCEGHGASPGMEASSG EREKRGTGEASPGDREKRGTGE ASSGEREKRRTGEASSGDREKR GTGKASSGEREKRGTGEASYG EREKRGTGAAGGQESCAHCGG WLMPRAKPSTHRETNPRGTEA TAMAMDHVGQQADTTDSTDG SQWDPSEHSPNCGIREVGAGDP DTQQTGRHHCYYPAKETNEKT NTNRNSNTFIEQLLHAKQQRGN SGVPFKPGHMVRALTTNALSW AKLYPDPWCLRMGGTGNEVFE NEIKTGSCWIKEQEGQPRPQSP RSQVRPEADPGPSPLTKMSAEN EYRPPSPPKLAAERDKPSPRLRP RGVPWRRESRVRAGRECALLR VAAEGARPPPAGMSYDRAITVF SPDGHLFQVEYAQEAVK\RGST AVGVRGRDIVVLGVEKKSVAK LQDHRPVRKICT\LHDN\VCMA FAGL/TPADARIVIQTGPGVEFQ\ SHRA*T\VEGPRVTVE\YITPLTF ASLKASVYTQSKWGARPFG\IS GPHRGFSTFDGTP*LYQTDPSG TY\HAWKA\NSIG\RGAKSSARS SWEKN\YTDKAIETDDL\TI\KLV IKALLEVVQSGGKNIE\LAVMR RDQSLKI\LNPEEIEKYVA\EIEK EKEEN\EKKKQKKAS
11783	42151	A	11854	12	432	

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11784	42152	A	11855	1	1775	MSYPADDYESEAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIPEVIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVYEIQDIYENSWTKLTERFFK NTPWPEAEAIAPQVGNDAVFLI LYKELYYRHIYAKVSGGPSLEQ RFESYYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSVLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLLRLHSLL GDYYQAIKVLENIELNKKSMYS RVPRVPRSPTYYYVGFAYLMM RRY\QDAIRVFANILLYIQRTKS MF\QRTTYKYEMINKQNEQMH ALLAIAL\TMYPMR\IDESIHLQL REKYG\DKMLRM\QKGDPQVY EELFSYSCPKFL\SPVVPNYDNI\ HPN\YHKE\PFLQ\QLK\VFSDEV Q\QQAQLSTIRSFLKLLHPPCLV AKPGLASLDLTEQEF\RIQLLVF KHKMKNLRVDSAVSQALDGEF QSASEVDFYI\DKDMI\HIADTK VARRYGDFFIRQI\HKF\EELNPN P*RRMG\QRPWMIFTTHSGNLV
11785	42153	B	11856	1	537	
11786	42154	A	11857	98	334	WATERWKGRKNHEISWKCFPG KAIS*MRSSKQMKPNFPRCSSIT VLSVRGMVLFLTLACPRFKMSS RTDFRFGNPQVT
11787	42155	A	11858	4	422	
11788	42156	B	11859	1	2567	
11789	42157	A	11860	2	364	
11790	42158	A	11861	1	501	
11791	42159	A	11862	1	402	
11792	42160	C	11863	30	673	
11793	42161	C	11864	195	1263	
11794	42162	A	11865	3	648	
11795	42163	A	11866	200	420	ILPSALRPPNPNWNVG/YVQTQ LVSKPLSLPTGIPCSTTSNILKPV ITKDARLHRVIVHGWGIKGTIPI AKIAIS

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11796	42164	A	11867	1	502	MQLPGRGHSFVCKANAGSTQA RQGASAGVAGCRGWLNYAAS EQIVLRVPHMRCEIPHKCVRRK SRIRPHSPFRLRNCWKGRSVRA FSLLRQLAKGGCAARRLSWVT PGFSQSRRCKTTASAKLACLQV RAQSEDISTVPIHYAYNMTRVG RMQMLGKYNPQSAKLVREAIL PTKATLDLSNQNNEDFSAFQLG LAQALHIKVHTMTREVMSDEL TKLLEGNLKPAIDMMVEFNTT GSLPENAVDVLNTALGDRKSF VALMALMEYSRYLVAEDKSAF VTPLYVEADGVTNGPINAMML MTGGLFTPDWIRNIAKGGL*FQ YTFTFNRNSRSQCFHIFQETSKK FFSMCF*SSLLTKHCHSSRDVW VFSTSFQHIRHTLIDGISNRTNQ LTCNTTSTRTIDGNSQRVLSNTT
11797	42165	C	11868	1	3831	
11798	42166	A	11869	1	5370	
11799	42167	A	11870	1	3999	
11800	42168	B	11871	1	12036	
11801	42169	B	11872	1	16395	
11802	42170	A	11873	1	19997	
11803	42171	A	11874	1	70	
11804	42172	A	11875	44	613	AGTHLRPFSPSLSAAMALRYPM AVGLNKGHKVTKNVSKPRHSR RR\GRL\TKHTKFVRDMIREVCG FAPYERRAMELLKVSKDKRAL KFIKKRVGTHIRAKRKREELSN\ VLAAMRKAAAKKDLGPSPCPL PEIKDKLDRSPGSPAVRGWVW VCRGPAVPCLVPALSHTLSGCC LVVNQKPWPAHPSRGSR
11805	42173	A	11876	1	150	FRGRCCVQRYRGCTLASA/CLL VGEAEAPSPVDPLERSRPYAVL RGQNLE
11806	42174	A	11877	447	725	
11807	42175	A	11878	2	206	RPVAYLLLQGWGRCCVQRYRG CTLASA/CLLVGEAEAPSPVDPL ERSRPYAVLRGQNLDQTLH*ST HQA
11808	42176	A	11879	1	413	
11809	42177	A	11880	122	268	
11810	42178	A	11881	1	555	

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11811	42179	A	11882	221	419	LQTILQGYSNQNSMVLVPKQR YRPMEQNRALRNNAAYLQKSP *ADKQLQQ/ECQDTKSMCKNH KHSYTPITDKQRAKSRVNSHSQ LLQRE*NT*ESNLQGA*RTSSRR TTNHCSMK*KRIQTNGRTFHAH G
11812	42180	A	11883	1	2464	MDEFLNTYTLPRLNQEEVESLN RPITGSEIVAIINSLPRKKSPGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTIKENFRPISLMNIDAKILN KIILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAFDKIQQP FMLKTLKKFGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKKWKNIPCSWVGRINIM
11813	42181	A	11884	2104	2637	MFQRGHISQWWVVVGALTVFT SVLDTDPMRDNKRSGSEILPFC REHGTSFTYNHAHSPLSCSPSCL FSGLALFSPENNSGFLCMTLPAS FTAGNRLFSSAGQPWWIQQGF KAHAKARRLILLAFHHYCCRPF LAVELKPSPVSTPTFLFA*LLPP CSVPGAILHESFGEAITWLDAE
11814	42182	A	11885	69	417	QTHSQHYTEWGKVESIPPENW NNTRMPIFTISIQHIIRSSSESNQT RERNQGHPNG*RGSQTVAFC*R YDRIPRKP*RLIQKTPRTASAAD TQANRVWSGPPASSNRPAAEGP DC
11815	42183	A	11886	376	597	ENKIPRNPTYKGCEGPLQGELQ TAAQGNKRGHKHMEKHSRLM DRKNQYPSAADTQANRVWSGP PANSNRPAAEGPD*PGQNFQYH VE
11816	42184	A	11887	5	292	LTVSCPCSRMLFLTTDVLLPLM FIKKLGANVASPSSKKPLFVIRL VITTLLPLACGTLPTSSVSRTTFF RTMLPQA\PEFAPPSTGTESHYY CCIW
11817	42185	A	11888	320	596	YPGKQGLEWTSSKLQQTCRKY RERHKDTP/TRRATPR/RHNCQV HQS*NEGKNVKGSQRERSGYS QREAHQTNSRSLGRNSTSQKRV GASIQRS
11818	42186	A	11889	3	239	EASRGRIRQQHLPFCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDC*KEN*QTERTSTPKPD LYITIIKDQSLL

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11819	42187	A	11890	3	278	EASRGRIRQQHLPFCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDC*KEN*QTERTSTPKPD LYITIIKDQRLIPGLFTSPWISARI
11820	42188	B	11891	394	1213	
11821	42189	A	11892	856	1217	VDRSRLQKVSNNKLVQAKGGC SNPLQGS*KLDNPKDANS/RQQ PERTWKWIFPQPHR*GAFGPRH C*ESHLYQFGLDLLNSAGSGIG KNEVQEQKRAEVGARAAPEKE LPEALSWFLKVLW
11822	42190	B	11893	1	894	
11823	42191	B	11894	93	938	
11824	42192	A	11895	149	508	LLEGKLTNKKDIHIKTPSVRHH HQRPKPKISLS**ATSAKSQDTK SMCKNHKHSYTTITDKQRA\NH E*TPIHNCFKESKIPRNPTYKRC *G/RSSRRTANHCSRK*KRTQTN GRTFHTHG
11825	42193	C	11896	1	1257	
11826	42194	A	11897	183	1065	YWRCNGFLS*\YAEAAEEIVDCI TESLSILKTPLPKKMNEEMLCQ EFGRFGPLASVKIMWPRTDEER ARERNCGFVAFMNRRDAERAL KNLNATAFRPALSHFPSLPMDT TSQIPKH\PVTVSSTNKLILIIKTH FQAQSSLNQNIHPMDPSHGIQY SAFSPSTPNPSHPALP*PLAIQVH HAVCDGFHVGRMLNELQQYC DEWQRDKLEEILRGLTPRKNDI GDAMVFCLNNAEAAEEIVDCIT ESLSILKTPLPKKMNEEMLCQE FGRFGPLASVKIMWPRTDEERA RERNCGFVAFMNRRDAERALK NLNATAFRPALSHFPSLPMDTT SQIPKHSSHRQFNKQAHSDHQD SLSGPVQSESKYPSHGSIPWDSI LSLLTLNTQPIPPSLALTHMEME SGLHFHCPFTASPPSAVPPPELE KTTLKFIWNQKRARIANSILSQ KNKAGGITLPDFKLYYKATVT KTAWTGSPTAIRQARTTRQEKE MKGIQIGKEEVKLSLFTDDVNL QVRENK
11827	42195	C	11898	138	644	

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11828	42196	A	11899	2	3088	ADKTPGGSQKASSKTRSSDVHS SGSSDAHMDASGPSDSDMPSRT RPKSPRKHNYRNESARESLCDS PHQNLSRPLLENKLKAFSIGKM STAKRTLSKKEQEELKKKEDEK AAAEIYEEFLAAFEGSDGNKVK TFVRGGVVNAAKEEHETDEKR GKIYKPSSRFADQKNPPNQSSN ERPPSLLVIETKKPPLKKGEKEK KKSNLELFKEELKQIQEERDER HKTKGRLSRFEPPQSDSDGQRR SMDAPSRRNRSSG
11829	42197	C	11900	413	823	
11830	42198	A	11901	263	1246	NPGKQGLEWTSSQTPADLQLR VLTVRRNTNKQKGHPHQNPICT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPVME DQMNEMKQEEKFREKRMKRN EQSLQEIRDYVKRPNLRLIGVPE SDGE\KEPSWKTLCRILSRRTSP A*QGRPTFKFRKYRECHKDTPQ GEQLQDT*LSDSPKLK*RKKY* GQPERKKYRLPSANT\KTSLRK* TRKSRRNG*ITGHIHPPKTKPGR S*IPE*TNSRL*N*GNN**PANQK KSRTRRIHSQILPEAQRGAGTIP SETIPINGKRGNPPKLIL
11831	42199	B	11902	67	2584	
11832	42200	A	11903	1	3793	MSDAEDERFLQFQLRYRVYLT GDCRTVGAGQWVQRTEREPKQ GEALPHPGSARGWGVPFPRDD GWHLENRVTPTLILRFSHSLSK QHTRRPYSAPGSEGPTPTEPCSL LAQQSEIKLQDGSEAGGGPLLLI PRQTGSGVDLRQTPTDMQLRV LTVRRKTNKQKGQPHQNPICTS PSSKTKAPHHTYSKTDHIVGSK ALLSKCKRSEIITNCLSDHSAIK LELRIKKRIQNRSTTWKLNNLL LNDYCVHNEIKAEI
11833	42201	A	11904	1	441	

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11834	42202	A	11905	312	3705	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECRLDRDEERAYVLYM KYVTVYNLIKKRPDFKQQQDY FHSILGPGNIKKAVEEAERLSES LKLRYEEAEVRKKLEEKDRQE EAQRLQQKRQETGREDGGTLA KGSLENVLDSKDKTQKSNGEK NEKCETKEKGAITAKELYTMM TDKNISLIIMDARRMQDYQDSC ILHSLSVPEEAISPGVTASWIEA HLPDDSKDTWKKRGNV
11835	42203	A	11906	1	609	
11836	42204	A	11907	3	755	LRVDNAPAHASGLFFCAGAAG TVLFAMAPSRNGMVLKPHFHK DWQR\RVATWFNQPAR\KIRR\R RPRQAKARRIGPAPRGGGPIRPI VRCPTGRVHNGSWRPGRGFQP GRSSRVAGHSPRKVAPDPSGIS VDPK\RRETSSHGSPLQAQRAS GLKE\YRSQTQSSSPRKPSAS/PL *GDSSAEELKL\ATQ\LTGPVMP VRNVYKKEKARVI\TEEV\KNF KAFASLRMARA\NARLFGIRAK RAKEAAEQDVEKKK
11837	42205	A	11908	1	327	
11838	42206	A	11909	1	756	
11839	42207	A	11910	1	219	
11840	42208	A	11911	2	227	
11841	42209	A	11912	1	567	
11842	42210	B	11913	99	799	
11843	42211	A	11914	61	342	
11844	42212	B	11915	1	945	
11845	42213	A	11916	92	133	DPPSQKLKTLRKD*TNG*LQ*P MKRSP*MT*WS*KP*HENYVTH AQASVPDSINWKKGYQ*LKIK* MK*SKKRSLEKKE*KETNKASK KYGTM*KD
11846	42214	B	11917	1	368	
11847	42215	B	11918	1	106	
11848	42216	A	11919	1	705	
11849	42217	B	11920	1	834	
11850	42218	B	11921	1	1305	
11851	42219	A	11922	1	1187	
11852	42220	A	11923	228	619	

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11853	42221	A	11924	1499	2238	KGKKKVINQISLGQRMRLSQSS HGKVQACQVPFHPNAPPAVQF QSRELQSGSRPRSCGEKATRCL RQGPREVPLPKNAWA*QRKQE KKRSRKGS/GREPGLRRPPNAQ ARDRSSRAPATHRKELKPEREH ISCSRSHIRYQEWSVLRDTVHR NLVLDTKRHPALILVEYKERTS SPATEQSCMENDFDELREEGFR RSVITNFSELKEDVQTHHKEAK NLEKRLDKWLTRINSVEKSLND WMELKTMA
11854	42222	A	11925	699	796	
11855	42223	A	11926	1029	1223	ERELPDPLRFPSEGNASALLSAS RTVRASTDLRPLSGTP*RDEPGT SDGNAEITRLLRRSGWEL
11856	42224	A	11927	186	1597	
11857	42225	A	11928	1	1200	
11858	42226	A	11929	1	600	
11859	42227	A	11930	1	663	
11860	42228	A	11931	908	1331	GDMRGRREGGFGLGRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLTMPLAPATFL RVNCWAG/RGR/C*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPEKRDLPL RVKDQGRHPCVV
11861	42229	A	11932	1	1707	
11862	42230	A	11933	1	1012	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLIDIYGTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITSYLSDHSAI KLELRIQNLTQNHSTTWKLNNL LLNDYWLHNEMKAEIKMFFET NENKDTTYQNLWDAFK/RSV*R EIYSTKCPQEKAGKIQN*HPNID QQN**TTSKANKEKKREDSNRC NKK**RGYHHRSHRNANYHQR ILQ/YTSMQIN*KI*KKWINSSTH TLSQD*TRKKLNL*IDQ*QELKL WQ*SIAYQPKRVQDQMDSQPN STRVASKRIKYLGIQLTRM*RTS SRRTTNHCSMK*KRIQTNGRTF HAHG
11863	42231	C	11934	1	1788	
11864	42232	A	11935	550	827	DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLLQQL PQEHTRKTLPLQQTSAWTYRLF HTSCEI

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11865	42233	A	11936	584	1094	NWIPSLHLTQKLIQDGLKT*ML DLKP*KP*KKT*AIPFRT*AWAR TSCLKHQKQWQQKPKLTNGI*L N*RVSA/PAKETTISMN/EATYR MGENFCNLLI*QRANIQNLQ*T QTNLQEKNKQPHQKVGKGHEQ TLLKKRHLCSQKTHEKMLIITG HQRNANQNHNEMPFHTS
11866	42234	A	11937	797	1044	EESIS*KWPYCPR*FVDSMPSPS SYR*VSSQNWKKLL*SSYGTKQ EPTLPSQS*AKRTKLEASHYLTS NYTTRLQ*PKQHGT
11867	42235	A	11938	176	374	LTNQKKSRTRWIHSQILSEVQR GADKQPNRE*TPIHNCFKENKIP RNPTYKGCEGPLQGELQTTAQ
11868	42236	B	11939	1	1843	
11869	42237	A	11940	3227	3391	DPLPGQRQLLLQKQRRP*TQAG LLSFQPGPQPHGSVPPTLSQPW LPGGWPELSG
11870	42238	B	11941	1	1479	
11871	42239	B	11942	1	2097	
11872	42240	A	11943	654	1341	KNRNYNKLSLRPQCNQTRTQD *ESHSKPLNYMETEQPAPE*LL GT*RNEGRNKDVL*NQREQRH HIPESLGRIQSSV*REIYSTKCLQ E/I/MQERSKIDTLTSQLKELEKQ EQTHSKASRRQE/DN*NQSRTE GNRDTKNPSKNQ*IQELVF*KD QQN**TASKTNKEKKREESNRH NKK**RGYHHRSHRNTNYHQRI LQTPLRK*TRKSRRNGYIPRHIH SPKTKTGRS
11873	42241	A	11944	471	611	
11874	42242	A	11945	1	585	
11875	42243	A	11946	3	1029	GRQHGGSQRMGGTASARASSG RLAPRGRGAFAFRRRCPSPRRW RLTCGPAAVEHSFCHNVGPGV RATADKYTCMFTYASQGGTNE QWQMSLGTSEDHQ\HFT\CTIW RPPRGKSYL\YFT\QFKAEVAGR LRFEYRHGLTFKAA/SLKRESD VPLENLRNFEVNQNSSGLTRPG GISKAELSKLVIVGQGIRALSCD QQPLLRGGTFSSPVKLKGACVP ERAQHITGFLGGTLKFSTWADV ALSRRGFSGWLKPWGREQRVQ GPPGSQQLFRFPLPVKLFWTQD RRSRGTKRVGNMGAMLGKAA MLPPTSSRASFMSLQNCFPMFT QGTSFQMNWEEMKCFFIFK
11876	42244	A	11947	1	1206	

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11877	42245	A	11948	1	654	
11878	42246	A	11949	849	1089	SPEGKHYRCYLVHMPSDTERSS L*MRPRAGRSSAEGPGCRQRSL ALDHMVQQAQRCWRYQWWR RFSKEFNQWWRRFSEEL
11879	42247	A	11950	5	1376	
11880	42248	A	11951	2	278	VPQPDTRKGSVLKWISKRGKPL AVEIEESHCL\CLPLRTECLGIKP \IVHLFSCTRPVIVPSLELNYDV DSIAHMFVADLLLMITLPSYDIP
11881	42249	A	11952	3	267	
11882	42250	A	11953	1152	1338	FKRGQYGRLLRPRFHHGQILYA RRQGA\EPLAIQVHHAVCDGFH VGRMLNELQQYCDEWQGGA
11883	42251	A	11954	394	615	ASDPLRGLLCGPSLLDERHPLL HGAQSHRPPKG*GVRANNAGL AGSSIYLQPRCGIHEVKPSGLLS REGLQLQS
11884	42252	C	11955	114	362	
11885	42253	A	11956	1	211	
11886	42254	A	11957	395	547	
11887	42255	C	11958	412	641	
11888	42256	A	11959	3	905	SNNSPTSASRVAGITGVRHCVR NWWVLGLTDFKNEAVDPRAW TTKSKTPPQNKTKQENKNEDV GRDQRVEWLVTEEVSELSLKG EKLHWKEKEVQSTGKETDARS SMRNYLMLLGPEVQEKEPVKR RLARGKAFVELAEPTRAPGNSG FPVSGGVFTPSLGALTWICKFR VKSWAILNSQLLLDTMKKGIV YKNGDRIQGNRSADNRNNGVP LTGARDMQPAMPEPPTHSMGS CAARAFPMSAASCFRAPSPIDH PKAEE\WGARRGTGGQ\PTCSP GAGIHWVKPAGLLSREGLQLH
11889	42257	C	11960	482	709	
11890	42258	A	11961	1	734	MRLESD/KHLVQFVPIHKSKG\L EYPIGPWLPFITNSRVQEQAFYH DRHSFEAVLDLNAAPESVDLAE AERLAEDLRLLYVALTLSAFAP LVRRRGDKKGDTDVHQSALGR LLQKGEPQDAAGLRTCIEALCD DDIAWQTAQTGDNQPWQVND VSTAELNAKTLQRLPGDNWRV TSYSGLQQRGHGIAQDLMPRL DVDAAGVASVVEEPTLTT\HQF PAGASRGTFW\HSLFEDLDFTQ PVDPNWRL
11891	42259	A	11962	21	898	
11892	42260	A	11963	1	1962	

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11893	42261	A	11964	1	313	MRFYGQLAEDPGQQKAGETTR HTEDYISQLPLQRQGIPELALQK DLFINKIYGKEFNVCRSTLEDPR VHVLCRDMDEAGNHHSEQTIA RTENQTPHVLTHRRELNNENT WTQGGEHHTPEPVMGWG*RPR AAKSWGNNKAY*RLYFSAAFA ETRDPRTCPSERSFY*QDLWK/ MSSMSAGRL*RIPEFMSFVGTW MKLETIILSKLLQGQKTKHRMF SLIGGN
11894	42262	A	11965	47	178	QQLVHTAFVIRLIRGTTEGAWR NCKQMAR*QSISLECKFMPRT
11895	42263	A	11966	2	223	
11896	42264	A	11967	2	133	
11897	42265	B	11968	179	6003	
11898	42266	A	11969	1	1125	
11899	42267	A	11970	1	360	
11900	42268	A	11971	677	1238	
11901	42269	C	11972	193	471	
11902	42270	A	11973	17	280	
11903	42271	B	11974	1	654	
11904	42272	B	11975	526	597	
11905	42273	A	11976	1	1261	
11906	42274	A	11977	170	998	
11907	42275	A	11978	1	1130	
11908	42276	A	11979	1	369	
11909	42277	A	11980	1	300	
11910	42278	C	11981	207	451	
11911	42279	A	11982	1	348	
11912	42280	A	11983	2	469	RGIREGEEFDVDLAGMEVAVG GWGRGLWLHRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFLSSNTTCQQFRDPGFR GRYPASPHTLSLPPETAHL*LLL CLPAAGVLPHTWPLLDRQGWH RGHAR

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11913	42281	A	11984	1	937	MAAPLVLVLVVAVTVRAALFR SSLAEFISERVEVVSPLSSWKRV VEGLSLLDLGVSPYSGAVFHER QYIPVKMKSKAFWIFSWEYAM MYVGS/HSGNHLPLLLPSQLLG FHPRSL/VALYFLFQISLQTLVIF WYFFAEMFEHFSLFFVCVFQIN VFFYTIPLAIKLKEHPIFFMFIQI AVIAIFKSYPTVGDVALYMAFF PVWNHLYRFLRNIFVLTCIIIVC SLLFPVLWHLWIYAGSANSNFF *GITLTFNVGQRPHRLKAPRASS AARSDRGPAASPASPGDAARPV SGRRPWDAPPHNYLNAVPPPSR
11914	42282	A	11985	1	521	
11915	42283	A	11986	1	207	
11916	42284	A	11987	1	867	
11917	42285	C	11991	1	225	
11918	42286	A	11992	72	425	
11919	42287	A	11993	1	354	
11920	42288	A	11994	460	752	
11921	42289	A	11995	93	401	PQKKYIHIFLDSLALLPRLECSG AISAHCKLHLLVSSDSPASASQ VAGITGARHHAWLIFVFLVEM GFHH/VGQAGLELLTSGDPPAL ASQRAGVSIFIYLFIF
11922	42290	A	11996	2	315	
11923	42291	A	11997	615	1180	
11924	42292	A	11998	3	151	
11925	42293	A	11999	2126	2241	
11926	42294	A	12000	1	765	
11927	42295	A	12001	924	995	
11928	42296	A	12002	1	789	
11929	42297	A	12003	2	132	FFFFFLVEMGFHHVGQAGLKLL TSSD\RPPWPPKVLGLQARAT
11930	42298	A	12004	504	755	

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11931	42299	A	12005	1	1322	MAILPKVIYRFNAIPIKLPVTFFT ELGKTTLRFIWNQKRACIGKSV LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT ESSEIMLHIYNHLIFDKPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTSHTKINSRWIKDL NVRPKTIKTLEENLGNTIQAIG MGKDFMTKTPKAMATKAKID KWDLIKLKSFCTAKETTIRLLG RPPALFTASSSVLKQLALEGILI LDSRALLGFLYEARHSHSNSPN HDAQNATSKKNIRDGYDKIYR QEQVLARMEEKTLITAGGNVK WCSHFRKQIGGQWLTLETKTK TPQPFSSTSQISTDKDKGLNPQL LKMDPGHMGWCPPGMGIPWQ LSSDDRVWVLAAAGSGRHPGS GFKSL/PGLLHEGSYGH****S*I *GGNS*GSSGGPQCISGEERVFR
11932	42300	A	12006	12	143	
11933	42301	A	12007	1	534	
11934	42302	A	12008	1	591	
11935	42303	A	12009	2	353	
11936	42304	A	12010	1	1923	
11937	42305	A	12011	1	465	
11938	42306	A	12012	1	784	PGWEKRMSRSSVVNTQEALPT AAIPRDAKGRVYYFNHITNASQ WERPSGNS\SSGGKNGQGEPA\R VRCSHLLVKHSQSRR\PSSWRQ EKITRTKEEALELINGYIQKIQS GEEDF\ESLASQFSDCKHQPKA RG\DLGAFQQKVRLQKPF*RTP RFALADGGR*AGPCFTD\SGIHII LPHLSEGWGAQAWPRGRAGRL GRPAPPCPPASGRTPHSLPPSHSI YCSHNGWEGALPDWGPFQTGG PGVPHSLSVPSWGCDLQTLH
11939	42307	A	12013	1	319	PRERAPRGSVGAGGEICHTSVC CCQPSWTRLLLLITWMLL/YYS ECKPFHCSREEPDNHILLLKI*EF GPPSTQGQHAAPLSRSRYSCCP DRYLLRKLGICQEHQLL
11940	42308	A	12014	1	1058	
11941	42309	A	12015	1	861	

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11942	42310	A	12016	1	431	IVLGGVATTVCQLNEFIMTDNA VPADVLVLTKPLGTQVAVAVH QWLDIPEKWNKIKLVVTQEDV ELAYQEAMMNMARLNRTGGL LICLPREQAARFCAEIKSPKYGE GHQAWIIGIVEKGNRTARIIDKP RIMEVA\HKWPLKM
11943	42311	A	12017	1	1020	
11944	42312	A	12018	247	1436	GERGPRTMSTRESFNPESYELD KSFRLTRFTELKGTGCKVPQDV LQKLLESLQENHFQEDEQFLGA VMPRLGIGMDTCVIPLRHGGLS LVQTTDYIYPIVDDPYMMGRIA CANVLSDLYAMGVTECDNML MLLGVSNKMTDRERDKVMPLI IQGFKDAAEEAGTSVTGGQTVL NPWIVLGGVATTVCQPNEFIMP DNAVPGDVLVLTKPLGTQVAV AVHQWLDIPEKW\NKIKLVVTQ EDVELGLPGRRLMNMARLNRT AAGLMHT\FNAHAAT\DITG\F\G ILGHAQNLGQASRRNDVSFVIH NLPGAWPRWLAVSKACG\NMF GLMHVTCPETSGG\LLICLPR\E QAARFCAEIKSPKYGEGHQAWI IGIVEKGNRTARIIDKPRIIEVA\ HKWPLKM
11945	42313	A	12019	219	380	RPLQIRSHSELLGVWTPTSEF*E DTTQSVTAGLLEVSWGRVVLC SKSFPALQS
11946	42314	A	12020	1	516	
11947	42315	A	12021	1	228	
11948	42316	B	12022	56	656	
11949	42317	A	12023	1	488	
11950	42318	A	12024	3	419	
11951	42319	A	12025	1	348	
11952	42320	A	12026	1	708	
11953	42321	A	12027	25	213	
11954	42322	A	12028	1	1165	
11955	42323	A	12029	1	411	
11956	42324	A	12030	1	996	
11957	42325	B	12031	1	744	
11958	42326	A	12032	1	444	
11959	42327	A	12033	1	555	
11960	42328	A	12034	1	2241	
11961	42329	A	12035	1	408	
11962	42330	B	12036	1	423	
11963	42331	B	12037	1	507	
11964	42332	A	12038	3	529	
11965	42333	A	12039	191	319	
11966	42334	A	12040	1	660	

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11967	42335	A	12041	1	579	
11968	42336	A	12042	1	2940	
11969	42337	A	12043	1	4280	MEYYAAIKKDEFMSFVGTWM MLETIILSKLSQGRKPKRRMLSL IGSQLLTNKGTSWMENEFDELT EVGFRRTLHPKSTTEYTFFSAPH CTYLKIDHIIASKTLLSKCKRTEI ITNGLSDHSVIKLELKIKKFTQN CTTTWKLKNLLLNDYWVNNEI KAEIKMFFETSENEDTMYQNL WDTFKPLCRGKFIALNAHKRK QRRSKIDIQTAQLKELEKEQQT NSKASRRQEITKIRAELKVTETR KTLQKINESRSW
11970	42338	A	12044	1	645	
11971	42339	A	12045	3	362	LDQLLDMSYE/QLMQLYSCAQ RRRLNPGLRRKQHSLLK\RLRK AKK/EAPPMEKPEVVKTHLRD MIILPEMVGSMVGVYNGKTFN QPEMIGHYLGEFSITYKPVKH/G RPGIGATHSSRFIPLK
11972	42340	A	12046	1	519	
11973	42341	A	12047	2	599	PPPRSSEDPAKMAEVEHEEGSG PFRKFTLPAAVDL\DQ\LLDIVPT KQFDAAVQVAAQRRRLEPGGL RRKQ\HSPA*KRLRKAKKGGPA PWRKPEVVKT/HTLRDYDHSYP EMVG\SMVG\VYNGK\TF\NQV GDQGVCGRPCRLGWAGVA*CR RDQLTPSFALGLPQPEMIGHYL GEFSITYKPVKHGRPGIGATHSS RFIPLK
11974	42342	A	12048	8	224	RTASYPRRFPWDHLLICPCQQL LICFLSLWIRLVFTKVSCT*NHN NMFSCVWLLLLSMIFLRFTHIA CIRNI
11975	42343	C	12049	65	163	
11976	42344	A	12050	3	187	
11977	42345	A	12051	3	689	HASDQKEIIIEPFQAVDEVERVP EDYYTGPVYLTEVTTLQQRLLQ PDFQPVCASQLYPRHKHLLIKR SLRCRKCEHNLSKPEFNPTSIKF KIQLVAVNYIPEVRIMSIPNLRY MKESQVLLTLTNPVENLTHVTL LECEEGDPDDINSTAKVVVPPK ELVLAGKDAAAEYDELAEPQD FQDDPDIIAFRKANKVGIFIKVT PQREEGEVTVCFKMKHDF\KNL \AAPISP
11978	42346	A	12052	1	882	
11979	42347	C	12053	152	404	

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11980	42348	A	12054	3	398	LRKIKIDLGKFSDNPDGYIDVLQ GLRQSFDLTWRDIMLLLDQSLT PNEKSAAKTAAREFGDLWFV/S FQN*SCKTTNRSSNGAPDAVHD *D/PTADPWTGPLAHALMLMTL KAPLTRKSQLHDPYYAPIQQEA V
11981	42349	A	12055	2	286	
11982	42350	C	12056	261	482	
11983	42351	B	12057	1	1133	
11984	42352	A	12058	438	575	NKTRMPSLTTPLQHSTESPSQSS QTREGNKGYPNW*RGSHTVTV C
11985	42353	B	12059	50	309	
11986	42354	A	12060	1	870	
11987	42355	A	12061	148	368	ELSSCSLMSHRAIHHPSEERATT T/NQQSEPGSW*GWVGANRWC HKMSSGGSLGTEPCGSCLACSA WTVTVQAQ
11988	42356	A	12062	405	707	RLSLQTAGCSDVPVFPSAPSGPP SPA*AP*SGSAASPWPPFAPSAA HVAMPAPPRHWPQLSLKMPPW PPDSPVPPGCLA*AEAPPPHCPV HLPASRSALS
11989	42357	A	12063	90	470	KSVHSLPPSFSSLLPWTCNRTLS KPPALPSPSRQPECRRRLLHCSG SRHSSCPSSSSSPSFSSSPSPSSSS SASASPPPPSPSPAPP*LWLQPL FCSQ*QLCHCQELVHLESRLTY PYHSSNQPF
11990	42358	B	12064	1	474	
11991	42359	A	12065	1	383	MEYYAAMKNDEFMSFVGTWM KLETIILSKLSQGQKPNTACSHS WMDPQRRGKRQSLSISEAGAN QFPKSVFRFFGLGDSKVGSKWS ATCACEPIHTSEYCGDRVICKTT SSLRGASFAWCSSGNGE*WFPA SSMSLQRT
11992	42360	A	12066	1	384	MIITGLEDYEMGLRMEGTLEIP GHYQKDKFLAQSTPDLLLPKTS LTNPFSINQILAERQIVTFTVYP DTERDRETRNLADLKQIKIDLG KFSDNPDGYIDILRGLRQSFDLT W\RDIMLLLNQTLAPN
11993	42361	A	12067	152	238	
11994	42362	A	12068	89	544	
11995	42363	A	12069	62	199	SWKPSFSANYHKDRKPNTACS HS*DPAFLAPSPVP*SRPLRPPQ D

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11996	42364	A	12070	1	655	SVSGLVEKVTFEQRLKGGEGDS TVGSSGNEIFRQWPCWELSNGC SLQGDAGCSCLVVHVTFPAGSL SGDGLPTAQWLQSLLVLAGGR RVNSTQGHRCHHWGSVAEPCV LVKRHHAAQEGLCSFQKTPRS QVPFHLFWDPGHHTLLCSYCPS \GVAGTQPAVQAVSTAV*TAAE GEPLPMSENMRCLVFCPCDSLL RMMVSSFIRVPTKDMNSSFFM
11997	42365	A	12071	1	987	MLVLGYNRKNTEGTQKQKGT NASDFHFLSQVLEQVVSPKGSK EAQCCVLRHLGCESSESAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLKGKERR QREGERRERKREREKRERESQR KERKREKKGKKREREKDRSDL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYYLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKP\IN*SMISTI TQGKEENPTAFLERLREALRKH
11998	42366	A	12072	1153	1379	CLASWKEKSLLHCPQRKQRLR GEELEKLKKWKETATQIKRSYC WI*PSKSPHYLTS*KR*WNY**L GNYNSIPAS
11999	42367	A	12073	1	864	
12000	42368	B	12074	8	441	
12001	42369	A	12075	62	332	TDSPHCTDPPSRPTVPASCLKRK CCGSTMPTARPIMPTLMETR*M PISPRVSWAGPRPTSWPALISST LFPRMANHWRD*SRITWFQGQ A
12002	42370	A	12076	34	409	TRAAGIRHEGKPEKTGLKRNFT N/DCRKS*TSG*RSTTSSRSRSPS PAPRSRSCSR\RDLPAPPPLSRSG DRPQTAPSCPMWRARLPSCPGS AIPIPRPAWTRSACCGAASTRLR PFSGSSTSPQWM
12003	42371	A	12077	1054	1368	
12004	42372	A	12078	298	514	PNWFKHDVSKSESFSNKMWIA KILKA/ARPAPLTQCV/RNSCFL QCRHLSSVSASDLT*DNVKRQF CVSPHTES
12005	42373	A	12079	2	1613	
12006	42374	A	12080	2	106	

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12007	42375	A	12081	42	305	YNTVLPKACLCGSLICWMN*SH SDQNMQVSVERSNLRVRLYAC CGLLLCTAYPQHFAHRYVDKIP GYPSRAGTLTGLHPMQVCRCR
12008	42376	A	12082	206	6038	
12009	42377	A	12083	1	4316	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN
12010	42378	A	12084	393	991	
12011	42379	A	12085	324	438	
12012	42380	B	12086	528	598	
12013	42381	A	12087	52	574	
12014	42382	A	12088	1235	1366	
12015	42383	A	12089	1	1800	
12016	42384	A	12090	1	513	
12017	42385	A	12091	3	77	
12018	42386	A	12092	1923	2171	GAFCPFTLLHGYQVLQWPGSSL PHKEGPAPALEGGHVYPRWI*A SADSQSTEAGRIGPASTG*RQYP GGEEHACCLPALLHS
12019	42387	A	12093	1	360	
12020	42388	B	12094	21	3636	
12021	42389	A	12095	1	936	
12022	42390	A	12096	1	599	
12023	42391	A	12097	1	248	VGKSSIVCRFVQDHFDHNISPTI GASFMTKTVLCGN/ELHKFLIW DTAGQER/SRQIPPLDPHENGNN GTIKVEKPTMQASRRCC
12024	42392	A	12098	1426	1572	
12025	42393	A	12099	367	513	
12026	42394	A	12100	31	661	APALPGCEHMMAIRELKVCLL GDTGVGKSSIVCRFVQDHFDH NISPTIG\ASFMTKTVPCENDFT KFLIWDTAGQERFYSLAPMYY RGSGAAVIVYDFTEAGFHFHPL KKWV\KRLKELGPE\NIVMAIA GNKCDLSDI\REVPLKGC*RNTA ESIGAIVVETSAKNA\INIE\ELFQ G\ISRPDPHPWTPHENGNNGTIK VEKPT\MQAS\RRCC

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12027	42395	A	12101	1	487	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNW KKLL
12028	42396	A	12102	1	1563	
12029	42397	A	12103	1	1449	
12030	42398	A	12104	3	1606	
12031	42399	A	12105	2	402	
12032	42400	A	12106	172	329	
12033	42401	A	12107	1	720	
12034	42402	A	12108	97	206	
12035	42403	B	12109	1	1248	
12036	42404	A	12110	1	1419	
12037	42405	A	12111	1	1387	MDKFLDTYTLPRLNQEEVESLN RSITGSEIVAIINSLPTKKSPGPD GFTAEFYQRYKEELVLLLLKLF QSIEKEATLPNSFYEASIILIPKP GRDTTKKENFRPISLMNIDAKIL SKILANQIQQHIKKFVHHDEVG FIPRMQGWFNIHKSKNVIQYIN RTKDKNYMIISIDAEKAFDKIQ QLFMLKTLSKLGIDGTYLKIIRA IYDKPTVKIILNGQKLEEFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGILLGKEEVKLSLF ADDMIVYLENPIVSAQNL\LKLI SNVS\KV*GYKINVQKSQAFLY TTNRQTESQIMSELPFTIASKRI KYLGIQFTRDVKDLFKENYKPL LNEIKEDTNKWKNIPCSWVGRI NIVKMAILPKPPLLIPRQTGSGV DLQQTPTDLQLSVLTVRRKINK QKGHPHQYLIWTSPSSKTKGRQ LLASNRTKLDGE
12038	42406	B	12112	1	711	
12039	42407	A	12113	1694	4489	IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKAIRSQKNKS GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYNYLIFDKPEKNEQWGKDSLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLIVRPKTIKT LEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLKSF CTAKETTIRVNRQPTKWEKTFA TYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDM

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12040	42408	A	12114	1	115	
12041	42409	A	12115	58	414	
12042	42410	A	12116	6	389	VMTTGTNSRVEPRVRGRVYKK KMDKKRQEKITEAKSKDKSQM DEEKTD/DEKPKLQVELEQEYQ DKFKRLPLEILEFVQEAMKGKI SEDSNHGSAPLSLSSDPGKVNH KTPSSEELGGDIPGKEFDTPL
12043	42411	B	12117	50	5137	
12044	42412	A	12118	1	1194	
12045	42413	A	12119	1	2559	
12046	42414	A	12120	3	406	
12047	42415	A	12121	119	423	TSSCSSEKFVITHLLKPTSVNSS KSFSFQLCSIG/VQGAAILWRRR GSLVFRIFSFSALVSPHLCGFIYL WSLTMVTYFSLSNGGRPSPCQA AAPQVNLGLLC
12048	42416	A	12122	3	597	ISASASDNVFMSVSSPSCSSCFF TLYRYLWKSEKPLYYSFVDKP VAYKKREMVVNLQKQFKHTG RVQ/SSNLLEKKAPSSFQFNWT EEDTDRTCF\HGHSLQGVLKEK GQSLLTKNSLYWLSTQKF*RCY GHHVPPYEESIYFLSNRFNLNLF SFLLRIKTSFL\HEEVSLVEK\KL FEEKIQCKKERNQDPRKVRTTL
12049	42417	A	12123	1	883	
12050	42418	A	12124	23	362	FAFNMPEPGKIVPAP*KGSKKA VTKAQNKDGEKRMLSRKESYS VYVYKVLKQVHPDTGVSSKG MGIMNSFVDDILERIAGEAFRL AHYNKRSTITSREIQTDVRLLLT REMVK
12051	42419	A	12125	2	405	
12052	42420	A	12126	1	398	LHSAMPEPAKSAPAPKKGSKK AVTKAQKKDGKKRKRSRKESY SIYVYKVLKQVHPDTGISSKAM GIMNSFVNDIFERIAGEASRLAH YNKRST\ITLPREI\QTAVRLLLP\ GELAKHAVSEGTKAVTKYTSA K
12053	42421	A	12127	1	401	
12054	42422	B	12128	48	424	
12055	42423	A	12129	3	462	DAWVSGRLTELPSSCFFPPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKKDGKKRKRSRKESYS VYVYKVLKQVHPDTGISSKAM GIMNSFVNDIFE\RIAGEASRLA HYNKRSTITSREIQTAVRLLLPG ELAKHAVSEGTKAVTKYTSSK

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12056	42424	A	12130	74	504	FAFNMPEPAKSAPAPK\KGS\KK AVTKAQKKDGKKRK/RSRQGR AYSVYVYKVLKQVHPDTWHL LLRPWGIMELLSFNDIFRNGIAG LRVSRLGRI*QQGVSTIHLPGEI HDGPLRLACLPGGVWPSKAVF RGAPRPFNQVNTSV
12057	42425	A	12131	53	471	
12058	42426	A	12132	1	241	FKDTCTRMFIAALFTIAKTWNQ PKCPTMWHIYTMEYYAAIK/SD EFMSFVGTWMKLETITLSKL*Q GQKTKHRMFSLIGGT
12059	42427	A	12133	1	244	
12060	42428	B	12134	1	2142	
12061	42429	A	12135	1	1962	
12062	42430	A	12136	3	393	IWMKLETIILSKLSQG*KTKHR MFSLTGGNLTMRTLGHRLLPSL PHRLRPCARLHLRCPPWPPPSR RRCARSTTPTATPPSTATSRWSS TPPTCTCLWPSTSTGTTWPWRT SSATSCACRTTKWSMPRS
12063	42431	A	12137	2	87	
12064	42432	A	12138	1	270	
12065	42433	C	12139	1	214	
12066	42434	A	12140	1	684	
12067	42435	C	12141	1	333	
12068	42436	A	12142	1	189	
12069	42437	A	12143	215	310	
12070	42438	A	12144	2	91	
12071	42439	C	12145	1	229	
12072	42440	A	12146	1	268	
12073	42441	A	12147	1	278	
12074	42442	A	12148	2	274	WMKLETIILSKLSQRQKTIHHLF SLIALFTIAKKWKPPRYLSVDK WIKKLWY/HTYTMEYYSAFKK EAILPIAIAWMGLKDIMLSEISQ TWP
12075	42443	A	12149	2	136	
12076	42444	A	12150	2	95	
12077	42445	A	12151	1	233	
12078	42446	A	12152	377	484	
12079	42447	A	12153	2	91	
12080	42448	A	12154	1	891	
12081	42449	A	12155	1	1194	
12082	42450	A	12156	785	892	
12083	42451	A	12157	191	317	
12084	42452	A	12158	410	520	
12085	42453	A	12159	683	796	
12086	42454	A	12160	830	927	

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12087	42455	A	12161	18	539	PTDP*LGIYQKE\YKSCYYKDIC T/RVCVPAALFTIANTWNQPKC TSMIDWVKKMWHIYTMEYYA AIKTDEFMSF\AGTWMKLETIIL RKLSQGQKTKHRMYSLIGGNL TMRTFGHSAGSHHTPGPIMRCG AGGGIALGEIPNVNDELMGTAN QHGTCIPMQQNCTLCTCTLKLK V
12088	42456	A	12162	1	108	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSL*GVSYYVAQAGLK LLGLSLSKCRDYRCEPPCPE
12089	42457	A	12163	1	701	
12090	42458	A	12164	274	435	
12091	42459	A	12165	1	3658	
12092	42460	A	12166	749	856	
12093	42461	A	12167	1	598	
12094	42462	A	12168	538	664	
12095	42463	C	12169	1	873	
12096	42464	B	12170	177	325	
12097	42465	B	12171	1	1245	
12098	42466	A	12172	1	3313	
12099	42467	A	12173	1940	2060	
12100	42468	A	12174	1	1213	
12101	42469	B	12175	155	559	
12102	42470	A	12176	2	321	PAPRGGAYRGRQTSLSCGGLHP V*ASWLLCLPKQAWAM/VGRP PQASLLPCSLISDCCASNQRDSV GVGPSEPCAGYNLLLCRFLSQS EKHSIRVGAVDCSCSYLAIL
12103	42471	A	12177	1	519	
12104	42472	A	12178	1	477	
12105	42473	A	12179	119	375	KRTQT*AIAGAPPPASLPPCSLIS DCCASNE*GSVGIGPSKPGAGY NLLLCHLISPSISPTSSPKSDTCPI ADFSNKSPDRSSAGDILLAMQS LGSMAIFLILILPTREHGKFFHLF VSSFISLSSGL
12106	42474	B	12180	1	363	

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12107	42475	A	12181	1	1309	MAEGEEGTSYMAAGERVVAIA LIDGFRPLTLESTFFNSGSCSKL EQHSTYLGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVPEP KQHGIGPKQKYRSTGPNRALR NNAAYLQFLIFGNLEKTKPWG KDSLLIKVFEAAVLWIECFAFIF YDARGVLIVVQVDSCSKLEQHS TLSRAILLIYKGFCRFRNHHQTG FSPAGANQRGPLAATLSGPGGE GQSAVARLTGEKKNHPGAQYA NRLSPRVGRFINAAGTTGFPTG KRAVSATQLMDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGHLISDCCASNQPDSVGVG PSEPGAGYNLVVRHFLSPSEKH SIRVGVTRFSRCRPSPLPLTQKG NSLTPCASQLRQCLALLRLR*R AISCCPSHW*KEKPPWRPIRKPP LPARWPIH*CSWHDRFPD/CESG HLISDCCASNQPDSVGVGPSEP GAGYNLVVRHFLSPSEKHSIRV GVTRFSRCRPSPLPLTQKGNSLT PCASQLRQCLALLRLRH
12108	42476	B	12182	1	1335	
12109	42477	A	12183	1	1675	
12110	42478	B	12184	57	1530	
12111	42479	A	12185	1	1419	
12112	42480	A	12186	1	574	RVDDFVRQTRPSAQAALAEKM AANQPPPLMMKHSQTDLVSRL KT\RKILGVGGEDDDGEV/HRSP ISQALGTEIKFTIREPLGLTVWQ FVSAVLFSGIAIMALAFPDQLY DAVFDGAQVTSKTPIRLYGGAL LSISLIMWNALYTAEKVIIRWTL LTEACYFGVQFLVVTATLAETG LMSLGIRLTRSSRRGR
12113	42481	B	12187	79	387	
12114	42482	A	12188	1	908	
12115	42483	A	12189	2	70	
12116	42484	A	12190	1	1158	

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12117	42485	A	12191	2	611	FVSVPSVLLGLQFWRSERD/TA RLQSARWRVERGRLKELLSRQ RPRRREEVVVGREVCRTEMEV RASLQKIVSNGDEQLEKAMEEI LRDFEKRPSSLLVDCQSSSEISD HSFGDIPASQTNKPSLQLILDPS NTEISTPRPSSPGGLPEEDSVLF NKLTYLGCMKVSSPRNEVEAL RAMATMKSSSQYPFPVTLYVP
12118	42486	A	12192	3	497	
12119	42487	A	12193	1	804	
12120	42488	A	12194	1	1243	MAPVEHVVADAGAFLRHAAL QDIGKNIYTIREVVTEIRDKATR RRLAVLPYELRFKEPLPEYVRL VTEFSKKTGDYPSLSATDIQVL ALTYQLEAEFVGVSHLKQEPQ KVKVSSSIQHPETPLHISGFHLP YKPKPPQETEKGHSACEPENLE FSSFMFWRNPLPNIDHELQELLI DRGEDVPSEEEEEEENGFEDRK DDSDDDGGGW\ITPSNIKQIQQE LEQF\DVPEDVRVWLA*PPDFA MQNVLLQMGLHVLAVNCMLI REARSYILRCHGCFKTTSDMSR VFCSHCGNKTLKKVSVTVSDD GTLHMHFSRNPKVLNPRGLRY SLPTPKGGKYAINPHLTEDQRF PQLRLSQKARQKTNVFAPDYIA GVSPFV\ENDISSRSATLQVRDS TLGAGRRRLNPNACRKKFVKK
12121	42489	C	12195	164	350	
12122	42490	A	12196	1	378	
12123	42491	B	12197	265	1539	
12124	42492	A	12198	1	2511	
12125	42493	A	12199	1	1077	
12126	42494	B	12200	38	1451	
12127	42495	A	12201	1	207	
12128	42496	A	12202	1	197	
12129	42497	A	12203	1	216	
12130	42498	A	12204	1	335	
12131	42499	A	12205	1	174	
12132	42500	A	12206	1	1309	
12133	42501	A	12207	1	1266	

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12134	42502	A	12208	1	590	IDRFDAPCGLEELEDHEDEFNE EDERAIEMYRRRRLAEWKATK LKNKFGEVLEISGKDYVQEVTK AGEGLWVILHLYKQGIPLCALI NQNLSGLARKFPDVKFIKAISTT CIPNYPDRNLP\TILVYPG\GDIN G\QFIGPLSV\GGMNLTRDELEW KLSESGAIMTDLEENPKKPIEDV LLSSVRRSGPHEEGQRFRG
12135	42503	A	12209	291	416	SHYLKIHAEKLSEYDQISPPNSQ PDKENPVLST**SIQRRHMTLFK MNLKIILKYRKPEA*SQRLVSK R*KHSIRGSGINLSFVPTGFQIVP FHLFETSLWL
12136	42504	A	12210	437	773	DYTITGELKTAIQRSKINFCPILH SHSSHNAKSFVI*TVTLLHRHLL *KVSVNKVQSLFIQCGIFSEAGA GVYNYCPPPRQRRQPGDKPRW RWRRGRNNRCSANSHGLQLYA
12137	42505	A	12211	1	1183	
12138	42506	A	12212	1	459	
12139	42507	A	12213	1	513	
12140	42508	A	12214	91	1168	
12141	42509	A	12215	323	429	
12142	42510	A	12216	870	1305	SPGLPHCWQPCRARSRGTDVW NVLVS\GSGSGAYKEPAILVGPE NLTLTVHQTAVLECVATGNPRP IVSWSRLGWPPNPTAKEQEQRA KTESQRKQPRDKARENQPKAA RPKRAAPKSHEAARKTNPPTAS TKRQAAPTNTPKESS
12143	42511	A	12217	1	2695	
12144	42512	A	12218	1	258	
12145	42513	A	12219	1	624	
12146	42514	A	12220	247	425	
12147	42515	A	12221	31	858	LLEIVNSSIQPEKQAGWLSQAV HGAPDGPNRPMLHPETSPGRG HLLAVLLALLGTTWAEVWPPQ LQEQAPMAGALNRKESFLLLSL HNRLRSWVQPPAADMRRLDW SDSLAQLAQARAALCGIPTPSL ASGLWRTLQVGWNMQLLPAG LASFVEVVSLWFAEGQRYRHA AGE*ARNATCTHYMQLVWATS SQLGCGRHLCSAGQAAIEAFVC AYSPRGNWEVNGKTIVPYKKG AWGSLCTASVSSLLKAWDHAR GLLGGPRETLGKEPTEPWTALK
12148	42516	A	12222	1	1519	
12149	42517	A	12223	1	789	

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12150	42518	A	12224	1	505	ATEDPGVAMGRRPARCYRYCK NKPYPKSRFCRGVPDAKIRIFDL GRKKAKVDEFPLCGHMVSDEY EQLSSEALEAARICANKYMVKS CGKDGFHIRVRLHPFHVIRINK MLSCAGAD/RIHISKKWGFTKF NADEFEDMVAEKRLIPDGCGV KYIPSRGPLDKWRALHS
12151	42519	A	12225	135	828	RFWVSPHGPAAPARCY\RYCKN KPLPKVLRFCR\GVP\DAKIRIFD PGAEKRQKVE*VFRFCGHMVS DE\YNQLSS*ALE\AARNLCPIS TMVKS\CGKDGF\HIRV\RLHPF HVIPHQTRCCSCAGADRLQTG MRG\AFGKPQGTVARVHIGQVI MSI\RTKLQNKEHV\IDALRRAK \FKFPGRQ\KIHISKKWGFTKFN ADEFEDMVAEKRLIPDGCGVK YIPSRGPLDKWRALHS
12152	42520	A	12226	2	367	
12153	42521	A	12227	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12154	42522	A	12228	1	714	
12155	42523	A	12229	122	939	YPGKQGLEWTSNKIQQTCS*GS SLLEGKLTNRKDIHTKTPSVRH/ RSSKAKERVSVIEDQMNETKRE EMFREKRVKRNEQSLQEIWEY VKRPNLRLIGVPESDGDNGTKL ENTLQDIIQQYFPNLARQANIQI QEIQRMPQRCSSRRAAPRHIIVR FTKAEMKEKMLRAARGKGRV THKGKPIRLKVDVLAETLQARR EWGPIFNILKEKNFQPRISFPAK LSFISKGEIKSFTDKEMLRDFVT TRPALQELLKEALNMERNNRY QPQQKHAKL

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12156	42524	A	12230	1	1043	MGDFLHSTDRNYLIKFWAKLS AKKTPANSSSPLGDHQHPCITK NLQIPEKWLIGLLLPLKADLLK EDAGTHCKEAKNLDERLDEWL TRINSVEKFLNDLMELKTMAQE LHYACTSFSSQFDQLEERVSVIE NQMSEMKREEKFREKRVKRNE QSLQKIWDYVKRPNLRLTGVPE SDWENGTKLENSLQDIIQENFP NLARQANIHIQEIQRMPQRYSS RRATPRHLIVRFTKFEMTEKMV RAAREKGQVTHKGKPIRITADI SAETLQARREWGPIFNILKEKN FQPRISYPAKLSFISEGEIKSFTD KQMLRDFVTTRPTLQELLKEAL /NMERNNQYQPLQKHAKL
12157	42525	B	12231	1	1275	
12158	42526	A	12232	1	1584	
12159	42527	B	12233	1	1023	
12160	42528	A	12234	1	2052	
12161	42529	A	12235	5160	6183	VSKHPQASAGDTQTNRVWSGP PANSDRPAAEGPDC*KEN*QTE RTS\NQNPICMSPSSKTKEAKNL DKRLDEWLTRINSIEKTLNDLM ELNTMARKLRDACTSFSSQFDQ VEERVSVIEDQMNEMKREEKF REKRIKRNKQSLQEIWDCVKRP NLRLIGVPESDGENGTKLENTL QDIIQENFPNLARQVNIQIQEIQ RTPQRYSSRRGTPRHIIVRFTKV EIKEKILRAAREKGRVTHKGKPI RLTAVLLAETLQARREWGPIFN ILKEKNFQPRVSYPAKLSFISEG EVKSFTDKQMLRDFVTTRPAL QELLKEALNMERNNRYQLLQK HATLSRPSMLG
12162	42530	A	12236	1	975	
12163	42531	A	12237	3	1186	
12164	42532	A	12238	1	906	
12165	42533	A	12239	1	1882	
12166	42534	A	12240	1	1394	

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12167	42535	A	12241	1	4935	MGPGARLAALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLLRRYLRGEEARLRDL TRCNDETITYLLDKRLTVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLRSRWAVGGATG SWVLSKGDRASLGERVVTGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLSPTSTRQRGQ SERSQDANGRRKQKT
12168	42536	B	12242	88	1014	
12169	42537	A	12243	686	1920	IKPQRWGKKQNRKTGNSKKQS ASPPPKERSSSPATEQSWTENDF DELREEGFRRSVITNFSELKEHV VTHRKEAKNLEKK\LDEWITRI TNAEKSLKDLMELKTTAQELR NECTNLSNRCDQLEETVSAME DQIN/EMNEMKQEGKFREKRIK RNEQSFQ\EIGDYVKRPNLH\LI GVPESDGQNGTKLENTLQDIIQ ENFPNLARQANIQIQEI\QRTPQ RYSLRRATPRHIIVRFTKVEMK EK\MLSAAREKGR\VTHKGKPIR LTTADLSAETLQAQKTEWG\PIF NIL\KEKNF\QPRIS\YPAK\LSFIS EGEIKYFTDKQMLRDFCHHQG LPLKELLKEEALKHWKGTTRY QPLAKTLPKYRSTRQKVNKDT QELNSALHQADLIDIYRTLHTK STEYTFFQHHTTPIPKLTT
12170	42538	A	12244	1	633	
12171	42539	A	12245	3	109	
12172	42540	A	12246	2	575	
12173	42541	A	12247	1	237	
12174	42542	A	12248	1	1065	
12175	42543	A	12249	2	338	
12176	42544	A	12250	1	1319	
12177	42545	A	12251	1	744	MQKALCAAPDLGTFVTVLTPPP GAQIGSRRERSKVPYIVRQCVE EIERRGMEEVGIYHVSGR\VAA DIQALKAAFDVN/NRTMHSSWE ESDELLKARDDPHSGQHSRDG ALAKAGMADKKDMSVMMSET DMNAIAGTLKLYFRELPEPLFT DEFYPSFAEGIDRLERVAEKEA VNKMSLHNLATVFGPTLLRPSE KESKLPANPSQPITMTDSRSLEV MSQVEVLLYFLRLEAIPALDSK RQSILFSTDV

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12178	42546	A	12252	1	507	
12179	42547	A	12253	1378	4280	STPMAVAGPLGRPWSTSPTRAS TSGASWKGRARARSCAARAPL SRRSALPGPAGPTPPGVLRIAEA AIPRTAAPMRTSPPARRTSPLAS PAACPQAPPPTACSGTKAALPR RTRNSPSTAAVPPRRSAISGTGT ARLSCPRPPSWASARPGRSGPT MTRAPSMETQMARSEHHLDTA ALQTGQRSSAGTKMGCPTLMT RPPHRPTSAARAGAAGMRWSR EP*SPLK/RSELDLEKGLEMRK WVLSGILASEETYL
12180	42548	A	12254	1	1109	MRTPYKTSPMRMLYMTSLMTP TRHANEDAVDDIAYKDTVQDI TSEDAVYDIANEDVVYDIANED ALQDIANEVAVYDIANEDIVYD IANEDALYDITNEDAVYNIANE DAVYGIANEDAVYEFANKHAV YDIANEDTVQDICKKEDAANK CYFPGFFPIRCRHEHLPVCIIDVI CSLIKCRHEHLPSSLIGQDRLGA QASRRERSKVPYIVRQCVEEIER RGMEEVGIYRMSGVAADIQAL KAAFNVSECRPAQDGMEVWA VVSAMRSQSAPRPRHVTSFSVS FLHLSGSSRRPLHFRALS\NNKD VSVMMSEMDVNAIAGSLKLYF RELPEPLFTDEFYPNFAEGIGEH WRPWPHGRRLLHVHCCPQRL
12181	42549	A	12255	1351	4308	WKGRARARSCAARAPLSRRSA LPGPAGPTPPGVLRIAEAAIPRT AAPMRTSPPARRTSPLASPAAC PQAPPPTACSGTKAALPRRTRN SPSTAAVPPRRSAISGTGTARLS CPRPPSWASARPGRSGPTMARA PSMETQMARSEHHLDTAALQT GQRSSAGTKMGCPTLMTRPPH RPTSAARAGAAGMRWSREPWS PLK/RSELDLEKGLEMRKWVLS GILASEETYLSHLEALLLPMKPL KAAATTSQPVLTSQ
12182	42550	B	12256	1	1017	
12183	42551	A	12257	2310	2834	EEKYNMQTRLRRAEDVFPPVIG VAAHKGGVYKTSVSVHLAQDL ALKGLRVLLVEGNDPQGTASM YHGWVPDLHIHAEDTLLPFYL MLR\LAIETVAHDYDVIVIDSAP NLGIGTINVVCAADVLIVPTPAE LFDYTSALQFFDMLRDLLKNV DLKGFEPDVRILLTKYSNSNGW

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12184	42552	A	12258	106	108	NFLFVLRRQLWVGGLCW*AAE LNKVCL
12185	42553	A	12259	1	901	
12186	42554	A	12260	23	482	KPRELGPISPVWLPPDRLPERPQ RRRPSGVDPGSWLGSGSCGSTG CSALMSCSCGSTPLLSLALKVT PGGVLGAPSGSEDGS*PNRKAC GSEMEICLTTRGVWGPEVALG VGGGLQQSCRAPCGGLPKLLRS WSQSSLSPNSPGRGASSGEAA
12187	42555	A	12261	1	1938	
12188	42556	A	12262	1	2235	
12189	42557	A	12263	43	1827	THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLLPLPAAGRVVVRRL AVVRSGSRSLSTADMTKGLVL GIYSKEKEDDVPQFTSAGENFD KLLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDPCG DAQAAAEGAVLGLYEYDDLK QKKKMAVSAKLYGSGDQEAW QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICSAIVS AAKLNLPINIIGLAPLCENMPSG KANKPGDVVRAKNGKTIQVDN TDA\EGRLILADALCYAHTFNP KVILNAATLTGAMDVALGSGA TGVFTNSSWLWNKLFEASI\ET GDRV*RMPLFDHYTRQ\VVDC QLAD\VNNIGKYRSAG\ACTAA AFVKEFVTHRKWAHLDIAGVM TNKDEVPQSTGKA*LGRPTRTL I\EFL\LRFSQDNCLVQILKNVFH SVLNWTVELKKVFE
12190	42558	A	12264	1	405	GIRSAEVGKHLAHILLSRQQGR RPVTLIGFSLGARVIYFCLQEM AQEKDCQGIIEDVILLGAPVEGE AKHW\SLSGRVVSGRIINGYCR GDWLLSFVYRTSSVQLRVAGL QPVLLQDRRVENVDLTSVVSG
12191	42559	A	12265	1	1072	
12192	42560	A	12266	105	514	

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12193	42561	A	12267	44	872	NARPWVRGLLIEFRRRGSLCRE RAREMEMGRRIHLELRNRTPSD VKELVLDNSRSNEGKLEGLTDE FEELEFLSTINVGLTSIANLPKL NKLKKLELSDNRVSGGLEVLA EKCPNLP\HLI*GGNKIKDLSTIE PLEKLENLKSLDLFNCEVTNLN DYRENVFKLLPQLTYLDGYDR DDKEAPDSDAEGYVEGLDDEE EDEDEEEYDEDAQVVEDEEDE DEEEEGEEEDVSGEEEEDEKGY NDGEVDDEEDEEELGEEERGQ KRKREPEDEGEDDD
12194	42562	A	12268	1	388	KRGAAMDGRVQLIKALLALPIR PATRRWRNPIPFPETFDGDTDR LPEFIEQTGSYMFVDENTFSSDA LKT\ALPQSLPSIASHRQTAAPS DLDSPRRYLGWPQSLDSDSDS WPPPKGSVTFSETYFLPTP
12195	42563	A	12269	1	127	
12196	42564	A	12270	5	434	ISLRYLDGLAGPTHASAATEAS DRSEDLRWT/VCAQLIQALLAL PIRPATRRWRNPIPFPETFDGDT DRLPEF\IVQTCSYMI\VDENTFS SDALKVTFLITRLTGPAL\QWVI PYIKKESPLLNDYRGFLAEMKR VFGWED\DEDF
12197	42565	A	12271	515	1137	
12198	42566	A	12272	1	762	
12199	42567	A	12273	1	468	
12200	42568	A	12274	2716	3411	KREEETKKKSKREMEVVKKKQ CTYSFKSQGKFLSTHARQFSIGS QPISASQTVEEIMKSILTLQSQI\ NSLAAVTLQNR*GLDLLTAEKG GLCTFLGEECCFYTNQSGIA*D ATQRLQEKASEIRRLSNSYTNL WSWATWLLPFLGPVAAILLLL AFGPRIFNLLVKFVWSRIEAIKL QMVLQIEPQMSSTNNFYRGPLD *PAGTSPGLESSPLKDTTTAKPL LRPYPAGSS
12201	42569	A	12275	8312	9221	
12202	42570	A	12276	74	471	
12203	42571	A	12277	4043	4159	LFCQSGFHSLLTPSTATCSTIR* VATSRLRPVFTCRRS
12204	42572	A	12278	1	1332	
12205	42573	B	12279	29	1316	
12206	42574	A	12280	1	580	
12207	42575	A	12281	2	710	
12208	42576	A	12282	1	1559	
12209	42577	A	12283	1179	1490	

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12210	42578	A	12284	2	313	
12211	42579	A	12285	599	743	GALART*PPQQRWVSCPR/GVP/GAL*REFTMFLSLQAENSIDFVSRELCAHSIRKLQAHVLLIK*VFIK
12212	42580	A	12286	208	398	
12213	42581	A	12287	716	1069	
12214	42582	C	12288	326	577	
12215	42583	A	12289	188	590	
12216	42584	A	12290	860	1121	VPFLTSWVNVGFKSSALHSSALLQFWLTLWE*LPAWARCCCCLPNGSFWGPRSSRLDVAWERPVAPGWREVSPLLSELWTAASGPYG
12217	42585	B	12291	1	1614	
12218	42586	B	12292	1	1080	
12219	42587	A	12293	3	219	
12220	42588	A	12294	890	1094	VESGTHLGQYKIYFGFLYQKKFSLQSHGYILFGCPQYW/ITSTDCPSIPCMWYSRTL*VTWSKKQVTSE
12221	42589	C	12295	1	3912	
12222	42590	A	12296	881	1151	
12223	42591	A	12297	1	1323	
12224	42592	A	12298	1817	2284	VWDGSILYQKLGALDGLSS*VIPLASSLQSLQYPLPSSFIQRILNTYSVKGLRSWTVNEDRVDAVSSGGIWLQVEASLVLY*MLYFSIITLLILGLVHVNFKILDSSSELITDKLCGGLGFTLYTGSKLI*SDVTFPRAFSASTQTSMLTKYTVE
12225	42593	A	12299	1	1109	
12226	42594	A	12300	1	367	
12227	42595	A	12301	1	531	
12228	42596	C	12302	1371	1746	
12229	42597	A	12303	1	645	
12230	42598	C	12304	387	680	
12231	42599	A	12305	655	2498	
12232	42600	A	12306	1	528	ENLGNTIQDTGMGKDFMTETPKAMTTKAKIDKRDLIKLKSFCTAKETTIRVNRQPTEWEKIFAVYPSDKGPISRIYKQLKQIYKKKSNNPIKKWAKNRNRHFSKEDIYVAKKHMEKSSSSLVIRKMHIKTTVGYHLMPVRMAIIKKSGNNRCWRGCGE\C*WEGQLVQPLWKTVWQ
12233	42601	A	12307	1	1359	

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12234	42602	A	12308	1968	2648	TQTNLQEKNKQLHQKVGKGYE QTLLKRRHLCSQQTHMQPTDT WKNAHHQLAIREMQIKTTMRY HLTPLRMAIIKKSGNNSCWRGC GEIGTLLHCWWDCKLVQPLWK TVWRFLKDLESEIPFDLAIPLLCI YPKDYTSFCYKDTCTCMFIAAL FTIAKTWN*PKCSSVIDWIKKM WHIY/TTMEYYGAIKRNKIMSF AGTWMKLDAIILSKLTQKQKT KLRMFLLISRS
12235	42603	A	12309	1	403	
12236	42604	A	12310	3	264	FFYAHIMFIAALF\TIAKTWNQS KCTSMIDWIKK\MWHIHTMEY YAAIKR\RGFMSFTRTWMKLEA IILSKLTQEQKTK\HHMFSLIRGS
12237	42605	A	12311	79	432	
12238	42606	A	12312	1	933	
12239	42607	A	12313	70	675	
12240	42608	A	12314	1	339	
12241	42609	A	12315	3	422	
12242	42610	A	12316	1	471	
12243	42611	A	12317	1	963	
12244	42612	A	12318	375	542	ENDKARRSDTPSML*WVEGMK *SVKAPHTLHLASDYVLEPWG GESATFIPASWDC
12245	42613	C	12319	1	2148	
12246	42614	A	12320	1	1881	
12247	42615	B	12321	1	1074	
12248	42616	C	12322	143	439	
12249	42617	C	12323	123	362	
12250	42618	A	12324	474	603	NHKNPRRKPRQYHSGHRHGQG LHV*NTKNNGNKSQNGQMGSN
12251	42619	A	12325	5169	5756	CPSLPPPHGKPAAACPRSPPGGC CTPRSARTVPRGLSENSQTKCH SADLPPEGPRVFWTPPGTGAAP APPAPAPGPARCGPRRCHAWPP QRRSSGAGRSPPPRHFAEFLKM VAFLRILILRAVSLLRSLDLEIS* G*RP*GPSWGGPPQSTPSAASA ASKTSSPRRWSTPAWAFLARA HPRWVAPSTAAQCTAAP

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12252	42620	A	12326	21	98	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMHRDSCPLDCKVY VGNLGNNGNKTELERAFGYYG PLRSVWVARNPPGFAFVEFEDP RDAADAVRELDGRTL\CG\CRV RV\ELVRMGEK\RSRNRGPPPS\ WGRRPRDDYRR\RSPPPR\RRSP R\RRSFS\RSRSRSLS*ERVGWC WAGGKREDSSERVDLSRRIF
12253	42621	A	12327	919	1043	
12254	42622	A	12328	460	657	CFSPGMWQKTHSRKHSPGAICP INPVGECLVRKIKQLD*ITWINA I*LPLRDGLFYFLNFPFCCRG
12255	42623	A	12329	1	2235	
12256	42624	A	12330	1	255	
12257	42625	A	12331	2	429	CRADLNSRIDDFVPNPSVAVSG ASYAVAAVTMAHYKAADSKR EQFRKYFEK\SGVLDTLT\KVLV ALYEEPE\KLNSALDF\LKHHLG AATP\ENPEIELLRLELAEMKEK YEAIVEENKKLKAKLAQYEP\P QEEKRAELGFFSV
12258	42626	A	12332	670	860	
12259	42627	A	12333	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLLKLHDERVLVAF GQRDGIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYP VSIRFGRPRLTSNEKLMLASMF HS\IKFVVLADP\RQAGIDSLLRK IYEIYSDFALKNPFYSLEMP
12260	42628	A	12334	1	2034	
12261	42629	A	12335	1	324	
12262	42630	A	12336	2	694	FGTRGKAAMAIFSVYVVNKAG GLIYQLDSYAPRAEAEKTFSYP LDLLLKLHDERVLVAFGQRDGI \RVGHAVLAINGMDVNGRYTA DGKEVLEYLGNPANYPVSIRFG RPRL\TSNEKLMLASMFHSLFAI G\SQLSPE\QGSSGIEMLETDTFK LHC\YQTLTGIKF\VVL\ADPR\Q AGIDSLLRKIYEIYSDFAL\KNPF \YSLEMPIRCELFDQNLKLALEV AEKAGTFGPGS
12263	42631	A	12337	2	1658	

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12264	42632	A	12338	3	997	VQKPNRQWRLVQDLRIINEAV VPLYQAVRNPYTLLSQIPEETG WFTVLDLKDALFCIAVHPDSQF LLAFEDPLNPTSQLTWTVLPQG FRDSPHLFGQALAQDLSQFSYL DTLVLRYVDDLLLAAPSETLCH QATQVLLNFLATCGYKVSKLK AQICSQQVKYLGLKLSKGTRAL SEERIQPILAYPHPKTRKQLRGL LGITGFCQIWIPRYSEIARPLHTL IKKTQKANTHLVRWTPEAEAA FQVLKKALTQAPVLSLPTGQDF \SLYVTEKTGIALGVLTQHYGE ERNS*LPTEYLSNIRKPLGDYY WLYRNLKRWQSYTARVIRKER
12265	42633	A	12339	3	421	
12266	42634	A	12340	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
12267	42635	A	12341	1	2223	
12268	42636	A	12342	1	3864	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN

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12269	42637	A	12343	204	963	DCACTFHCRSATKIVKDLKAQ GLVKPCNSPCSTPILGVQKPNG QWRLVQDLRIIDEVVVYVDDL LLAARSKTLCHQATQALLNFLI TCDYKVSKPKAQLCSQKVKYL GLKLSKGTRVLSEERIQPIPAYP HPKTPKQLRGFLGITGFCRIWIP RYSEIARPLYTLIKKTQKADTH LVEWTPEAEVAFQALKEALTQ APVLSLPMGQDVPLYVTEKTGI ALGVLGVLTQVRG/LSLQPMAY LSKEMDVVAKGWPH
12270	42638	A	12344	1	1178	MPESPTPLLGRDILAKAGAIIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQQGLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCLPLRNQQECHQATQV LLNVLATCGYKVSKQKAQLCS QQVKYLGVKLSKGTRAL/QQ*R TDRT*LSTSNCSNLRHSRGPSRG SLD*SQPQLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIRRRKKGL IRIYMLPLILSAPYDHLH
12271	42639	A	12345	1	841	
12272	42640	A	12346	3	1428	
12273	42641	A	12347	2	268	
12274	42642	A	12348	1	897	
12275	42643	B	12349	1	1650	
12276	42644	A	12350	232	1002	TPGSTVHAPEADQGLQKIVKDL KAQGLVKPCNSPCSTPILGVQK PNGQWRLVQDLRIIDEVVVYV DDLLLAARSKTLCHQATQALL NFLITCDYKVSKPKAQLCSQKV KYLGLKLSKGTRVLSEERIQPIP AYPHPKTPKQLRGFLGITGFCRI WIPRYSEIARPLYTLIKKTQKAD THLVEWTPEAEVAFQALKEAL TQAPVLSLPMGQDVPLYVTEK TGIALGVLGVLTQVRG/LSLQP MAYLSKEMDVVAKGWPH
12277	42645	A	12351	1	2217	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12278	42646	A	12352	1	6530	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
12279	42647	A	12353	1734	4349	MPNRACFQCGLQGHFKKDCPS RKPQVCLTIESQEVNCLLDAGA AFSVLLSCPGQLSSRSVTIRGVL GQPVTRYFFQPLSCDWGALPFS HAFLIMPESLTPLLEREILVKAG AIIHLNIGEGTPICRLLFEEGISPE VWATEGQYGQAKNAHFVQVK LKDSTSFPYQRQYPLRPEAQQR LQKIVKDLKAQGLVKPYSSPCN TPILGVQKPKRQWRLVQDLRII NEAVFPLYPAIPSPYTLLSQIPEE AEWFTVLDLKDAFFCIPVHPDS QFLFAFEDPSNPTSQLTWTVLP QGFRDSPHLFGQALAQDLSQFS YLDTPVLQCMDDLLLAARSET LCHQATQALLNFLTTCGYKVS KPKAQLCSQQVKCLGLKLSKV TRALSEERIQPILAYPYPKTLKQ LRGFLGITGFCRIWIPRYGKIAR PLYTLIKETQKANTHLVRWTPE AEAAFHALKKALMQAPVLSLL TGQDFSSYVTKNKQTKKKK\T* IALRVLALV*GTSLQPVAYL/SK EIDVVAKGQPHCLRVVVAVAV LVSEAVKIIQGRNLTVWTSHDV NGILTAKGDLWLSDNHLLKYQ ALLLEGPMLRLCTCAALNLDTF LPHNEEKIEHNCQQVIAQTYAT RGDHLEVPLTDPNPNLYTDGRS FVEKGLQKVGYAVVSDNGILES NPLTPGTSAQLAKLTRALELGE GKRVNIYTDSKYAYLVLHAHA
12280	42648	A	12354	5	138	
12281	42649	A	12355	1	909	
12282	42650	A	12356	3	245	
12283	42651	A	12357	1	1080	

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12284	42652	A	12358	3	955	VPRKSVHSGDAEYHKVLKEEA SDSRENKVGTTWLQILSGSFAS RVTEHITQPLQESVSLWISSEQN IPPKFMGRLNKLRKATYKRKYS AAKSKVEKKKKEKVFATVTKP VG\GDKNGGT\RVVQTR\KLPR YHPTEDVPRKIVEPPQKNLFSQ HVRKTAKTALPPGTILIILTG\RH RGK\RVVFLK\QLASGLILV\TAP LVLNRVPLRRTHQKFVIATSTKI DISNVKIP\KKKDKTPLLTDAYL \KKKKLRKPR/HPRKGEIFDTVK RGNMRITE\QRTIDQKAVDSQIL PKIKAIPQA/LQGYLRILCLL*RN GIYPHKLVF
12285	42653	A	12359	1	555	
12286	42654	A	12360	1	300	
12287	42655	A	12361	1	588	
12288	42656	A	12362	1	264	
12289	42657	A	12363	1	870	
12290	42658	C	12364	239	400	
12291	42659	A	12365	9	98	SWKPSFSAN*HRNRKPNTTCSH SQVGVDL
12292	42660	A	12366	9	81	
12293	42661	A	12367	3	169	
12294	42662	A	12368	134	481	GCCGGTIKNSFSFPPLPNWPRFV MFPSLCVLIVETCETWICTLIVQ LPLMSENMRCLIFCSCVSLLRM MVSSFVHVHDHKVKSHSRPS/G NLRSKEASPSPKTSKVGKLTVQ PSVCG
12295	42663	A	12369	41	388	SYGQMMKCQPFTFPSPGYGAG VFSSDKIGQMTFMERT*RMSCK EAAQDHTAREKEKVELKFPSLP FRRKELL*PCTWLGSPISLVTLD FPWPQGSGRLSMPVLWTCLIPG SLEIG
12296	42664	B	12370	1	909	
12297	42665	C	12371	295	2025	
12298	42666	A	12372	14	260	
12299	42667	A	12373	1	142	TCTCVFIAALFTIAKTWN*SKCP SMRDWIKKNVAHTHHGILCSH KKE
12300	42668	A	12374	1	395	

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12301	42669	A	12375	2	976	REHLAEGMAVGTASADLNISA CWLRREQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQRK EQAAIFAVLQPPLVIPRKTGSGV DLEQTPADLQKRGLTVTRKTN KQKAIASTSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSSPAR EQNWMEN\EFDELTEVGFRRW VITNSSELKKHVLTQCKEAKNL EKRDMDEAGNHHSQQTNTGTE NQTPHVLTHKWELNNENTRTRI YKKHGAAICLASGIYHSVDLPF WGLDLPFWDLEDSGSTILGSGG QWPSSHSSTRQCTSVDSVWGL
12302	42670	B	12376	1	111	
12303	42671	A	12377	34	346	
12304	42672	A	12378	1	585	
12305	42673	A	12379	3	14703	
12306	42674	A	12380	1	636	
12307	42675	A	12381	1	1626	
12308	42676	A	12382	1	3246	
12309	42677	C	12383	62	202	
12310	42678	A	12384	1	286	
12311	42679	A	12386	1	1176	
12312	42680	C	12387	1	942	
12313	42681	A	12388	785	892	
12314	42682	A	12389	2	91	
12315	42683	A	12390	1	708	
12316	42684	A	12391	3	96	TWMKLETIILSKL*QRQKTKHR MFLLIGGN
12317	42685	B	12392	1	1954	
12318	42686	A	12393	1550	1830	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKKMW HIYTMEYYAAIK/SDEFMCFAW TWMKLETIILSKLSQEHKTKHH MFSLTSGS
12319	42687	A	12394	3	553	
12320	42688	A	12395	1	1428	
12321	42689	A	12396	642	753	
12322	42690	B	12397	1	759	
12323	42691	B	12398	1	900	
12324	42692	A	12399	623	775	
12325	42693	A	12400	992	1156	
12326	42694	A	12401	86	349	

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12327	42695	A	12402	1	2521	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NIVQHINRTNDKNHMIISIDAEK AFDKIQQRFMLKTLNKLGIDGT YLKIIRAIYDKSTANIVLNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGIQLTRDVKDLFKEN YKPLLNDIKEDTNKWKNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKGARIAKSILIYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKWGNDS LFNKWCWENWLAICRKLKLDP FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNTIQDIAMGKDFMS KTPKAMATKAKIDKWDLINLK SFCTAKETTIRVNRQPIEWEKIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSSLAIREMHI KTTMRHHLTSVRMAIIKKLGN DWCWRGCGEIGRLLHCWWDC KLVQPLWKSVWRFLRDLELET PFDPASPLLGIYQKE\YKSCYYK DICT/RVCVPAALFTIANTWNQP
12328	42696	B	12403	80	5612	
12329	42697	B	12404	68	505	
12330	42698	A	12405	1	471	
12331	42699	A	12406	194	430	IAIMRLLLQISIIILSSCLREVKSM QAYRKALRKLKLADVKRYQKS LVVQKRS*ER*SLVLILILPARTF QSYLAPIC
12332	42700	A	12407	1	546	
12333	42701	A	12408	2	418	
12334	42702	A	12409	302	746	ETSHQVMDRSNPVKPALDYFS NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGQLKV LGANLWWPYLMHEHPAYLYS WEDGDCFTPKALDPLPACDLC DQL\HLRSRQGGSVCGCDPCEQ LLLL\VSQLQAPAIDSAAAGRPV
12335	42703	A	12410	83	552	
12336	42704	A	12411	1	459	
12337	42705	A	12412	34	588	

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12338	42706	A	12413	1	466	
12339	42707	A	12414	950	1230	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ
12340	42708	A	12415	497	847	
12341	42709	A	12416	1	337	MGVVPEELFLEELNLSGLKWD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPR\ALADS LMQLARQVSRLESGQHPEFAPP SHGD
12342	42710	A	12417	716	961	
12343	42711	A	12418	1	1218	
12344	42712	A	12419	1	1104	
12345	42713	A	12420	548	1078	
12346	42714	B	12421	83	345	
12347	42715	A	12422	1	681	
12348	42716	A	12423	1	1431	
12349	42717	A	12424	566	871	
12350	42718	A	12425	145	980	
12351	42719	A	12426	2	702	
12352	42720	B	12427	1	1156	
12353	42721	A	12428	188	584	
12354	42722	A	12429	1	1194	

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12355	42723	A	12430	170	1855	LLEGKLTNRKDIPHQNPICTSPS SKTKGILPISEPPSNRIFACWGK PAWTACCN/FSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQINHTPNSF HIGAGGSWCLSESPCVVLNYK YPLVCGYTDGNAEVSKFGNFFL DLSRTRCLAEGNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGT ENGYQGEESLFNKAYYGGGTN FFRKESQKLQQSAKKRDAELA NGALGIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKMNGKW YLFTDSRGSKMTIDGINSNDIY MLGYVSNSLTGPYKPLNKTGL VLQMGLDPNDVTFTYSHFAVP QAKGNNVVITSYMTNRGFFED KKATFAPSFLMNIKGNKTSVVK NSIRREGFCRFRNHHQTGFSPA GANQRGPLAATLSGPGGEGQS AVARLTGEKKNHPGAQYANRL SPRVGRFINAAGTTGFPTGKRA GFCRFRNHHQTGFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGFPTGKRAV
12356	42724	A	12431	851	2237	
12357	42725	A	12432	2	2346	
12358	42726	B	12433	329	479	
12359	42727	B	12434	656	2404	
12360	42728	B	12435	486	834	
12361	42729	A	12436	1	693	
12362	42730	A	12437	1	114	
12363	42731	A	12438	152	391	AGGWALPSLGLPSWTSRCPWR RGSAGLLLEASVPVQQ*PKLLD RLSRRWPGEGHPRPARVRSCM ALGPRRLGVLCQEPS
12364	42732	A	12439	1	1707	
12365	42733	A	12440	1	897	
12366	42734	A	12441	36	420	
12367	42735	A	12442	2	217	
12368	42736	A	12443	1	903	
12369	42737	A	12444	1	1626	
12370	42738	B	12445	107	757	

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12371	42739	A	12446	1	1655	MGTVPRSAGQETWVLCEHIIGG ERSFTEYSLCHRIESSTSSIKLEL GGNNVEPLESSRVFDSTVQNEE ADAVSTGEEGVTHEGTQGGKV IPQMHMGSGLQPKSFSQNRSQV NNDMIVTDNNGAVKFPQLCKF CDVRFSTCDNQKSCMSNCSITSI CEKPQEVCVAVCWMSEEICTN VMYSPLPCKFLHLSPIEVLPIIRS PVNQSGRCKIRHIGSNNRLQRS TCQNTGWESAHVMKTPGFREY NTSNPDLLLVIFQVTGISLLPPL GVAISVIIIFYCYRVNRQQKLSS TWETGKTRKLMEFSEHCAIILE DDRSDISSTCANNINHNTELLPI ELDTLVGKGRFAEVYKAKLKQ NTSEQF*DSGQFKILFPIE\EYAS WKTEKDIFSDINLKHENILQFLT AEERKTELGKQYWLITAFHAK GNLQEYLTRHVISWEDLRKLGS SLARGIAHLHSDHTPCGRPKMP IVHRDLKSSNILVKNDLTCCLC DFGLSLRLDPTLSVDDLANSGQ CYEVCSSGRFLVTIFKGNRLRE RTEKNTRITPRDWVYEWLW
12372	42740	A	12447	1555	3277	RAAGSAMGRGLLRGLWPLHIV LWTRIASTIPPHVQKSVNNDMI VTDNNGAVKFPQLCKFCDVRF STCDNQKSCMSNCSITSICEKPQ EVCVAVWRKNDENITLETVCH DPKLPYHDFILEDAASPKCIMK EKKKPGETFFMCSCSSDECNDN IIFSEEYNTSNPDLLLVIFQVTGI SLLPPLGVAISVIIIFYCYRVNRQ QKLSSTWETGKTRKLMEFSEH CAIILEDDRSDISSTCANNINHN TELLPIELDTLVGKGRFAEVYK AKLKQNTSEQFETVAVKIFPYE EYASWKTEKDIFSDINLKHENIL QFLTAEERKTELGKQYWLITAF HAKGNLQEYLTRHVISWEDLR KLGSSLARGIAHLHSDHTPCGR PKMPIVHRDLNSSNILVKNDLT CCLCDFGLSLRLDPTLSVDDLA NSGQVGTARYMAPEVLESRMN LENAESF\KHTDVYSMALVLWE MTSRCNALGEVKDYEPPFGSK VREHPCVESMKDNVLRDRGRP EIPSFWLNHQGIQMVCETLTEC CDHDPYARLTAQCVAERFSELE HLDRLSGRSCSEEKIPEDGSLNT

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12373	42741	A	12448	3	1354	
12374	42742	A	12449	1	168	
12375	42743	A	12450	2	147	
12376	42744	A	12451	3	523	LQFFRRSEVKMKNHLLFWGVL AVFIKAVHVKAQEDERIVLVDN KCKCARITSRIIRSSEDPNEDIVE RNIRI\IVPLNNRENISDPTSP\LR TRFVY\HLSDLCKK\CDPTEVEL\ DNQIVTAT\QSNICGWMTVPQS TCYTLSTGNKCYTAVVPL\VYG GETKMVETALTPDACYPD
12377	42745	A	12452	3	274	
12378	42746	A	12453	1	120	
12379	42747	A	12454	119	461	PVPQDLQAAVLGRTTALFK\AV KTGTLQVCKRLLLSF\VCL/CPA PRGRQASLSCGGLHPVRASWLL CLPKQAWAMAGAPPPAWLPPC SLISDCCASNQRDSVGVRPSEPG VGYSLV
12380	42748	A	12455	2	370	
12381	42749	A	12456	1	3135	
12382	42750	A	12457	1	942	
12383	42751	A	12458	1	462	
12384	42752	A	12459	1	297	
12385	42753	A	12460	935	1338	CTDGFLVWMSFLFVSFPLPPCS LISDCSASNERDSVGVGPSEPG AGYNLVVRRFLSPSEKRSIRV* VTRFSRCRPSPLSLTRKGNSLTP CASQVRQCLALFRLAHGVRTH SPAPTVWHSLPKVGPFLENSVP
12386	42754	A	12461	1	268	
12387	42755	A	12462	3	479	
12388	42756	A	12463	1	262	
12389	42757	A	12464	1	304	MAGAPAPASLPPCSLISDCCAS NQRDSMGVGPSEPGAGYNLVP V\EKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLALL QLAHGRGSPNPRP
12390	42758	A	12465	1	512	
12391	42759	B	12466	1	1257	
12392	42760	A	12467	1	705	
12393	42761	A	12468	1	3039	
12394	42762	B	12469	66	467	
12395	42763	C	12470	360	747	

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12396	42764	A	12471	3771	4703	SFQFFCSVFSPSLWFYLLLVFDD GDVQMRFRCGCPFCLLVFLLTD RTLSCRSVGIPCRVRCQCA\LLG GASQLGCSGVKGSRDPLEEAV CPFS\DL\QLRAGGNTALFKAVR QGHLSLQRLLLSF\VCLCPAPRG GAYRGGQASLSCGGLHPV*AS\ RLLCLPKQAWAMAGAPPPASL L\PCI\LISDCCASNQRDSVGVGP S/ERPGVGYSLVVRRFLSRSEKR NIRGG\VTRFSRCRPSPLSLTRK GNSLTPCASQSEGNAIGPAFGF AHGARTHWALRPTVWHSLCE MNPVPQMEMQKSPVFCVAHA GGCRPEL
12397	42765	A	12472	1	1038	
12398	42766	A	12473	27	428	LADRSAIPGFAIFAVTFLLALVG AVLYLYPWTLLKPC*SHY*GIN LVVAV*VKTT*GKNCMKMV*L IL*RVTLPSS*RFGLRLEKAF*M GHLIKT*LGKNNMKMPSCNWS LF*GTS*KNEKEGTSVNIFSLTP
12399	42767	A	12474	107	362	NKPCEEFYFLAALIYLLYHGRK KADTKIPP*ISRFFLILYPSHELTI FIVIHIMCDLGCTWAICFLTTSE EVQKKLYEEINQVFG
12400	42768	A	12475	193	637	TSSEVVKKQIAQVHNFAVIMQL ARENIILSS/EDLLVIKVPLY*GV NENMLTEVPSFSFFYDVP*NRL QLHEGIFILFFPSHVFIK*PI*KAF SNLRPNCAMILLEANDFLIIFKC TTHYHLCNRLHSKTKHMLAEG HVLGLWVGEPFI
12401	42769	A	12476	1	1930	
12402	42770	A	12477	1	362	
12403	42771	A	12478	58	160	GVSLQSTSEEGRGMRQE*TERE IKVTCRSHYRLA
12404	42772	A	12479	3	410	
12405	42773	A	12480	1	807	
12406	42774	A	12481	154	375	
12407	42775	A	12482	2	512	
12408	42776	C	12483	29	455	
12409	42777	A	12484	209	433	
12410	42778	A	12485	1	1546	
12411	42779	A	12486	3	931	
12412	42780	A	12487	1	363	
12413	42781	A	12488	1	351	
12414	42782	B	12489	82	263	
12415	42783	A	12490	1	1878	
12416	42784	A	12491	24	242	
12417	42785	A	12492	1	3558	

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12418	42786	A	12493	2	478	HNSLKSDENKENSFSADHVTTA VEKSKESQVTADDLEEEKAKA ELIMDDDRTVDPLLSKSQSILIS TSATASSKKTIEDRNIKNKKSTN NRASSASARLMTSEFLKKSSSK RRTPSTTTSSHYLGTLKVLDQK PFTETEA*EPDRADNIRGSCLFR
12419	42787	A	12494	1	1047	
12420	42788	A	12495	1	1055	
12421	42789	A	12496	212	611	
12422	42790	A	12497	2	195	YVMGRNDGGYLMIDSKTAEIK FVKNMNRDSTFIVNKTITAEVL AID\RYSGKNCLLISWSYICG
12423	42791	A	12498	1	429	
12424	42792	A	12499	1	503	
12425	42793	A	12500	3	825	GTTKWQTVRRQKREWIKFAAA CREGEDNSKRNPIAK*SDLQNS LLPALY*KH\IRSDCESNQKITY RISGVGIDRPPYGVFTINPRTGEI NITSVVDREITPLFLIYCRALNS RGEDLERPLELRVKVMDINDN APVFSQSVYTASIEENSDANTL VVKLCATDADEENHLNSKIAY KIVSQEPSGAPMFILNRYTGEV CTMSSFLDREQHSMYNLVVRG SDRDGAADGLSSECDCRIKVLD VNDNFPT/FRENFKQNSSRFSNS LLSSFDQWRKL
12426	42794	A	12501	986	4030	KQRLTWTFSPGKSETMMGLFP RTTGALAIFVVVILVHGELRIET KGQYDEEEMTMQQAKRRQKR EWVKFAKPCREGEDNSKRNPIA KITSDYQATQKITYRISGVGIDQ PPFGIFVVDKNTGDINITAIVDR EETPSFLITCRALNAQGLDVEKP LILTVKILDINDNPPVFSQQIFM GEIEENSASNSLVMILNATDAD EPNHLNSKIAFKIVSQEPAGTPM FLLSRNTGEVRTLTNSLDREQA SSYRLVVSGA
12427	42795	B	12502	1	3572	
12428	42796	A	12503	1	594	
12429	42797	A	12504	1	612	
12430	42798	B	12505	200	532	
12431	42799	A	12506	2	735	
12432	42800	A	12507	5	400	

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12433	42801	A	12508	2	1260	GQAASPASPASPASPAMAWAA LLGLLVALLLLLLLSRRRTRRP GEPPLDLGSIPWLGYALDFGKD AASFLTRMKEKHGDIFTILVGG RYVTVLLDPHSYDAVVWEPRT RLDFHAYAIFLMERIFDVQLPH YSPSDEKARMKLTLLHRELQAL TEAMYTNLHAVLLGDATEAGS GWHEMGLLDF/CLQLPAQSRLP DSLRN*GAATHP*KPGPGPRPLS *CLPHLSPARPAAPQTGPWLPV SGGQGPHVQCQKSPVEAAIPSQ AGQAGPPEQMAGELPAAPGGD GCVRGDAGTGPGAAAVGHTGE YGSRCLLAPALPSQES*SPGCCP RRAREYPLASGAACLADDHSPT EGSRQHTC/DLIAC*VRASGLQL PPSSPARL\GGPGHAHGRRERIQ PATW*PPPPLPLPEPPERPRNLH RPRGI
12434	42802	A	12509	3	466	
12435	42803	A	12510	1	1134	
12436	42804	A	12511	2	1211	
12437	42805	A	12512	2	405	HEMLLASEIKHLPRRLLIGQERE TQTSELKIKRRGNEEAPS/PPPSS AYERGTKRPDDRYDTPTSKKK VRIKDRNKLSTEERRKLFEQEV AQREAQKQQQQMQNLGMTSP LPYDSLGYNAPHHPFAGYPPGY PMQA
12438	42806	A	12513	191	898	
12439	42807	A	12514	1	270	
12440	42808	A	12515	2	1328	
12441	42809	A	12516	1	2868	
12442	42810	A	12517	1	1254	
12443	42811	A	12518	1	576	

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12444	42812	A	12519	1919	3044	HQGPSTPPSWAMSGPPTPLSRE DWHQGPSTPPSWAMSEPPT/SSI QGLASGAVHTILLGDVRATYTS IQGVTSGVSQVSRAAQMAVPSS RILQLSKPKAPATLLE\EWDPVP KPKPHVSDHNRLLHLAKVPRK EGSGKKVGAFPEIKGPEAFRDK ARAMESQSNDMPFDELLALYG YEASDPISDRESEGGDVDPNLP DMTLDKEQIAKDLLSGEEEEET QSSADDLTPSVTSHEASDLFPN RSGCLLAGEAESSRGLLPRAQP VPRGAGLADNSRGALLRAHGT VRVGTTATVKPADAPPESPRDR RSRNDSHRPTGPSESERQPQSN QPTLLLRGHGTIRVRTTATVKP ADAPAESPRDRRSRNDSHGQSS
12445	42813	A	12520	413	1412	
12446	42814	A	12521	293	412	NHLSVAGNGSSPCGL*AGALGL LLWLLASSGHRVLSGMI
12447	42815	A	12522	2	181	
12448	42816	A	12523	1	277	
12449	42817	A	12524	1	739	
12450	42818	A	12525	1	326	
12451	42819	A	12526	3	566	
12452	42820	A	12527	1	465	
12453	42821	A	12528	1	1167	
12454	42822	A	12529	260	395	EVATATPTLSNHYPDQSAAIN/D QG*PLHQQKDHILQKAQMNISI F
12455	42823	A	12530	209	958	FRCVLISFWSHKLHLWYHEGRI VPSDRIVPPHGIVSSHGVALPQR ILMRQFTLLEGLNKDGRFLIQLS GTAPWSSYFNSVAKFGVIHRIH SFFLSHNGHKAVAPLDLLSNVG GSCLCGDASSF\TTPSRITMTSK SWLARSVAEMSYR/WTALVNH VADDQRGHQKNVIALDWVINR NVQLVNRNHLPFRCSCFLDHLD AHRGTNDHAFPQVTHSEHEAQ LAISDGNHSMAAENQSFCPSVS LSCFHENAA
12456	42824	A	12531	1	1965	
12457	42825	C	12532	520	684	

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12458	42826	A	12533	701	1307	GRHLTTNHTAAVVVFPFRPLCS SFFRYSGFRGVAGATASGRGQG PAG*DNCQRAWRGAFYKFQAT LSAGAGTRAEEGSDGDGEAAE PGAGTAREPARLRGYRSRRFVL DGRRCCLCYFKNPHDPLPLGHL DIAEACFSYQRADEAAEQPAHF QVRSAGAATVLEVGTRALRGV HLLRAHRGIWAQAWSPVSFLQ AVLPAWLL
12459	42827	A	12534	1	1356	
12460	42828	B	12535	1	1449	
12461	42829	A	12536	3	2449	
12462	42830	A	12537	1	3327	
12463	42831	A	12538	1	1359	
12464	42832	A	12539	1	672	
12465	42833	A	12540	1	1281	
12466	42834	A	12541	1	399	
12467	42835	A	12542	1	399	
12468	42836	A	12543	171	426	PVSCATGEEEDNVLFPKGDDLP R**PGKLWCEFHASSISQALGQ HPRRSVLDTDQSHVPLVRRKTT CFSQRAMISPDDDPSQEAGALS RNNLLAPYSALTFMENGNCLL QLFQLGKLLVQASHLHGQLLV FVQKIIISM
12469	42837	A	12544	1	988	
12470	42838	A	12545	3	129	LFHPCQDSQQHH*CVCCRLTGH GAA*VHGPCQAVQTYRASH
12471	42839	C	12546	532	1101	
12472	42840	A	12547	197	355	
12473	42841	A	12548	1	1275	
12474	42842	A	12549	3	131	

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12475	42843	A	12550	1746	3504	ESDPSNSTTSMDRTLL/MSSIVP RLPSACRILPTGFTIPE*SCVHRT ASLIPPLPPGSRKYSPPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTSPDISHQQAAALLRTY LKNLSPYINSTPPIFGPLTTQTTI PVAAPLCISWQRPTGIPLGNLSP SRCSFTLHLRSPTTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCISLHPWLSSPCSSDSP PRPSSCLLIPSPENNSERLLVDT RRFLIHHENRTFPSTQLPHQSPL QPLTAAALAGSLGVWVQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAGISTSVMTFRSLSNDFS ASITDISQTLSVLQAQVDSLAA VVLQGQLRGLDLLTAEKGGLCI FLNEECCFYLNQSGLVYDNIKK LKDRAQKLANQASNYAESPWA LSNWMSWVLPIVSPLIPIFLLLL FGPCIFRLVSQFIQNRIQAITNHS IRQMFLLTSPQYHPLPQDLPSA
12476	42844	A	12551	2	394	
12477	42845	A	12552	1	882	
12478	42846	A	12553	45	409	
12479	42847	A	12554	1	1035	
12480	42848	A	12555	118	312	
12481	42849	A	12556	1	1083	
12482	42850	B	12557	1	1122	
12483	42851	A	12558	97	439	
12484	42852	A	12559	1	450	
12485	42853	A	12560	1	471	

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12486	42854	A	12561	2	1407	WGKNRAEKLETLKSRVPLLLQ RNAVPHQQWNKAGRRMTLTS* EKKASDD/PNYSKLQEEIQTKG KEVKHFEKNLDECITRITNREK CLKELMELKAKARELREECRSL RSQCDQLEERVSVMEEIQTTIRE YYKHLYENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPITGSE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELIPFLLKLFQSIEKEGI LPNSFYEASIILIPKQGRDTTKK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSRNVIHHINRTKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDETYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLFELISNFSKVSGY KINVQISQAFLYTNYRQSAKS
12487	42855	A	12562	1	846	
12488	42856	A	12563	1	1281	
12489	42857	B	12564	1	274	
12490	42858	B	12565	1	2265	
12491	42859	A	12566	1	2742	
12492	42860	A	12567	1	1272	

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12493	42861	A	12568	222	2130	RKKNKKK*TKPPRNMGLREKT KSMSDWCT*K*RGEWNQV/AK TLCRILSRRT/YPNLARQADIQIQ EIQRTPQRYSSRRATPKHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLTADLSAETLQARRE WGQIFNILKEKNFQPRISYPAKL SFISEGEIKPFTDKQMLRDFVTT RPALKELLKEVLNMERNNRKK LNRPITGSEIVAIINSLPTKKSPG PDGFTAEFYQRYKEELVPFLLK LFQSKEKEGIHPNSFDEASIILIP KAGRDTTTKDNFRPISLMNIDA KILNKILANQIQQHIKKLIHHDQ VGFIPGMQGWFNICQSINVIQHI NRTKDKNHVIISIDAEKAFDKIQ QRFMLKTLNKLGIDRMYLKIIR AIYDKPTANIILNGQKLEAFPLK MGTRQGCPLSPLLFNIVLEVLA RAIRQEKEIKHIQLGKKEVILSL FADDMIVYLENSIVSAQNLLKLI SNFSKVSGYKINVQKSHAFLHT NNRQTESQIMSELPFTIASKRIK YLGIQLTKDVKDLFKENYKPLL NEIKEDTKKWKHIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRAHT AKSILSQKNKAGGITLPDFQLY CKATVTKTAWY
12494	42862	A	12569	1	474	
12495	42863	A	12570	1	1197	
12496	42864	A	12571	1	1518	
12497	42865	A	12572	1	3189	
12498	42866	A	12573	1	2199	
12499	42867	A	12574	3	2820	ENKDTTYQNL\WDAFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKREK NQIDTIKNDKGDITTDPTEIQTTI REYYKHLYANKLKNLEEMDKF LDTYTLPRLNQEEVESLNRPITG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFR
12500	42868	B	12575	1	1593	

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12501	42869	A	12576	1	3549	MGDFNTPLSTLDRSRRQKVNK DTQELNSALHQVDLIDIYRTLH HKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWIHNKMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EVTKIRAELKEIETQKTLQKINE SRSWFFERINKIDRMLARLIKK KREKNQIDTIKNDK
12502	42870	A	12577	1	2724	
12503	42871	A	12578	1	3567	
12504	42872	B	12579	709	2064	
12505	42873	A	12580	1	3370	
12506	42874	A	12581	1	2024	MGFYHVGQAGTELLTSNDPLT SASQSARITGKALQKPTEVPVP YEKMLQDQSALIVQGLPEGVA FKHPENYDLATLKWILENTAGI SFIINSATIEPPAAQPMSFTHMG HSLCVLVVETHAKPVAVQSSSF TRNPEVISLEVAAVTVKEESED PDYDYITFKDLPGIAYETKAYV LWPQLSKICSKNGDKNKAYRG QQCRLRQQNPLAALTGKISVSV YVSHPSLRSVSIGWTRQVARQT MQKDRDGPLKNEGEKNCAGSE KNTLTSQLKELEKQEQTHSKAS RRQEITKIRAELKEIETQKTVEK INESRSWFFERINKIDRPLARLIK KKREKNQVDAIKNDKGDITTDP TEIQTTIREYYKHLYANKLENV EEMDKFLDTYTLPRLNQEEVES LNRPITGSEIVAIINSLPTKKSPG PDGFTAEFYQRYKEELVPFLLK LFQSIEKEGILPNSFYEASIILIAK PGRDTTKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHIN RAKDKKHMIISIDAEKAFDKIQ QPFMLKSLNKL/DIGKNYFKVH MGPKKSPCRQVNPKPKEQSWR HHST*LQTILQGYSNQNSMVLV PKQRYRSMEQNTALRNNATYL QLSDL*QT*EKQAMGKGFPI**
12507	42875	A	12582	722	4214	

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12508	42876	A	12583	228	1152	KNRDYNKLSLRPQCNQTRTQN *ESHSKPLNYMETEQPAPE*LL DT*R\MKAEIKMFFETNENKDT TYQNLWDAFKATASKTNKEKE KNQIDTIKNDKGDITTDPTEIQT TIREYYKHLYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGAEIVAIINSLPTKKSPGPDGF TAEFYQRYKEELIGWLRESVSK ICLKFDHQVQVITGRLIIRFQIAF GTVVLCQLTRHIDVFVGKRLA NARFAPSLGGAPDLFTLKPCFV AVETQGDLPQATTVVDIDGCL GKPANVQVALDLDVKGFQQW
12509	42877	A	12584	1	2028	
12510	42878	A	12585	2	2264	
12511	42879	A	12586	1	2130	
12512	42880	A	12587	1	2900	MENDFDELREEGFRQSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERVSAME DEMNEMKGEGKFREKRIKRNE QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLYTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPITGAE
12513	42881	A	12588	1	2745	
12514	42882	B	12589	1	3288	
12515	42883	A	12590	1090	2526	
12516	42884	A	12591	1	3242	
12517	42885	A	12592	3862	8976	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
12518	42886	A	12593	1	1000	

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12519	42887	A	12594	1	979	MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFGVDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGRNQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRQLVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDLMEL KTMARELRDSCTSFSRQFDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLFADNMTVYLENPI IS\PKISLS**ATSAKSQDIKSMC KNHKHSYTPITDKQRAKS
12520	42888	A	12595	1140	2210	KPWHKNFVTHAQASIADLIKW KKGYQ*LKIKLMK*SKKTRNTN YHQNTINISMQIN*KI*KKWRNS WTHTLSQY*TRKKLNL*IDQ*Q ALKL/QAIIYSLPTKNVQGQMD SQSNTTRVWGILARAIRQEKEI KDIQLENEEVKLSLFADDMTVY LENSIVSAQNLLKLRIKYLGIQL TTDVKDLFKENYKPLLNKIKED TNKWKNIPCSWIRGINIMKMAI LPKLIYRFNAIPIKLPMTFFTELE KATLKFIWNQKRAHIAKTILSK KNKAGGIMLPDFKLYYKATAT KAAWYWYQNRDIDKKLTQIYK KKTNNPIKKWAKDMNRHLSKE DIYGANRHMKKCSSSLVIREKQ IKTTMR
12521	42889	A	12596	520	697	GLCSVPLLCISVLVPVPCCFGYC SLVV*FEVR*SDASSFVLLA*DF LGNAVSFLVPYEL
12522	42890	A	12597	1	1410	
12523	42891	A	12598	1	1461	
12524	42892	A	12599	77	457	QALKLRQ*LIAYQPKRVQDQM DSQTNSARGTKRSWYHSF*NYS N/PTEKEGILLNSFYEAGIILIPKP GRDTTKKENFRPISLMSINAKIL NKILANRILQHIKKLINITIKSASS LGCKAGSTYANQ

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12525	42893	A	12600	1	919	MGDFNTPLSTLDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNCSTTWKLNN MLLNDYWEHNKMKAEIKMFF ETNKNKDTTYQNLWDTLKAVC RGKFKALNAHKRKKERSQIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKETETQKTLQRLMN PGAVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIVYLENP\ MSQPKISLS**ATSAKSQDIKSIY KNHQHSYTPIRDKQRAKS
12526	42894	A	12601	1	1264	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLPTQKSSGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RYTHKKNNFRPISLMNIDAKIL NKILANRIQQHIKKLIHQDQVGI IPGMQSWFNIHKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLENKIPKNPTYKGCE GPLQGELQITAQRNKGRHKQM EEHPMLMDRKNEYHKNGHTPK VIYRFNVIPIKLPMTFFSELEKST LKFIWNQKRARIAKTILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEM TPHIYNHLIFDKPDKNKQWGK DSLFNKWCWENWLAIGRQLKL DPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNTIQDISMGKDF MSKTPKAMATKAKMDKWDLI KLKSFCTAKETTIRQSWPEMTK FTFSSNTDVKNWKHGKNNIGR HKTSVNTCKMDSGLVLERWM EWNPGFPLSIDAKCHKDLPRDI QFDSEKGVDFVLNYSKANMR WAGSMFL*FIESF*HEWLLNFV KGLFCIY*DNHVVFVFGSVYML
12527	42895	B	12602	1	1827	
12528	42896	B	12603	13	1377	
12529	42897	A	12604	557	664	KTPLSQPKISLS**ATTAKSQDT KSVYKNQQHSYT

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12530	42898	A	12605	77	1866	QAPKLRQ*LIAYQPKKVQDQTD SQPNSTRGTKKSWYHSF*NFSN/ PIEKEGIFPNLFYEANIILIPKPGR DTTKKENFRPISLMNVNAKILN KLLANQIQQHIKKLIHHNQVGFI PGMQGWFNICKSINVIQHINRT KDKNHRSISIDAEKAFNKIQQPF MLKTLNKLDDMIVYLENPIVSA KNLLKLISNFSKVSGYKINVQK SQAFLYTNNRQAESQIMSAVSF TIASKRIKYLGIQLTRDVKDLFK ENYKPVLNKIKEDTNKWKNIPS LWIGRVNIMKMAILPKVIYRFN AIPIKLPMTFFTELEKTTLKFIW NQKRAHIAKTILSKKNKAGGIT LPDFKLYYKATVTKTAWHWY QNRDIDQWNRTEPSEIIPHIYNH LIFDKLDKNKTLGKDYLFNKRC WENWLAICRKLKLDPFLTRYT KINSRWIKDLNIRPKTIKTLEEN LGDTIQDIGMGKDFITKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTIRVNRQPTEWENIFAIYPSDK GLISRIYKELKQIYKKKSNNPIK KWAKDMNRYFSKEDIYAANR HMKKCSSSLALREMQIKTTMR YHLIPVRMAIIKKSGNNRCW
12531	42899	A	12606	67	243	GLCCVPLIYISVLVPVPCCFGYC SLVV*FEVR*HDASSFVLLA*D* LGDVGSFLVPYEL
12532	42900	A	12607	1554	1692	
12533	42901	A	12608	640	816	GLCSVALVCISVLVPVPCCFGY CSLVV*FEVR*HDASSFVLFA*D *LGNVDSLLVPYEL
12534	42902	A	12609	1626	1739	

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12535	42903	A	12610	1	2014	MKREGSLEKKRIKRNEQSLQEI CDYVKRANLRLIGGPESDGENG TKLENTLQDMQEKFPNLARQA NIQIQEIQRTPQRYSSRRATPRHI IVRFTKVEMKEKMLRAAREKG QVTHKGKSIRLTADLSAETLQA RREWGPIFNILKEKNFQPRISYP GKLSFISEGEIKSFTDKQMLRDF VTTRPALKELLKEALNMEKNK QYQPPQKHAKLTREARANTFK PSRRREITKIRAELKEIETPKTAQ KINESRSWFSERINKIDRPLARL RKKKREKNQIDTIKNDEGDITT HPTEIHTIIREYYKHLYANKLEN LEEMDKFLDTYTLPRPNQEEVE SLNGPIAGSEIQAIINSLPTKKSP GPDGFYQRYKEELVPFRLKLFQ SIEKEGILPNSFYEASIILIPKPGR DTTKKENFRPISLLNINAKILNKI LANRIQQHIKKLMHHDQVGFIP GMQGWFNIRKSINVIQHINRTK DKNHMIISIDAEKAFDKIQQPF MLKTLNKLGIDGTYHKIIRANY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAIR QEKETEGIQLGKEEVKLSLFAD DMIVYLENP\MSQPKISLS**ATS AKSQDTKSMCKNHKYSYTPIT DKQRAKSSVNSPFTIASKRIKYL GIQLTRYVKDLFKERSMK
12536	42904	A	12611	1	700	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLSTKKSPGPD GFIAQFYQRTKDKNHMIISIDAE KAFDKIQQHFMLKTLNKLGIDG TYLKIIRAVYDKPTASIILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLGKE EVKLSLFADDMIVYLENP\MSQ PKISLS**ANSAKSQDIKSMCKN LKHSYTLITDKQRAKSSVNSHS QLLQRE
12537	42905	A	12613	1	1765	
12538	42906	A	12614	1	2310	

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12539	42907	A	12615	1	836	MENEFDELTEVHFRRWVITNSS ELKEHVLTQCEEAKNLARRNK LENLEEMDKFLATYTFPSLNQE EVESLNRPITSSEIEAAINSLPTK KHPGPDGFTAKFYQRYKEELHI NRAKDKNHMIISIDAEKAFDKI QHPVKLKILNKLGIDGTYLKIIR AIYDKPTANLILNGQKLEAFPL KTGTRQGCPLSPLLFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSL FADD\RLYI*GTPLSQPKISLS** ATSAKSQDTKSMYKNHKHSYT PTTDKQRAKS
12540	42908	A	12616	355	4502	QSARFRGRRTLRRPGVGYSLVV *FEVR*CDASSFVLLA*DCLGN AGSFLVPYEL
12541	42909	A	12617	248	362	
12542	42910	A	12618	529	680	YYTRCSKWWNCSVLP*IYIYNF HLPHGKLKNTDYIKKKLHDFFF KNSKHI
12543	42911	A	12619	1	641	
12544	42912	B	12620	36	48	
12545	42913	A	12621	1	326	
12546	42914	A	12622	1	444	PGSTHASAHACERLQTRTLRAF SSQRRFPATASRASLSSNMAKIS SPTETERCIESLIAVFQKYAGKD GYNYTLSKTEFLSFMNTELAAF TKNQKDPGCP*PHDGRKLGQPT VDGQLDFSEFLNLIGG\QAMAC HDSFLKAVPSQKRT
12547	42915	A	12623	2	6008	
12548	42916	A	12624	530	856	

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12549	42917	A	12625	1	952	MAARGTGDKVKPGCEEAGAAF ELPPSVYAAALHESHQHQPCPA GGARAQRVPGGIVTEPLTCTPP KDMVFLSDDGDDDDDDDNDD GGGDDDNDGNDNDGDNDNGD DDDGDDNDDDGGDDDNDGNG NDGDNDNDDGDNDDSNGNDD GDGDDDGVDDDDDNSDGNDG DDDDSDDDDGDSNGYDDDGD GNDDDDGDSDDDDSDNGDGD NGDGDDDGGGGDDDDNGHDD DGDMMMMIVMMVMVMMVV MMVMVMMVVVVQLRKRAEA SVSEAKCSINVSDDNDDGDGN DGDDDDSDGDDDDGGGDGGD SELTNQFPTNHSGMKASKLRK DSDHREW*W**WWWWCN*GR EQRPVFLKQSAQLMSVMIMMM VMVMMVMMMIVMVMMTMV VVMVVIVNSPINSRLITQA
12550	42918	A	12626	3	380	
12551	42919	A	12627	5	765	RQWEVGRWSGTTIFSCFCKKTL YFTNPSPSSSSLVTVILRREVTH/ CGGAPEQRYQIIPVCVAARLPT RAQDVLDAHLSEVNAVRFGPN SSLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDFDPS VRNSAPVAWDCALSDLHTGQG YQVLAATYNQAAQLWKVGEA QSKETLSGHKDKVTAAKFKLT RHQAVTGSRDRTVKEWDLGRA YSPKRQRPSRTGHDDDGGFVE KKRGKCGEKRDQIVTVSV
12552	42920	B	12628	1	2802	
12553	42921	A	12629	458	708	QNRHRHHGPFSMVAVSSQLLD TPAERLSLHTWKIAQRPGRGTP HFPDGAV/VQAETLPQTGRPGR GTPHFPDGAASSFGYCSLVA
12554	42922	A	12630	2300	6491	EGLEALIHQERLSYWANQVSED RPVCKAIIQGKQFEGLVDTGAD VSIIALNQWPKNWPKQKAVTG LVGIGTASEVYQSMEILHCLGP DNQESTVQPMITSIPLNLWGRD LLQQWGAEITMPAPLYSPTSQK IMTKMGYIPGKGLG\KNEDGIK VPVEAKINQEREGI\GYPFLGAV TVEPPKPIPLTWKTEKPVWVNQ WPLPKQKLEALHLLANEQLEK GHIEPSFSPWNSPVFVIQKKSGK WHTLTDLRAVNAV

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12555	42923	A	12631	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDKEKACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
12556	42924	A	12632	1	642	
12557	42925	A	12633	260	534	
12558	42926	A	12634	1	438	
12559	42927	C	12635	391	750	
12560	42928	A	12636	199	451	
12561	42929	A	12637	120	992	RDRIPGPVCKGKWKNKERILIFS SRGINFRTRHLMQDLRMLMPH SK\HDTNMARSDNLSVINEGCE MNNWLRCIYFEAKKKQDLYM WLSNSPDGPSAKFLVQNIHTLA ELKMTGNCLKGSRPLLSFDPAF DELPHYALLKELLIQIFSTPRYH PKSQPFVDHVFTFTILDNRIWFR NFQIIEEDAALVEIGPRFVLNLIK IFQGSFGGPTLYENPHYQSPNM HRRVIRSITAAKYREKQQVKDV QKLRKKEPKTLLPHDPAADVF VTPAEEKPIEIQWVKPETKVDL KASV
12562	42930	A	12638	1	342	
12563	42931	A	12639	1	580	PGWEKRMSRSS/GVNTQEALPT AAIPTDAKVRVYYFNHITNASQ WERPIGNSSSGGKNGQGEPARV RCSHLLVKHSQSRRPSSWRQEK ITRTKEE\ALELINGYIQKIKSGE EDFE\SLASQFSDCSSAKA\RGD LG\SFSRGQMQKPF*RTPRFAL\ RTGGDERGPCFTD\SGIHIILPHL SEGGKPRPGLGAGQGG
12564	42932	A	12640	3	116	
12565	42933	A	12641	2	253	
12566	42934	A	12642	3	512	EDYLERKRQ/VPTECQTHSKLG GPMTLKREVKP/KVDVSPSKKG PL\QHHTLL\VCHVRIFYPGSIQ/ VRWFLNGRKKTAGVVSPNLIR NGDWT/FQILVMLEM/TPQQGD VYTCQVEHTSLDSPVTVEWKA QSDSARSKTLTGAGGFVLGLIIC GVGIFMHRRSKK\FNEDLHKQG
12567	42935	A	12643	1	363	
12568	42936	B	12644	70	1229	
12569	42937	A	12645	1	430	
12570	42938	B	12646	1	1321	
12571	42939	A	12647	3	446	

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12572	42940	A	12648	1	417	
12573	42941	A	12649	269	452	TILRSFGYFFRRINIMLTEEKIKS DHRKISQLIFLQKLCQTLQSENV SQGGMLYRAKA*H*T*TLVWV *HVMSYPHKGLGLMLSLCSVK HSTLRDVFTL
12574	42942	A	12650	83	1385	
12575	42943	A	12651	1	974	MNPLECVDRSSQPWGNPTWTS SGMRSVTFLVGFKLTFLALAQT LNAAASLTGQELLAGFPPGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLFKANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCVIGLQMGTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGFLPPCLGPSQE
12576	42944	A	12652	1	1103	MNPLECVDRSSQPWGNPTWTS SGMRSVTFLVGFKLTFLALAQT LNAAASLTGQELLWNFPLLMF AWKIAPALCCGNTVVIKPAEQT PLSALYMGALIKEAGFPPGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLFKANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCVIGLQMGTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGFLPPCLGPSQE
12577	42945	A	12653	1	729	
12578	42946	A	12654	259	390	SFCSANFEVFRLTAQQ*FVR*H ALSHIF*G*V*SFPKSTKRVNF
12579	42947	A	12655	68	735	
12580	42948	A	12656	1	825	
12581	42949	A	12657	3	470	
12582	42950	A	12658	1	1683	

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12583	42951	A	12659	1	1748	MNKPYIRNLSENAAPLDLEGIL KDAKIPVSGPFLVKIGYAFVDC PDEIWALKAIEALSGKIELHGKP IEVEHSVPKRQRIRKLQIRNIPPH LQWEVLDS*LVQYGVVESCQQ VNTDSETAVVNVTYSSKDQAR QALDK/LLDKLNGFQLENFTLK VAYIPDEMATQQNPFLQPRGRR GLGQRGSSRQGSPGSVSKQKPC DLPLCLLVPTQFVGAIIGKEGAT IRNITKQTQSKIDVHRKENAGA AEKSITILSTPEGTSAACKSILEI MRKETQDVKFTEEIPLKILAQN NFVGRLIGKEGRNLKKIEQDTD TKITISPLQELMQYNPEHTITAK GNVETCAKAEEEIMKKIRER*E NDITSM/N/LQAHLIPGLNLNAL GLFPPTSGMPPPTSGPPSAMTPP SPQSEQSESETVHLFIPALSVRA LISKQGQHIKQLSRFAGASSKIA PVEAPDAKVRMVMIAGSPEAR FKAQGRIYGKIKEENFVSPKEE VKLEAHIRVPSFAAGRVIGKGG KTVNELQNFSSAEVVVPRDQTP DENDQVVVKITGHFYACQVAQ RKIQEILTQVKQHQQQKALQSG
12584	42952	A	12660	3	803	
12585	42953	B	12661	1	330	
12586	42954	C	12662	127	342	
12587	42955	A	12663	324	491	
12588	42956	A	12664	1	891	
12589	42957	B	12665	1	1869	
12590	42958	A	12666	2	136	
12591	42959	A	12667	108	355	
12592	42960	A	12668	2	811	FGMRGSRGGWAGEMAASGES GTSGGGGSTEEAFMTFYSEVKQ IEKRDSVLTSKNQIERLTRPGSS YFNLNPFEVLQIDPEVTDEEIKK RFRQLSILVHPDKNQDDADRA\ QKAFEAVDKAYKLLLDQEQKK RALDVIQAGKEYVEHTVKERK KQLKKEGKPTIVEEDDPELFKQ AVYKQTMKLFAELEIKRKERE AKEMHERKRQREEEIEAQEKA KR/EEREWQKNFEES\RDGRVD SWRNF\QAQFRRGKKEKKNRTF LRPPESKNGSNVE
12593	42961	A	12669	731	850	
12594	42962	A	12670	201	377	LMTLPCKIPSPGSSWLKISPIEHL MTPTPASQRTTPFDCNFPLPTQI L*NGPTPISLH

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12595	42963	A	12671	742	2982	KIFPFDASFLPCLHKFNLKGKG NSKGFKMAEKFESLMNIHGFDL GSRYMDLKPLGCGGNGLVFSA VDNDCDKRVAIKKIVLTDPQSV KHALREIKIIRRLDHDNIVKVFE ILGPSGSQLTDDVGSLTELNSV YIVQEYMETDLANVLEQGPLLE EHARLFMYQLLRGLKYIHSAN VLHRDLKPANLFINTEDLVLKI GDFGLARIMDPHYSHKGHLSE GLVTKWYRSPRLLLSPNNYTK AIDMWAAGCIFAEMLTGKTLF AGAHELEQMQLILESIPVVHEE DRQELLSVIPVYIRNDMTEPHK PLTQLLPGISREALDFLEQILTFS PMDRLTAEEALSHPYMSIYSFP MDEPISSHPFHIEDEVDDILLMD ETHSHIYNWERYHDCQFSEHD WPVHNNFDIDEVQLDPRALSD VTDEEEVQVDPRKYLDGDREK YLEDPAFDTNYSTEPCWQYSD HHENKYCDLECSHTCNYKTRS SSYLDNLVWRESEVNHYYEPK LIIDLSNWKEQSKEKSDKKGKS KCERNGLVKAQIALEEASQQLA GKEREKNQGFDFDSFIAGTIHL\ SSQHEPTDVG\DKLNDLNSSVS QLELKSLISKSVSQEKQEKGMA NLAQLEALYQSSWDSQFVSGG EDCFFINQFCEVRKDEQVEKEN TYTSYLDKFFSRKEDTEMLET\E PVEDGKLGERGHEEGFLNNSGE
12596	42964	A	12672	826	1041	WKITVKGGVFLWWAGVGDTK VLSGGAF*ARMSQEEDFHKVM SSVKARTGHLHFFCGGMSSVK AGQGPFSVLL
12597	42965	A	12673	1	1482	
12598	42966	A	12674	3	488	
12599	42967	A	12675	2	114	

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12600	42968	A	12676	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSITRRIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDEDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGKLFSKYL ADPSNLFVVSSDFCHWGQRFR Y\SYYDESQGEIY*SIEHLDKMG MSIIEQLDPVSFSNYLKKYHNTI CGRHPIG\VLLNAITELQKNGM NMSFS\FLNYAQSSQC\RNWQD SSVSYAAGALTVH
12601	42969	A	12677	2	114	
12602	42970	A	12678	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSITRRIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDEDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGKLFSKYL ADPSNLFVVSSDFCHWGQRFR Y\SYYDESQGEIY*SIEHLDKMG MSIIEQLDPVSFSNYLKKYHNTI CGRHPIG\VLLNAITELQKNGM NMSFS\FLNYAQSSQC\RNWQD SSVSYAAGALTVH
12603	42971	A	12679	1	912	
12604	42972	A	12680	1	156	
12605	42973	A	12681	112	1120	
12606	42974	A	12682	33	415	NMNKPITPSTYVRCLNVGLIRK LSDFIDPQEGWKKLAVAIKKPS GDDRYNQFHI\DAVPKTANTLP SKEAITVQQKQMPFCDKDRTL MTPVQNLEQSYMPPDSSSPENK SLEVSDTRFHSFSFYELKN
12607	42975	A	12683	3	311	
12608	42976	A	12684	1	1125	
12609	42977	A	12685	1	1365	
12610	42978	A	12686	3	141	VVSTVVPDS/AHKLFIGGLPNYL NDDQCHGLSKGYAFCEYVDIN VTV

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12611	42979	A	12687	1	1255	GTRSTSSLRRQMKNIVHNYSEA EIKVREATSNDPWGPSSSLMSEI ADLTYNVVAFSEIMSMIWKRL NDHGKNWRHVYKAMTLMEYL IKTGSERVSQQCKENMYAVQT LKDFQYVDRDGKDQGVNVRE KAKQLVALLRDEDRLREERAH ALKTKEKLAQTATASSAAVGS GPPPEAEQAWPQSSGEEELQLQ LALAMSKEEADQEERIRRGDDL R\RRWQSRRARGRLGARRSRPS WTLLTSSRPQLLPRPQTPGGAQ HPWLLPSPRLPPPRTPGAAPLSL QLLIPGEVQPPRRPLGTPGGLLP LQDPQLTLGVGPQPLQLGRGPR LIHGEVPMVGSRSVGPQPPIPGH RPRPSQIPGEGHLPSPAPMAQQ QPGDSTRSPTSSLTLTDSARHCR PPGAAQESWSCWQERCRPEAL
12612	42980	A	12688	116	1541	
12613	42981	A	12689	3	415	
12614	42982	A	12690	1	1440	
12615	42983	C	12691	117	314	
12616	42984	A	12692	3	120	
12617	42985	A	12693	1	729	
12618	42986	A	12694	79	870	EWSSVRRSLVEKRALRRPHPQC LCFRMKTILSNQTCRPFPE\NVD \ITLKGRP\VIV*GPAEGTLR\RDF \NHLQW*NLSLSWKEKKRGSR VDK\WWGNRKGNWPT\VRTYL VVHVQN\MIKGVLPLGLPVTKD EGLVYA\HFPHPTLVIPGRNGSS LLKSRNFLGVKNTSRRVSG*RP G\VACS\VSSSPRKDEFNPLKGN DIGACFQISAGFGFQQAPHTCL KTRDIQGNFWDGYPMVLWKK GTVSARAGWNKDLKEFTWATE RKMPG
12619	42987	A	12695	2	293	
12620	42988	A	12696	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS
12621	42989	A	12697	1	1308	

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12622	42990	A	12698	124	1135	DKNSMGLPGVIPSCAAVLWSSI HLSSSALSPTISACRHPMEDSM DMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTV SLGAGAKDELHIVEAEAMNYE GSPIKVTLATLKMSVQPTVSLG GFEITPPVVLRLKCGSGPVHISG QHLVAVEEDAESEDEEEEDVK\ LLSISGKRSAPGGGSKVPQKK\V KLAAD\EDDDD\DDEEDDDEDD \DDDDF\DDEEAEEKAPVK\KSI\ RDTPAKNAQKSNQNGKDSKPS STPRSKGQESF\KKQEKTPKTPK GPSSVEDIKAKMQASIA/EKGGS LPKVEAKFINYVKNCFRMTDQ EAIQDLWQWRKSL
12623	42991	A	12699	201	416	
12624	42992	A	12700	2	678	
12625	42993	A	12701	3	2149	
12626	42994	A	12702	1	219	
12627	42995	A	12704	267	437	
12628	42996	A	12705	507	845	
12629	42997	A	12706	426	704	SRRWGGVHSCPPSPPPTAGHWT LLILCAKARRSEAAMVLASRRR RPGPRPRRRRRLPVLGSRGGAG PARGRGPSGWPGPLRAAPSP*P SSTV
12630	42998	A	12707	195	892	
12631	42999	A	12708	1	893	
12632	43000	A	12709	1	777	
12633	43001	A	12710	1	439	KTQVAPSTDGIQP\PSSNSRTDE REFFIASYNRKKEDGEGNVWIA KSSAGAKGEGILISSEASELLDFI DNQAQVHVIQKYLEHPLLLEPG HRKFDIRSWVLVDHQYNIYLY REGVLRTASEPYHVDNFQDKT CHLTNHCIQKKKKK
12634	43002	A	12711	1	394	SGTRPVFLVPHTIGIP\HPAIVTP QVKQEHPHTDSDLMHVKPQHE QRKEQEPKRPHIKKPLNAFMLY MKEMRANVVAECTLKESAAIN QILGRRWHALSREEQAKYYEL ARKERQLHMQLYPGWSARDN
12635	43003	A	12712	1	789	
12636	43004	A	12713	1	870	
12637	43005	A	12714	1	729	
12638	43006	A	12715	1	828	
12639	43007	A	12716	1	213	
12640	43008	A	12717	1	664	
12641	43009	A	12718	1	695	
12642	43010	A	12719	96	269	

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12643	43011	A	12720	3	241	
12644	43012	A	12721	213	660	EGPARHRLLSPVRASKMTKKR RNNGRAQKRAARHVRGPSPLK/ CFPSGPLPPNCAR\CVPK\DKAIK KF\VI\RNIVEAAA\AR\DISEASV FDAYL\LPKL\YVKLH\YCVSCAI HKQK*SGNRSS*SPAKTRTPPPR FR\PGG*LPHGPPTKSP
12645	43013	A	12722	1	303	
12646	43014	A	12723	610	928	FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFFLRWSFAVVAQAV\ VQWHNLSSLPFGFKQFSCLSLP SSWDYRCPPPRPANFCIFTRDG VSPCCPGWSRTSDLR
12647	43015	A	12724	1	2775	
12648	43016	A	12725	1	6039	
12649	43017	A	12726	2	3661	
12650	43018	A	12727	1	1173	
12651	43019	A	12728	1	1632	MPNPKNSKGGRKNKRANSSGD EQENGAGALAAAGAAGAAAG GALAAAAGCGAAAAGAPGAG GAAGAGGAGTGAANAAAAAG AAAAGDAKNEAPCATPLICSFG RPVDLE\KDDYQKVVCNNEHC PCSTWMHLQCFYEWESSILVQF NCIGRARTWNEKQCRQNMWT KKG\YDL\AFRFCSCRCGQGNL KKDTDWYQVKRMQDEKKKKS GSEKNTGRPPGEAAEEAKKCRP PNKPQKGPSHDLPRRHSMDRQ NSQEKAVGAAAYGARSPGGSP GQSPPTGYSILSPAHFSGPRSSR YLGEFLKNAIHLEPHKKAMAG GHVFRNAHFDYSPAGLAVHRG GHFDTPVQFLRRLDLSELLTHIP RHKLNTFHVRMEDDAQVGQG EDLRKFILAALSASHRNVVNCA LCHRALPVFEQFPLVDGTLFLSP SRHDEIEYDVPCHLQGRLMHL YAVCVDCLEGVHKIICIKCKSR WDGSWHQLGTMYTYDILAASP CCQARLNCKHCGKPVIDVRIG MQYFSEYSNVQQCPHCGNLDY HFVKPFSSFKVLEAY
12652	43020	A	12729	1	1485	
12653	43021	A	12730	1	1074	
12654	43022	A	12731	2	3394	
12655	43023	A	12732	1	2190	
12656	43024	A	12733	1	1251	
12657	43025	A	12734	1	1710	
12658	43026	A	12735	3	679	

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12659	43027	A	12736	209	337	
12660	43028	A	12737	365	538	
12661	43029	A	12738	2	196	
12662	43030	A	12739	1	2639	
12663	43031	A	12740	3	173	
12664	43032	A	12741	1	1479	
12665	43033	A	12742	1	921	
12666	43034	A	12743	1	798	
12667	43035	A	12744	2	773	
12668	43036	B	12745	75	321	
12669	43037	A	12746	321	738	
12670	43038	A	12747	1	3190	
12671	43039	A	12748	287	1636	ACGAMERAPPDGPLNASGALA GDAAAAGGARGFSAAWTAVL AALMALLIVATVLGNALVMLA FVADSSLRTQNNFFLLNLAISDF LVGAFCIPLYVPYVLTGRWTFG RGLCKLWLVVDYLLCTSSAFNI VLISYDRFLSVTRAVSYRAQQG DTRRAVRKMLLVWVLAFLLYG PAILSWEYLSGGSSIPEGHCYAE FFYNWYFLITASTLEFFTPFLSV TFFNLSIYLNIQRRTRLRLDGAR EAAGPEPPPEAQPSPPPPGCWG CWQKGHGEAMPLHRYGVGEA AVGAEAGEATLGGGGGGSVA SPTSSSGSSSRGTERPRSLKRGS KPSASSASLEKRMKMVSQSFTQ RFRLA\RDRKEAKSLAVIVSIFG LCWAPYTLLMIIRAACHGHCVP DYWYETSFWLLWANSAVNPV LYPLCHHSFRRAFTKLLCPQKL KIQPHSSLEHCWK
12672	43040	A	12749	1	2142	
12673	43041	A	12750	3	711	VWWNSDLMVINRSTTELPLTV SYDKVSLGRLRFWIHMQDAVY SLQQFGFSEKDADEVKGIFVDT NLYFLALTFFVAAFHLLFDFLA FKNDISFWKKKKSMIGMSTKA VLWRCFSTVVIFLFLLDEQTSLL VLVPAGVW/AAAIELWES*RK/ VI*RWTIFWRGLMPEFQFGTYS ESERKTEEYDTQAMKYLSYLL YPLCVGGAVYSLLNIKYKSWY SWLINSFVNGVYAFGFLFMLPQ
12674	43042	A	12751	1	2025	
12675	43043	A	12752	494	747	ATVKWITLCRNRNIKLPTFIKKE GTGKAPKKSRKSVLGLGP*VHT SPGDPAEGEGLPAGERPDGNLS QSPNSLRFYIKKKKAYK
12676	43044	A	12753	9	731	

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12677	43045	A	12754	143	641	RSWVLLGVGARGSTPRTYQVP SPSLAPSALC*VS*VPLESLSCSH ADNWKQELTKFISPDQLPVEFG GTMTDPDGNPKCLTKINYGGE VPKSYYLCKQVRLQYEHTRSV GRGSSLQVENEILFPGCGLR\VL RFYNTYSLVHSKRISYTVEVLL PDQTFMEKMEKF
12678	43046	A	12755	1	1506	
12679	43047	A	12756	2	526	CQPVRAA*RHGNTPLATV*PAS T/WWKWSEKQKEEQEMQNWR ESAS/VSGYPQDILSCAMSQNPR KRKRPRNVSAPPVHQMAQMNI SVEQMETSKTHQATPLTWGQM KRLAHVAEENLRSQNKPLTTSN LMVAMMVVISLAVSLPVAGAD QNYIYWAYIPFPH
12680	43048	A	12757	1	1443	
12681	43049	A	12758	3	766	
12682	43050	A	12759	29	253	
12683	43051	A	12760	34	252	
12684	43052	A	12761	1362	1611	SSVLHPWDARLVQHT\KSIHIIH HINRTNDKNHMIISIDAEKAFD KIQQDFMLKTLNKLGIDGTYLK IVRATYDKPTASIILNG
12685	43053	B	12762	1	1755	
12686	43054	A	12763	1	2109	
12687	43055	B	12764	1	1497	
12688	43056	B	12765	1	1527	
12689	43057	B	12766	1	1746	
12690	43058	B	12767	1	2853	
12691	43059	B	12768	1	1479	
12692	43060	B	12769	1	1932	
12693	43061	A	12770	1269	1581	NTGKPNPAAHQKGYPPRSSGPH PWDARLVQHT\KSINIIHHINRT KDKNHMIISIDAEKAFDKIQLPF MLKTLSKLGVSYNMFTRLTIPI AQVDTRGNQLPSYLI
12694	43062	B	12771	1	4404	
12695	43063	B	12772	56	2080	
12696	43064	B	12773	1	5445	
12697	43065	B	12774	295	2831	
12698	43066	A	12775	89	459	
12699	43067	A	12776	2	980	
12700	43068	A	12777	1	378	
12701	43069	A	12778	1	363	PGVALPGRCRQAPADLLP*MR AYWPDVIYSFANRSRFWKHEW EKHGTCAAQVDALNSQNKYFG TSLELYRELDLNSVLLKLGIKPS INYYQVADFKDALARVYGVIP KIQCLPPSQDEDRQ

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12702	43070	A	12779	1	577	QRFKNDCRDPRDTGPIHGLWPD KSEG/CNRSW/PFNLEEIKDLCP EMRAYWPDVIHSFPNRSRFWK HEWEKHGTCAAQVDALNSQK KYFGRSLELYRELDL/NQVADF KDALARVYGVIPKIQCLPPSQD EEVQTIGQIELCLTKQDQQLQN CTEPGEQPSPKQEVWLANGAA ESRGLRVCEDGPVFYPPPKKTK
12703	43071	A	12780	1	624	MRPAALRGALLGCLCLALLCL GGADKRLRASVSRPFSLEHPEP GHCLDLHLRAYPAR\WSS*PWP QDFWVR*PTWES/VSDLLPEMR AYWPDVIHSFPNRSRFWKHEW EKHGTCAAQVDALNSQKKYFG RSLELYRELDLNRGERVPTQFP RELVVNRSLAPPPTPGFLSGHVI SVHTSSPLPSAMSGSFLRPLPEA ESGSMLLGQPADP
12704	43072	A	12781	1	612	
12705	43073	A	12782	113	1149	RGAPRGPGRQGCCGHSRSPAR GPRDTGLGRPRAPGAPGGRCCS GGSAAARGLGDSVSPGSLPRAA GGKWEPERQLAAFSPQVGTMR PAALRGALLGCLCLALLCLGG ADKRLRDNHEWKKLIMVQHW PETVCEKIQNDCRDPPDYWTIH GLWPDKSEGCNRSWPF\NLEEI KDLLPEMRAYWPDVIHSFPNRS RFWKHE/WPKRHGTCAAQ\VD ALNSQK\KYFGRSLELY\RKLDL NSVL\LKLGIKPSINYYQVADFK DALARVYGVIPKIQCLPTSQGE\ EVQTIGQ\IDLCLIKARTRQLQN\ CTEPGEQP\SPKQEVWLANGA\ AESRGLRVCEDGPVFYPPPKKT
12706	43074	A	12783	2	515	
12707	43075	B	12784	62	359	
12708	43076	B	12785	219	523	
12709	43077	A	12786	1010	1550	DTENIPSSRRRERSKVPYIVRQC VEEIERRGMEEVGIYHVSGR\V AADIQALKAAFNVSECRPAQD GMEVWAVVSAMRSQSAPRPRH VTSFSVSFLHLSGSSRRPLHFRA LS\NNKDVSVMMSEMDVNAIA GSLKLYFRELPEPLFTDEFYPNF AEGIGEHWRPWPHGRRLLHVH CCPQRL

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12710	43078	A	12787	2	951	GSNLYCTLEGDSFGYFVNKAK TRVYRD/THADPNWNEEFEIEL EGSQTLRILCYEKCYNKTKIPKE DGESTDRLMGKGQVQLDPQAL QDRDWQRTVIAMNGIEVKLSV KFNSREFSLKRMPSRKQTGVFG VKIAVVTKRERSKV\PYI\VRQC VEEIEPPKALEGGWASTACPAG VATDIQALKAAFDGNNKDVSV MMSEMDVNAIAGTLNLYFREL PEPLFT\DEFYPNFAEG/IRVAEK EAVNNM\SLHNLATVFGPTLLR PSEKESKLPANPS\QPITMTDSW SLEVMSQVQVLLYFLQLEAIPA PDSKRQSILFSTEV
12711	43079	A	12788	3	644	
12712	43080	A	12789	168	378	
12713	43081	A	12790	1	486	
12714	43082	A	12792	83	536	
12715	43083	A	12793	1	662	
12716	43084	A	12794	3	357	
12717	43085	A	12795	2	421	
12718	43086	A	12796	2	908	
12719	43087	A	12797	1	846	
12720	43088	C	12798	87	413	
12721	43089	A	12799	1	508	MCQGDTYAWGGHMCRGGHLR RGHSHERDTPRGPERPPRPPAR DRESKDERRRPPPKDPPAVRTC\ PDSPSTATPPPPPPPPPPPPPPP PAAPSAFAALRLRGPGRKWTA RGQLPLPATAPEARVRALPRGG YSSPGRATSARGPAPWPLPSRT GKPPRPCSANTQEHC
12722	43090	A	12800	1	393	
12723	43091	A	12801	1	582	
12724	43092	A	12802	1	1422	
12725	43093	A	12803	1	1080	
12726	43094	A	12804	2	261	SCPFGGNCFYKHAYPDGRREEP QRQKVGTSSRYRAQRRNHFWE LIEERENSNPFDNDEEEVVTFEL GE\MLLMLLAAGGDDELTNS
12727	43095	B	12805	60	802	
12728	43096	A	12806	2	238	
12729	43097	A	12807	1	1017	
12730	43098	B	12808	1	939	
12731	43099	A	12809	1	708	

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12732	43100	A	12810	1	2653	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDIYRNLHP ESTEYTFFSAPHHTYSKIDHILG SKAPLSKYRRSEIKINCLSDHSA IKLELRIKKLTQNRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLLARLIKKKR EKNQIHAIKNDKGDMSTNHTEI QTTIREYYKHLYANKLENLKEI DKFLETYSLPRLNQEEVESLNR PITGSEIEAIINSLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNIPCSWVGRINIVKMAIL PKNWKKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEIMPHIYNHLIFDKPDK NKKWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENPGNTIQDI GMGEDFMSKTPEAMATKAKID KWDLIKLKSFCTAKETTIRLNR PPTEWEKIFAIYSSDKGLISRIYN ELQQIYEKKTNNPIKKWAKDM NRHLSKEDIYAAKRHMKKCAS
12733	43101	B	12811	1	2748	
12734	43102	A	12812	1	1962	
12735	43103	B	12813	1	1833	
12736	43104	A	12814	176	421	QQPASPTRSVLLFPKTAHISGSP APPNVGLLNPSTGAAQKKTMT SAGLGRLSL*K*LNLPECVACA GETWVTSMMSGNQCN

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12737	43105	A	12815	1	1615	LISNFSKVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKR MKYLGIQPTRDMKDLFKENYK PLLNEIKEDTNKWKNIPCSWVG RINIVKMAILPKNWKKTTLKFI WNQKRARIAKSILSQKNKAGGI MLPDFKLYYKATITKTAWYWY QNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGKDSLFNK WCWENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTIKTLE ENPGNTIQDIGMGEDFMSKTPE AMATKAKIDKWDLIKLKSFCT AKETTIRLNRPPTEWEKIFAIYS SDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYAA KRHMKKCASSLAIREIQIKTTM RYHLTPVRMAIIKKSGNNRCW RGCGEIGTLLHCWWDCKLVQP LWKSVWRFLRDLELEIPFDPAIP LLGIYPKDYKSCCYEDTCTHMF IVALFTIAKTWNQPKCPTMIDW IKKMWHIYTMEYYADIKKDEF MSFVRTRMKLETIILSKISQ\EK KTKHRMFSLIGGN
12738	43106	A	12816	1	996	
12739	43107	A	12817	1	756	
12740	43108	A	12818	1	1428	

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12741	43109	A	12819	1	2377	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NIVQHINRTNDKNHMIISIDAEK AFDKIQQRFMLKTLNKLGIDGT YLKIIRAIYDKSTANIVLNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGIQLTRDVKDLFKEN YKPLLNDIKEDTNKWKNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKGARIAKSILIYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKWGNDS LFNKWCWENWLAICRKLKLDP FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNTIQDIAMGKDFMS KTPKAMATKAKIDKWDLINLK SFCTAKETTIRVNRQPIEWEKIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSSLAIREMHI KTTMRHHLTSVRMAIIKKLGN DWCWRGCGEIGRLLHCWWDC KLVQPLWKSVWRFLRDLELET PFDPATP\LLGIYPKDYKSCCYK DICT/RVCVPAALFTIANTWNPT
12742	43110	A	12820	1	4840	
12743	43111	A	12821	578	630	EYKNR*GLSLNPWGKTVHISW DVWSVGSSKAKRNWESWES*C RGIQKKASLRSRTGNHSASSGI* ESRV*GLGTTGYRGITASLMSL RSCTRLH
12744	43112	A	12822	8	214	EEWPKRKSEIRERPRP*SWPSDK QTLVVQRGQKMEQANHPDPTD HMSQLMWTACPKGLGIALICL VRH
12745	43113	A	12823	33	240	GGGRNTWLQAVPGFPGW*RTL RTAVWDRRLTLRKPHHCPGGS QFPGPQRQVIGLLHFLSSLNHQ GWFV

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12746	43114	A	12824	1	411	MSTITQRKEENPSVFLEWLWEA /CKKIYSPVTRLTRGSIDPKR*V YYAISHRYQQKAPKPSPGP*TK SGGIIKPGNLGVLY*GPRGTGQ KGKARSEKGCSLSHGPQTNKP WWFREDRKWSRPITWYGFLSV WFARTP
12747	43115	A	12825	1	611	
12748	43116	A	12826	120	493	KYRAQRRMIARWLPQDLERGE AMLPNSSGWYKSLKGI/VLISEA FSCKCRAASLTIADWLV*KQHS SPKKVQSPPFSAVRRSKPWQFW RVTAAKQSIWDCRVRIDFVISC KLRNPLRVCGSRILK
12749	43117	A	12827	1	2195	VGEEGPAGVEGLNFPAQSRRLP GPQQCSPGAEQGASARARRPRP RPRPAAMVPGVPGAVLTLCLW LAASSG\SWRPAPARL\CAAAG RVAVCRERPARS\CASRCLSLQI TRISAFFQHFQNNGSLVWCQNH KQCSKCLEPCKESGDLRKHQC QSFCEPLFPKKSYECLTSCEFLK YILLVKQGDCPAPEKASGFAAA CVESCEVDNECSGVKKCCSNG CGHTCQVPKTLYKGVPLKPRK ELRFTELQSGQLEVKWSSKFNI SIEPVIYVVQRRWNYGIHPSED DATHWQTVAQTTDERVQLTDI RPSRWYQFRVAAVNVHGTRGF TAPSKHFRSSKDPSAPPAPANLR LANSTVNSDG/AV*TVTIVW\DL PEEPDIPVHHYKVFWSWMVSS KSLVPTKKKRRKTTDGFQNSVI LEKLQPDCDYVVELQAITYWG QTRLKSAKVSLHFTSTHATNNK EQLVK\TRKGGIQTQLPFQRRRP TRPLEVGAPFYQDGQLQVKVY WKKTEDPTVNRYHVRWFPEAC AHNRTTGSEASSGMTHENYIIL QDLSFSCKYKVTVQPIRPKSHS KAEAVFFTTPPCSALKGKSHKPI GCLGEAGHVLSKVLAKPENLS ASFIVQDVNITGHFSWKMAKA NLYQPMTGFQVTWAEVTTESR QNSLPNSIISQSQILPSDHYVLTV PNLRPSTLYRLEVQVLTPGGEG
12750	43118	A	12828	1	1410	
12751	43119	A	12829	2	299	
12752	43120	B	12830	81	510	
12753	43121	A	12831	3	436	
12754	43122	A	12832	1	769	

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12755	43123	A	12833	15	413	ERMCAGPWRKGAETGPYFCND TVRHRKASLLCPF*RMNGDQN SDVYAQEKQDFVQHFSQIVRVL TEDEMGHPEIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFREL VEPRKQDADSLQRAWTVGWC VELLQA
12756	43124	A	12834	1	795	MNGDQKSDVYAQEKQDFFQHF SQIVGVLTEDEMGHSEIGDAIA RLKDVLEYNAIGGKYHRGLTV LVAFQELDAINYAILLEACIYYL LKLYCQAQPYYLNLIELFLQISC QPEIGQTLDLITAP/QDNVDFGR FT/EKQHANA*KILLEI/GEFFQI QDGYLDLFGDPTVTRKVGTDIQ DNKCSWLVVQCLQRSTLEQYQ ILKENYGQKKAKKVVQVKALY EELDLPAVFLQYEEDGYSHIMG LTEQYAAPLLPAMFLGLVYKIY
12757	43125	B	12835	1	328	
12758	43126	A	12836	2	868	
12759	43127	B	12837	118	1138	
12760	43128	A	12838	100	374	KHISPALKALELPFERNLII/PLQ LLKVRILKEGEML/DI*HWFL** GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV
12761	43129	A	12839	1	1035	
12762	43130	A	12840	13	600	INPPPPPFRPELPSSSNSPKMTDH KGERGEATRYMFSRPFKKTMG VVPLGHNN*RF\YKKGDIVD\IK GMGYCVQNGMP\HKCYPWPKL EGVLQLLPQHA\VAIVVNQPVL GQSFFPRE*IVRIEHIKHF*EPEIS FLK/RVLKENDSEKERSPNEKG TWGSNLKRHLAPPQKKHTL*R TNGKEPEL\LEPIPYEFHGHN
12763	43131	A	12841	1	317	QRPSEAKEIKLYAQIPPIEKMDA SLSMLANCEKLSLSTNCIEKIAN LNGL\EAVGDTLEELWISYNFIE KLKGIHIMKKLKILYMSNNLVK DWGTPVIKGDEEEDN
12764	43132	A	12842	155	588	
12765	43133	A	12843	1	954	
12766	43134	A	12844	1	486	
12767	43135	A	12845	1	367	
12768	43136	A	12846	1	190	LISRAKEDDMTLNIAEGVHPSY NIVLNTLHT/CGISVKSTWRPSK GAAP*ARMPGGTAGPCLAS

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12769	43137	A	12847	1	2376	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA\WQQLPC*YKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
12770	43138	A	12848	1	636	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA\WQQLPC*YKKQIS
12771	43139	B	12849	180	811	
12772	43140	A	12850	1008	1265	FLGVPTLGGWRPIQHELRK/PRE VTPVLLRDLIRRFRPPLWIGSDN GPAFLAALVQKTAKGIQNNITG GVYTLCDIDSHIILFRSGY
12773	43141	B	12851	1	996	
12774	43142	A	12852	1251	1424	DSPRGEAES*A*LPEKLLEMSG NRLVDNKDPGKKQTQRRIPHSP SQIPVPLPEIWCT
12775	43143	A	12853	1	1121	
12776	43144	A	12854	189	621	
12777	43145	A	12855	2207	2308	
12778	43146	A	12856	1	762	
12779	43147	A	12857	1	678	
12780	43148	A	12858	3	496	
12781	43149	A	12859	107	258	NALGKRTSFTNRNFLASGRLFD SVTYARRLQQYPAPL*KTAI*SF SLLNH
12782	43150	A	12860	2	410	SPDPWVSTYKSTCHIAQEIAEKI HLRNQYERKGE*AP\RSNLMSE DANGGAPNPWLFEEPEETIGW GFDEIRQQQHNIIR*QDAGLDA LSSIISRQKQM\GIEIGNELHEQN EIIDDLANLMENTDEKLRNETR RVN
12783	43151	A	12861	3	1402	

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12784	43152	A	12862	1	711	MAPDPWFSTYDSTCQIAQEIAE KIQQRNQYERKGEKAPKLTVTI RALLQNLKEKIALLKDLLLRAV STHQITQLEGDRRQNLLDDLVT RERLLLASFKNEGAEPDLIRSSL MSEEAKRGAPNPWLFEEPEETR GLGF\DEIRQQPQKII\QEQDARL DALSSIISSQKQ\MGQEIGNELD EQNEIIDDLANLVENTDEKLRN ETRRVNMVDRKSASCGMIMVI LLLLVAIVVVAVWPTN
12785	43153	A	12863	1	936	
12786	43154	A	12864	1	1023	
12787	43155	A	12865	1606	2238	
12788	43156	A	12866	3	347	
12789	43157	A	12867	1	1665	
12790	43158	A	12868	1	589	
12791	43159	A	12869	19	1677	
12792	43160	A	12870	1	906	
12793	43161	A	12871	1	228	
12794	43162	A	12872	1	320	
12795	43163	A	12873	1	398	TSKAPGAQGEQGFEECFLAVAL AGRPLPSLWALFQATTPV\LQG LKEAFFRPEVP\LRRDLPLLLFR\ TQTSDPAMLP\TMIGLLAEARR AGCLSYQTSLVSDGETWHVMG ISSLLP\SLEG\WKQ\HVTEAFQF HF
12796	43164	A	12874	3	322	SAGGSGRRTLHSRTMAQFVRN LVEKTPALVNAAVTYSKPRLAT FWYYAKVELVPPTPAEIPRAIQS LKKIVNSAQTGSFKQLTVKVTT G*MKTDVHNRKCLPLGFF
12797	43165	A	12875	91	425	WTFHPTTMAPFVRDLGEKTPA LGKAAVTYLKPRLAAFWYYH\ QVELVPPTPA\EIPRAIQSLKKIV\ NSAQTGSFKQLTVKEA\LLNDL VATEVSTWFYVREITGKRGIIG* NV
12798	43166	A	12876	179	664	HSSPAVPGRTDFSHSQNPWPQF CPVTLVGEDPRALVNAAVT/YT RKPRIGLHFWYYA\KVELVP\PT P\AEIP\RAIQSLKK\IVNSAQTGT LANSSHVKEAV/L*NGLVATEV\ LMWFLCSERLLGKRGHSLGYG CFEDQSFNIWIIFWILFILELFVW DHVVDPDC
12799	43167	A	12877	25	164	
12800	43168	A	12878	2110	2260	
12801	43169	C	12879	32	1429	
12802	43170	A	12880	172	322	

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12803	43171	A	12881	1060	12039	
12804	43172	A	12882	1	810	
12805	43173	A	12883	3	146	
12806	43174	A	12884	1	1211	GPQDGNQQPAPPEKVGWVRKF CGKGIFREIWKNRYVVLKGDQ LYISEKEVKDEKNIQEVFDLSD YEKCEELRKSKSRSKKNHSKFT LAHSKQPGNTAPNLIFLAVSPEE KESWINALNSAITRAKNRILDE VTVEEDSYLAHPTRDRAKIQHS RRPPTRGHLMAVASTSTSDGM LTLDLIQEEDPSPEEPTSCAESFR VDLDKSVAQLAGSRRRADSDRI QPSADRASSLSRPWEKTDKGAT YTPQAPKKLTPTEKGRCASLEEI LSQRYAASAHTLQLRAEEPPTP ALPNPGQLSRIQ\DLVARKLEET QELLAEVQGLGDGKRKAKDPP S/RSPPDSES\EQLLL\ETER\LLG EASSNWSQAKRVLQQVRELRD LYRQ\MDLQTPD\SHL\RQTTPH S\Q\YRKSLM
12807	43175	A	12885	617	1041	TTLINPGGPAPLLSLPTSSITGFT TFYHPNLKPLRTCPS*VQAWPC RHPI*SRDYQRDAEPTTCISKLL GENIRRDEFWKVQIKARSGETE QNPRSTAFAFGELPLANREELN LLLNKGILPLCDQRQEIESECAF TIFCAGDANCFPPSPTHLPLTAL QQRPCGLSGSASKEAWGNSLV CGPRGDTLPMAIAKPHRSASKH STLHQYPTPPRSLCHQHRDEQP TNHLQTLNTIPAWIHTKWVPGL DHINKPWRSCSSSQSAYLFYHW LHYFLPPKLKTSKDLSILSAGLA MSAPHLIFRVSAITSNSSCKPSS TSKACEELFKEHQCLGSTDIPIH IQGGAPFSAVSPQRLVLRGSQD GSHMVRPRLPFPDSAGLANFHL FSKLFLD
12808	43176	A	12886	1	606	
12809	43177	A	12887	174	350	VSWRFVQVFI*V\AGGSRICAAA GLSPGTPPPCATSLIGACSLIFIP RLLSLFCGDEAL
12810	43178	A	12888	3	265	
12811	43179	A	12889	1	1209	
12812	43180	A	12890	53	369	VAHQEKGIAEPGLRPTGDSRQT HRRLDVERSTSVQEHMGGCHF SPFPEREKLSTLRGIHQQAPAL WQATDQWIDIEF/GLGQPEESL GR*ITRLQGKTILPFGSPIC

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12813	43181	A	12891	1	345	
12814	43182	A	12892	2	451	
12815	43183	A	12893	2	286	
12816	43184	A	12894	217	1071	GENPRSENTRLATILEVACCHF GSSPPPS\GSSGRKDPPLTFGDH EGTSKAEPSPALGLTPEHKGNV GHAARIQQPGPLSLWSRKAGK GVQDCYIDLKQIKIDLDKFSDN PDGYIDVLQGLGQSFDLTWRNI MLLLNQTLTPNERSATITAARE FGDLWYLSQVNDRIAAEKREK FLTGQQAVPSVGSHWDTESEH GDWCCRHLLTCMLEGLRKTRK KPMNYSMMSTITQGKEENPTA FLERLREALRKHTSLSLDSIEGQ LILKDTFITQSAADIRK\NFKSPP
12817	43185	A	12895	1	756	
12818	43186	A	12896	473	1015	
12819	43187	C	12897	152	322	
12820	43188	A	12898	146	1079	PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRAA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPSLPLCSGVS PRAGLGSAWPKIPFLGIREAKN PRSENTRLATILEAGHRHLGTS VSKDHPVTFWRPRRDLQSDLK QIKIDLGKFSDNPDGYIDVLQEL GQSFDLTWRDIMLLLNQTLTPN ERSATITAAREFGDLWYISQVV AAVAGLVSEAVKIIQGSYCVDI HDVNGILTAKGDLWLSDNHLL KYQALLLEGPVLRLRTCATLNP ATFLPDNEEKIEHNCQQVIAQT
12821	43189	A	12899	189	1798	

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12822	43190	A	12900	194	1729	NPAAQTPFFVVKKGGKRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSSPCNTPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEAEWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDTLVLQ YMDDLLLVTHSETWCHQATQA LLNFLATCGYKVSKQNAQLCS QQVKNLGLKLSKGTRALSEERI QPILAYPHPKTLKQLRGFLGITS FCRIWIPRIKAVKLQIILQMEPQ MQSMTKIYHGPLDRPTSPSSNV NDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYYLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKP\IN*SMISTI TQGKEENPTAFLERLREALRKH
12823	43191	A	12901	1	642	
12824	43192	C	12902	54	254	
12825	43193	A	12903	32	221	NGVGHNRMGTNGSGGGEWG\P PAPASA*GCSLASAFASASPRW WFEMGCRGIYDAQQVALSRSF
12826	43194	A	12904	203	538	
12827	43195	B	12905	131	536	
12828	43196	A	12906	1	1251	
12829	43197	A	12907	38	475	ESERRGEFCLCKIISEQGRAVCV EDEQTSHFALTGNNGIYRKSQQ QWQQELSDLARDPPAQCSAGP VGDDMFHWQATIMGPNDSPYQ GGVFFLTIHFPTDYPFKPPKVAF \TTRIYHPNINSNG\SICLDILRSQ WSPAFNQFPKSS
12830	43198	A	12908	282	849	QSCPAAGIIKSFGRTFEHTPREV RKPDDKHTLLALKRINKDLSDL ARDPPAQCS\AGPV\GDDMFHW QATIMG\PNDSPYQGGVFFLTIH F\PT\DYPFKPP*GLHFTTRFY\HP \NINSKWAAFCLRYS*DSQW\SP ALTFSKVLLSI\CSLL\CDPNP\D\ DPLVPGDWHGSY*NRTGDKYN RISREWTQKYAM
12831	43199	A	12909	1	397	
12832	43200	A	12910	245	535	
12833	43201	B	12911	68	333	
12834	43202	A	12912	265	562	

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12835	43203	A	12913	1	872	MVNTECQLDWIEGCKVLILGVS KEASQGLGGRSRGRNVRQSTD ADIRPTSEKDARSLMTTRQEDN ISVDQRGFLSGVQKKSGCANGL KGSVCGGFYWVMAVIRMGVG KAMGLNLKLGIKFEIKKGYLKG CRDSLRLSPTGFGKFTATSHEV AATVPIKVVLELTLQTHKILRG VFAHLTSCLQLHSLPPGSSMDS AKARRQLQVAGQGHSLVKQK GFHVEAPDHHPVQLSDISCKSY RWGHKLIKINFLIPPLWWYYDL EEVKREQSEEKQQAKIMADIIG DALNAQKAFKGNPKGHKPLPF SAGQMENW*CPECPKSI
12836	43204	A	12914	7	231	
12837	43205	A	12915	1	223	MEILTTCDKGLIFTGNTRKSETS TSECTCPLDINCSLSHSPPSPSDE ETQHHTDSLHVRPRKGYLLCIY HIPDIVAVMVNIQCQLDWIEGC KVLFLGVSVKVLPKEINTGISGL GKADPPSIWKS*QHVTKDLYLQ VILENQKLVPANALVRWILTVP FPTLLRALQMRKHSTTLTVCMS DRGKDIYCASTIYQI
12838	43206	A	12916	1083	1273	NKMSFKLKEDCFGRSKCNL*T* CWKSINEA*K/DLELQLQFGPQE KLFALEQQVKKKLNLVPDA
12839	43207	C	12917	1	1506	
12840	43208	A	12918	3	1219	
12841	43209	A	12919	1	735	
12842	43210	A	12920	2	94	
12843	43211	A	12921	362	460	WLILSVNLIGLKDAKYCSCVCL *GCCQRRLTF
12844	43212	A	12922	1235	1474	
12845	43213	A	12923	1	250	
12846	43214	A	12924	1	261	
12847	43215	A	12925	2	85	
12848	43216	A	12926	1	291	
12849	43217	A	12927	1	321	
12850	43218	A	12928	1	370	
12851	43219	A	12929	1	684	
12852	43220	C	12930	1	210	
12853	43221	A	12931	2	91	
12854	43222	A	12932	1	243	
12855	43223	A	12933	2	353	WMKLETIILSKLS*GQKTKHRM SSLIGSTDQQRLVVKNVQGRVC PGSTGHGAWEAWTAMRKVDS PLQTGSLRPGWCRQVGSHARS GSAEAAGNPGLHPGICPRVEDG IQVAENFPEV

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12856	43224	C	12934	1	289	
12857	43225	A	12935	1	1194	
12858	43226	A	12936	140	237	
12859	43227	A	12937	1	292	
12860	43228	A	12938	2	178	
12861	43229	B	12939	1	1245	
12862	43230	A	12940	2	241	
12863	43231	A	12941	1	675	
12864	43232	A	12942	1515	1920	TPTNLQEKNKQPHQKVGEGYE QTLLKRRHLCSQKTHGKNAHH HWPSEKCKSKPQ\WIPSISHQLE WQSLKSQETTGTWMKLETIILS KLLQGQKTKHHMFSLIGGNRT RRTHGHRKGNITLWGLLSDSV NCASSSG
12865	43233	A	12943	608	891	
12866	43234	A	12944	1	3956	MGSCPGGFTAEFYQRYKEELVP FLLKLFQSIEKQGTLPNSFYEAS IILIPKPGRDTTKKENFRPISLMN IDAKILNKILTNRIQQHIKKLIHH DQVGFIHGMQGWFNIRKSINVI QHINRTNDKKHMIISIDAEKAF DKIQQPFMLKTLNKLGTWMKL ETIILSKRSQGQKTKHRMFSLIV NIIPTIKILIKQNMTAMETLCPIF KLEGDTMDNPIANRRVRTAVP TSVVCLHVGTEPEARLPHGPMI TAQSPFG
12867	43235	A	12945	1	855	
12868	43236	A	12946	1	255	
12869	43237	A	12947	273	3484	
12870	43238	A	12948	3	377	
12871	43239	A	12949	85	333	
12872	43240	A	12952	22	308	
12873	43241	B	12953	30	383	
12874	43242	A	12954	3	448	
12875	43243	A	12955	1	453	
12876	43244	A	12956	3	491	
12877	43245	A	12957	2	749	
12878	43246	A	12958	155	637	
12879	43247	A	12959	1	510	
12880	43248	A	12960	2	559	RPHASAHASGRQRSQDVTTMV WALLLLTLLTQGTGSWAQSAL TQPPSASGSPGQSITISCTGLIND VASYNFVSWYQQHPGKAPKL MIYEVTKRPSG\VPDRFSGSKSG \NTASLDHLWGSRLEDEADYYC LLICRRLHPGGGIRRWDPRVTV LGSAQRPTPTVTSGSRPSSEGAP SQQGHTSVSDQ

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12881	43249	A	12961	1	1958	MSVQRKDRVRTQQGGSVASSM LTQEPVGSVALGQSARDRDPD CSDSVSVYLMDTWQSVIIGFAE SAATLGDPPELPMHPEGSEASY ELTQPPSVSVSPGQTARITCSGD ALPKQYAYWYQQKPGQAPVL VIYKDSERPSGIPERFSGSSSGTT VTLTISGVQAEDEADYYCQSAD SSGTYPTVTQADRETPTHQYSR HPSYAKGFVFLWGSWAQSALT QPASVSGSPGQSITISCTGTSSD VGSYNLVSWYQQ\PQGKAPKL MIYE/VDSKRPSGVSNRFSGSKS G\NTASLTISGVPGLRDEG\DYY CCSYAGSVASYELTQLPSVSVS PGQTARITCSGDVLGENYADW YQQKPGQAPELVIYEDSERYPG IPERFSGSTSGNTTTLTISRVLTE DEADYYCLSGDEDNPSVTQAD GEDTGIRSHYEGTLALYLYPEP VKATCSVTSYVLTQPPSVSVAP GQTARITCGGNNIGSKSVHWY QQKPGQAPVLVVYDDSDRPSGI PERFSGSNSGNTATLTISRVEAG DEADYYCQSLSTLGPKTLGDTV LRPMIYSVSIQASGVPDGFSGSK SGNTASMTISGFQAEDEADYYC NSHRRGSVVSSELTQDPAVSVA LGQTVRITCQGDSLRSYYASW YQQHPGKAPKLIIYDGH
12882	43250	A	12962	2	367	
12883	43251	A	12963	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12884	43252	A	12964	2	1178	
12885	43253	A	12965	1	732	
12886	43254	B	12966	99	716	
12887	43255	A	12967	1	1011	

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12888	43256	A	12968	3	1263	GRTIQTKGKEV\ENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERVSAM EDEMNEMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTPQRYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRAILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQEIQRTPQR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK
12889	43257	A	12969	1	1392	
12890	43258	A	12970	1	1224	
12891	43259	A	12971	1	970	
12892	43260	A	12972	1	954	MDGDLHKGVAVFWPPDAAGG HTCCRSMVCRSLLGGAQWKFH SFRCRIRFELILHMIQERNSINIS QKDVHTETPSETHHHQRPKVD KSMKMRRNQCKKAENSKNQK ASSPPKEHNSWRAREQNWTEN EFDKLTEVGFRRWVITNSSELK EHILTQCKEAKNLEKTLEELLT RITSLEKNINDLMKLKNTA*EL REAYTSINSQISQAEERISEIEDQ LNEMKHEHRIREKRMKRNKQS FQEIWDYVKRPNLRLISVPESD GENGNK*ENILQDII\QENFPNL ARQANIQIQEIQRTPQRYSSRRA TPRHIIVRFTKV
12893	43261	B	12973	1	1346	
12894	43262	A	12974	1	318	GSRGELLLSLCYNPSANSIIVNII KARNLKAMDIGGTSDPYVKVW LMYKDKRVEKKKTVTMKRNL NPNFNES\FAFDIP\TEK\LRETTII ITVMDKDKLSRNDVIGK
12895	43263	A	12975	17	389	SWGPHCTHKLKKSFSLMPEMT DAMDRERM/RGSKKDV/R*VLG GCAATWTPRAGGRQQSPGTTV DKREDTPDCAMCDQSTSHPISA SSPSLLPGSSFTTQTFPPGIAHYR ASFLIVAYYPSNKNSK

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12896	43264	A	12976	84	282	GEGQVGWPQGEVQQDEEVIEE VGA*DAGSGYQEEEEGPQSLRR EVVGVELVVGADPSGEGPKED
12897	43265	A	12977	1	1179	
12898	43266	A	12978	3	634	
12899	43267	A	12979	234	619	CYVVQEVLPSLLCHCLVICSRP GRTAEWPPG*GF*SPPHRGWW GC*GHD/HRRGTSIFPTH/V*SPP ASYPGSLCRPGGQEEREREGEW QREGRRPGTR*CGAEAEARGW RAAAKATAVAGARNRRPGISG
12900	43268	A	12980	1	1182	
12901	43269	A	12981	3	763	
12902	43270	A	12982	32	949	
12903	43271	A	12983	1	1299	
12904	43272	A	12984	1	1176	
12905	43273	A	12985	1	421	
12906	43274	A	12986	81	404	VKFGPEIWCRDSDQGRGGVGT SLGRSIPCPPALCSVRKIYLRPL VLRPTSPRNISPILNRDPTVQLT WQPLPEPLELWPKAL*LTPSQIY SA*RLKTDAARLPRKPPR
12907	43275	A	12987	1	378	
12908	43276	C	12988	1	751	
12909	43277	A	12989	302	629	ICLSYPAPPCKRFPHYTRVLYH* SLFNENTSQSCFTSR/WKLESFT TRAIERHQIPLL*ATLTLIRWLD KKLAFQLLSLTASFSPSYQSLPP TPPLKLPPIISSHTRQMV
12910	43278	A	12990	14	380	
12911	43279	A	12991	189	608	QSDLSASQHGLFPLATEVRSSG AASCPDSDSICPAPTIAPGRATP PQANCWASEGTLRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLFSNLQGP RSRPVAFLSKQLDLTVLGWPSC L\VQQLLPP
12912	43280	A	12992	1	513	
12913	43281	A	12993	2	462	WSMGLPRRSGCVSLQPLSQEDL GRSQSESLGPEFQGLWEWLPEQ LPRSFIQALGSLSYFPRTLMNLS WPLCLRKWGYL/SLYLPFQVGL PSTVPWPLILPSKVPEEEGQLQS TLPCGIKLLPVFTSHHAFLGVFC NQWVSDVFLALFLMKLLGAQ
12914	43282	A	12994	59	213	
12915	43283	A	12995	1	1159	
12916	43284	C	12996	1	864	
12917	43285	A	12997	1	1155	

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12918	43286	A	12998	879	1163	SRRPLFMGLVRVLCKMSGRGP LCFPGGHWIVFLWGGTVLWLW T*SPHWHRKAN*DLFLQKLPRL *VSHQCDPCLPVCHLWNCLFLL PLWGPPAG
12919	43287	A	12999	1	179	
12920	43288	C	13000	1	410	
12921	43289	A	13001	42	365	FGLRLSLAPPFCMFPLTT*HS*P SVLPASFPAALGIPQARAVTPFV SP*LLASLSFWAPPCSLCLDASV *HGSHLWHAQSSCRLRWSFGL AASQMQPEEPSHGPRRK
12922	43290	B	13002	1	741	
12923	43291	A	13003	8	265	
12924	43292	B	13004	1	646	
12925	43293	A	13005	1	1158	MKLVTIFLLVTISLCSYSGYWPE NEQMSVGGGDDNGEVLYSALR GASEVIGQCQSSATKPRRSGKE SVREPWARVPGALGVGVREID QTLGIDTILCHHHERLLQSHYGI HKSSLMSVGNSQVAALYQLNV YVVADTVGLIIKSNSILDSVQPN YCSNKHIELRTQVGGARNLRA NSPMTSSYNQESSSMENVSALS LLTVESPTSMFDYCDDSLERVK SALDIFSMIIYTVTFFLGLAGNG LVIWVVGFHMSCTVNTCLPSDP HLHGPLTCDPVANLVLEQLHTS KGNSGALEDLAFGNLFLCSLLD LQGNSWWKVSPSLYNQYDLQ NETQGSHQLWKEIIIPW*PSAFV V/SSGYWPENEQMSVGGGDDN GEV/RVFRPEGGFRGDRAVSVF SH*AEKIWEGISQRAL/VPEFQG LWEWV/CREIDQTLGIDTILCHH HERLLQSHYGIHKSSLMSVGNS QVAALYQLNVYVVADTVGLII KSNSILDSVQPNYCSNKHIELRT QVGGARNLRANSPMTSSYNQE SSSMENVSALSLLTVESPTSMF DYCDDSLERVKSALDIFSMIIYT VTFFLGLAGNGLVIWVVGFHM SCTVNTCLPSDPHLHGPLTCDP VANLVLEQLHTSKGNSGALED LAFGNLFLCSLLDLQGNSWWK VSPSLYNQYDLQNETQGSHQL WKEIIIPWHQTLVTTAHFFFGFF

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12926	43294	A	13006	3	371	AGARFNVRSH*RNDRVRPHRD VYSLQGRLSDHSPTFQGCQTTQ GRLPWSFTLSGKFRFSGEGATT SPAHKNFQTPEPQWPGIPPEPPP TGACYTCRKSGHWAKECPQAR IPPKPHPICVGPH
12927	43295	A	13007	77	332	RWKKNCLSPPRMS*QR*WKP* MQQAACSVGETQPPCTQVK*T ALLLTQSLFGGLFTRTHMKFGA VTRIGGPPLGDQSPVLLLFAP
12928	43296	A	13008	1048	1349	RVVEQDDAERLFRRFRAA/GDL PYGAFGEIF*ETQCQEMQQLAE DHASVTMISLEAWRLYRKMVC RIWASMLRLSVCHLCAPKRVW SLISRNGYHLPGSIH
12929	43297	A	13009	213	499	PEQRTSHRQQQRRQPPPQSRS*P FCPSLPRSALSLSFLCDGYAAP* AYRE*IPVTEDHFAE*I/ISWCPC *YREALGQLLAKMRR*SARKRF QLSP
12930	43298	A	13010	2	431	
12931	43299	A	13011	2	367	
12932	43300	B	13012	1107	2083	
12933	43301	B	13013	1	627	
12934	43302	A	13014	712	2671	AHVGRGST*ALPRAMGSDAF*C PLQ*MTPASFGSKAALSRVFIKE ALMMEDPCVVRKPLSAHMTA WWCRIWKAYLESV
12935	43303	A	13015	50	1362	WEQIPHGLVLSLQQLPRRSGSIS LQPLSQEDLGRSQSESLGPEFQ GLWQWLSDFQT*HQWFVSGFQ AFSDRLKAALSASLLLRFGDSD WLPSSSACKCLMLGLHFVIVGN ICATLKEKYSSMLHLDVTMKK NGEKRTRLQKRKKGMPPHPAY EDLNIAAITLPANVVLHQPSGFR TSGQLDPVWWSLDTDAHEIWC QDPGLGSGDFPWEITPLSSYSLL HEKDPPTTSGPQTDQPKKHLTN FKSKTKETGFIHGPKTPAPVTD WEGSLPLVFNHCRDTSLIIHPCF KGVRPRRDACLGPSPLAASPAF LEKGQDLINLAFKVYNNRKKL QFLASTVRQTPATSPAHKNFQT TEPQQPGVPPEPPPTGACYMCR KIWPLGQANARSPGFLLSRVPS VWDPTGNRTVQLTWQPLPEPL ELWPKALCLTDSFPDLLGLAA
12936	43304	A	13016	1	507	
12937	43305	A	13017	5	271	
12938	43306	A	13018	1	618	

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12939	43307	A	13019	1	429	
12940	43308	A	13020	1	3567	
12941	43309	A	13021	1	353	
12942	43310	A	13022	1	338	
12943	43311	A	13023	1	1175	
12944	43312	A	13024	3	326	
12945	43313	A	13025	150	494	PSPSLGYLVGTRGTALRL*DAR AAMRPFDPSTLLPTCWDYWTY AGSLTTPPLTESVTWIIQKEPVE VAPSQLSAFRTLLFSALGEEEK MMVNNYRPLQPLMNRKVWAS FQATNEG
12946	43314	A	13026	2	975	DSREHHPLQTGVSGNRPKMLG RNTWKTSAFSFLVEQMWAPLW SRSMRPGRWCSQRSCAWQTSN NTLHPLWTVPVSVPGGTRQSPI NIQWRDSVYDPQLKPLRVSYE AASCLYIWNTGYLFQVEFDDA TEASGISGGPLENHYRLKQFHF HWGAVNEGGSEHTVDGHAYP AELHLVHWNSVKYQNYKEAV VGENGLAVIGVFLKLGAHHQT LQRLVDILPEIKHK\DARAAMR PFDPSTLLPTCWDYWTYAGSLT TPPLTESVTWIIQKEPVEVAPSQ LSAFRTLLFSALGEEEKMMVN NYRPLQPLMNRKVWASFQATN
12947	43315	A	13027	1	1233	
12948	43316	A	13028	761	1000	IPFISFSCLIALARTSNTMLNKSG ERGHPSLVPVFIGNASSFCPVSM ILAVGLS*IALIILRYVPSIPNLLR VFSMKGC
12949	43317	B	13029	697	1527	
12950	43318	A	13030	1	1695	
12951	43319	A	13031	434	925	VAKIFSHFVCCLFTLMVVSFAV QKLFSLIRSHLSILSFVAIDFGVL DMKSLPMPMS*MVMPRFSSRV FIVLGLTFKSLIHLELIFV*GVRK GSSFSFLHMASQFSQHHLLNRE SFPHCLFFSGFSKIR*L*ICGIISE GSVMFH*SISLFWYQYHAVLVT VAL
12952	43320	A	13032	1124	1234	KITPKKQIRQSPNLTQNTGQQ*S LQLWEHFQISTHF
12953	43321	A	13033	929	1261	
12954	43322	A	13034	1118	1354	IPFISSCLIALARTSNTMLNRSGE RGHPCLVPVFKGNASSFFPFSMI LAVGLS*IALIILRYIPSIPSLLRV FSVKGC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12955	43323	A	13035	2	348	HQHLLFPDFLMIAILTGMRWYL IVVLICISLRASDDEHF/YHVSV GCINVFF*EISVHILRPLFDGVV* FFLVNLFKFFVDSGYEPFVRWV DCKNVLPFCRLPVHSDGSFFCC AEAL
12956	43324	A	13036	578	712	LISNFSKVSGYKINVPKSQAFLY TKNRQTAKS*VNSHSQLLQRE
12957	43325	A	13037	1	1833	
12958	43326	B	13038	1	1587	
12959	43327	B	13039	1	1851	
12960	43328	A	13040	1349	1444	
12961	43329	A	13041	953	1277	MVLPRFSSRVFMVLGLTFKPLI HLELIFV*GVNFV*GSSFSFPHM ASQFSQHHLLNRESFPHFLFLSG LSKIR*L*MCGIISEGSVLFHWS ESLFWYQYHAVLVTVAL
12962	43330	B	13042	804	4236	
12963	43331	A	13043	1	744	
12964	43332	A	13044	137	797	
12965	43333	A	13045	210	418	
12966	43334	A	13046	1	927	
12967	43335	A	13047	1	1415	MGFLGTGTWILVLVLPIQAFPK PGGSQDKSLHNRELSAERPLNE QIAEAEEDKIKKTYPPENKPGQ SNYSFVDNLNLLRAITEKEKIEK ERQSIRSSPLDNKLNVEDVDST KNRKLIDDYDSTKSGLDHKFQ DDPDGLHQLDGTPLTAEDIVHK IAARIYEENDRAVFDKIVSKLLN LGLITESQAHTLEDEVAEVLQK LISKEANNYEEDPNKPTSWTEN QAGKIPEKVTPMAAIQDGLAK GENDETVSNTLTLTNGLERRTK TYSEDNFRDFQYFPNFYALLKSI DSEKEAKEKETLITIMKTLIDFV KMMVKYGTISPEEGVSYLEGL DEMIALQTKNKLEK\NATDNIS KLFPAPSEKSHEETDSTKEEAA KMEKEYGSLKDSTKDDNSNPG GKTDEPKGKNRSPIWKPIRK\NI EWLKKHDKKGNKEDYDPFQR* EVSFNNKADA\YVEKGILDKEE AEAIKRIYSSL
12968	43336	A	13048	1	879	
12969	43337	A	13049	3	640	
12970	43338	A	13050	134	382	DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPWMN/WPPH*IKHIQS
12971	43339	A	13051	87	500	

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12972	43340	A	13052	1	1356	
12973	43341	A	13053	1	447	
12974	43342	A	13054	3	107	
12975	43343	A	13055	3	2377	
12976	43344	A	13056	1	2193	
12977	43345	A	13057	1	2724	
12978	43346	A	13058	253	490	QSSIPAIMSSFLGTGAETMPVPL GAGMRRTSTEPQRVCFCTGIIF KTSSLREAPRKKSMISDSLMGR E/WMPVTKLGRLVKDMKIKSLE EIYLFSLPIKESEIIDFFLGASLKD EVLKIMPVQKQTRCGSVLVRLI PAPRGTGIVSAPVPKKLLMMA GIDDCYTSARGCTATLGNF/AK ATFDAISKTYSYLTPDLWKETV FTKSPYQEFTDHLVKTHTRVSV QRTQAPAVATT
12979	43347	A	13059	1	819	
12980	43348	A	13060	1	623	MARRKNGKWESEIIDFCLGGSL KDEVLKIMPVQKQTRAGQCTR FKAFVAIGDYNGHIGLGIKCSK E/LATAIRRAIILAKLSIVPVCRG YWGNKISKPHIVPC\RGTGIVSA PVSKKLLMMASINDCYTSARG CTAILGNFDKATFDAISKTYSYL TPNLWKETVFTKSPYQEFTDHL VKTYTRVSMQSTQAPALAKLP RVAVQPRAEV
12981	43349	A	13061	1	949	KWRITPVPTGRP/GGPGGPGMG KPRCF/RGEVFGIVIRAGSPGPG TGPGRG\GEAAGAKAED*E\WM PV\TKLGRLVKDMKIKSLEEIYL FSLAIKKSEIMSFLLGGLLSRDE VFE*LCPVQEQ\TRAGQ/RATRF KAFVALTTLGTTNG\HVGLGC* VPPREVATGNSWGPFILGQALH SSPVRRGLLGGTKNSAKPPTLV PWQR*PRAACGLCAGYAFIPLQ PRGQLASVSA\PVP\KKLLMMA GTDG\CNNSQRRGCTATVG\NL AKATTFDAISKTYSYLTPDLWK ETVFTKSPYQEFTDHLVKTHTR VSVQRTQAPAGATT
12982	43350	A	13062	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE

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12983	43351	A	13063	2	797	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKVPKTAENFR/A L*SIEEKGFGL*GVPCFHRLFPR VLCVRGGDFHTAINGT\GGKSI\ YGEK\FEDENFI\LKHTGPGILSH GKMLDPNTNGSQFFICTAKT\E WLDGKHV\VFGKVKEGMNIVE AMEA\FGSRDCKTSKKITIA\DF GQLRIKFDFVFLSLTTKIISFCAL LSGEHPLHPIWLGVILESMWLS LAVPFWVPCFPCSLPCLAGLQS
12984	43352	A	13064	1	720	
12985	43353	B	13065	98	2074	
12986	43354	A	13066	596	841	
12987	43355	A	13067	66	326	
12988	43356	A	13068	1	441	
12989	43357	A	13069	2	325	WCPSQAAAAGARATRDMPEGS MTCLCRALWWLFSWLKVHR*R QGQQGRPAAPSAGPAKPTPTRN SSWLLLAAPVPTRTSPSTPPCKL REPAPALASPERGSHSAAVG
12990	43358	A	13070	38	1066	
12991	43359	B	13071	1	324	
12992	43360	A	13072	2	680	
12993	43361	A	13073	2	165	
12994	43362	A	13074	1	1110	MASLLKSARPQTHWKEETPETS KRLKEQTPDIPSLRAVTLIAKVH SFIPEVCETKNPLEGIHSGHILAP NVGPSPSRRQARVQVFENVSVR ATKSDLPQSSLWSRRKTTVSAA ASKKTSKEISKGPQKPPGY/PVT SPSSCRGRGIWPNP/EYMSTSPS LI*/SQIKVDLGKISDDPDRYIDV LQGLGQTLDLSWRDVMLLLDQ TLAFNEKNAALAAAQEFGDTW YLSEVNDRMTAEERDKFPTED GEPIKCDCQQIIVQTYAAQDDIL EVPLANPDLNLYTDGSSFVENG IRRAGYAIVSDVTILERPNLFRA IQQVVKACEVCQRKNPLVHPP NYLYKTLNLTHSLLNQSNPSLA NDCWLCSSLSVSAEPYN

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12995	43363	A	13075	450	1776	RGGRACLRP*AA/SPGPSTP*WP PPRGVQAAAILSGPPRPAPPKG AASQRLCGGFVEARQAWVGRR GGRRGPVGETQPPPSVIQPPSRG AG/PRDQQPAMPEPPTPSVGSC AARASQISAAPCSTAPSPIDHPR AEECRRTVWDWQAAPPAAQV RDPLGEASWAPESGGDVENLY VLLRDCKYTSQHPVSSSGSVNA PIDTLYLATLLRDCKYTNRHSV SSSRFVNTPISTVSSSEFANAPID TLHLATLKEETPNTSEHQKEQT PDMPPLRTVTVTARVRGFILDV SETKNPPIPDTFWRPRWDLRQS PSNQTLAFNEKNAALAAAQEF GDTWYLSQVNDRMTAEERDKF PTEFIPSSGFLVLLTSRMKPQTF AASVTALKDGVSRVCSFRCVQS FFLPSADWCIYKPLARYRALIG AFLQSAHWCVYKPLARHSVLI GAFTNL
12996	43364	B	13076	1	1999	
12997	43365	A	13077	3	469	
12998	43366	A	13078	224	410	
12999	43367	A	13079	478	675	
13000	43368	C	13080	55	237	
13001	43369	A	13081	109	239	
13002	43370	A	13082	2	88	
13003	43371	A	13083	2	178	
13004	43372	C	13084	278	460	
13005	43373	C	13085	50	217	
13006	43374	A	13086	3	251	
13007	43375	A	13087	1	759	
13008	43376	A	13088	2	604	
13009	43377	A	13089	1	558	
13010	43378	A	13090	3	1055	
13011	43379	A	13091	1	466	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPK
13012	43380	A	13092	2	848	
13013	43381	A	13093	458	625	
13014	43382	A	13094	482	745	

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13015	43383	A	13095	1	742	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIWHINRTKDKNHMIISIDAE KVFDKIQQPFMLKTLNKLGIDG TYLKILRAIYDKPTANIILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLGKE EVKPSLFADDVIVYLENPIISVQ NLLKLISNFSK\IKYLGIQLTRNV KYLFKENYKSLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPK
13016	43384	A	13096	1	1458	
13017	43385	A	13097	2	1624	
13018	43386	A	13098	1	1095	
13019	43387	A	13099	1	2913	
13020	43388	A	13100	2	1887	
13021	43389	A	13101	1	972	
13022	43390	A	13102	1	873	
13023	43391	A	13103	1	1365	
13024	43392	A	13104	1	867	
13025	43393	A	13105	1	591	
13026	43394	A	13106	1	990	
13027	43395	A	13107	1	2109	
13028	43396	A	13108	1	843	
13029	43397	A	13109	1	1203	
13030	43398	B	13110	1	1221	
13031	43399	A	13111	1	1092	
13032	43400	A	13112	1	931	
13033	43401	A	13113	1	1293	
13034	43402	A	13114	1	544	
13035	43403	A	13115	3	718	
13036	43404	A	13116	693	1397	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFFIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATKAKRA SAQQKKLPSE
13037	43405	A	13117	1	2814	
13038	43406	A	13118	1	1302	
13039	43407	A	13119	1	1542	
13040	43408	A	13120	3	1327	
13041	43409	A	13121	1	1023	
13042	43410	A	13122	1	1448	
13043	43411	A	13123	1	1038	
13044	43412	A	13124	3	1711	

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13045	43413	B	13125	1	1756	
13046	43414	A	13126	1	923	
13047	43415	B	13127	1	1515	
13048	43416	B	13128	1	1560	
13049	43417	A	13129	1	4032	
13050	43418	A	13130	1	2684	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTPWKLN NLLLNDYWVHNEMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDTIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEFYQRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQLMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYR FNAIPIKLPMTFFTELEKTTLKFI WNQKRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIIPHIYN HLIFDKPEKNKQWGKDSLFNK WCWENWLAICRRLKLDPFLTP
13051	43419	A	13131	1	1149	
13052	43420	A	13132	127	329	
13053	43421	A	13133	1	1132	
13054	43422	A	13134	1	1020	
13055	43423	A	13135	803	2009	
13056	43424	A	13136	1	1944	
13057	43425	A	13137	1	1282	
13058	43426	A	13138	1	2423	
13059	43427	A	13139	1	2694	
13060	43428	A	13140	1	1195	

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13061	43429	A	13141	6082	6984	KLAQDRDALSPPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPIV\SAPKSPL RLISNVS\KV*GYKINVQKS\QA FLYTNNTDKQESQIMSELPFTT ASKRIKYLGIQLTRDVKDLFKE NYKPLLKE\IKEDTNKWKNIPCS WVGRINIMKMAILPKVN\YRFI NSMPSIPIKL\PMTFFTELEKNYF KVHMEPKKSPHCQVNPKTKEQ SWRHQRYLTSNYILQGYSNQK STISMVLVPKQHGTGTKTEIIDQ WNRTEPSEITPHIYNYLIFDKPL LEKNKQWGKGFPI
13062	43430	A	13142	193	335	MVEEKLTLPKDEK*KSKQRSIY RKTLQELKNKNEKRNRKNKW QVKTH
13063	43431	A	13143	131	427	
13064	43432	A	13144	1	360	
13065	43433	A	13145	2	376	
13066	43434	A	13146	1	360	
13067	43435	A	13147	2	376	
13068	43436	A	13148	3	469	
13069	43437	A	13149	224	410	
13070	43438	A	13150	478	675	
13071	43439	A	13151	32	161	
13072	43440	A	13152	1	1671	
13073	43441	A	13153	1	1656	
13074	43442	A	13154	62	1295	
13075	43443	B	13155	149	320	
13076	43444	A	13156	12	89	
13077	43445	A	13157	28	417	
13078	43446	A	13158	2	440	
13079	43447	A	13159	190	553	EIVREGASFSIRHLRWSRHRKC RFSVKTLTGEDPSTLEV\EPS\DT IE\NVKAK\IQDKEGI\PPDQQRL/ VSFAGKQL\EDGRDSLSGY\NIQ KGSLLLHPCV*DFRGGAKKKEE ESLYTTSPRKD
13080	43448	A	13160	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVIFPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY

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13081	43449	A	13161	5	405	HCCGIPHSIASEQDTYFMAKEV WQWAHAHGIHWSYHVPHHLE AAGLIEQWNGLLMSQLQHQLG DNTLQGWGKVLQKVVYALNQ RSIYGTVSPIARIHGSRNQGVEV EVALLTVTPNDPL/GKY*LPVPV TLHSDR
13082	43450	A	13162	138	387	
13083	43451	C	13163	184	297	
13084	43452	A	13164	1	430	
13085	43453	A	13165	1	867	
13086	43454	A	13166	35	601	CLSRRASPVYLASMSGRGKTG G\KARA\KAMSRSSRAGRPSSQ VGR\VHRLLRKGHYAERV\GRR QPCCYLGG*CMEYLTS*ESWS MAG\NAARNN\KKTRIIP\RHLQ\ LA\IRNDEELNKLAWAALTIAQ GSR/VLPNIQARCCGPR*TSATV G\PKAPSGGEERATQASARSTK RARAAAGRPSVPMPPQRPF
13087	43455	C	13167	11	313	
13088	43456	B	13168	1	552	
13089	43457	A	13169	1	621	
13090	43458	A	13170	55	296	
13091	43459	A	13171	959	1182	WVYLF*PSCKGVIYP*AAGFESI FWWVTINKNIDWINYIYYNQQ QFMNYTRDAVKGIAEQLGTNC QMAWENRIALDMILAERGGVC IMIKTECCAFIPNNTAPNGSITK ALQGLTALSNELASSSGVNDPF TGWLEKWFGKWKGITASILTSL TAVMGVLILVGCCVIPCICGLV QRHRGPPLVVIETKPLGLERLA GLPVGHALKLGSGIQATPQNGE NADRREAFPAAS
13092	43460	A	13172	1	540	
13093	43461	A	13173	2	142	
13094	43462	A	13174	42	384	
13095	43463	A	13175	102	329	
13096	43464	A	13176	1	1257	
13097	43465	A	13177	1	378	
13098	43466	A	13178	1	1143	
13099	43467	A	13179	1	481	SDSELNRPRVTMKFNPFVTSDR SKNRKRHFNAPSHVRRKIMSSP LSKELRQKYNVRSMPIRKTDEV \QVVRGHYKGQQIGQGSPRCTR KKYVIYIER\VQREK\ANGTNCS TWGISPKARWLFTRLKLDKDR KKILERKAKSRQVGKEKGKYK EELIEKMQE

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13100	43468	A	13180	39	556	AAAGYFAEDCEASCVCVKHPP SVKKARCFLSELIKKPSGGSVTL SESTAIISHGTTGLVTWDATLYL AEWAIENPAAFTNRTVLELGSG AGLTG/VAICKMYRPRAFIFSDC HSRVLEQLRGNVLLNGLSLEAD ITANLDSPRVTVAQLDWDVAT VHQLSAFQPDVVIAADVLY
13101	43469	A	13181	46	231	
13102	43470	A	13182	1	1503	
13103	43471	A	13183	3	340	FFFANTFYCVFNVLVNAPLRFL SLPSTQSLEAKLRDSSDSELRRD ILQKVRIPESLGLMTLPPESLRK T*EKNRRCACTL*K\TPVQRTKP LSQHCRWVWAPPTAPALSFSKT
13104	43472	A	13184	2	594	
13105	43473	A	13185	1	1470	
13106	43474	B	13186	79	1355	
13107	43475	A	13187	248	540	
13108	43476	A	13188	386	1388	
13109	43477	A	13189	386	1334	
13110	43478	A	13190	3873	4070	
13111	43479	A	13191	146	510	PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRAA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPSLPLCSGVS PRAGLGSAWPKIPFLGIREAKN PRSENTRLTT
13112	43480	A	13192	21	95	KCSSNGAPDAVHE*DLPWTPGP AC
13113	43481	B	13193	1	477	
13114	43482	A	13194	228	935	PLSSSMAAELEFAQIIIIVVVVTV MVVVIVCLLNHYKVSTRSFINR PNQSRRREDGLPQIMHAPRSRD RFTAPSFIQRDRFSRFQPTYPYV QHEIDLPPTISLSDG\EEPLLYQV PCTLQLRDPEQQMELNRESVRA PPNRTIFDS\DLIDIAMYSGGPCP PSSNSGISASTCSSNGRMEGPPP TYSEVMGHHPGASFLHHQRSN AHRGSRLQFQQNNAESTIVPIK GKDRKPGNLV

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13115	43483	A	13195	526	1629	FYSFDSARGEPARPWRVRGLEG RVELGQQLGLLTLGPAFPGGLG GTQRVGLPGPAGPGAGEEGQA GPAEAGQVPVGGLADEAVEHG VGDAVEAGEQEGEVVGVENAL GEVAAGLPDAAHQQQHVVGQ EAGQEDDHGAEHQPLDLVLAA LLGAVAPAHGAQDALVGRQQ QADGEEEA/LPGSGSS*WHAAM PGWGSAQSTRGAGSRPR*PPRA SGSRCWSAAPWPR*PR*RRRPP SGSGTGGSGRDGPQPGSGPR/T MQQRKPTLM*MFSYRR\IRTPG RTGRRETSCRAAARTAARRAA SRCRRGRPPSGCTGTRPARSGP* SAGS\EVEGQAVGREAHHQHG NIDHRGQRLVDGMVDGTAHRG VVCSDVPH
13116	43484	B	13196	2699	7361	
13117	43485	A	13197	67	1523	
13118	43486	A	13198	1	287	
13119	43487	A	13199	2	563	
13120	43488	A	13200	96	401	
13121	43489	B	13201	1	480	
13122	43490	A	13202	1	924	
13123	43491	B	13203	13	1512	
13124	43492	A	13204	1	402	
13125	43493	A	13205	609	803	RDPRHNPSSA\FQAGGIALLMLI TRGEDLTGGVIHQYPGPGMNL WMQGTAGNQRRAAENAAQQQ
13126	43494	A	13206	3	526	VTETALTLPYLVAKHGYFLPQD LAKRTETMNWLFWLQGAAPFL GGGFGHFYHYAPVKIEYAINRF TMEAKRLLDVLDKQLAQHKFV AGDEYTIADMAIWPWFGNVVL GGVYDAAEFLDAGSYKHVQR WAKEVGERPAVKRGRIVNPTN GPLNEQLHERHDPSDFQTNTE\ NNRQG
13127	43495	A	13207	1	250	
13128	43496	A	13208	1	489	
13129	43497	A	13209	209	601	
13130	43498	A	13210	1	96	
13131	43499	A	13211	1	1110	
13132	43500	A	13212	1	595	
13133	43501	A	13213	1	240	
13134	43502	A	13214	1	675	
13135	43503	A	13215	1766	1957	
13136	43504	A	13216	1	426	
13137	43505	B	13217	94	3238	
13138	43506	A	13218	1	2370	

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13139	43507	A	13219	1	2796	
13140	43508	B	13220	43	566	
13141	43509	A	13221	1	903	
13142	43510	A	13222	3	110	
13143	43511	A	13223	2	755	
13144	43512	A	13224	1	1338	
13145	43513	A	13225	1	807	
13146	43514	A	13226	1	918	MARADTVSVPMFMGLAAKPC WRDTEPNTGYRGPHVRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDAC\LSNAILVHNKKGGP LADGIVITPSHNPPEDGGIKYNP PNGGPA\VPTSLKWWKTGPTHC WPMA*KA*SVSP\RRSDGIRSKN DVIDTSDDDM**QCLSRRSN\G HPGAKVANLVPKTTFIDGVDQT SFFLGTNGQSNRKAEHYFLNGK LAAVRMDEFKYHVLIQQPYAY TQSGYQGGFTGTVMQTAGSSV FNLYTDPQESDSIGVRHIPMGV PLQTEMHAYMEILKKYPPRAQI
13147	43515	A	13227	1475	2904	FWRAAAPIPDCWRSGAVKKQH VEVTQLDWTPPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGFTGTV MQTAGSSVFNLYTDPQESDSIG VRHIPMGVPLQTEMHAPGLPLA SSMKRWIRRATGFIFGKEQFED VVPVLGSKVNGVQFNAELVAD SLGISQIRCRCAIFLTVVFFPVLH KQAFDLISLLLQQPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFTT LVQGSLPELHQAWQAVDERPH ANRFLPPDEIEQSLNGVHYQHH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRILTRSQLQRLQ LAWPQQQGRYPLTYHLFLGVI
13148	43516	A	13228	215	525	LAWARRCRRLLAKATSLIRAPS SEMRASTPCRGQRRPSGYSWY GRSPRAVLEGLRVGAHLSRAN CPWPSR/SQVVELIPDGFPVFLD FTKIPGRDTQNEHIVLLH
13149	43517	A	13229	1	942	
13150	43518	B	13230	1	1201	
13151	43519	A	13231	685	921	

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13152	43520	A	13232	2	251	
13153	43521	A	13233	2	100	
13154	43522	A	13234	5	1093	
13155	43523	A	13235	2	482	
13156	43524	A	13236	1	2496	
13157	43525	A	13237	572	912	RCRPDKAFTPHPAIGARCLMRR LRVLSCLQPLPNVGWIRRLRRIR QFSAPDEGAKCRVAILQ/DFDA QYGRFLEVTSGAQQRFEQTD*K HAAALPFFFPSSAYSLAAISVVF GFR
13158	43526	C	13238	5	127	
13159	43527	A	13239	1	444	
13160	43528	A	13240	17	261	
13161	43529	A	13241	173	397	
13162	43530	A	13242	169	421	LKPKNLDEKLLPASSSSCRIWA TSPVHHLWQVLKKILFGWNPT KSPRCLS/TRQAMFSLSKKASLP WTIAARSADQRCRTRIAEL
13163	43531	A	13243	17	744	RPHQEQRIAGCGVNALSSLRSA TAVGMIRRASVASG/DRAPIAG CGVNALSGLHRHFIEVTCTHFL LVRYEGIAIFRGGKFRLLHFLN VVLHTLALGIGVCQVKHVEPH AVDTCQGDELELVAHIRQLLLE AGNSFVVEVYLPVERRRAVISQ QFARIFRVDSLCKATRQFQIRRG RSHQTGQHMGIRRQVDAAHAD DRRTSGRVPPLIQVCPAHSSEA VVVVDVDVDVDVDVDVIGAV
13164	43532	A	13244	954	1104	
13165	43533	B	13245	54	1169	
13166	43534	A	13246	35	3066	VGHSTRPAASPGPAAGIGRSPA RLVQQPQRSLAKPLNRPAQQR GLLPQRRHPKRTRKRRKQAQN PQKRLPHRQPVRRRHRHHRRLL QKMRRPDKRQQRRAAPRRHPR RRQRLLAVRRRQLRAKVRRNP RQRAPRQQLNGQRILHPPWRLR MQVRRKRG*YSSAVRPTVRLK RWRQRQRQ*NQPMTMQRNVC RKTRTALIYP/YKGCFLNNINAV SKTDFADKRGMRYVRVNAPAG ATSGKYYPVVVMRSAGSFHI
13167	43535	A	13247	1	2919	

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13168	43536	A	13248	1	3211	MEFTSLTPDDLRVLELYRTPFS DGYVFHSMQFHIFDLLKSGQN VVLSAPTSMGKSAIVDSLLGMG TLKRLVLVVPTVALADETRRRL QERFGDRYQIIHHSSQVCHSDQ AVYVLTQERVNERDDIVDIDLF VIDEFYKLAFRQLKSGDIDHQD ERVIELNIALSKLLKVSRQFYLT GPFVNSIRGLEKLGYPHTFVST DFNTVALDVKTSASKRMTTKP SSKRWGKSRTCVDADHIKNGIG LHFGALPRALQQYT
13169	43537	A	13249	486	3882	LRLRGEALPVASGCLANATDTP AGTTLWADTERHAVQ**TCEA DTLGSCGYAAKPCLSPVAVWQ MLLTRLLEQHYGLTLNDTPFSD EPVLTAPIDAAALRGIEFGKFQL GNMVVGDIIECGSDVTDYAVG DSVCGYGPLSETVIINAVNNYK LRKMPQGSSWKNAVCYDPAQF AMSGVRDANGARRGFWWGGL GAIRVQLAFKWLNAAGRLPGG GLGGPIPYSAHRCDIARRHGAD FCLNPIGTDVGKEIKTLTG
13170	43538	B	13250	1	1116	
13171	43539	A	13251	729	985	SAPPQLAPSLPDRATDPDTCWP PG*RP\RYLPSRQIDCFNTRFRLL QRLTASQCAEAVDVAFFRLTV QQTPHFRCAQLRQRAFRID
13172	43540	A	13252	395	605	
13173	43541	A	13253	1	1140	MIYVFVTVKHRNDHFTKNTLA SYRGRTLLGTLFKGVYHLYKD ETYLYQSGKGHTIQEVRIVKGL NNPDLDAAVGEDLAQQLRDEL ELVKGASNEFDKELFLAGEITP VFFGTALGNFGVDHMLDGLVE WAPAPMPRQTDTRTVEASEDK FTGFVFKIQANMDPKHRDRVA FMRVVSGKYEKGMKLRQVRT AKDVVISDALTFMAGDRSH/AY PGDILGLH\NHGTIQIGDTFTQG EMMKFTGIPNFAPELFRRIRLK DPLKQKQLLKGLVQLSEEGAV QVFRPISNNDLIVGAVGVLQFD VVVARLKSEYNVEAVYESVNV ATARWVECADAKKFEEFKRKN ESQLALDGGDNLAYIATSMVN LRLAQERYPDVQFHQTREH
13174	43542	A	13254	1	1495	

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13175	43543	A	13255	372	1365	IRYFENRGLFAHCATRTGQFPP HCILASYKCGEQPDSSSNHPRN LFVWRSNLLGSSG\KGHEYMQ KYLLGTESGIQGEELGASDGIKP EEVEWQTAAIEGKLDLLVTLDF RMSSTCLFSDIVLPTATWYEKD DMNTSDMHPFIHPLSAAVDPA WESRSDWEIYKGIAKAFSQVCV GHLGKETDVVLQPLLHDSPAEL SQPCEVLDWRKGECDLIPGKTA PNIVAVERDYPATYERFTSLGP LMDKLGNGMDLTDYANMALSI PSANTDIWNLEQDTVGTRLTNS RHGLADNGGAWVSYFGGNFN GDNGTINYDQDVNGIMVGVDT KIDGNDG
13176	43544	A	13256	3	1444	
13177	43545	A	13257	61	1058	LPYLIALLARAWFNGLLTSRTR LYIKGNGIVDLPKLQEMVADVS HHFPLRLPAPTPKALYSPCEIRH LAINVNLEYDPTAAFRNQVVHF DFRKLDVFSFGENQNCLVGNV DLL\YRNSWNEVRTLHFNGEQS MIEALKTILGKMHQDAAPPDSV EVFCYSQHLRGLIRTRVQQLVS ECIELRLSSTRQETGRFKALRVS GQTWGLFFERLNVSVQKLENAI EFYGAISHNKLHGLSVQVETNH VKLPAVVDGFASEGIIQFFFEET QDENGFNIYILDESNRVEVYHH CEGSKEELVRDVSRFYSSSHDR FTYGSSFINFNLQDPYLRARVSI
13178	43546	A	13258	1	1133	
13179	43547	A	13259	2	240	ISSARHFGALACTLELGKALTF GQNDLRQFAVTASAIAALL/SR HSPSFEMHMASDTLNFMPFEK GTLLAQDGEERFTVTH
13180	43548	A	13260	1	358	LPFLPSGLRGLAAENKIRRPHSA GSFLGPPCGLRGKLV/ISAAALM STTIPISRVQGLLQFLNSKSPISR AERSWSTFGASAAFLTTLASLL FLFPPLAISSLANSFAKVFPPTPC AGSP
13181	43549	A	13261	1	1635	
13182	43550	A	13262	1	1363	
13183	43551	A	13263	5	249	
13184	43552	A	13264	15	280	
13185	43553	A	13265	6	363	

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13186	43554	A	13266	78	346	TRYAMLTRHDNHLSKFYLARG RYRADFHAPETNTGERCYRYK PLPYWLE*RRGRNRYPALQ*TM FLPADGPARCLSRQAAILKESV LPK
13187	43555	A	13267	568	831	ELQRHVLVVFAGFWIVKNSRN LFLVCRAEHKRSVVKGLLRQQ GQGFWFHFQDGFAVEVGNAN VIGSE*IVFGIVFPHRERCLVDK
13188	43556	A	13268	3	419	
13189	43557	A	13269	1	561	
13190	43558	A	13270	1	741	
13191	43559	A	13271	2	1040	
13192	43560	B	13272	1	1974	
13193	43561	A	13273	2111	2340	EVFIRDKLMERRNRRTGRTEKA /RDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPVKVLQSQCI
13194	43562	A	13274	470	813	KTTSFPAKLFNACRISLLASAEV NPNISAYLATWISQIPSCSCRVP SDFLIWSTNRYSIRF*SRERLVG EAVA/AAAADGVTFSVPVTPHT FRHSYAMHMLYAGIPLKVLQS LMGH
13195	43563	C	13275	440	1180	
13196	43564	A	13276	1	1290	
13197	43565	A	13277	1	1036	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMENSRDRFEQRGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KDPRPLPYLGHDEPYTFDINLS VNLKSMVVGGTDMGQEPLKQ MGAWGPLSLKAMFGFFIRGYG FFTPFGRTLFPLGFGSTPPFTFPL LTKTIGVFILDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA GAAAAADGVTFSVSVTPHTFR HSYAMHMLYAGIPLKDLQSLM GHKSISSTEGYTKDFSLDVG\AR HRVQF\AMP\ESDAV\AMLKQLF
13198	43566	A	13278	366	672	RNGTHPRYIEAVPWGALPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSRLALRELQQAV HAGLPQQAKILFDGGSEIGKIPH IVLYKPVQCSLWAFVH
13199	43567	A	13279	2602	2976	
13200	43568	A	13280	982	1347	
13201	43569	A	13281	1	780	
13202	43570	A	13282	568	891	

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13203	43571	A	13283	1	718	MKEKPSSPRQYSYSFLSSMILLG GGESWNLLRADQRLIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEAVAAAA ADGVTFSVPVTPHTFRHSYAM HMLYAGIPLKVLQSLMGHKSIS STEVYTK\VFALDVAAPHPESTP VHLPSRENKIPPPIMRIPCGLPTS PIEQKQGKISATGTQWRRLKQE TRLSSVSARLMSYVGVMC
13204	43572	A	13284	1	496	AMFGFFIRGYGFFTPFGRTLFPL GFGSTPPFTFPLLTKTIGVFILDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEAGAAAAADGVT FSVSVTPHTFRHSYAMHMLYA GIPLKDLQSLMGHKSISSTEGYT KDFSLDVG\ARHRVQF\AMP\ES DAV\AMLKQLF
13205	43573	A	13285	2	545	
13206	43574	B	13286	1	735	
13207	43575	A	13287	1	1599	
13208	43576	A	13288	583	1005	
13209	43577	B	13289	31	1239	
13210	43578	A	13290	1	1023	
13211	43579	A	13291	1	933	
13212	43580	A	13292	1	1278	
13213	43581	A	13293	1	705	
13214	43582	A	13294	2	893	
13215	43583	A	13295	88	429	
13216	43584	B	13296	1	1419	
13217	43585	A	13297	1	2784	
13218	43586	A	13298	163	416	RNGTHPRYIEAVPWGALPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSRLALRELQQAV HAGLPQQAKILFDGGSEIGKI
13219	43587	A	13299	740	1431	CCQTLPVFHPPHPSHLGPRPCPP TH/HLPSEHRSLFLEAACHDSDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRHRLHR PQQPSPPLGIPHPSLL\TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13220	43588	B	13300	1	858	
13221	43589	B	13301	1	1098	

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13222	43590	A	13302	1	1047	MNRQLSDSYTEDTKEPSDVTTS ERTRSPPGSAKTTMIDTLKKLQ DVLKTEDSKNPTKSAADLLEQ YVKATGPIIEILQKATKTMEMI MIVEEKASDELQPDPELQQRYI HSVRGKPGLVKQRTQEIETRLR LAGLTVSSPLKRSHSLAKLGSL TFSTEDLSSRPPGPPPGPPPGLHP GPPPRRPPPKLPPPAPPGCSVHC CHYPLHFVVSPLEGFYCSLMRI QIVFVTAFVHHDSALLPLDASL APEALQNFQRYTGIQHVHRIGM AERMWCDRNRERHTVSSSGGN RLPNPAPLPNPGVLSAPPNLIQR PKADDTSAATIEKKATATISAK PQITNPKAEIT*NPRVWQGSWI GEAVAAAAADGVTFSVPVTPH TFRHSYAMHMLYAGIPLKVLQ SLRSQ*SVRGKPGLVKQRTQEI ETRLRLAGLTVSSPLKRSHSLA KLGSLTFSTEDLSSRPPGPPPGP PPGLHPGPPPRRPPPKLPPPAPP GCSVHCCHYPLHFVVSPLEGFY CSLMRIQIVFVTAFVHHDSALL PLDASLAPEALQNFQRYTGIQH VHRIGMAERMWCDRNRERHT VSSSGGNRLPNPAPLPNPGVLS APPNLIQRPKADDTSAATIEKK ATATISAKPQITNPKAEITRFCPL
13223	43591	B	13303	1	1185	
13224	43592	A	13304	529	774	
13225	43593	B	13305	1	1089	
13226	43594	A	13306	712	1024	GVESNLVVVVALCHRLIYLVW GTRTVRTWIGEAVAAAAADGV TFSVAVTPHTFRHSYAMHMLY AGIPLKVLQS\RVVALDVAARH RVQFAMPESDAVAMLKQLS
13227	43595	A	13307	556	1040	
13228	43596	A	13308	1	984	
13229	43597	A	13309	95	428	
13230	43598	C	13310	1	426	

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13231	43599	A	13311	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KARLTWGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
13232	43600	A	13312	1	1593	
13233	43601	A	13313	1	2536	
13234	43602	A	13314	887	1205	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
13235	43603	A	13315	79	351	
13236	43604	A	13316	1	2320	
13237	43605	A	13317	187	798	
13238	43606	A	13318	2089	2610	
13239	43607	A	13319	1	1407	
13240	43608	B	13320	154	3682	
13241	43609	A	13321	1	1206	
13242	43610	A	13322	1	255	

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13243	43611	A	13323	3058	3160	GSAA*LPPPLPAAFSGSCWLSQ RHPELHV*NEIYHLLH*KSFTSC *HNLSS*PRYPYLSSERVLW*CL SFISKI*SVTMP*SDLISLW*KLE PLTCRSTSHFRQKLAQ/RLP/AY QQGHQDLFILRSDLPSQVFIRDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEAVAAAAADGVT FSVPVTPHTFRHSYAMHMLYA GIPLKVLQSLMGHKSISSTEVYT KVFALDVAARHRVQFAMPESD AVAMLKHYPEINALALYLKCG TEWIC
13244	43612	A	13324	1	1812	
13245	43613	B	13325	1	1776	
13246	43614	A	13326	583	751	
13247	43615	B	13327	826	2097	
13248	43616	A	13328	1810	4163	
13249	43617	A	13329	686	2939	
13250	43618	A	13330	1085	1690	SYFIMVKVGTSYVPINVSFSPKV GPGASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGR\IYK ARIW\EV\TDRTVR\TWICRGGL PAAAADGVTF\SDPGPP\HTFRH SYAMHMLYAR*YR*KFLQSLM GHKSHPINGKATPKVFGPGMG LARA/HRGAGWQWPKSDAVG\ MPKQLSLRINALGLYMETGKPE GIMLFFGC
13251	43619	A	13331	3	327	
13252	43620	A	13332	3	337	
13253	43621	C	13333	167	413	
13254	43622	A	13334	1	1256	
13255	43623	A	13335	1	1078	
13256	43624	A	13336	3	976	
13257	43625	A	13337	1	1004	
13258	43626	A	13338	2	291	WRKIYEANGKKRKQRLQS*SL MKQTLNQQRSKETKKASA/SM RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIPCSWVG RINIVKMAIPPK
13259	43627	A	13339	1	2022	
13260	43628	A	13340	1	2262	
13261	43629	A	13341	5	283	
13262	43630	A	13342	1	1245	
13263	43631	A	13343	1	1203	
13264	43632	A	13344	1	687	
13265	43633	B	13345	1	1371	
13266	43634	A	13346	1	2241	

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13267	43635	A	13347	1	832	LKKCIKTPEIPSKHVRNWVPKV LEQRRQGLETYLQVASITLIPKA DEDTPKKKTTDKNSWTGTDAK VFNKILEIKFSSILKRLYWPVLE VLARAMRQEKEIKGIQLGKEEV KLSRFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQ\TESQIRIKYLGIQ LTRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKRYPFCQLCHQSAISTTKG VFTSILPLLMIEQLVSGRSCPSV AWSSMECTTV
13268	43636	A	13348	1	1314	
13269	43637	A	13349	1	843	
13270	43638	B	13350	1	1011	
13271	43639	A	13351	1	173	
13272	43640	A	13352	1	323	
13273	43641	A	13353	3	2020	
13274	43642	A	13354	1	1473	
13275	43643	B	13355	1	636	
13276	43644	B	13356	1	456	
13277	43645	A	13357	1	619	
13278	43646	A	13358	1	1293	
13279	43647	B	13359	79	1041	
13280	43648	A	13360	3	718	
13281	43649	A	13361	1	612	
13282	43650	A	13362	1	992	
13283	43651	A	13363	1	1236	
13284	43652	A	13364	1	1071	
13285	43653	A	13365	359	1250	KLPMGVAVVKLLHLPKVIIVFW LASWMMSRWLHYPDWVTIIAQ QVLMNVVSVMQADCRMNLLEI FLRWLMRKIFHVRLLPAVSTPP NCLNQLLLFFLTPVNYLPGQVM HFKKPLQIKRNYLSSRHLTFMS RKKLGKVSG\YKIHVQKS\QAFL SANSGQTESQIMSELPFTMASK RIKYLGIQLTRDVKDLFKEKYK SLLNEIKEDTNKWKNNPCSWV GRINIMKMAILPKVIYRFNAIPI KLPMTFFTELEKTTFKFIWNQK RAHIAKSNLSQKNKAGGITLPD FKLYYKATVTKTT
13286	43654	A	13366	1196	2132	
13287	43655	A	13367	1	2271	
13288	43656	A	13368	2	1105	
13289	43657	A	13369	1	2117	
13290	43658	A	13370	1	1447	
13291	43659	A	13371	1	1669	
13292	43660	A	13372	1	2823	

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13293	43661	A	13373	1089	2539	
13294	43662	A	13374	1	1787	
13295	43663	A	13375	1205	1207	
13296	43664	B	13376	1	2745	
13297	43665	A	13377	1	2063	
13298	43666	A	13378	1	4380	
13299	43667	A	13379	1	3347	MGDFNIPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNCSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDAIKNDK
13300	43668	A	13380	1	2367	
13301	43669	A	13381	1	1116	
13302	43670	A	13382	1	1095	
13303	43671	A	13383	670	1500	QTESSSTSKSLSTMIKWASSLG WQGWFNIRKSINVIQHIKGIQR QKPHDYLNRCRKSL*QNSTTLH AKNSQ*I\AQNLLKLISNFNKVS GYKINVQKSQAFLYTSNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFTELEK TTLKFIWNQKRAHIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNMCYRSMEQNRALS YYVAYLQPSDL
13304	43672	A	13384	441	3131	
13305	43673	B	13385	1	5688	
13306	43674	B	13386	916	2165	
13307	43675	A	13387	1	1529	MDPPAGAARRLLCPALL*LPAG *PLRPRLAGAAPAPGTALLHER AMPL*LRPGLHDVHGVPDL
13308	43676	A	13388	1	714	
13309	43677	A	13389	3	457	
13310	43678	A	13390	2	492	
13311	43679	A	13391	3	1201	
13312	43680	A	13392	1	309	
13313	43681	A	13393	2	1073	

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13314	43682	A	13394	3119	6984	CIVKHAAMRSAMTSLAARITVL NPTRATTPNT/RVADDQGFLRQ WSKVAKERKLQRLYIGEPSAEA VAAQMPDLILISATGGDSALAL YDQLSTIAPTLIINYDDKSWHPR LSFNKADEITTVFCGSKKSLAN GIPMANILFPTSVIATQQTQHFR FVDDFNAQFLRFASLDPAASPA ITISGKATLEIPGTELVFYAALE KKLNIKPGQTTFDGRFTLLPTC CLGNCDKGPNMMIDEDTHAHL TPEAIPELLER
13315	43683	A	13395	3	587	
13316	43684	A	13396	1	315	
13317	43685	A	13397	430	636	
13318	43686	A	13398	1	84	
13319	43687	A	13399	1	1647	
13320	43688	A	13400	1	2652	
13321	43689	B	13401	1	1494	
13322	43690	A	13402	1	750	
13323	43691	A	13403	1	513	
13324	43692	A	13404	1	2254	
13325	43693	A	13405	1	746	
13326	43694	A	13406	3	428	LGDDFVRAANIILHCEGKVVVS GIGKSGHIGKKIAATLASTGTPA FFVHPAEALHGDLGMIESRDV MLFISYSGGAKELDLIIPRLEDK SIAL\GKPTSPLGLAAKAVLDIS VEREACPMHLAPTSSTVNTLM MGDALAMAV
13327	43695	A	13407	1	1431	
13328	43696	A	13408	943	2481	
13329	43697	B	13409	1	783	
13330	43698	A	13410	3	729	
13331	43699	A	13411	1	843	
13332	43700	A	13412	3	128	
13333	43701	A	13413	1	136	
13334	43702	A	13414	1	492	
13335	43703	A	13415	3	619	

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13336	43704	A	13416	1	1600	GQACHASSSPLKGSRGSPPNFEI LYGPIFEDSLAPD*PKVIAGQ\IT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLFDFALYFFHNYQA LLAKGSGPYFYLPKTQSWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDEILHALR DHIVGLNCGRWDYIFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTCHKRGAFAMGGM AAFIPSKDEEHNNQVLNKVKA DKSLEANNGHDGTWIAHPGLA DTAMAVFNDILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKGQSQNLWKFA VYSGLRHGELAALAWEDVDLE KGIVNVRRNLTILDMFGPPKTN AGIRTVTLLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFIA SQMGHETAQMVYEIYGMWID DMSDEQIAMLNARVM
13337	43705	A	13417	2	278	
13338	43706	A	13418	3	662	GHLWIRIDLSQSAVSHSVKELE NHTGVRLLDRTTREVVLTDAG QQLALRLERLLDELNSTLRDTG RMGQQLSGKVRVAASQTISAH LIPQCIAESHRRYPDIQFVLHDR PQQWVMESIRQGDVDFGIVIDP GPVGDLQCEAILSEPFFLLCHRD SALAVEDYVP\ALPLPEGSPLVV KRITPVVERQLMLVRRKNRSLS TAAEALWDVVRDQGNALMAA
13339	43707	A	13419	1	646	GQQLSGK\VRVAASQTISAHLIP QCIAESHRRYPDIQFVLHDRPQ QWVMESIRQGDVDFGIVIDPGP VGDLQCEAILSEPFFLLCHRDSA LAGGDYVPWQALQGAKLVLQ DYASGSRPLIDAALARNGIQAN IVQEIGHPATLFPMVAAGIGISIL PALALPLPEGSPLVVKRITPVVE RQLMLVRRKNRSLSTAAEALW DVVRDQGNALMA\GRE
13340	43708	A	13420	1	1068	
13341	43709	A	13421	1	381	
13342	43710	A	13422	3	938	

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13343	43711	A	13423	595	1630	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGHYDHDYEFELGTR FRAVIIKLCNGDSLRHFMTSVY ALVKCFHEGDPLHKTGCQHLIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVEMLLREAGKAGFC RFRNHHQTGFSPAGANQRGPL AATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGNSYDHDYEFELGTHQ RLGAVARIVGDDLLNELRRDV VDARAGDVDQHAHAEKGDFR
13344	43712	A	13424	1	1395	

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13345	43713	A	13425	1307	1992	DKLNPVAHQKAYLAQSSQCHP QNARLVQHTQIRILPISEPPSNRI FACWGKPAWTACCN/FSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQLKHKEVESPNRPI TSSEIQVLIKSLPIKKSPGPDGFT AEFYERYKEELVPFLLKLFQTIE QERLLPNSFYEASIILTSKPSRD ATKKDNFRPTSLMNIYAKILNK IGQTESSSTSKSLFSTIKSVSSPE CKAGSTYANQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQETTPWSPFSDPVLAFDY KVFMAFVYNVVRVSQRMVVA GCISAFNDKLLNDLICFPVAPVS SKQIFPSDVKVAEPDHSCVSSY RIGSMAPNLTLSEMPRHNYFPA GNSVDHDNEFEL
13346	43714	A	13426	560	844	
13347	43715	B	13427	200	1519	
13348	43716	A	13428	950	1230	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ

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13349	43717	A	13429	695	1060	FRQRSVAFPPTVPNACVSVRSR ERDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQ*AQR N*CRKHRLSIPRK
13350	43718	A	13430	1	1558	MRDIFWVPDICKVMLYLVFFRS MGTPLRAVAMGLVITSWKIAQ KPRDFADFGTTINQDFRLLGQT SVDRLLQLSQGQAVKGNQLLP VSLKTDTKAKNLYLTKAYYGG GTNFFRKESQKLQQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTGFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN
13351	43719	A	13431	391	1676	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQ*AQR N
13352	43720	B	13432	1	1638	
13353	43721	A	13433	1	2430	
13354	43722	B	13434	1	1282	
13355	43723	B	13435	1	1225	
13356	43724	A	13436	350	709	
13357	43725	A	13437	1	2236	
13358	43726	A	13438	548	1698	RSWLRSSLSGSIPIATEISCTSCE ASTSS/VRDFPGVKDLTFQWHD RLIFAIARLLGRSACGVTFHKEQ LGTVKVLRGTISQFARQRRAAG QLFTHHFFGRTHTALGAGNRH LRQQFSRLNVLVQPQDKGIFHH ARNECRALTRRETPAFFRIRAVF NSQLSQTQLHIFFTARPAGLAS KCRKPPQACYLWDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMQLARQV SRLESGQNIESAKGLHVWDSW PLHNADGTVDEYNGYHVVFAL AGSPKDADDTSIYMFYQKVGD NSIDSWKNAGRVFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGEHYG
13359	43727	B	13439	448	1116	
13360	43728	A	13440	97	1636	
13361	43729	A	13441	1	1296	
13362	43730	B	13442	1	2160	

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13363	43731	A	13443	485	865	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQS*NSS KTKNTKCLNSINQRLKILSLQK DLMCGTAGRCKTLTEQ
13364	43732	A	13444	816	1194	SLILFLRRRRAVEKRGKVWKDS CPNGTTLTLSGAIFLFIRDFADF GTPITQDFRLLGQTSVDRLLHLS QGQAVKGNQLLPVSLVKRKTT LAPNTQTASPRALADSLMQLA RQVSRLESGQ*AQRN
13365	43733	B	13445	1	2710	
13366	43734	A	13446	2027	2934	NPRILPISEPPSNRIFACWGKPA WTACCN/FSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRAL ADSLMQLARQVSRLESGQDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLVKR KTTLAPNTQTASPRALADSLMQ LARQVSRLESGQSRVHSHSLGP LPTTTTGSLINQKKGGVSGGPG SKEQAEISCLKERKDLGLGILGS TVGILKVKHQGASTKQGHSQD LIKILLSDTSLSTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQYMNLLPIFLRWLMR KIFHDEHGVPQDQQEEEPISETII EEEIPSINSDLGNELYFVKLPKF LSIEPKDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQP HSTDSATHRKMTLSLADRCSKT QKIRILPMAGRDPECQRTEMIK SSDLMAEIIQEHKEDQLPELEQL EHIGLFSHAEIKAIIKKASDLQY RIQERALFKDDFINYVLHEIPLF EQIQRRTRIGYSLKHGIRAVKA TIVRALYGRIKPAGVVVTRSVP
13367	43735	A	13447	1	5240	
13368	43736	A	13448	4733	4753	

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13369	43737	A	13449	299	761	LNTTAITLCLLLREARKTLMTH QSTCFIKRDFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN**PVPKEKRRRGDRQE HQQPCRNTEGTALRVWAARDQ
13370	43738	A	13450	3925	4190	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQ*AQR N
13371	43739	A	13451	2	1040	
13372	43740	A	13452	58	350	HLASWVVALVLHWGCVWVTA ESSTSKTRSPFRARSWIGEAVA AAAADGVTFSVPVTPHTFRHSY AMHMLYAGIPLKVL\QSLMGH KSISSTGVPSSNS
13373	43741	A	13453	1	1290	
13374	43742	A	13454	289	1338	
13375	43743	A	13455	1	732	
13376	43744	A	13456	982	1347	
13377	43745	A	13457	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KARLTWGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
13378	43746	A	13458	1	780	

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13379	43747	A	13459	116	396	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHR
13380	43748	A	13460	3	514	
13381	43749	A	13461	2	545	
13382	43750	A	13462	1	1110	
13383	43751	A	13463	1	870	
13384	43752	A	13464	1	1422	
13385	43753	A	13465	1	1599	
13386	43754	A	13466	614	1236	TARVAAARRRCQCWGSGACGS ALTLPRTSSLTLTETPIVQQTRM VVRCPTASLPSQWRSCPSSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVTDRTVRTWIGEAVAAAAAD GVTFSVPVTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13387	43755	A	13467	1	1023	
13388	43756	A	13468	1	699	
13389	43757	B	13469	1	1281	
13390	43758	B	13470	77	751	
13391	43759	A	13471	1	705	
13392	43760	A	13472	2	893	
13393	43761	A	13473	206	837	CAGAGGIARRRAEKEKALSAV NLDPTSRRLSSTSLPGAPPNPRV AAAGLSRRRPTPESAGRKS/GR WPRASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAVAA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEVYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13394	43762	A	13474	1	1416	
13395	43763	A	13475	1	765	
13396	43764	B	13476	1	519	
13397	43765	A	13477	1	2784	
13398	43766	A	13478	1	624	
13399	43767	A	13479	2089	2454	

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13400	43768	A	13480	740	1431	CCQTLPVFHPPHPSHLGPRPCPP TH/HLPSEHRSLFLEAACHDSDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRHRLHR PQQPSPPLGIPHPSLL\TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13401	43769	A	13481	2	2309	
13402	43770	A	13482	1	603	
13403	43771	A	13483	1	762	MVPHSTGKSWNGCDPTSATLD QLVTVFFMKLFSIGDARIPCLGP RSHSYRRSDYYSGTTIHSCCRA DYWSGTTAHLYCRSDYHPVPS FILVTSTTNHQPLKPSISEASWN PLFASL/HHLQLITES/W/YMSLA TTVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAVAA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEVYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13404	43772	A	13484	1	762	
13405	43773	A	13485	1	615	
13406	43774	A	13486	887	1203	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
13407	43775	A	13487	1	855	
13408	43776	A	13488	1	927	
13409	43777	A	13489	1	921	
13410	43778	A	13490	1	3216	
13411	43779	A	13491	1	1974	
13412	43780	A	13492	1	1221	
13413	43781	B	13493	1	2337	
13414	43782	A	13494	1	1273	
13415	43783	A	13495	1	1251	
13416	43784	A	13496	1999	3237	
13417	43785	A	13497	1	1773	

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13418	43786	A	13498	1	633	AQALIATYGRDRDPGRPLWLG SVKSNIGHTQAAAGVAGVIKM VMAMRHGQLPRTLHVESPSPE VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEAVAAAA ADGVTFSVPVTPHTFRFSYAMH MLYAGIPL*VLQSLMGHKSISS TEVYTKVFALDVAARHRVQFA MPESDAGGPGTCACSQQGCRL RGSSVSPGRQHPQPHVRV
13419	43787	A	13499	101	1943	
13420	43788	A	13500	686	3925	
13421	43789	A	13501	1	2084	
13422	43790	A	13502	734	834	
13423	43791	A	13503	1	1075	
13424	43792	A	13504	1	357	
13425	43793	A	13505	795	1273	SHPFFSTDWSTDTGFRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVVSVMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLLFFLTPVNYLPG QVMHFKKPLQIKRNYLSSRHLT FMSRKKLG
13426	43794	A	13506	344	449	SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASCMMSRCPHYPDWVTI IAQQVLTPRKDVMQADCRMNL LEIFLRWLMRKIFHGFGM
13427	43795	A	13507	1197	1511	WHYREPLLLRAQLTNPPSGQLV SITKYLQPVEY*AYVLE*QAHL HYQLKSVDQWPVQKQFSSGSD LYQLHPFHVQHFLEPCFPRHPE FAPPSTGTESHYYCCIW
13428	43796	B	13508	1	1494	
13429	43797	A	13509	1	554	MTARKARKITRRWRIGEAADL VGVSSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVFGTRLRRAEDVFPPVIGVAA HKGNDPQGTASMYHGWVPDL HIHAEDTLLPFYLGEKDDVTYA IKPTCWPGLDIIPSCLALHRIETE LMGKFDEAQPNLGIGT/N*CRM CC*CADCSHAC
13430	43798	A	13510	1771	2068	DTYSVSWIGEAVAAAAADGVT FSVPVTPHTFRHSYAMHMLYA GIPLKVLQSQYPIFKLSYKNPVT QTAWF\WFPNRIFGPVPINVSFS PKVGPGLPGII
13431	43799	A	13511	65	277	

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13432	43800	A	13512	327	748	VHQFHGSLHEGFCAGCGCPAP GTVCDAGGFCRFRNHHQTGFSP AGANQRGPLAATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AKSIWCHRNCRW/RVAVVKLL HLPKVIIVFWLAS
13433	43801	A	13513	512	580	
13434	43802	A	13514	2096	2272	EWRNVCGVTGTENVTPSAAAA QPPPQSRPFSWILRPF*RP*RKIS TSFIRPLFTFLPA
13435	43803	A	13515	402	2784	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQSD F*RRRKNISERSAAYR*RQLYIR RQPYAERPS\HVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSAKK RDAELANGALGIIELNNDYTLK KVMKPLITSNTVTDEIERANVF KMNGKWYLFTDSRGSKMTIDG INSNDIYMLGYVSNSLTGPYKP LNKTGLVLQMGLDPNDVTFTY SHFAVPQAKGNNVVITSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQGQLTWLQVA KRAGLGGGQSGRTVLRERLPN YKNFKGTIQELGQNQYAVSGEI FVVDRNTVEITELPVRTWTQVY KEQVLEPMLNGTDKTPALISDY KEYHTDTTVKFVVKMTEEKLA QAEAAGLHKVFKLQTTLTCNS MVLFDHMGCLKKYETVQDILK EFFDLRLSYYGLRKEWLVGML GAESTKLNNQARFILEKIQGKIT IENRSKKDLIQMLVQRGYESDP VKAWKEAQEKCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRLS
13436	43804	A	13516	2	199	WRKKSLDIPPLIIPNGIVKNILRH FSQLLNVPITRPFSWILRPF*RP* RKISTSFIRPLFTFLPA
13437	43805	A	13517	1	1887	

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13438	43806	A	13518	125	828	ECRKHTKLKLQPTIWHVLKI/Y NSEKLLVYRKLLQVLTGLYKRS NLGVRLYACCGLLLCPAYPQH FAHGYVDKIPGYPGRAGTLTGL HPMQCDNLKTCHTSHGSVMAE TAVINHKKRKNSPRIVQSNDLT EAAYSLSRDQKRMLYLFVDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEAILRYFIKHSADMEA ITNGMMNLNRQRHQHLVALRII FAHGENGGEEVVHIGHV
13439	43807	A	13519	504	755	EPCFPAHPEFAPLSTGAESHHY CCIW*AKYVHQARTL*DQRS*A DHEAYRKTAVRRCSQTTQQAW EQLVHQQHILPSSCRYPG
13440	43808	B	13520	1	1980	
13441	43809	A	13521	923	1063	
13442	43810	B	13522	1	1932	
13443	43811	A	13523	383	1383	RKVFFIALKRMPAMKKAMNLF LGLSNVRTVHPEGFTVYISTHIS FPSLSGYKTRLRSFGLVKQKKS PILLEVLAREIRQE/KEIKGIQFG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKLSRM HGRPHQPPNAASTLPFPKRRSH YGQKSERLSRSGDNRKSHPECR HWQSCAKKSRCLAFTRTVRHT PRSAYLLTRTIELLESSALWHV QTQRIYAPLYETLDPGNRTHCE
13444	43812	B	13524	107	1000	
13445	43813	A	13525	1778	1897	
13446	43814	A	13526	273	421	SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFSSAS
13447	43815	A	13527	273	697	SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVVSVMQADCRMN LLEIFLRWLMRIIFHVRLLPAVS TPTNCLNQLLLFFLTPVNYLPG QSGTTVPLVSSV

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13448	43816	A	13528	273	688	SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVGSVMPADCRMN LLEIFLRWLMRKIFTTGLRSFGL VKQKKSPIRMPCVYTNPCVSIV SRMGQASSL
13449	43817	B	13529	1	1053	
13450	43818	B	13530	1	1869	
13451	43819	A	13531	120	430	EDLSDTGVRSKSIWCHRNCRW/ RVAVVKLLHLPKVIIVFWLASW MMSRWLHYPDWVTIIAQQVL MNVVSVMQADCRMNLLEIFLR WLMRKIFHSSLEDPRNWHL
13452	43820	B	13532	148	334	
13453	43821	A	13533	2	147	TSMDKGLQGALKKKI*DL*KK* L\KNIPVDKWITPREVFSGIVCK QNI
13454	43822	A	13534	151	325	KAICHNTFSKPSMDKGL/LRRS KKEGFKTYKKNIYKNIPVDKWI TPREVFSGIVCKQNI
13455	43823	A	13535	283	406	HRTKISIVPEGIFKSFSLPLAGIM TEQYFL*TLHRLLRLIM
13456	43824	B	13536	1	1902	
13457	43825	A	13537	508	1041	LWREASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPW/C YQT\WHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIDWIIERYQLPQSYQRMPDF RRRFLQVCVNEINSRTPMRLSYI EKKKGRQTTHIVFSFRDITSMTT
13458	43826	A	13538	1	1422	
13459	43827	B	13539	1	1002	

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13460	43828	A	13540	1	160	MVLIVAATVVVVVVVGLCWM AKSECRSAMRLSSLQVRIFTYLI GREAAFADNLKWMACANKES ALLDRFIFLILLLCKEPWECHCL PLFKVAMPSKCDIPVICAHINIG FTLRQLRGFGPCNIGSFEAKDS KNPQVRVISQKHKALRCIWFIT CSICNPEFTEGALQGNKQRKRQ CLQWFRAKALESNEPGFEFIQD KLLTQSLCFFPYTFLWLTGPHPS GSSYTDPCSSKADVTPSSTAVQ EHSSALELKTKIVSPITRQQHGF FTQISTLADVQENVMEYLHVLS RPKVIDQEHDVVWTEAYIDSTV CRVKRRQLLLQQVPLTRKQQF LPAPYVDLDSARTRTNKQQQN PIIYTGSKQGSHVILFHYGESWN LLRADQRLIFAKSWPRASRYQQ GHQDLFILRSDLPSQVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEVYTK VFALDVAARHRVQFAMPESDA VAMLKQL*QPQWWWWSW*D CAGWRKVNAAQPCVCLPFRFA SSHTSLDERLRLQTI
13461	43829	A	13541	48	668	
13462	43830	A	13542	1	1278	
13463	43831	A	13543	100	157	
13464	43832	A	13544	1	1122	
13465	43833	B	13545	1	1131	
13466	43834	A	13546	273	812	SHPFFSTDWSTDTGVRSKSIWC HRNCRWESPS*SC/WHLPKVIIV FWLASWMMSRWLNYPDWVTII AQQVLMNVVSVMQADC\KRIC WKYFCAG*CGKIFTYQ**TW\N NTETSMSQKPCKMKRI/YSREE LAV*KMDHHSDLISLW*KLEPL TCRSTSHFRQKLAQGFPVSTGT PGFIYSAK
13467	43835	B	13547	1	987	

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13468	43836	A	13548	246	2065	LVGWLDGWLDGWLIVALPFM MIPWHSSIQPFTIHPFNWNFG*M PELCPQI\GMDSWLAGWM/CWL DGWLDGW*MAKLRKPVL*PD KEGNEIWVDMYTVKPSGWTVR TFDKPRKRFIAFFIAGILFRAIKN HFLPRETLQCLPYILTGFRRGQS EYFSIFSNMDLADTVMFLIVAL PFMMIPWHSSIQPFTIHPFNWNF G
13469	43837	A	13549	2	118	
13470	43838	A	13550	397	729	THGIRIGDFFCFTKRKLRKPVL* PDKEGNEIWVDMYTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFSIFSNMDLADTVMFL
13471	43839	A	13551	147	417	SSSWGRSSPQLVCGIFQTAGPQS LCKWNQ*VLAQTNKKTAGTSA DLYVPV*QL*RKAVVLPTNAP WRFWRTRQEWFSSRGRSGYQS QET
13472	43840	A	13552	1	2418	
13473	43841	B	13553	1	1848	
13474	43842	A	13554	188	490	EWRNVCGVTGTEKVTPSAAAA ATASPIQVLTVLSVTSQIRAFSV LPVRRLRRSMSLSRINTCVNRF CNPIKKGMRYGLICPL*SLLDGL CARLINQGKDS
13475	43843	A	13555	83	440	SLLFKCSGVIVLRRPLGYRQVM NVTRRCLLRTHWMISSLLFY*L VNRHRRSVEEYLVSYTLPMGV AVVKLLHLPKNFVSLITPRGRL EKERAFLFQHMRSISTGLKIFV MHTSCPMVVC

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13476	43844	A	13556	1337	2583	QQRR*MCQNLMTH\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEVYTK VFALDVAARHRIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLIPFFIGLQNRF TQFRLSETKEITNPYAMRVTNP CVSIVCVNEINSRTPMRLSYIEK KKGRQTTHIVFSFRDITSMTTG
13477	43845	B	13557	1	696	
13478	43846	A	13558	326	1577	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRF*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHIRH
13479	43847	B	13559	1	3822	
13480	43848	A	13560	848	1476	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
13481	43849	A	13561	1	2196	
13482	43850	A	13562	326	3746	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRS*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHIRH*SCRYPS*ARCQ*LTG QIVHRGEKKEQQLI
13483	43851	A	13563	3802	4075	IRCFTYSPAPGYFPRFRAVIIKLC NGDSLRHFMTSVYALQEAAAE VRHTLVTLRQLVTLYDPVDFQ RDDA*AIRAYDTDTGIRINAWH TDW
13484	43852	A	13564	1708	3198	
13485	43853	A	13565	1	1401	
13486	43854	A	13566	1214	1357	NKINMFIAALFTIAKT\WNQPK\ CPTMIDWIKKRGSSRVASSSSPT RTR

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13487	43855	A	13567	3363	3852	SHPFFSTDWSSDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVVSVMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLLFFLTPVNYLPG QGFAGFRNPPSNRIFACWGKPA WTACCNSLRARR
13488	43856	B	13568	350	742	
13489	43857	A	13569	248	599	HRDSYKRMAYGLVISVVSLSR KLRKPVL*PDKEGNEIWVDMY TVKPSGWTVRTFDKPRKRFIAF FIAGILFRAIKNHFLPRETLQCLP YILTGFRRGQSEYFSIFSNMDLA DTVMFL
13490	43858	B	13570	1	2148	
13491	43859	A	13571	3064	5069	RSDPDENCC*TGH*STLFNWC\ WRNALSIWEPVCNEIFYRLIKPR WEIRWGKRAPVIPKHTLNTQPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLLTGQQTP AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGELDDEQMAA LSRLGNDYRPTSAYERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSHPRQ APCMKSNNALIVILGTVTLDAV GIGLVMPDLALKGLRVLLVEG NDPQGTASMYHGWVPDLHIHA EDTLLPFYLGEKDDVTYAIKPT CWPGLDIIPSCLALHRIETELMG KFDEGKLPTDPHLMLRLAIETV AHDYDVIVIDSAPNLGIGTINVV CAAHALIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDV RILLTKYSNSNGSQSPWIEEQIS DAWGSMVLKNVHAIVTGDAV GMDDIPQEARQYRHNQAYAYS IQGDGAEDDDERIVRFHTRVTV DSDTLASDAARLTCRHGLGNQ RNGGVLIEDKFECFFSLTAVFA TRAYYAVYHLTGARHSDIVVA HGYAGCNVRFVALLGTNTTLE TYLSNQGSNGFSCLHFGEDVGQ

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13492	43860	A	13572	1408	5578	CSHLLIIQLANQNTIITFGKCSSF TTATPIGNFYDTRYSSTERRCLL TSQ*KRRDEIIQCVLSKQL\RAR SLPDPTRKVFSTLSPRSTFRVNF TSRPHTGKVWAFREPFLLPPHL RKPDTDTGYLYKRMAYGSVIS/ ICFTKPKLRKPVL*PDKEGNEIW VDMYTVKPSGWTVRTFDKPRK RFIAFFIAGILFRAIKNHFLPRET LQCLPYILTGFRRGQSEYFSIFS NMDLADTVMFL
13493	43861	A	13573	2678	2884	SAPLQRNTARRFLLFLKACSNR FCYR\WRHMTAIPSYNRSKLREI KGGLYHMGIFRRFLASKETPTF CY
13494	43862	B	13574	1	7903	
13495	43863	A	13575	1	880	
13496	43864	A	13576	1	996	
13497	43865	A	13577	763	778	NRCEPPV*GTRFSQQLLLALKA TLLIEELYALTVHSWRPKW
13498	43866	A	13578	2	254	
13499	43867	A	13579	1	2358	
13500	43868	A	13580	206	382	
13501	43869	C	13581	1	1137	
13502	43870	A	13582	79	906	
13503	43871	A	13583	2	383	SPPEVVRLGYHPPRHGHQ\HLF ASCRKGDVGRVRP*TRPDPGSD LLPAQVPAGAARRGGTMPACV GTRSWYSTFWPMEPAARPTPS MVSAASMGH*VTPSAGLYAITS RSRLPAGGGITMTTSCSGF
13504	43872	A	13584	1	1092	
13505	43873	A	13585	173	262	
13506	43874	A	13586	898	1391	QLGILRVNLLGIDLRVTGHQAA PPLHLLDLLQMH/SSPPCRPQ*A TSSPPPSLRCRAPHR*SLAAP*A PPPRPSLSAGSPHRKGPPGPAPT GSWSSGNQAGLPCCLGWASVF LCPSHLPPPHLPQSSASLAFHRV KHLIHLHNSVIDKMKYQLKFLC LLGEYLSV
13507	43875	A	13587	1	960	
13508	43876	A	13588	1318	1369	RDFHPK*HTIGIQYIWQQLEINQ CDTSLSMVLP\R*RDFHPKSHLL PGAAQIQ
13509	43877	A	13589	212	385	
13510	43878	A	13590	377	505	
13511	43879	A	13591	69	193	CSLRSLAQMLPFYPRRSLCLSCS L**PHCCLWLAALRSESK
13512	43880	A	13592	1	230	
13513	43881	A	13593	2	341	

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13514	43882	A	13594	1	2421	
13515	43883	A	13595	1	623	
13516	43884	A	13596	1	906	
13517	43885	A	13597	1	568	
13518	43886	A	13598	107	199	
13519	43887	A	13599	42	328	GGASGVCSF*CSE/LSSFWWVR GLAGSGVKLQTFATQEPSWLH PVDPVPGLQVELPASPAPCART PQPLGGRWDSAPWSRGRRSSG AHGIDVALLP
13520	43888	A	13600	5	124	IWILWFFVSLT*RSRGPSQ*VLQ LIKAPHVDLLVVTFGC
13521	43889	A	13601	827	973	IHQSALCI*LKFYTSLTHPVISLV VETLVWW*YLKM*KKLWSWI RGRG
13522	43890	A	13602	2	503	
13523	43891	A	13603	56	792	
13524	43892	A	13604	1	411	
13525	43893	A	13605	1	1554	
13526	43894	A	13606	1	363	
13527	43895	A	13607	1	966	
13528	43896	A	13608	932	1189	
13529	43897	A	13609	146	323	
13530	43898	A	13610	1	1827	
13531	43899	A	13611	2	412	
13532	43900	A	13612	1	2238	
13533	43901	A	13613	2	411	GATDCVCYYTVGFNDTKTSAL HMVVGDSLAMDVSSVHHNSTL LRYSVTLLGYGFYGDIIKDSDK KRRLGLARYDFLCIKTFFSHH* YEGTVTFLPAQHTVGSPRDRKP CRAGCFVCRQSKQQLEEEQKT ALYGLEL
13534	43902	A	13614	3	2185	
13535	43903	A	13615	206	1568	
13536	43904	A	13616	165	417	TWDYIRPNE*YM*MAKKKMP MD\VWCNGKNWRPAG\EFVDD G\TETHFSIGNHDCYIKAVSSGK RKEGIIHTLIVDNREIPEIAS
13537	43905	A	13617	463	837	
13538	43906	A	13618	1	765	
13539	43907	A	13619	3	510	AGVHKIEFEHGTTSGKRVVYV DGKEEIRKEWMFKLVGKETF\Y VGAAKTKATINIDAISGFAYEY TLEINGKSLKKYMEDRSKTTNT WVLHMDGENFRIVLEKDAMD VWCH\GKKIRRPAGEFVDDGTE TPLQYPGPMTCYIKAV\SSG\KR KEGIIHTLIVDNREIPEIAS
13540	43908	A	13620	342	585	
13541	43909	A	13621	1	1119	

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13542	43910	B	13622	48	1104	
13543	43911	A	13623	656	916	GWRKYLQGAADMGIAEGGGS VWSSWASSSLISVPVR*LCESTQ RSAPGWPPLTGGSCSESVALWL CVNDFEFQMRLMPSRDSEPAC
13544	43912	A	13624	179	682	
13545	43913	A	13625	1	7511	
13546	43914	A	13626	56	8669	
13547	43915	A	13627	42	8716	
13548	43916	A	13628	1	2457	
13549	43917	A	13629	3	571	
13550	43918	A	13630	1	867	
13551	43919	A	13631	1	2238	
13552	43920	A	13632	171	396	
13553	43921	A	13633	1	3940	
13554	43922	A	13634	554	619	
13555	43923	A	13635	1	1359	
13556	43924	C	13636	208	359	
13557	43925	A	13637	2	513	PSHDHSKLGTRASGKVILHGEH AAVHGKVALAVSLNLRTFLRL QPHSNGKGDLSLPNIGIKRAWD VARLQSLDTSFL/RWTKEDLELI NKWAFQGERMIHGNPSGVDNA VSTWGGALRYHQGKISSLKRSP ALQILLTSTRG\PRNIRALVGGG RNRL\LEVPDMGGPLLLSW
13558	43926	A	13638	3	1331	RVDDFVGELLRLRRGGAADVE AAAAAGFPGAMLSQVLLVSAP GKVILHGEHAVVHGKVALAVS LNLRTFLRLQPHSNGKVDLNLP NIGIMRAWDVARLHSLDTSFLG ECKEEKPEQGDVTTPTSEQVEK LKEVAGLPDDCAVTERLAVLA FLYLYLSICRKQRALPSL\DIVV WSELPPGAG\LGSSAAYSVCLA AALLTVCEEIPNPLKDGD\CVN R\WTKED\LELINK\WAF\QGER MIHGNP\SGV\DNAVQHLGEGA LRLPSRGRFSFL*RGSPVFQI/LG LTNTKVPSAITRALVAGVRNRL LKFPEIVAPLLTSIDAISLECERV LGEMGEAPAPEQYLVLEELIDM NQHHLNALGVGHASLDQLCQV TRARGLHSKLTGAGGGGCGITL LKPGLEQPEVEATKQALTSCGF DCLETSIGAPGVSIHSATSLDSR
13559	43927	A	13639	1	950	
13560	43928	A	13640	1	1653	
13561	43929	A	13641	1	2601	
13562	43930	A	13642	2	513	
13563	43931	A	13643	47	367	

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13564	43932	A	13644	1	633	
13565	43933	B	13645	1	1110	
13566	43934	A	13646	172	1095	
13567	43935	A	13647	1	855	
13568	43936	A	13648	3	440	
13569	43937	A	13649	2	230	
13570	43938	A	13650	2	606	AEFDLCCSPCRRRLLGREEAGE EPTSPVTQYLQPRSPEECKMFA CAKLA\CTP\SLIRAGSRVAYRPI SASVLSRPEASRTGEGSTVFNG A\QNGVSQ\LIPKGSFKTSAISKK TLDTA\AKFIG\AGAGNS*GVG WFLVAGIG\TVFWASLIHWVM ARKPFRWKQQL\FSY\AILGICL VLKAMGSPFVLMVAFLILFAHV TEITA
13571	43939	A	13651	200	2320	
13572	43940	A	13652	224	640	
13573	43941	A	13653	1	357	
13574	43942	A	13654	43	183	
13575	43943	A	13655	3	478	SSAGREPDPSDLPRRLCFTHRLP AARRWVQLCVHASPEPGGQGV CPGRSERMVIRVFIASSSGFVAI KKKQQDVVRFLEANKIEFEEVD ITMSEEQRQWMYKNVPPDKKP TQGNPLPPQIF\NGDRYCGDYD RLFESKESNTVFSFLGLKPRLAS KAEP
13576	43944	A	13656	2	428	CRDGKDVVSLVRATVWALSKR KLQPTRA/ALTPTPSAVNKIKQF LKDKPELVDVKVGVRTRGCNG LSYTVEYTKTKGNSDEVIQDEA RVFIEKKAQLTPLGTEMDYVED KLSSE/FMFNNPT*TCGCGAPGK LVETLGLTEEIM
13577	43945	A	13657	1	1377	
13578	43946	A	13658	1	1215	
13579	43947	A	13659	1	452	REAEAADLRSEAPGRRDGEDV GFLSSGQLSGLCSKRKLQPTRA ALTLTPSAVNKIKQLLKE*P*AC R\LKVGVRTRGCNGLSYTLEYT KTKGDSDEEVIQDGVRVFIEK\K AQLTLL*TEMDYVEDKLSKGV GVH\SPNIKGTCGCGESFNI
13580	43948	A	13660	3	763	
13581	43949	A	13661	1	306	
13582	43950	A	13662	738	1022	GQHHPETKAWQRHNKKREF*T NILDEH*CKNPH*NTGKPNPAT HQKAYPP*SSGLHPWDARLVQ HTKINKCNPAYKQNQRQKPHD YLNRCRKGL

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13583	43951	A	13663	2	516	QKIDLPEYQGEPDEISIQKCQEA VRQVQGPVLVEDTCLCFNALG GLPGPYIK\WFLEKLKP\EGLHQ FLAGVEGKS\AYALCTFALSTG DPSQPVRLFRGRTSGRI\VAPRA CQDFGWD\PCFQPDGYEQTYAE MPKAEKNAV\SHRFRA\LLE\LQ EYFGKFGQLDFCKLEAGPFR
13584	43952	A	13664	7	227	
13585	43953	A	13665	1	415	
13586	43954	A	13666	234	510	
13587	43955	A	13667	2	402	
13588	43956	B	13668	530	1544	
13589	43957	A	13669	1	603	
13590	43958	B	13670	1	1527	
13591	43959	A	13671	1	1179	
13592	43960	A	13672	2	413	
13593	43961	A	13673	100	374	KHISPALKALELPFERNLII/PLQ LLKVRILKEGEML/DI*HWFL** GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV
13594	43962	A	13674	1	1035	
13595	43963	A	13675	2	564	GPFGRNRHLPVIRQNDGPQRGK RRGTPKYVF*/RPFRK\HGGGPL GPPYM\RI\YRKGDIVD\IKGMG\ TVQNGMPH\KCYHGKTGRVYN VTQHAV\GIVVNK\QVKGKILA K\RINVRIEHI\KHSKSPR*ASLK/ RVLKENDQEKERSPKKKGTWG SNLKRHPAPPQKKHTL*RTNGK EPEL\LEPIPYEFHGHN
13596	43964	B	13676	68	391	
13597	43965	A	13677	1	404	PTRTWTRGRIPRLSAPPSRGAR GTMADPRVRQIKIKTGV\VKRL V\KEKVLYEKEPKQ\QEEKIEKM RAEDGENYDIKKQAEIL\QESR MMIPDCQRRLEAAYLDLQRILE NEKDLE\EAEEYKEARLVLDSV KLEA
13598	43966	A	13678	1	436	LLLACRSMDCYLAIVHATRTLT QQRHLVKFICLGLRNLFLLLSL RILLFRRTFYPSNVSPVCYEDM GNNTANWWMLLRILPQSFGFIV PL/LIMLFCYRFTLHTLFKAHMG QKHWTMWVIFADVLIILLCWL PYNLVLLADTIMGT
13599	43967	A	13679	1	705	
13600	43968	A	13680	292	1489	
13601	43969	A	13681	434	1205	
13602	43970	A	13682	1	390	

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13603	43971	A	13683	21	479	TYPEAWKLYYRSR*SRDLRKY HAHSVSP*QDQRYTS*KILKCD EHIQKLGSCITDPGNRETSGNT MHTVFHRDKTKDTHPESCCSSE KGGQPLPWFEHRKNVPQFAEP TETLFGPDSGKGAKSLVELLDE SECTSDEEIFISQDEIQSFMANN QSFYSNREQYRQHLKEKFNKY CRLNDHKRPICSGWVDNGWEA
13604	43972	B	13684	32	438	
13605	43973	A	13685	533	1226	
13606	43974	A	13686	1	1566	
13607	43975	A	13687	215	453	
13608	43976	A	13688	1	553	RRPARAAVIKQPPAPGASQHAA TPTQTPLCTPARPLPPMAHVQQ LEGRWRLVDS\KGF**NTMKE\L GVT\IALRKMGRNAQAQICIIT\S DG*NPSPLKTESTLKT\TQFSCT/ LWGEKFEETTA\DGQKKLTNCL STFPDG\AL\VQHQEWDGERKS T\ITKKN*KDGEISWLECVMNN\ VTCTPDSMKK
13609	43977	C	13689	11	106	
13610	43978	A	13690	3	155	LCELQKAIDLFTDAIKLNPRLAI LYAKRASVFVKLQKPNAAIRD CDRAIEINPDSAQPYKWRGKAH R*ILAWPFCMPRGPVSSSNYRS QMLPSETVTEPLK
13611	43979	A	13691	1	1732	
13612	43980	B	13692	95	1715	
13613	43981	A	13693	1	446	
13614	43982	A	13694	1	786	
13615	43983	A	13695	88	828	

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13616	43984	A	13696	157	1515	RREKMAELKYISGFGNECSSED PRCPGSLPEGQNNPQVCPYNLY AEQLSGSAFTCPRSTNKRSWLY RILPSVSHKPFESIDEGHVTHNW DEVDPDPNQLRWKPFEIPKASQ KKVDFVSGLHTLCGAGDIKSN NGLAIHIFLCNTSMENRCFYNS DGDFLIVPQKGNLLIYTEFGKM LVQPNEICVIQRGMRFSIDVFEE TRGYILEVYGVHFELPDLGPIG ANGLANPRDFLIPIAWYEDRQV PGGYTVINKYQGKLFAAKQDV SPFNVVAWHGNYTPYKYNLK\ NFMVINSVAFDHADPSIFTVLT AKSVRPGVAIADFVIFPPRWGV ADKTSGPPYYHR\NCMKRFME LIRGQFEQKQGWFLPGGRG/SL HSTMTPHGP\DADCFEKASKVK LALKRIADGTMA\FMF*SSFNLA GPKWGLQAP\RVLDKNYPKCW EPLKSPF\TPNSRNPAEPN
13617	43985	A	13697	1	156	
13618	43986	A	13698	8	306	
13619	43987	C	13699	1	1143	
13620	43988	A	13700	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSSLGADAI AKQRKTSVSAAASVSATIPIRR VQGPTVVGSWARGVSAAASGP RGTGPKGKARSEKGCSLSHGPQ TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSHP LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAIIYMNMGNKL PIWCHLLEEGIYLEVWALEGQF GRAKNACPVQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAEWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPQGFR DSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSEASCQQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYLGLILARGTRTLGK ERIQPILAYPHPKTLKQLWGFL QIT/GFCQLWIPR*SKI
13621	43989	A	13701	188	688	

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13622	43990	A	13702	636	2628	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKD
13623	43991	B	13703	302	619	
13624	43992	A	13704	1	5172	
13625	43993	A	13705	1	2091	
13626	43994	A	13706	1	1754	GPRGTGPKGKARSEKGCSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIIYMNMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAEWFP VLDLKDAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGLILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIARPLYT LIKETQRANTHLVEWESEAETA FKTLKQALVQAPGLSLPTGQNF SLYVTERAGIALGVLTQTRGTT PQPVAHLSKETDVVAKGWPHC LRVVAAVAVLVSEAIKIIQGKD LIVWTTHEVNGILG/AKGSLWL SDKRLFRYQALCLEGLVLQIRT SCGSHLAVTRLWALYF
13627	43995	A	13707	2	887	

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13628	43996	A	13708	3	1750	GWAVPRPGPRGLTVATEAAAA AAAAAAAAISSRTRAPQAPEGR NRRLEKMADDIDIEAMLEAPY KKDENKLSSANGHEERSKKRK KSKSRSRSHERKRSKSKERKRS RDRERKKSKSRERKRSRSKERR RSRSRSRDRRFRGRYRSPYSGP KFNSAIRGKIGLPHSIKLSRRRS RSKSPFRKDKSPVREPIDNLTPE ERDARTVFCMQLAARIRPRDLE EFFSTVGKVRDVRMISDRNSRR SKGIAYVEFVDVSSVPLAIGLTG QRVLGVPIIVQASQAEK\NRAA AMANNLQKGSAGPMRLYVGSS HFNITEDMLRGIFEPFGRIESIQL MMDSETGRSKGYGFITFSDSEC AKKALEQLNGFELAGRPMKVG HVTERTDASSASSFLDSDELER TG\IDLGTTG\RLQLM\ARLAEG TGLQIPPAAQQALQMSGSLAF\ GAVGRNLFCYRFAKQDFSHQT\ ETSALSAAAS\VQPLATQCFQLS NMFNPQTEKEVGWDTEIKDDV IEECNKHGGVIHIYVDKNSAQG NVYVKCPSIAEAIAAVNALHGR WFAGKMITAAYVPLPTYHNLF PDSMTATQLLVPSRR
13629	43997	A	13709	141	343	LHEGLLP*RGHALLSGALHG*C VGSCLFSTPRCLTSSTACGYPSS CTPGSCTAWCPSASRRLSCWT
13630	43998	A	13710	5	426	
13631	43999	A	13711	1	1188	
13632	44000	A	13712	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDQEAVI DGRRKPEESRTTSHICRCRS
13633	44001	A	13713	1	700	
13634	44002	A	13714	3	483	
13635	44003	A	13715	2	361	RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNSLKIISNA SCTTNCLA/PPASTGAAKAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13636	44004	A	13716	2	249	SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV

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13637	44005	A	13717	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQER\YPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPSADAPM FVMGVNHEKYDNSLKIISNA\S CTTNCLT\PLAKVIHDNFGIVEG LMTTVHAITATQKTVDGPSGKL WRDGRGALQNIIPASTGAAKA VGKVIPEL\NGKLTGMAFRVPT ANVSVVDLTCRLEKPAKYDDI KKVVKQA\SEGPLKGILGYTEH QVVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13638	44006	A	13718	3	483	
13639	44007	A	13719	2	361	RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNSLKIISNA SCTTNCLA/PPASTGAAKAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13640	44008	A	13720	2	249	SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
13641	44009	A	13721	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQER\YPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPSADAPM FVMGVNHEKYDNSLKIISNA\S CTTNCLT\PLAKVIHDNFGIVEG LMTTVHAITATQKTVDGPSGKL WRDGRGALQNIIPASTGAAKA VGKVIPEL\NGKLTGMAFRVPT ANVSVVDLTCRLEKPAKYDDI KKVVKQA\SEGPLKGILGYTEH QVVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13642	44010	C	13722	40	243	
13643	44011	A	13723	2	2972	
13644	44012	A	13724	1	602	

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13645	44013	A	13725	1	325	MGRNQSRKAENTKNESASSPP KDRNSSPVREQSWTENEFDELT EVGFRKLVITNFSELKEHVLTD HKEAKNLEKS\LEVVAREISQE KEIKVFN*EKRKSNCPCLQMT
13646	44014	A	13726	1	981	
13647	44015	A	13727	1	739	MGRNQSRKAENSKNQSTSSPPK DCSSSPAREQNWTKNEFDELTE VGFRRSLIANFSKLKECVLTHR KEAKNLEKSDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RIPQRYSLRRATPRHIIVRFTKV EMKEKMSRAAREKGRVTHKG KPIRLTADLSAENLQARREWGP VFNILK\NFQPRIPYPAKLSFISG GEIKSFTDKQMLRDFFTTRPAL QELLKEALNMERNNQYKPLQK HAKW
13648	44016	A	13728	1	1277	MKEQNGGGGREEDHKDKGIRQ LPSLLPSAGEAKSDKPEHHNRY RKEIASFEDEKRAMGVAKMAE QEQLQSAAPSMTNAEVGTAHG GRAEAGRGVDSPGKRKVLGDF PFLAKGSRDRLPGKAGHSLPKY YAFTKVLATGRQERNSINISKK VIYTKTTSTGHQHQRPKIDKTT KMGRNQSRKAENSKNESTSSPP KGHSSSPATEQSGTENDFDELT EVGFRRSVTTNFYELKEDVQTH RKEAKNLEKRLDKWLTRINSV EKTLSDMMELKTMARELRDTC SSFKSRFNQVEERVSVIEDPIY\E LSREDKVRDKKVRNKQSLQEI WDYVKRPNLRVIGVPESDGEN GTKLENMLQDIIQENFPNLARQ ANIQIQEIQRTPQRYSSRRATPR HIIVRFTKVEMKQKVLRAAREK GPVTHKGNSGSLS
13649	44017	A	13729	1	1584	
13650	44018	A	13730	493	575	SHLPMNPANTRSQRNPTKKKQ KKNVC/DNIRELEQQMEDAYR GTKRKMLPSSSSRMRSDGFDEE SQRYYWRPKNEISGTLEDDFLK AKSWNRKFYDYEANMPDRWG\ QVAIKSYTLKNLKQTVVISKILP TGRKHLPR*SHLPMNPANTRSQ RNPTKKKQKKNVCG
13651	44019	A	13731	1	655	
13652	44020	A	13732	2	1664	
13653	44021	A	13733	1	2364	
13654	44022	A	13734	1	224	

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13655	44023	A	13735	1033	7511	
13656	44024	A	13736	56	8669	
13657	44025	A	13737	42	8716	
13658	44026	A	13738	1	5046	
13659	44027	A	13739	1	2298	
13660	44028	A	13740	1	2362	
13661	44029	A	13741	1	2046	
13662	44030	A	13742	1	1503	
13663	44031	A	13743	1	813	
13664	44032	A	13744	185	735	
13665	44033	B	13745	317	910	
13666	44034	A	13746	1	867	
13667	44035	B	13747	1	2325	
13668	44036	A	13748	1	430	
13669	44037	A	13749	1	867	
13670	44038	A	13750	35	518	CLSRRASPVYLASMSGRGKTG GKARAKAKSRSSRAGLQFPVG RVHRLLRKGHYAERVGAGAPV \YLAA\VLEVAQPLRVLELAGN AA\RSN\KKTRIIPRHLQLAIRND EEL*KLPGLP*RIAQGSR/VLPNI QA\VLLPK\KTSATVG\PKAPSG GKKATQASQEY
13671	44039	A	13751	1	937	
13672	44040	A	13752	1	1096	
13673	44041	A	13753	85	1512	
13674	44042	A	13754	3	2377	
13675	44043	A	13755	1	1134	
13676	44044	A	13756	49	408	
13677	44045	A	13757	47	2603	
13678	44046	A	13758	1	378	
13679	44047	A	13759	1	696	
13680	44048	A	13760	3	401	
13681	44049	A	13761	882	1106	KLHPYTTRQYCHFRI*TDVMAK RSRNAVKGLSALVWCALSDFA AGFTPDDGCTRATFFTGGWRK RDCRGAVAGG
13682	44050	A	13762	688	1100	
13683	44051	A	13763	476	552	
13684	44052	B	13764	178	1107	
13685	44053	A	13765	1	198	
13686	44054	B	13766	94	625	
13687	44055	A	13767	1	732	
13688	44056	A	13768	1	4443	
13689	44057	A	13769	216	575	PGAGDRYVGKPVSAGVTAVSC GVWSSMPDATLIASYQAYTSH VGRIRRSRRIR/TNTARADYPAL TALPFNNFRTHNRFGFNAASVL ASIGIGSSLICAARISAHSGAEH KPREPKAANIK

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13690	44058	A	13770	1018	1489	KLPGQRRFVQTPSHVLHTTLSY PTAPAQSSYPAPLSPSQDRAPTL AHQTT*FSASYTANAQWQRVA ADHLKSVRETYAHVRQFSPAL GNAPPDLQPLS*ASCVPKSGAR YSSVIRQNRRDFFRATDHMYVT VPTNRPKMWNPVNTQMNSFRA DTCER
13691	44059	A	13771	1013	1755	GSPGLRPGGAAGKALAPSGCT GNSHRAPM*PGAQAQTRPEKW A*QRP/HVSTGARGARVRALAA VAAAEAQRAGAAVRAAALHT RAAVSAGAARAVVQVVLAAR TREAGAAAAAQGVAQVQAES AIAAWLQAAPVHPLLTVGALE TGWAVADVGRVRVCTPDTQA AVEAGSICTCHPAHLTPQPVEP TRAGAFKGPGCLTTAASIGTRV PVTGPRPRDKASGGSRGRAPGA EAAAGGDRDRAEGSSPAL
13692	44060	A	13772	1	1236	
13693	44061	A	13773	1	456	
13694	44062	A	13774	1	219	
13695	44063	A	13775	1707	1853	
13696	44064	A	13776	1	615	QLATFFFGGGLPGGSAPWDPPG EACLWVLVRLPGRTVWVIQFV QLRSFFAPPFAHNGRASSGRVS VHYGIAQTAEWAAEICGVGAR KIRELAAIFHQNTIMHFANGG/N PTRRSAVLSSMQGSLPGGC\DA VDIHPVARIVEALENPGGAYQH NGMNRHFPDIRFIWWAGGANF THHQDTNRLIRAWQNDSYFRK GRIKAKMGPKLF
13697	44065	A	13777	407	661	ANWIKWRWHRAMHSSSSMWQ TANSLASFISAPVTSSSACRSTL PATRYWCI*WRSSAIWKWVILS GPVATRICTATIWIQLICN
13698	44066	A	13778	1	2448	
13699	44067	A	13779	3	1612	
13700	44068	A	13780	1	1626	
13701	44069	A	13781	3	118	
13702	44070	A	13782	1175	1396	
13703	44071	A	13783	197	933	
13704	44072	A	13784	2	64	IILLNSAPAWM*TFKLGPGVDV NYMLHTQNK
13705	44073	A	13785	1	855	
13706	44074	B	13786	1	1605	
13707	44075	A	13787	1	588	
13708	44076	A	13788	1	2769	
13709	44077	A	13789	813	1341	

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13710	44078	B	13790	1	999	
13711	44079	A	13791	1	281	
13712	44080	A	13792	1	1332	
13713	44081	A	13793	1	1384	MPITLRRSVEKEQLIEIANTIMPF GKYKGRRLIDLPEEYLLWFARK DEFPAEARYTHIDLHVPAPLLV MFTLDTRQSACDRNPHLPIHVC SSWTSPKCAPRLWTRALLPRTR TPPYATGTTIGSRASWFVTFPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLIHKM VEVNACLKQLDNKDIADYEHN QLMRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSAVVEETR EAVDTTSQPVAT
13714	44082	A	13794	1	2004	MTQQITLIKDKILSDNYFTLHNI TYDLTRKDGEVIRHKREVYDR GNGATILLYNTKKKTVVLIRQF RVATWVNGNESGQLIESCAGL LDNDEPEVCIRKEAIEETGYEV GEVRKLFELYMSPGGVTELIHF FIAEYSDNQRANARGGVEDEDI EVLELVQCGGQIGVPDTVLAVF ATGIGFLAMSVTKPRINAQPYP MPWRNLAQLVEHINRTRIHRNL QFTDAFKRRLIDNICRKNNIIGT HTGQSKFSGQTQQIFGEIPQVVP ASELAAAMKQIKELQRLLGKK TMENELLKEAVEYGRAKKWIA HAPLLPGDGERTDDWMDGRRS RHTDDTDVLLRIHHVIGELPTY GYRRVWALLRRQAELDGMPAI NAKRVYRIMRQNALLLERKPA VPPSKRAHTGRVAVKESNQRW CSDGFEFCCDNGERLRVTFALD CCDRLSSRGRNAAAKRQRDDP LRWKFRLPSGGTKLLMPLDQQ APARFAPFVTCTLTILCGTGHV VYTILPIIYDVAIKNNIRPERPM AASSIGAQMGIIASPVSVAVVSL VAMLGNVTFDGRHLEFLDLLAI TIPSTLIGILAIGIFSWFRGKDLD KDEEFQKFISVPENREYVYGDT ATLLDKKLPKSNWLAMWIFLG AIAVIALLGADSDLRSSF/GGKP

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13715	44083	A	13795	3	918	DKTRKRRIRQ*IPNATSFLYQNS PNGLSE*L\PAGTWFAGNAPASS CGFRDRYLIVCSHQTPHVPGQI TVAAPDARAQAILRIVRQLQRF FHRFEGGHRQHRAKNLLLEHP HIVLTKQNRRFEADALQPDPA WQQGTLSNGLQWQVLTTPQRP SDRVEIRLLVNTGSLAESTQQS GYSHAIPRIALTQSGGLDAAQA RSLWQQGIDPKRPMPPVIVSYD TTLFNLSLPNNRNDLLKEALSY LANATGKLTITPETINHALQSH DMVATLVFRYLKKGWWRYRL KGSTLLSHDPAHPLKQPVEAEK
13716	44084	A	13796	1	1368	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAVYGIAWMA ETMFAPACYGYYILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPFQSVKAD IATNPFKRPGGAFIRITQTFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTEGAIPFAAADPLR/PSFGG KPLSMVLVIQMFMLLTGALIIIL TKTNPASISKNEVFRSGMIAIVA VYGIAWMAETMFAPACYGYYI LPTYPSDLAAIQFDRSGTTHIGR FVINHSFILPGLIGVSVSCVFGWI FAAIKRDAAAGRAKENVIFHHF PFQSVKADIATNPFKRPGGAFIR ITQTFRTVQTFRLSAYRLDFAG DRLRISTPRAKMRTAFKKDHLR QRRRCIRQRAPPARHNLVGAV ALPATVAGVNFTFSNVPLDSSV LSSLLTDFSTAVGSIVMLAVIM GLMLAFDMGGPVNKVAYAFM LICVAQGVYTVVAIAAVGICIPP LGMGLATLIGRKNFSAEERETG
13717	44085	A	13797	3	2185	
13718	44086	A	13798	1	920	

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13719	44087	A	13799	251	479	TQRVDWRSRSSISPGDGLHAFP AFGKEGGKMLDRLRERRDVKT LQQSGSAAGAEFALAGAHPHT GTTA*IQQAINV
13720	44088	A	13800	1	939	
13721	44089	A	13801	1	386	
13722	44090	A	13802	3	524	
13723	44091	A	13803	1	548	
13724	44092	B	13804	67	1144	
13725	44093	A	13805	811	974	VSRRIKLDVTEEFARAGDNKRC ICQ*RHGLAERDIARLLVEIVVI WCDIGVIQA
13726	44094	A	13806	1164	1262	
13727	44095	A	13807	2	894	
13728	44096	A	13808	1	1587	MVKEGTFREDLFYRLNVIHLIL PPLRDRREDISLLANHFLQKFSS ENQRDIIDIDPMAMSLLTAWSW PGNIRELSNVIERAVVMNSGPII FSEDLPPQIRQPVCNAGEVKTA PVGERNLKEEIKRVEKRIIMEVL EQQEGNRTRTALMLGISRRAL MYKLQEYDATGFFRDGMTIMV GGFMGIGTPSRLVEALLESGVR DLTLIANDTAFVDTGIGPLIVNG RVRKVIASHIGTNPETGRRMISG EMDVVLVPQGTLIEQIRCGGAG LGGFLNPTGVGTVVEERQTSID TSTRKRPFELGRPSRNNDKGIRP \DQALDRKNIRE/ALHDSLKRLQ TDYLDLYQVHWPLRPFYCFGK LGYSWTDSAPAVSQLDTLDAL AEYQRAGKIRYIGVSNETAFGV MRYLHLADKHDLPRIVTIQNPY SLLNRSFEVGLAEVSQYEGVEL LAYSCLGFGTLTGKYLNGAKP AGARNTLFSRFTRYSGEQTQKA VAAYVDIARRHGLDPAQMALA FVRRQPFVASTL\LGATTMDQL
13729	44097	A	13809	1	618	

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13730	44098	A	13810	80	952	RPGIVALNAILPLSRTRQSKPTR LKKRAIANCAPTWKKRFVALV YRTA*RFPSITLSVAVT*PASAK NKAIKMTQKIEQSQRQERVAA WNRRAECDLAAFQNSPKQTYQ AEKARDRKLCANLEEAIRRSGL QDGMTVSFHHAFRGGDLTVN MVMDVIAKMGFKNLTLASSSL SDCHAPLVEHIRQGVVTRIYTS GLRGPLAEEISRAYCADSHHGP FAMVNNMTDLTAQEPAWQTR DHLDDPVIGELRNRFGPDAFTV QATRTGVPVVWIKREQLLEVG DFLKKLPKPYVMLFDLHGMDE RLRTHREGLPAADFSVFYHLISI DRNRDIMLKVALAENDLHVPT FTKLFPNANWYERETWDLFGIT FDGHPNLRWIP
13731	44099	A	13811	92	735	RLLRPLPQPRSSVLPGLTTFHAS STSETRQSKPTRLKKRAIANCA PTWKKRFVALVYRTA*RFPSIT LSVAVT*PCVNIITIGCQVKTVT TIATAQIQRFTRFNHFSRFQYFR NSPKQTYQAEKARDRKLCANL EEAIRRSGLQDGMTVSFHHAFR GGDLTVNMVMDVIAKMGFKN LTLASSSLSDCHAPLVEHIRQG VVTRIYTSGLRGPLAEEISRGLL AEPVQIHSHGGRVHLVQNGEL NIDVAFLGVPSCDEFGNANGYT GKACCGSLGYAIVDADNAKQV VMLTEELLPYTDNPEA
13732	44100	A	13812	1	1113	
13733	44101	A	13813	5121	6228	LRRDSGRLRSCWHPRSPTSMGS LGQREDLQDEDRNSGADPGQR GRCSIHLEGPGQQPCLQRAVQG EGDPVLAKEEIQDQCHPHGQV QLLLVPAAEPVRAVPPRVQPVL PHHHHPAELSGIREE*GNQNDA EN*TISTTRTGSGLESSR*M/SILP LSRTRQSKPTRLKKRAIANCAP TWKKRFVALVYRTA*RFPSITL SVAVT*PYWSGAPGGPCRRPYC HFRHRGARGSGAPGDGGEAPP AAAFLGGDVGFGL
13734	44102	A	13814	56	196	CRGDGGKLIIQCQRRMGI*PCG* LRQRKAELFQHLPLC*FWRPEI GTVCSGSIDNGSDRLRR
13735	44103	B	13815	64	2373	
13736	44104	A	13816	3	403	
13737	44105	B	13817	55	1040	

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13738	44106	A	13818	587	1533	VLLTAKFFPSMYSPIKTAGGPA ST*VL*MIISIDAEKAFDKIHQPF MLKALNKSENKIPRNPTYNGCE GPLQGELQTTAQGNKRGYKQT QQHDMHMSTKNQYHENGHTA QGMKGITQPSAFIPTAESNSFQP QVKTLPSPIDAKQQLQRKIQKK QQEQKLQSPLPGESAAKKSESA TSNGVTNLPNGNPSILSPQPIGIV VAAVPSPIPVQRTRQLVTSPSP MSSSDGKVLPLNVQSHQNCW WTRFNMSSLNVVKMTTISLTPS NSNTPLKHSASFISATGTTEESR SVPQIKNGSVVSLQSPGSRSSSA GGTSAVEVKVEPETSSDEHPVQ CQENSDEAKAPQTPSALLGQKS NTDGALQKPSNEGVIEIKATKE RRSSPATEQSWMENVFEEQREE GFRRSNHSQIREDSQTKGKEEK RLKELMELKTKVRELREECRSL RSRCDQLEERVSAMDDEMNEM KREGNFREKRIKRNEQSLQEIW DYVKRPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLARQANI QIQEIQRTP
13739	44107	A	13819	590	817	
13740	44108	A	13820	107	410	KGRNIQLNGPSSRVSLWRSLYF LNLNTGLPC*IGEVLLDNILQSV FQLGSILPITFRYTNQT*IWSFHI VPYFLEALLISFYSFFSKLPFSLH FIHFIFHR
13741	44109	B	13821	1	3735	
13742	44110	A	13822	922	1137	HFFLHFNFGESDNYVSWSFSSR GVSLWRSLYFLNLNVGLPC*IG EVLLDNILQSVFQLGSILHITFR YTNQT
13743	44111	B	13823	1	954	
13744	44112	A	13824	3	156	
13745	44113	A	13825	683	972	SHRLLRLLHSSRSSPGLVSSSISS FKHFSVLVILFTLMIVSFAVQKL FSLIRSHLSILALVAIAFGVLVM KSLPTPMSSMVLSR/SFF*GFYG FRSYI
13746	44114	C	13826	1	895	
13747	44115	C	13827	372	1727	
13748	44116	A	13828	705	1072	LALLVELIPLPLCNGLLCLF*SL LV*SLFYQRLGLQPLPFFVFHLL GRSSSILLF*AYV*LFWHDFAA AGTGCSFPCLALPSGALVGQA WW*QKSLSICLSVKDFISPSLM KLSLAGYEILG

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13749	44117	A	13829	1	1136	
13750	44118	A	13830	547	675	
13751	44119	B	13831	144	1877	
13752	44120	A	13832	1	441	
13753	44121	A	13833	27	344	
13754	44122	A	13834	287	600	GPGSLQSSPLLSPPWPRASSPLL LRPSVRGWHLGEP*NCFPSPLA AS/EQAPKRSS*PQCNHR*RETA ARGLAYPPDRPLPSMLSCESPE TPAKAGPGRERGCEKC
13755	44123	A	13835	2	226	
13756	44124	A	13836	2	226	
13757	44125	B	13837	45	518	
13758	44126	B	13838	1	699	
13759	44127	A	13839	3	362	
13760	44128	A	13840	2	130	
13761	44129	A	13841	3	96	
13762	44130	A	13842	1	545	
13763	44131	A	13843	2	144	
13764	44132	A	13844	2	91	
13765	44133	A	13845	1	370	
13766	44134	C	13846	1	214	
13767	44135	A	13847	215	310	
13768	44136	A	13848	2	91	
13769	44137	A	13849	1	289	
13770	44138	A	13850	1	997	
13771	44139	A	13851	1	192	
13772	44140	A	13852	2	267	
13773	44141	A	13853	2	181	
13774	44142	A	13854	1	171	MESYAAIKNDEFMSFVGTWMK LETLILSKLSQGQK\TKHCMFSL TDVIARRRSWTSI
13775	44143	A	13855	92	244	KRRRRRGQIRKMKEEEGNRRT WMKLETIILSKL*QRQKTKHRM FLLIGGN
13776	44144	A	13856	146	382	
13777	44145	B	13857	124	1215	
13778	44146	B	13858	1	628	
13779	44147	A	13859	377	484	
13780	44148	A	13860	2	220	WARTSCLKHQKQWQQKPKLA NGI*LN*RASAQQKKLPSEWTG TWMKLETIILSKLLQGQKTKHR MFSLIGGN
13781	44149	A	13861	965	1150	GVDQRAVCSSRIW*SHLFLFHS VVVHLPWAGTWMKLETIILSK LSQGQKTRHRMFSLIGGN
13782	44150	A	13862	254	571	YSYKLEIIIGKQPEIYRDPCYRP AV*SQTAVLAISEAPWA*DLPS QVSDTISWWTVC*AHWKSAVL GWE*PGFPGTWMKLETVSLSK LSQGQKTKHHMFSLIGGN

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13783	44151	A	13863	62	214	
13784	44152	A	13864	274	435	
13785	44153	A	13865	1	294	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN
13786	44154	A	13866	663	1266	PPLTCQCSHLCVTLVGH/WIKLE TIILSKLSQGQKTKHRVFSLIGG AGALAKECMSLYPGCKITVFDI PEVVWTAKQHFSFQEEEQIDFQ EGDFFKDPLPEADLYILARVLH DWADGKCSHLLERIYHTCKPG GGILVIESLLDEDRRGPLLTQLY SLNMLVQTEGQERTPTHYHML LSSAGFRDFQFKKTGAIYDAIL
13787	44155	A	13867	1	681	
13788	44156	A	13868	1	247	
13789	44157	A	13869	2	178	
13790	44158	B	13870	1	2042	
13791	44159	A	13871	1	378	
13792	44160	A	13872	1	683	
13793	44161	A	13873	1	972	
13794	44162	A	13874	308	406	
13795	44163	C	13875	177	653	
13796	44164	A	13876	1	465	
13797	44165	A	13877	3	1175	FFSSQAAALLVVLGSSHTLQRA RKHSAPGLPDTCALLQPPAASA AAAPSMSGPDVETPSAIQICRIM RPDDANVAGNVHGGTILKMIE EAGAIISTRHCNSQNGERCVAA LARVERTDFLSPMCIGEVAHVS AEITYTSKHSVEVQVNVMSENI LTGAKKLTNKATLWYVPLSLK NVDKVLEVPPVVYSRQEQEEE GRKRYEAQKLERMETKWRNG DIVQPVLNPEPNTVSYSQSSLIH LVGPSDCTLHGFVHGGVTMKL MDEVAGIVAARHCKTNIVTAS VDAINFHDKIRKGCVITISGRMT FT\SN\NSMRFKVLLDPAPVVDS FQKRYRGRQCLSST*VSLSQER QV/PLPVPQLVP\ETEDEKKRF\E EGKGRYLQMK\AKR\QGHAEPQ
13798	44166	A	13878	121	361	SLFELENRSKFSVATAGLVPSR RLSINCIRRAFITSSNGFPLWFCL HQKGPVDCCVAVY*CGTEDGS WAPTHPGVGPSLP
13799	44167	A	13879	1	462	

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13800	44168	A	13880	3	287	PCSLSSDCCASNQRDSVGIGPSE PRVGYNILVIRFLSPSEKRSPR\V GVTRFSSAWEPSQLAGILPISEP PSNRIFACWGKPAWTACCNSLR ARR
13801	44169	A	13881	1	1332	
13802	44170	A	13882	1	753	
13803	44171	A	13883	1	516	
13804	44172	A	13884	71	277	IYFNTQESFCPPRPLK/LCDGRG CHKGL*NAFKAFSPFSWPLALG SFLLMQISAACLNSFPENGLFFS TT
13805	44173	B	13885	1	1095	
13806	44174	A	13886	1	741	
13807	44175	A	13887	264	2880	WLLQKHKLHVSR*LGL\PDTSW ILPSRPDAGGRFPIRTPPCVLVV HKPSRHCREWTANTVLPKGAL AKWLLEPKADLQGWHLPADG QYTKPSISYNIKLYINCYNRTVT TAAQHQQVQRKHGASIFLAEN VAVREKDKEERKVTRAPTEQA WTAGSWIETAYREIKGVGQES VCITVMHLEELVYELAWIIMSA VVEAFDPVAPSSKCRLNPDPDP YCCTPYTLHTSPPPPSCCTPYT LHTGPPPQTPFCCTPYTLDTSPS PQTHSCCTPYTLHTVPTFHLPA AHPIHLHTIPPPQTQGQGFVSED EYLEISDIKRDQSGEYECSALND VAAPDVRKVKITVNYPPYISKA KNTGVSVGQKGILSCEASAVP MAEFQWFKEETRLATGLDGMR IENKGRMSTLTFFNVSEKDYGN YTCVATNKLGNTNASITLYVD HIVGSKALLSKCKRTEIITNYLS DHSAIKLELRIKNLTQNHSTTW KLNNPLLNDYWVHNEMKAEIK MFFETNKNKDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKI DTLTSQLKELEKQEQTHSKANR RQEITKIRAELKEIETQKTLQKI NESRSWFFERINKIDRLLARLIK KKREKNQIDAIKNDKGDITTYP TEIQTTIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVES QNRPITGSEIVAIINSLPTKKSPG

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13808	44176	A	13888	1	629	AMAGSPPPASLLPC\LISDCCAS NQRDSVGVGPSEPGVGYSLVV RRFLSPSEKRSIRVGVTRFSRCR PSPLSLTQKGNSLTSWASQVLT PAPEKQPDNKLPLPRRGSRDPT EYFHGQEVRDKSDEHVDHVSQ IHSFRDEVKRLGAEDSSNAETP TELHEFNTGGVYRPPNSTSVIQP LDQGVIRTFKPCYTKYSLEKIVS AVEENPDRT
13809	44177	A	13889	1	1452	
13810	44178	A	13890	167	309	
13811	44179	A	13891	3	386	SVGALQKQQGWHQRRCISLHF PSFLCVFSLAKSRRADHNQDPR ASRMAFSLTSSPLARSAASAVA AFGCGTSGNGRFSSVP*AYRQV FQRIAIAVYGPLMRDR*AHPVK TPDAIDCRIRQPAIPRLQ
13812	44180	B	13892	121	298	
13813	44181	A	13893	473	1826	
13814	44182	A	13894	1	270	
13815	44183	A	13895	3	3706	
13816	44184	A	13896	1	1464	
13817	44185	B	13897	591	729	
13818	44186	A	13898	1	1326	
13819	44187	A	13899	1	1152	

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13820	44188	A	13900	1	2524	MREEFAHRWLARAGEKTPPDA LEKLTDPLMFAAAMVSAGKAD VCIAGNLSSTANVLRAGLRIIGL QPGCKTLSSIFLMLPQYSGPAL GFADCSVVPQPTAAQLADIALA SAETWRAITGEEPRVAMLSFSS NGSARHPCVANVQQATEIVRE RAPKLVVDGELQFDAAFVPEV AAQKAPASPLQGKANVMVFPS LEAGNIGYKIAQRLGGYRAVGP LIQGLAAPMHDLSPCIAATDAG SAAAQRIGDLVSVHVIPRPHVD LEQVFPIGLKAYTATCNHPVSL RFTIKSSSDRIKLSNQTLQSKNL FIMRFYCFSLCLSLSAFYHCRGV IVNIQAVFWLQKGTEAADILTT CAQLWIMMYALLSVFSLLDVIL NLAQKFPAASQLPLKGIFQGIKL IGAILVGILMISLLIGQSPAILISG LGAMAAVLMLVFKDPILGLVA VRNWDNTITTIPTWSLVSDSFK NWSGMSASGGRRIKRSISIDVTS IRFLDEDEMQRLNKAHLLKPYL TSRHQEINEWNRQQGSTESVLN LRRMTNIGTFRAYLNEYLRNHP RIRKDMTLMVRQLAPGDNGLP LEIYAFTNTVVWLEYESIQADIF DHIFAIVEEFGLRLHQSPTGNDI RSLAGVTINKAPGDDEILKNTV DFVSFSYYASRCASAEMNANN SSAANVVKSLRNPYLQVSDWG WGIDPLGLRITMNMMYDRYQK
13821	44189	A	13901	1	2370	
13822	44190	A	13902	1	282	
13823	44191	A	13903	1	714	
13824	44192	A	13904	3	506	
13825	44193	A	13905	459	551	
13826	44194	A	13906	401	492	
13827	44195	B	13907	479	702	
13828	44196	A	13908	120	256	

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13829	44197	A	13909	16	1249	SKSGAIEIARLAGRVHGVVVQI TSEIGPLTLLTANFAFSAS*STA WKATSMDGEVLS*YSTSASAS AERQSTHQ*TGFAPLCR*PLPMI /VAQRADDVGFSFEVHGQVRV RPVAQHAQTDKVFALTVNLGR RVFAALGAELGGARSAVRPVP ECYAVRETLALLQKIFPIRQCEN SVYRNRSRPCLQYQIGRCLGPC VEGLVSEEEYAQQVEYVRLFLS GKDDQVLTQLISRMETASQNLE FEEAARIRDQIQAVRRVTEKQF VSNTGDDLDVIGVAFDAGMAC VHVLFIRQGKVLGSRSYFPKVP GGTELSEVVETFVGQFYLQGSQ MRTLPGEILLDFNLSDKTLLAD SLSELAGRQINVQTKPRGDRAR YLKLARTYAATALTSNFRSIYR SPATDRACQRVETAGNER
13830	44198	A	13910	1	438	
13831	44199	A	13911	1	1200	
13832	44200	A	13912	1	300	
13833	44201	A	13913	1	431	
13834	44202	A	13914	2	1465	
13835	44203	A	13915	1	513	
13836	44204	A	13916	3	535	RDKILVFKDENFWMIRGYAVLP DYPKSIHTLGFPGRVKKIDAAV CDKTTRKTYFFVGIWCWRFDE MTQTM\EKGFPQRVVKHFPGISI RVDAAFQYKGFFFFSRGSKQFE YDIKTKNITRIMRTNTWFQCKE PKNSSFGFDINKEKAHSGGIKIL YHKSLSLFIFGIVHLLKNTSIYQ
13837	44205	A	13917	1	876	
13838	44206	A	13918	23	414	
13839	44207	A	13919	2	425	QERGPHQVIQRKECLREYSPVV S*AKGTGVAVGQKGTLQCEAS AVSSAEFHWYKDDKRLIEGNK GVKVENRPFLSKLIFFNVSEHD YGNYSCVASNKLGHTNASIML FGPGAVSEVSNGTSRRAGCVW LLPLLVLRLLLKF
13840	44208	A	13920	1025	1270	
13841	44209	A	13921	370	701	
13842	44210	B	13922	1	660	

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13843	44211	A	13923	1	432	RFSRVDDFVLTMDDGPPPRRAR GDLTHSGLWRVCCIEGIYKGHC FRINHFPEDNDYDHDSSEYLLRI VRASSVFPILSTILLLLGGLCIGA GRIYSRKNNIVLSAGILFVAAGL SNIVGIIVYISSNTGDPSDKRDE DK*NHYN
13844	44212	A	13924	1	1093	
13845	44213	A	13925	1	1203	
13846	44214	A	13926	1	1353	
13847	44215	A	13927	2	445	
13848	44216	A	13928	1	227	
13849	44217	A	13929	1	840	
13850	44218	C	13930	120	356	
13851	44219	A	13931	40	342	
13852	44220	B	13932	403	473	
13853	44221	A	13933	70	2169	
13854	44222	A	13934	1428	1905	RCAATSGYGERVQRTV/PTHTV W*ASLSQSSAHRVVAINSIANK RSSMPPKSWATVALTSTKLKCR FMAKVRNKSFSVLHNV*MTISI/ SPWVILSSGVDEKLFPRAVRVA MTAGASGFLAGRAVWASVVG LPDNELMLRDVCAPKLQQLGDI VDEMMAKRR
13855	44223	A	13935	227	342	VHSWQRYSGR*RGY*PQNQSA TDQTRRWQSLKTAGAVA
13856	44224	A	13936	480	928	FFADLQQPVCADSYPLLVQMK LAPHKS*NAVLWQRSATKSFSV L/AQGLNDHINMPWVILSSGVD EKLFPRAVRVAMTAGASGFLA GRAVWASVVGLPDNELMLRD VCAPKLQQLGDIVDEMMAKRR FIPLLRRWVDLALTRWLITVSK
13857	44225	A	13937	564	1185	WLHASAALLRW*YQLPGQPHH RRCRSADGSHVPSLCAAVPDQR \PLITVRRIGMQAMTTSTTGDRQ RSWQIAMDGSQKLPQRMLDSV RWHLAHDSKFDLLALGVAGW MRYVGGVDEQGNPIEISDPLLN RMAANRFVHITQLPVIYRAFRN SFTQVARLQLCHKRFQQRHTSV REQIVTVLSGIRDNHVHFVQTL TGDGVGNQRQLVQ
13858	44226	A	13938	228	424	HRFCPAARH/RSWSGLREMAVS ISMPRRIINSGRYCAICWYKRRS RCARNMLIFPVARSTPIPGPS
13859	44227	B	13939	128	1670	
13860	44228	A	13940	2	2367	

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13861	44229	A	13941	1	921	ELPASPAPCARTPQPLGGRWEA ARRKERVLCLFDVDGTLTPAR/ QGRTLKIGSSHRECHADTPEAE CGVCSSVTEVRAKWRSQTC*KP ECYASPLPP*KIDPEVAAFLQKL RSSYLPVGSQTWSHTLSSSCPLC DPEVIGRDTVPVSGSGSPGHAQ SPVFLGQTIQNHLGPGGARFEF RA/CSGSLWLPALPHH\RGTFIEF RNGNCVPSQGLAHSRSSELPSA PSPLQKEQAALLLALSAPPSRE* QSPPLPTGGMISFDVFPEGWDK QVRSSQCGEGLHLNIPPLPILCV QGGNDFEIFADPRTVGHS
13862	44230	A	13942	105	416	HSVLEVGPWWEVFGSWGQILH SLVSSHHVRHWLLPSPSAMTES SLTFQQKPSRCQHHASCKAYHS HQLLLVPTAGRLEDRSHH*IPC KHSPAPAWSLAAPVGN
13863	44231	A	13943	191	573	SSSGGYQQQLMRVIGTRDTAV NKASNVPSFGA*I/PSGRGQQAK LIALTRALTLAKELHVNIYADC KYAFHILHQHDVIWAERGFLTV QGSSSIINASLIKTLLKATLLPKE AGVIHYKGHQKASAPIA
13864	44232	A	13944	1	1065	
13865	44233	A	13945	321	537	
13866	44234	A	13946	346	1260	GGPARAEFSRHLGCKGHHPLPK DVASEVPAGSSTSVSSLIRTNGC PGLGSWEPP*FFSENKRLSTLMS FTLRDSKMFSPQSGLFLGCSAG EHSALRDPTASGLPGTASGVRP GR/RQRVGSDIEASTQGESKPCI LSI*TLPNA*LKTKTLTPLEIAAC TNPHSFSITARIGPAHLAAPRPV TPAGRGGARAPGR*CAAARPPP ASQ*VSGSPAPGGGPSYAPAAR TS*PSSLAPGAKRLRFSRVATFC CSFLAWSSSSNKAFCT*EHMSL LSSWISQSLEKVASCCPCEQFDS WKRLENILLFS
13867	44235	B	13947	1	459	

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13868	44236	A	13948	63	1263	VEAAKKAHHAACKEEKLAISR EANSKADPSLRPQAHTYALSPL FLTAMPSV*QGEHVIYTRVRHS DQVSESSGKPLSLPLLEPGIWAF EAAQVPPRWDQVRSLEPTTEW EAPGLKKRRVSQGLNGNEPLSC AWIFL*TKEKYEKSLKELDQGT PQYMENMEQVFEQCQQFEEKR LGWDKG*LAPAF*KSHVSL*FS YKAIYHDLEQSIRAADAVE/DR RGF\RK**TFGFSPSAPVA*EWS ADLNRTLSRREKKKATDCQDP HGPLQSWDPLKALSLHSTLNVP SNPAQSAQSQSSYNPRGPHTLC RPVLRALWPPLSCSVSSYEKTQ SYPTDWSDDESNNPFSSTDANG DSNPFDDDATSGTEVLCSPPSV SYLSWRRLPLCLAGDELTKME DEDEQGWCK
13869	44237	A	13949	2	485	AAAFGTRLSRRGRGCGVTGSG GGRRRVPAPRRPRSPLQPPHQ/P PRRPSRRTPGCGSRGA\PSRGRR LVPPPPEPPRAAQQRARH\HRTS \RPAARQPPRRPPAQPRSCPRRV RPTPAWSPPGRRGPRRSRRRRR RGGRARARRPRRRGQVPRPQS ATGAGHAR
13870	44238	A	13950	1	207	
13871	44239	B	13951	1	5297	
13872	44240	B	13952	1206	1360	
13873	44241	A	13953	46	369	NEGKNAKGSQRERSGYPQREA HQTNSGSLGRNPTSQKRVGANI QHS*RKEFSTQHFISSQTKLHK* RRNKILYRQANAERFCHHQEGS TKHGKEQPVPAAAKSCQNVK
13874	44242	A	13954	476	868	KYDCCISSTFCRALVHFSRTTFQ VNSPLSPNISAFGYMPLKYSIYF LHHLRPNIL*AASYFLKYKGTL KLPALRGCLS*STRCWCKIHICI *ND/ECLQFLGPWFENEFCFLPS TSQFVEFVLDILVLQNEP

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13875	44243	A	13955	1770	3003	PANIIMTGS\NSHITILTLNVNG\ LNAPI*RHRPAIA/S/WLKSQDPS VV\CIQETHLTCRDTHRLEIKG WRNIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMAK GSIQEEELTILNIYAPNTGAPRFI KQVLSDLQRDLDAHTIIMGDFN TPLSTLDRSTRQKVNKDIQELD SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALL SKCKRTETITNCLSDHSAIKLEL RIKKLTQNHSATWKLNSLLLND YWVHNKMKAEIKMFFETNENK DTAYQNLWDTFKAVCRGKFIA LNAHKRKQERSKIDILTSQLKE LKKQEQTNSKATRRQEITKIRA ELKEIETQKTLQKKQPNKDPAM EKNNKTDRVLARLIKKKREKN EFSAHILYKFSKQNGS
13876	44244	A	13956	105	392	RSRKPRGNPKSHPEDTDPTKAP RKRQISSRGHRSHR*EPGPQSAA PGFREQRRRGQMG*IWYLTPTP PGGQRPSSAASPRGFPPTNNSSR LPAEPE
13877	44245	A	13957	55	403	SEGMSGKASEKQEAFACPRHLT RAVDGPS*SGLLGSRLPPSCSPG KEAPGGSELYLCLMRGLQTL*A RSGTGLR/PNPAEIR*EPGPQSA APGFREQRRRGQMG*IWYLTPT PPGGQ
13878	44246	A	13958	217	444	RSRKPRGNPKSHPEDTDPTKAP RKRQISSRGHQSHR*EPGPQSA APGFREQRRRGQMG*I*TPCRP ALPKSKPRPL
13879	44247	A	13959	309	670	PCPRASSQGLKATH\GQR*SSEP PGASFPGLQDGGRREPRRPD*D GPSTGLVRCLGHANVGDPCLK VFVFFKNLSPTYLRASAEQTLP LLLPHLHGLCLHQPLHLGFTAA WAQLTFWEASQ
13880	44248	C	13960	392	760	

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13881	44249	A	13961	24	915	HAGRHARGSLFPGARPSETRAH CVRTARPNCKEEDTPMVRGKN SGGEHCTWGPSLAAGG*GIGDP GGLPGT\PHPGLQLLLHGFAGP HMASLCCGVSSPAGVRQWPA* GSGNHQVKSWLGLPKNVS*AP SML*NPKMQRLMKAQPHGRCE VRRGRVCSALGP/IGMSGKASE KQEA*DEGHPHLHAPGT*QDQ VDGPS*SGLLGSRLPPSCSPGKE APGGSELYLCLMRGLQTL*ARS GTGLRANPAEIR*EPGPQSAAP GFREQRRRGQMG*IWYLTPTPP GGQRPSSAASPRGFPLV
13882	44250	A	13962	397	612	RPQHHTFCCDGRVMMARQKGI FYLTLFLILGTCTLFFAFE/CSFG *VELPDYGYFGSRGRTCFLGSL GLVLG
13883	44251	A	13963	125	1298	FQSWAQPLFLLSCNRKTHFGTR IPI\MSVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKGIF\ YLTLFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSM\AT L\LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGQRPPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHCPW VGNCVGKRNYRYFYLFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTVLEVLICFFTLWSV VGLTGFHTFLVALNQTTNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVLCGPLPPSVLDRRGILPLE ESGSRPPSTQETSSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPPEP PEPPQEAAEAEK
13884	44252	A	13964	44	647	DYSAQHGKASQKHVARLISSGT FQGATVSRPFQLSTSSSSFCSSSS SLSSSSSLSSSLLLSCSSESVFLS LSFFFCSEASFLPFCSRLYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFPFIAKLLAQDVAYSTKT LAAREIGAPGLLGDVDTVRELR GDRG*AKLPFQHLLPSCPFVRPP RAAHRLLDDPGDHGIGQV
13885	44253	B	13965	158	1075	

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13886	44254	A	13966	125	1297	FQSWAQPLFLLSCNRKTHFGTR IPI\MSVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKGIF\ YLTLFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSM\AT L\LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGQRPPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHCPW VGNCVGKRNYRYFYLFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTVLEVLICFFTLWSV VGLTGFHTFLVALNQTTNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVLCGPLPPSVLDRRGILPLE ESGSRPPSTQETSSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPPEP PEPPQEAAEAEK
13887	44255	A	13967	247	850	DYSAQHGKASQKHVARLISSGT FQGATVSRPFQLSTSSSSFCSSSS SLSSSSSLSSSLLLSCSSESVFLS LSFFFCSEASFLPFCSRLYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFPFIAKLLAQDVAYSTKT LAAREIGAPGLLGDVDTVRELR GDRG*AKLPFQHLLPSCPFVRPP RAAHRLLDDPGDHGIGQV
13888	44256	B	13968	298	380	
13889	44257	A	13969	48	252	QRAGSPHSPRSLSAPPLPELPLW RHLRSPSAHRCTVGAPFWDGQ G/LEPAPSAALAAFPRSRARDLQ LA
13890	44258	B	13970	1	447	
13891	44259	A	13971	236	559	MWLEPMQMGFLHMMEKMAA RTSAILD*GTLK*FHFTLTTSLK ALSSHTPIFPGTGELQLPVSPSV CLDQGMQLKPSTSSHLLKTVKP RMKRQSLLHMKQSFEPKIYL
13892	44260	A	13972	1	645	MKPQTLTVSVTAFKVAHLEFVP SDVQMCSEFLPSGGFVVSLASG VKLQTFAVSFTAHKSSVDPKNS EAQLASPSGFCTRAADGAACQS \LPCTCTPQPLGGRWDWALWS RGW/LLVEEAWAAQEPTEELRE RALALASPERGSHSAAVGQRAP QVPPKWEPRQRRRRERARAVR TASTLSPLNPPSKQDTLTAVGN LADDHSSYFLLDRGEEGALQL
13893	44261	A	13973	28	322	
13894	44262	A	13974	1760	4426	
13895	44263	B	13975	942	3414	

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13896	44264	A	13976	1	274	
13897	44265	A	13977	545	1150	RISGPGAVLLPVMPALWRLRHR MFSLTKK*HLPAHRSLAEGYLL YQPQLDTLKARLTQKYQELQV LFEAYQIKKTKLDRQSSSASLET LLALLQAEGAKIEEDTENMAEK FLDGELPLDSFIDVYQSKRKLA HMRRVKIEKLQEMVLKGQRL/S TRPWPRCPPGCPNWHLPPPFPT LPQSQWASCRCTSAHPPPTTPG AAGRL
13898	44266	B	13978	213	611	
13899	44267	A	13979	1	639	MEAVTVVPVGTEEGMGEEEQD SGTTTGCGLPSVEKMLATNPGK TPISLLQKYGTRIGK\TPVYYLL KAEG\HQPNFTFWV\VGNTSCT AQGPRKKVVKHKAAEVALRHL KVESMLEPAPEDSSSFSPLDSSL PEDFPVFTAAAAATPVSSVFLT RSTPMEKQPPLLP\QQSECIPVG ALQKLVVQKGWWLPEHTVT*E SRPDQHEELT*RVERFT
13900	44268	A	13980	361	894	AFFPMSTAGVCGNVEGEPETP WSLPLSQVPFSPNA/CPQGTLGR S*AGVAGAPGPGVPGRSPAA\GI PEPAARPGRPALSRLPGLGGAG ARSGAA*G*GSRPGG/PLPAADP VQSWGP*EAPSHP*PGT\SADSP PSGVSGATGDCLWGSGRAELF GFATTSSAAPFPGLPTFFFIPVSP
13901	44269	B	13981	1	3842	
13902	44270	A	13982	3	407	DAWAAARPGRSCALPPPGA/PE EPGHVPGAA*G*GSRPGGRFQL PDPVQSWGP*EAPSHP*PRNFPQ TRRHLGVKQHGCSQPSPHGSRA SQAHPGISGLF/GPHHPGPPLFIH GPRCCCAQATASNHLFACGTSS DP
13903	44271	C	13983	127	297	
13904	44272	A	13984	3	1920	

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13905	44273	A	13985	3	2271	GQGRRTAGGGGGGGAGVGAG AGAMEAERGPERRPAERSSPGQ TPEEGAQALAEFAALHVWSGE GIGVGSPAHTPADGNSGPQVFD AGEVFGIMQVEEVEEEEDEAAR EVRKQQPNPLAPPTSLCPMPTR QPHIVACARSIFLIDHAWTCRV EHARQQLQQVPGLLHRMANL MGIEFHGELPIWVPEGSSGGW MGEREVPYVLCLQTAEEKMPV WYIMDEFGSRIQHADVPSFATA \PLEEGPQPSVPSPPLMGTH/DL GTEEVTRDFAYGETDPLIRKCM LPLSSSHRGMETPCVHTSRASL PLQACELPSWSLLLINEPPRPAF PSLP*PHLYFRCVSF*AIPGLVLE SRLDTWEPGSPSSGSPHRVYTD VQQVASSLTHPALPVRASRHCR PPLELAHLPPPCRKLSQERPGVL LNQFPCENLLTVKDCLASIARR AGGPEGPPWWVLGWHHLGTQ APGAPQTALLLPRGEDNHWICK PWNLGLCVLGSPRGLCPGHQR ACTCVLQVVSKYIESPVLFLRE DVGKVKFDIRYIVGGTSLAGTR PLKNPYVSAHLSSRAFAQGRRG RGGPTWSGWLLARDPARV*DL LSSLVHSVERCPMQWALSEWQ LHHLSTWSSGLCGLAG**VFQM HRTPTPP**QAACSRPSGGLYR A*WALCLLPGAADPLLRGCSEQ AS*LRLPGPQAEIFRAFTELFQV
13906	44274	A	13986	1	600	MEEQRVQFTLWLHFSPHGICQF ESGRQEAKKLKGSGQPLKTGEI KTGIQKYRREALLQHYLGPASL AGRSKALTGTAERSCSSGSDSSI FTLCVNYNDSRAIMKTLAAIGT GFDCASKAEIQLVQILGMPPER FMYANSCKQMSQIKYTANNGV QMMIFGNEVKLMSVARTHSKQ P/CHISVKSGAMLKASRLLLE*A KEL
13907	44275	B	13987	1	2040	
13908	44276	A	13988	205	438	LYFLETGVFCVQVPAQQC*CSV PGSCRRPLEEAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLS

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13909	44277	A	13989	284	632	KTGVFCVPGPRPTVLM*CSFVG GKKNQYCLTGDAGCLQEKHSL GPAGV/HLEEAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSPFEP
13910	44278	A	13990	594	1003	VRKGHHAVRGLCGRAQFRCIS GDPGKRPLG/LPGGNAPKSGSL ARRPQPVRIPGSRPQ/RGSVSHL GPAGVH*R/RAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSPFEP
13911	44279	A	13991	1	1500	VRVAHIPIAAAEIAAIPDRGGHL SVGKRKLTFWFFYGVLPFRDV AIEFSPEEWECLDSAQQHLHRD AMLENYGNLVSLAAGDQSLPG DAAASAVCRQLSPSACGAILGL PPVNGVAPVRLRGEIVTYTWSQ LTGLALALSKDGADGLRRLTRP TRRAPPALLLAPQTAAERWRG KCDPRHGGGCALALQGWTLYP RESPSRESKELGGLWSFRADLD SRRQGFEEQWYPRPLRELRGRG GRRPEARRWEGGSPGPCRLLPL SAPELAPYRKLKVNGLRGAGL GDGETGGTGEGRGGRRRKRCC RTLSRDEGFNDICQDWWLRQF VGWVLYEQEVTLPEQWTQHLR TRVVLRIASAHSYATVVSAARS RQGRGIGGLIYTLGMPFFLSGW QVPEPHAAGYVRECLIAGPLLM P/TTCCPLLISPVSAVGEWGRHA RA*GADSSSLVQNTDFDFFNYA GLQR\SVLLYTTLTTYIDDITITT GVEHDSAEIPIFPEYLRVNTGN
13912	44280	A	13992	2	307	
13913	44281	A	13993	220	427	MSTLPFPSLQMFRRPPYGSPSTC RSQDNRSYSRVTEELQERRRW NSGDAN*DQSPEARRQRPRHIE EAA

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13914	44282	A	13994	1	2832	MGKYYTQGDKVLMPLAIQVH HAVCDGFHVGRMLNELQQYC DEWQGGAYPKGYFVQNTDFDF FNYAGLQRSVLLYTTPTTYIDDI TITTGVEHDSAAAPMVDSLIAR VGVMARGNAITLPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADA
13915	44283	A	13995	1	2934	MITFDFMSHIQVTLMQEVSFHG LGQLRPCGFAGYSPPPGCFHRL ASSVCSFSRCTVQAAVDLPFWG LEGTSPLLAASLGSAPVGTLCG GSDPTFPSWTALADVLHEEGHT PASNFCLRNLAGEASQSWRKE GLGTPRPTASSTEELQTLNEDSR LMTSPHNLEETRDCDTELPKKS LGWKEIRVYGQNKTLGFWLQA QLLICDGGNLRMFRLLPYGSPS TCRSQDNRGYGGVTEELMERK RWNSTDGFHIQGVLE
13916	44284	A	13996	68	425	SHILPGAPGAPAWWTRWPSTLP EPFPRGRGSPAGTSPISRPGLVQ SS*ASRGSDSRLPV/GPASCQAS GPGPDSRRPPPCTPA\GPHHGSL PSAGRVGASAAAAGPPSPAVPL PPAERPAP
13917	44285	A	13997	324	723	TAFSLNFQGGVEGEVWAGTRA ARGACAGERGLGGSRTRSGW/P GTAGPGQAGHGTCSLPCPSLPP AMGSCVSEPPRQAPPPAPWRLV PSTAQGLRSVGTQCGTGGSSAC GPC\GDPGF*THQSAPCQNGPIS SL
13918	44286	A	14000	39	383	

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13919	44287	A	14001	181	1446	EDLLQEAQALAEVTAQGKGLG QVRSLDLSLEACAGSPPLQVLD LQDREPRSLTSLPSSAANRGKL EKAQSNPCGHRRHQAAGLKLP LFSAQAPQGQPTPAPRFRAATR KPGTAQSHAPLWSPAMSFFPEL YFNVDNGYLEGLVRGLK/ALGE LSQADYLNLVQCETLEDLKLHL QSTDYGNFLANEASPLTVSV\ID DRLKE\KMV\VEFRPHEGTMPY EPTSPSFP*TSITLQFT*FDNVI/L WLIHRARLHQRSIAELVPQVAH PLG\SFEQMEAVNIAQTPAELY NAILVDTPLAAFFQDCISEQDLD EMNIEIIRNTLYKAYLESFYKFC TLLGGTTADAMCPI\LEFEA\NR RAFINT\INFFG\TKTVPKKDRCP AFFPH/CGAGFFPEGPAAMGFG LNNLLTGAKKRGPYNFPEVQL AFLRGDG
13920	44288	A	14002	1	1182	
13921	44289	A	14003	26	342	ARFLAGP*LPSRRTGLRDLQPA MPEPP\PTPWAPVRPEPPRRAPP PAPRRPVPSTGKEQTTQGLRSA GAGHRDWQAAPPAAPVRDPLG EASWAPESGGDVESLYV
13922	44290	A	14004	66	463	
13923	44291	A	14005	3	1446	
13924	44292	A	14006	221	852	NSFLMVGFFPFFSL/CAAFDTKT GLRVAVKKLSRPFLRPDGYYTE FNIYLLFNFYILTSSAV*VVLSH SVVIECLLSIRHCSRYFRKSSED KNFLRGSRLLCNFSLISRYLVTH LMGADLNNIV*RYR*YK**FFK MNSPFLPLPVGGELIMHHKVDP VCFVFFSLPVSKS*QFVCSSSAL *ILDFGLARHTDDEMTAKGQPE CFVRWACAS
13925	44293	A	14007	55	784	RHIQDPASQRLTWNKSPKSVLV IKKMRDASLLQPFKELCTHLME ARGAGGGHDARSLTTAPVSRE PPCRRVGSAGGMSRLALCFQEN MIVYVEKKVLEDPAIASDESFG AVKKKFCTFREDYDDISNQIDFI ICLGGDGTLLYASSLF/QGNAA VVLRSRLKVRVVKELRGKKTA VHNGLGEKGSQAAGLDMDVG KQAMQYQVLNEVVIDRGPSSY LSNVDVYLDGHLITTVQGDGVI VSTPTG

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13926	44294	A	14008	155	1592	PESRHQCFSDRSANFLTMEMEQ EKMTMNKELSPDAAAYCCSAC H\GDETWSYNHPIRGRAKSRSL SASPALGSTKEIRRTRSLHGPCP VTTFGPKACVLQNPQT\IMHIQD PASQRLHVEQRPPRTVLVIKKM RDASLLQPFKELCTHLMEENMI VYVEKKVLEDPAIASDE\SFGA VKKKFCTFREDYDDISNQIDFII CLGVDGTLLYASSLFPGQPSPP VMAFHLGSLGFL\TPISFENFQS QVTQVIEGNASCCSSGSRLKGQ GW*RSLRGKKTA\VHNGLGEK G\SQACRPGTMDVGKA/QAMQ VPRS*NEV\VIDRGPSSYLSNVD VYLDGHLITTVQGDGKARSTV LGP*ASLGRE*RLRLSLSGVIVS TPTGSTAYAAAAGASMIHPNVP AIMITPISRSVLPTAGGPHLSLL DPQIMLSPEARNAGGGPFWKP WLRLLLSRPSISITTSCYPLPSIC VRDPVSDWFESLAQCLHWN
13927	44295	A	14009	327	466	
13928	44296	A	14010	2	196	
13929	44297	A	14011	923	1776	WRKCGCETAGSASATRAAATE KMEAPRNKMCRDQENSAWRN AVPGP*E*RQPEEFPRTTSILAEP TVLSRRKCRPSEKRGSATEKFG ATSAVTENPPLGAAGERANKTL GAATVTPTLGPRPRMEKGGTR CPSTL*PSVQERQPESPSGNHPE TQKIEFAGRRVTFQHRWATTLR TRISGTGASPRDRSAFFGFPWC G/AAQPSDEESTPATQEEAQAQ AGVAAAASSEEPGHCAPRPPHA PRSALFEDWSREPERSDDGDLS ECRRPATEPWRPPGSAWRLPCA A
13930	44298	A	14012	568	1223	SARGLLPGSGPLSHAGPQLQVE WFGCLPPPDSTLELVVCGTVAI SRVRMSAVCVLRTWS\RNAG\Q LI\CFTVFQPCSNVHVL/KGPNY VCFFG\YPSF\KYSHP\HNFLKTI NAVCGQ\LVQFRFPDTEEGIRK VTV/KCYVKEGDTVSQFDNIGK VQSDKASVT\IASPYDGVI/RKL* HSLDDIAYVGKPLVNIETEALK GTVNLFYQIDYCPPFVIGSQLK

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13931	44299	A	14013	5	296	LFSRVPSKGPPRYHHTSSRG*TR AD*LISS\GNS*AHCIPSGLQGM LNLLPTPRAPVRPEPPRRAPPPA PRRPVPFDHPRACGTGRQLHLQ PRCGIH
13932	44300	A	14014	1	376	MQAVLLTVLQKHNQSVIYWY MKYIYYEGLVIMDDYDYVIMD YMTMETEKSHDLQAGGPGKPV VQFQFKPKILQASRGNGVKSWS KSKGLRTRCANVQGQENREGP AKHSPFLCLFVLFGSSTGRMIPN HTGDTSKVIAGTEERGVPKKVT LKFDACAAIDRPWAHQLDCTY HFKGSNDEHDSRLHTNAG*L*L C/RLWIT*LWRLRNPMICRLEA QESQWYSFSSSPKSCKPVEAMA LSPGPSPKA*EPGVLMSKGRKI GRAQLSIHLSSAFLFFSAPQQVE
13933	44301	A	14015	1638	2289	VEKKKKPMSAPALRLPDLTKLF TLYVSETKKMAVRVLTQTVGP WPRPVAL\LSKQLDEVSKRWPP CPKSLVAIALLAQEADKLTLRQ NLNIKSPCAVVILINTKGHH*LM NARLARYQSLLCEHPRITLGSL QHLNPATFLPVSESPVKHNCVE VLDSVYSYVGPNHRDHPLNISR LGAVTWMGSSFHQPLQSDTLK KTTSPGSSHTRKLTGPRTAEA
13934	44302	A	14016	1	675	MAPPLRPLARLRPPGMLLRALL LLLLLSPLPGLREGIGELITPIGT SLPDLDPARRRWEGGIGRVGSE VADLCPGKEGGKVPEAEKEGV WCFSELSFVKEPQDVTVTRKDP VVLDCQAHGEVPIKVTWLKNG AKMSENKRIEVLSNGSLYISEV EGRRGEQSDEGFYQCLAMNK\F *AILNQKAHLALSRIGST*RRRP DRP*EDEAFVMTTHCFQDLLTS
13935	44303	C	14017	18	329	
13936	44304	A	14018	391	895	WASSDTPTGFTQRWRPDWAGG GGGEERGDGTGVVWEGEKVY RFRRVTGGSSFPSPAVLVRAPN TGMPKLTYIQT*GPLGERGKEP VPPN\PTLPQTFGGLLNASVVRK TEIPSPSPPPVCYLRASAERQ/PA GGSPQAKWRRAASSPPPLPPVH LPPPPPPPRPPPPPPP
13937	44305	B	14019	1	1110	

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13938	44306	A	14020	282	710	YPEPQGWRVAHTVQYPIHIQPL KPGPRGR*SIMDIQVPPKEGGV LILKN\SSRLLNSWTQGCLQISA FSPTSSTLPGTPWSNVGPYKIAP ITSFGE\PFIRVIWKQLPSWISIIQ V/SHKQ*QIHRSVDIGWSPGQEC GPKGCFV
13939	44307	A	14021	1	1416	MIILIDAEKAFDKIQQPFMLKTL SKLGTDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILP\R DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFHKWC WENWLAVCRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLKSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL
13940	44308	A	14022	1	3450	
13941	44309	B	14023	1	3171	

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13942	44310	A	14024	1	2433	MRTKTQHTRISGTHSKPVCRGK FIALNAHKRKQEKSKIDTLTSQ LKELEKQEQTHSKASRRQEITKI RAELKEIDTQKTLQKINESRSW FFERINKIDRPLARLIKKKREKN QTDTIKNCKGDITTDPTEIQTTI REYYKHLYANKLENLEEMDKF LNTYTLPRLNQEEVESLNRPITG AEIVAIISSLPTKESRTGWIHSRI LPEVQGGTEKEGILPNSFYEASII LIPKPGRDATKKENFRPISLMNI DAKILNKILAKRIQQHIKKLIHH DQVGFIPGMQGWFNIRKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQRFLLKTLNKLGIDGTYF KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSGYKINVQKSQAF LYTNNTQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKDDTNKWKNIPCSWVG RINIVKMAILPKNWKKTTLKFI WNQKRAHITKSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHTY NYLIFDKPEKNKQWGKDSLFN KWCWENWLAICRKLKLDPFLT PYTKINSKWIKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLKSFC
13943	44311	A	14025	1	1023	MGAIYDKPTANIILNGQKLEAF PLKTGIRQGCPLSLLLFNIVLEV LARAIRQEKEIKVIQVGKEEVK LSLFADDMIVYLEDPIISAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKE\KEDTNKWKNIPCSWVG RINIVKMAILP/KAICRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMDKDFTSK TPKAMATKAKIDKWDIIKLKSF CTAKETTIRVNRQPTEWEKIFAI YSSDKGLISRIYNELKQIYKKKS NNPIKKWAKDM/NRHFSKEDIY AAKRHM
13944	44312	B	14026	1	2206	
13945	44313	A	14027	1	1689	

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13946	44314	A	14028	1	2523	MKQFLLYLDESNALGKKFIIQDI DDTHVFVIAELVNVLQERCHTR LGYTEFLVAWRVTFGLCVEAV TLHLKYQILIRGLLEMMSFSDA DILKQLPVTVPGLFPASLSPSSL LGNSPPSWLRHNSESKVSAVSS PSATKTLSTGIGKLDPGHKEMA EESELLKNKMQAPPLSRCPESQ KCQHQLRLHHWKPSVRHQVKR RSPAVLRSAMPPADCPAVLEAT TATHPEKGTALSKHLPSSDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKEQGKGDLKKKKK GKLPKNYDPKLTPDPERWLPM QECSFYQGRKKGKKKDQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIPPRH QRPAGAPATKKKQQQKKKKG GKGFPVLREITVVKVDTLVVFQ ILEERLSVFHIQYDTSYPFSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQQPFMLKTLNKFGVDGTY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNTV LEVLARAIRQEKEIKGIQLGKEE VKLSLFAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTESQIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL
13947	44315	A	14029	1	2868	
13948	44316	A	14030	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
13949	44317	A	14031	2	3419	

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13950	44318	A	14032	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD
13951	44319	A	14033	845	1616	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFFIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATKA/KKS FCTAKETTIRVNRQPTEWEKIF AIYPSDKGLIS

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13952	44320	A	14034	707	2878	TLMQKSSIKYWQNESSSTSKSL STMIKWASSLGCKAWFNIRKSI KVIQHINRAKDKNHMIISIDAEK AFDKIQQPFMLKTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLIRNFSKVSGYKINVQES\Q AFLYTINRQTESQIMSALPLTIA SKRIKYLGIQLTRDVKDLFKEN YKP\LLKEIKEDTNK\WKNIPCS G\EGRINIVKMAILPKNWKKTTF \RFIWNHKRACIAKTILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNIDIDQWNRTEPSKIIPRI YNNLIFDKPDKNKKWGKYSLF NKWCLENWLAICRKLKLDPFL TSYTKINSRWIKDLNVRPKTIKT LEGNLGNTIQDIGMGKDFMSKT PKAMATKAKIDKWDLNNLKSF CTAKETTIRVNMQPTEWEKIFA IYPSDKGLISRIYNELKQIYKKK TT\NPIKKWAKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN RCWRGCGEIGTLLHCWLDCKL VQPLWKSVW*FLRNLELEIPFD PAIPLLGIYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTII DWIKKMWHIYTMEYYAAIKND EFVSFVGTWMKLEIIILSKLSQE
13953	44321	A	14035	869	3869	RHKKPFKKLTNPGAEIQTTIREY YKHLYANKLENLEEMDKFLNT YTLPRLNQEEVESLNRTITGSEI EARINSLPTKKSPGPDGFTAEFY QRYKEEMVPFLLKLFQSIEKEGI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANQI QQHIKNLIHHDQVGFIPGMQG WFNICKSVNVIQHINRTKDKNH MIFSIDAEKAFDKFQQLFMLKT LNKLGIDGMYLKIIRAIYDKLT ANIILNGQ
13954	44322	A	14036	2	99	

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13955	44323	A	14037	1	914	TVTVIHTVARVGNLDIQIQRKS ELFLSLVVCEAIKNEMNVMLKS SPVDLVTATDQKVEKMLISSIK EKYPSHSFIGEESVAAGEKSILT DNPTWIIDPIDGTTNFVHRFPFV AVSIGFAVNKKKKVDETYLGL VKETCFPLQIEFGVVYSCVEGK MYTARKGKGAFCNGQKLQVS QQEDITKSLLVTELGSSRTPETV RMVLSNMEKLFCIPVHG\IRSVG TAAVNMCLVATG\GA\DAYYE MGIHCW\DVAGAGIIVTEAGGV LMDVTGGPFDLMSRRVIAANN RILAERIAKEIQVIPLQRDDED
13956	44324	B	14038	91	1959	
13957	44325	A	14039	28	152	LPSPSSKDTDS/AASCCAPRGRA KGSVSNSRLSFPPSSVPLP
13958	44326	A	14040	35	879	GSQCSSPPPASRCGSCSSAPSRH CPCRDFEPAVAGLARTPVLTTK TNPSPPARTGLNAPSMGTSLI/P ALCCFPLYQGSTELQCKAP**LP SPSSKDTDS/AASCCAPYFLVLL KVLSSVDNSSIWCSAGPPAQS/S SLYTIPMSSMSAKNCSVLRSGT WASFTCS*GSQRVSLGTPEALG TEDHTSRSLGHSHVCHVDLSPA TASCSFQTASSEVSPPATASCSF QTASSEVSPPATASCSFQTASSE VSPAATASCSFTFSFFFVCALWF GICPSCSAAVLST
13959	44327	A	14041	3	159	EHQCENPQ*NTGTPNPAAHQK AYPP*SSGLHPWDNQRQKPHD YLNRCRKGL
13960	44328	A	14042	54	245	GGGGGEAEDRLREPETEKALSS SL/RRAPDQC/RALIMQLFQAHC FFLST/QATAALQAHYAHIFPSK
13961	44329	A	14043	903	1205	WDVSQNNKSYL*QTHSQYHTE WAKTGSIPFENWHKTGMPSLT TPIQHSVGSSGQGNQTNREPNH E*TPIHNCFKENKIPRNPTYKGC EGPLQGELQTTAQ
13962	44330	B	14044	1	339	
13963	44331	B	14045	1	1547	

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13964	44332	A	14046	807	1440	NTGKPNPAAHRKAYPPRSSRLH P*DLQQTPTDLQLSDLTPGRKT NKQKGIASPSTKRTSTPKPHLQ ANAQRFCHHQACVTRVPKGST KHGKEQLVPATAKTCQIVKNIN AMKKLHQLTEIQITIREYHKHL YANKLKNLEEMDKFLDTYTLP RLKQEEVESLNRPIMGSEIEAIIN SLPTKKSPGPDGFTAKFYERYK EELVSFLLKLFQSIEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLKNIDAKILNKILANRIRQPIEK LIHHDQVGFIPEMKGWFKKCKS INVIHHINQTNDKNHMIISIDAE KAFDKTQQPFMLKTLNKLGTIR QKKEIKGIQLGKEEVKLSLFAD DMIVYLENSIVSAQNLLKLISNF SKVSRYKINLQKSQAFLYTNNR HMESQITSELPFTIDTKRIKYLGI QFTRDVKDLFKENYKLLLNEIK EDTNKWKNIPCSWIEESIS
13965	44333	A	14047	603	764	LPLFLIEYPLFLSLA*LPWPKLPT LC*IGVVREGIPVLCCFSKGMLP VFAHSV
13966	44334	A	14048	1566	1865	MQSIRKTIGIHAKYDKACRNGE DICLRETNSAADTQAKRV*SGP PANSNRPAAEGPDC*KEN*QTE RTSTPKPHLYVTIIKDQRGTQLL TNNGTKLDRE
13967	44335	B	14049	1	1932	
13968	44336	A	14050	711	1575	TRKFRRNG*IP*HIHPPKTKSGR SRI\FNRPITGSEIEAIINSLPTKKS PGPDGFTAEFYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPGMQGWFNIRKSI NVIQHVNRTRDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDG MYLKIIRAMYDKPTANIILNGQ RLEAFPLKTGTRQGCPLSPLLFN IVLEVLARAIGQEKEIKGIQLGK EEVKLSLSADDMIVYLEKPIISA QNLFKLISNFSKVSDTKSMYKN HKHSYTPITDKQRAKS

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13969	44337	A	14051	1	1579	MQGWFNVRKSLNIIHHINRNND KNHIIISIDAEKAFDKIQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRQ GCPLLPLLFNIMLEVLARAIRQE KEMKGIQLGKEEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKINVQKSQAFLYIINRQTESQ IMSELRFTIATKRIKYLGIHLTR DVKDLFNENYKPLLNEIKEDTN KWKNIPCSWTGSINIVKTAILPK VIYRFNAIPIKLQLTFFTELEKTA LKFMWIQGYSNQNSMVLTLLV IPRKMRSAVELQQTSTDLQLRD LTVRKKTNKRKATASTSQKGH LHQNPICRSPTSKTKEVGFRRSV ITNFSELKEDVRTYHKEAKNLE NRLDEWLTRINSVEKTLNDLKE LKTMARDLHDACTSFNRRFDQ VEERVTVTEDQINEINDGENGT KLENTPQDIIQENFPNLA\SRPTF KFRKYREHYKDTPREEQPQDT* LSDSPRLK*RKKC*RQPERKVE LPTKGSPSD
13970	44338	A	14052	50	1105	TRKSRRNG*IPGHIYPPKTK\QE EGESLNRPITGSEIEAIINNLPTK KSPGPDGFTAKFYQSTNNKNH MIISIDAEKAFHKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLPFNIVLEVLARAIRQEKEIN CIQLHNEEVKLSPFADDMIAYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTINRQTESQI MSELPFTIATKRIKYLGIQLTRD VKYLFKENYKPLLNEIKEDTNK WKYIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTLSSQNWKKT TLKFIWNQKRARIAKSILSKKN KAGSIMLPDFKL
13971	44339	A	14053	1	764	MQGWFNVRKSLNIIHHINRNND KNHIIISIDAEKAFDKIQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRQ GCPLLPLLFNIMLEVLARAIRQE KEMKGIQLGKEEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKI*FPLFLIEYPSFLSLA*LPW PALPTLC

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13972	44340	A	14054	1	344	MGINQRRKAENSKNQSASSPTK DCSSSPAKEQSWTENDFEELTE VGFRRQANAERFCHHQVCPKR APEESTKHGKKQ/RSISHCKNM PNCKDHRCYEETASTDSLAETQ QQKREF
13973	44341	A	14055	301	370	DDGVF*IDNHVICKQRQFDFLFS
13974	44342	A	14056	1	1418	MVREGFPEEVTFELKNELEISK GQQMGKNIPDTGASSAKALGE RELGTLDKMKNSPSDGSKKDIR THRKEAKNLEKRLDEWLTRINS VEKTLNDLMQLKTMARELHDA CTSFNSQFDQVEERINKIDVRLA RLIKKKREKNQIDAIKNDKGDIS TDPTEIQTTIREYYKHLYANKL ENLEEMDKFLDTYTLPRLNQEE FESLNRPIIGSEIEAVSNSLPTKK SPGPDGFTAEFYQRYKEELVPF LLKLFQSIEKEGILPNAFYEASII LIPKPGRDTTKKENFRPVSLMNI DAKILNKILANRIQQHIKKFIHH DQVSFIPRMQGWFNICKSINIIH HINRTNDKNHMIISIDAEKAFDR IQQPFMLNTLNKLGIDGMYLKII RTIYDKPTANIILNGQKLEAFPL KTGTRQGCPLS/ATPVQHSVGS SDQGSQARERNKGYSIRK*GSQ IVSVCR*HDCIFRKPHRLSPKSP
13975	44343	A	14057	1240	1596	CYSFLFVRCPSDSQVPQLQVC/C EFAGGPLQTVFAWVSPAEVVE MFLQG*RKPFYMSY/TSFEMAL MKVWTMVRTSASPVGDVFGR GWSPFPTSTVGALTVFGVSPGS CRSSPLPSERLWV
13976	44344	A	14058	507	971	PANQKKSRTRRIHSQILPEAQR GAGTIPSETIPINGKRGNPPKLIL *SQHHPDTKAWQRHNRKREFY TDIPDDH*CKNPQ*NTGKPNPA AHQKAYPPRSSWLHLWDARLV QRTQISKRNSSYKQNQRQKPHD YLSRCRKGLQQNSAALHAKNS
13977	44345	A	14059	561	758	
13978	44346	A	14060	2364	2663	DGQLTLVSILNHYSLAQSCEY* DGECFCLHCSASPFL*EGAQST ACTAPPECFASDLGAV*LPQHS WCSTLLLEGAPWPGTLGTAPQF QHRKLGTNLAG

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13979	44347	A	14061	1	64	MPIGKVGEYYIKGTLRATKESE QQSSALELSSDRVYLNEKEPGD QPWNAAFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSLTLIIQGCKQEGFYS PSMRPRVVPKRGSAPKVRAEEN AALPSRCPPGPLPVAQP/TGPAD GGSCEQCPSCGCGCCQLPPPLP WFPR*TPCDKRV
13980	44348	A	14062	1	774	MFVWSNVEGHSVAMFPWYSIP FLNPPCSHTRPSNLPVTQWPPTR ENNLPSWQLLLTSIHQAQFLSA LHKEQGSSSEKDGRSPNKWDK DHIRCPMS\AVMIFSKRHQAL/V RAHQGHPNQDNWTVSQMLSK WWYTLGPNERQKYHELAFQAT AALQAHYVHIFPSKGRWELLH GSQRLDWGRCQLKLLGQQGQ DVLHTNLGKEENSSCWGYKME CEEGFGPQGGDCGLGGVHAPL LSPEGLDSEQNTLIMGDIFHCA KKLP
13981	44349	B	14063	1	753	
13982	44350	A	14064	2	1457	YPRRRPSRAGVLAGPAVLAGPP SSPGRRPRRAAFFAEPPFSARRS PRRAAVLAVPPSSPRRRPRRAA VLAAPRVLAAPPSSPRRRPR\PP PSSPRRRPRRAAAGSLPGAELP QSSRLAAHL\AAD*PDS*IAAGA VPRGWEGLTIMAEGKEEQVTF YVDGSRQRAYAEKPPVVKTIRS CTV/SGHSRHNSSSGM*/SSPNSP /IPFQFTFQIPSLLQAALWLCL*V TWHFFVR*PVLSSRHCFSPGGLF SLSLQSAGCPAGSLQAEFVALP PGGQSRLHRTRAS*VPGAFQEK CPLERVWPFHPSKQHPRNGLAF PLP*APQRTQPAEDTLPRHPEM GLILSQGTAG/PGRECQATQLPA QHSHAEVLHFGGAMSGQLSLV GPQDSKRTARLTDSQHLGSPT* QPPGLTEGTSLEQG**S*MGWM VGVIAGAPSGWSGSSGPSEGTP LFSSPA*LPWPELPTLC*IGVVR EGIPVLCQFSKGMLPVFAHSA
13983	44351	B	14065	72	1235	
13984	44352	B	14066	1	2715	

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13985	44353	A	14067	50	1304	TRKFRRNG*IP*HIHPPKTKSGR SRI\FNRPITGSEIEAIINSLPTKKS PGPDGFTAEFYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPGMQGWFNIRKSI NVIQHVNRTRDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDG MYLKIIRAMYDKPTANIILNGQ RLEAFPLKTGTRQGCPLSPLLFN IVLEVLARAIGQEKEIKGIQLGK EEVKLSLSADDMIVYLEKPIISA QNLFKLISNFSKLSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ATKRVKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKCKTVGLLS NISTHKSAVHALVEAGGIPSLIN LLVCDEPEVHSRCAVILYDIAQ CENKDVIAKY
13986	44354	A	14068	1	1155	MFVWRNVEGHSVAVFPWYSIP FLTPPCSHMRPSKLPVTQWPPT RENNLPSWQLLLMSVHQAQSL SALRKEQDSSSEKDGRSPNKW DKDHIWWPMS\AVIIFSKQHQA L/VRAHQGHPNQDNRTISQMLS EQWYTLGPNEMQKYDLAFQN VEARIRY/CHRPRKRARFLSHAS PPWRQLPAAGAEASGAWNLPA GGG*HDYNRCSVPVFRTEVSTR PRPSEICGLTQE*TLLSAKSQVG NTFGFAGHTISDTTTPCGLCTSK AAIEVPEADTLPHICSWHKGEE CGLRGPEPSSPPPRPSLAARVSA GRGALRRRRRPEVPP\SRAPRSA ATATPANEQRAVADVGQWAR ARGGRVRAAGRSGLLRVKMM KMKTVMIHFHLMKDEYIFSS
13987	44355	A	14069	1331	1584	SLQRKAARFASSSTVPRRPQGIL PIISFSNVPVGSRRLKAPLVFIGP G*ITLNRIPYLPHSAARDPFTWN TFSFLLPCEEVPST
13988	44356	B	14070	1	1248	
13989	44357	B	14071	1	459	

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13990	44358	A	14072	1	2156	MGKKQSRKTGNSKNQSASPPP KERSSSPAMEQSWMENDFDDL REEGFRQSNYSELKEEVRTHGK EVKNLEKKLDEWLTRITNAEKS LKDLMELKTTARELHDECTSLK RVSVTEDQMNEMKREEKFREK RIKRNEQSLQEIWDYVKRPNLH LIGVPESDRENGTKLENTLQDII QENFPNLVRQANIQIQEIQRTPQ RYSSRRATPRHIIVRFTKVEMK EKMLRAAREKGRVTHKGKPIR LTADLLAETLQARREWGPIFNI LKEKNFQPRISYPAKLSFIDRST RQKVNKDTQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHHTY SKIDHIVGSKALLSKCKRTEIIT NCLSDHSAIKLELRIKKLTRNHS TTWKLNNLLLNDYWVHNEMK AEIKMFFETNENKDKTYQNLW DTFKTVCRGKFIALNAHKRKQE RSKIDTLTSQLKGLEKQEQTHS KASRRQEITKIRAELKEIETQKT LQKINESRSWFFEKINKIDRPLA RLIKNKREENQIDAIKNDKGDIT TDPTEIQTAISEYYKHLYANKL ENLEEMDKFLDTYTLPRLNQEE VESLNRPITGSEIEAIINSLPTKK SPGPDGFM/RRILPEGQGGAGTI PSETVPINRKRGNPP*/PHFM/SA SIMLIPKPGRDTTKKENFRPISL MNIDAKI/RQ*NTGKPNPAAHQ KAYPP*SSGLHPWDARLVQLTQ

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13991	44359	A	14073	3	1794	AMLPMELGCGPLPEPLPVGCSR FSLFK*QTCISTVP/GYMVTAQS MSSTPPPPSPSTLPSSPSPPPPLPQ PLPPPPPSPPTLSSLSSPSPPRPPL VSPSTLPSPQPSSPQPLLPPSSSPP SLPSPPPPSPPLPSPSPSAIPSLPPP SPQPLPPPPPSSPPPSLPSPLLPPP PLSSSPSSPLSPSPPPPSPPPSLPPS PPPSPPPPPPPQPPSPPSSPLSSPP LSSSQPSLLPPSLSSLPLPSSPSPL LPLSLPLSISPP*LSLLSPLPPSPS LPPSSFQST*TIGQCFSL/VMWH VAPCTYLALAGNTLMAWPLMS ASSKASGGVSMFVWRNVEPCS VAVFSWYSVPFLTPPCSRVRPS NLPVTQWPPTRAKNLPSRQLLL TSVHQAQSLSALCKEQDSSSEK DGRSPNKWDKDHIWWPMSGG HDLQQAAPGPGRAHQGHPYQD NWTISQILSERWYTLGPNEMQK YHDLAFQHMAGEDIASDEEHM VIHEEEGVMVSLLMTALAPLTL ISSSRIFGKVYGPTPSSSYTYSD ASSSTLAPTSFLLGPGAFKAQES GEEAEDGLRELETEKALSSSL/R RALDQ/*LALIMQLFQAHCFFLS T
13992	44360	A	14074	1	2496	MLLSIDAEKAFDKIQQPFMLKT LNKLGHGYEQHHLHTTNDVDE EDLSDAASKGDDFALSEQSQD AHFLQPEAYGLGEGAETATGT AHQGNHVRVEECGRSLCGCVP LVLHPLPDPSLQPHEAQQPASH SVACNQRKQPAKLPAVAHERP PGGTGSVDPGRPPGATCPESPG PATPHTLGVVEPGKSSPPTMEE EPWAPQGSPCWTAQSLSALRK EQDSSSEKDGRSPNKWDKDHI WWPMS\ALMIFSKRHQAL/V
13993	44361	A	14075	4317	5099	KMFVFLCISAQLSLQCFRGSFHF IKIYDFSFQLFFLFLELPYLLLLN HFKMLELVLQQGHPNQDNWT VSQMLSKWWYTLGPNERQKY HELAFQVKVAH\CNKD*KKFSS EAKPTSQGLAG\GNKGSWEWS MSETGTATAPGVSSELLSVAAQ TLQSSDTK\SSFCGAEWGHP*GI GCDDVIADDGFSTTDTDLKFKE WVTD\ESGDNSGEEPEGNKGFG GKVFAPVIPSSFT/HCRPLLDPE/ PPGSPDPPAAFGKVYGPTLSSSY

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13994	44362	A	14076	1	637	MSRVGSCRWVCGLADFKNGAT DLCDKSLHNRELSAERPLNEQI AEAEEDKIKKTYPPENKPGQSN YSFVDNLNLLKAITEKEKIEKER QSIRSSPLDNKLNV/EKDVDFNQ EFGKLIDGY\DSTKEWDWVHKF QDIPNVLVGTAFNVDDGNGGF VVHWLNNKEFHFTSSTEVFMH QLRKLSDKQVDHENDDADRED EEHSQEDRERGLHMKLDH
13995	44363	A	14077	448	464	KKRA*GSVSQRFPAET*LAD*VI NTGSQEAKRREQR
13996	44364	A	14078	179	382	NTPNQRSVASNRFVKCTHQHS VKCTQSALCKMHQSAGFLKVD NHRED*KKGHSDRAKTEHGRG QIRE
13997	44365	A	14079	697	1654	PKPSVGRMGFLGTGTW\ILVLV LPIQAFPKPG\GSQ\DKSL\H**ED LSAERPFELNRLLEAEGRTRFK KTYPP\ENKPG\QSNYSFV\DNL NLL\RAITEKEKIEKERQSIRSSP LDNKLNVEDVDSTKNRKLIDD YDSTKSGLDHKFQENETADNSF SQEEEPVVAGEDLPPPSPQESD VQPVQPEEVSARDFLQRLDLQI KLSTQAAKKLKEESSSLERMRE ETSLSPTVPTKRWDTRILLIGAF YRVLIGAFYRVLMGAFYKPIAS YRALIGVFYRALMGAFYNPLV RQKSSPRPHSTQEVQLASPLTN TQITYYVIFTV
13998	44366	A	14080	72	1117	ILENHLSDRVAEGGPLQGLRLG VQGEAVPPGLVHQRGGLGPLD GELIGSVGQQVSDVEGAGSHR G*RHTGRTPAVSAGPAA*SATH TAPMWLAGW\YEPAQPGPVLV SPPTPFGQTRQASWCSA*ARCA GSWWH*HQTPGGA*RVAAPAP SWSRSCP*RPTRSPAAAPPAPSR PGRAVGLATGAGHPAQHGHGR AVPTGPRAAGAGSWSELCPPSS CAGTSRGR*AGTRR*AAPAGSG RPGPGAWAGPRCSRSTYAAAA CGRGGA*AGADSGPRSGTHAG HCGARCRSSTPLVPAAAGHLPP PGPGRTGDCPASSCPGPGLPHG CSLSGSWGEGWVSAARQAGLP WAVA
13999	44367	A	14081	2	269	
14000	44368	A	14082	1	591	
14001	44369	A	14083	2	477	

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14002	44370	B	14084	237	419	
14003	44371	A	14085	2	1220	LPPGFVMAAAAAARWNHVWVG TETGILKGVNLQRKQAANFTA GGQPRREEAVSALCWGTGGET QMLVGCADRTVKHFSTEDGIF QGSETLPG\GEGMFRGLAQTDG TLITCVDSGILRVWHDKDKDTS F*PTPGTESGPWGCVGCAKTQA HPHVVCHRLGKRMLLKIWDLQ GS\GNLCFKAKNVRNDWLDLR VPIWDQDIQFLPGSQKLVTCTG YHQVRVYDP\ASPQRRPVLETT YEEYPLTAMTLTPGGNSVIVGN THGQLAEIDLRQGRLLGCLKGL AGSVRGVAV\HPSKPLT*PPVRL DRVLRIHRIQNPRGLEHKVYLK VSIE/RALLLSGRDNLGG*APEP SKTQTRCP*EDTEDR*TLGDPW RQLPSGKLFGVWSSPKELSKRD GERRSGLGPPAPDAPVPTL
14004	44372	B	14086	96	592	
14005	44373	A	14087	102	612	HCAGSPHSPRSLSGTPLPGLPL WRHLRSPSAHRCTVGAPFWAG QDRSQLP*LAGRCGGRGPSGNP GCA\PACGPAGVPGGRGLGGPR TRSSQPALPAPGNEGLSTRASG CRGRTGSPSSASPPLGLSCLPAG QGWGP/GSPPCVSLPPTPWAPV RPEPPG*AAPPAPRRPVP
14006	44374	C	14088	1	636	
14007	44375	B	14089	31	612	
14008	44376	A	14090	234	504	SFYHLGAGE*PGKSRVPIPQFQS PWGPYCQGRARGGEVCHLQAV PPRGAGAARTLSGHPLGSPEQL PQPGPAAELPGGVVPRSTPPCP
14009	44377	B	14091	1	924	
14010	44378	A	14092	11	354	RLSTSPPDSGAQLASPSGSHTRA AGGAACQSRAVRS/PFPSPWVV DGTGCGGAGGGARWGGSGCT GAHGVGGR\PGMAG*GPEPCP EGRQLRPLAPVGCGQ*REP\G*K NSMGETTT
14011	44379	A	14093	147	513	GSASGVVRLSRWARGLAGFRS EAADLRGECYSS*GSASGVVRL SRWARGLAGFRSEAADLRGEC YSS*KQRGPKELRSPAGFT*WIP /LPGLQVELPASPAPCAPTPQPL SG*WD\GRRGAGGGARRGGSG RTGALGVG\GGSGMAGCRSRA LPPREGS

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14012	44380	A	14094	418	1026	WNPHQGCRWSCLPVPRHALAF LSPWVIDGTGRHGAGGGALWG GSGRTGAHGVGG\S*GMAGCR SRALPHGKAAKAR*EIERSASG/ TGTAGGPSTPSAATGPGAKSLI ARGQQGWPAAPSAGPAKPTPT GNSSWPASAAGSSGSCSRLS/SP HLPAS*GSGLQPWPAQKGAPTV QQQAEGLPIPRLPEEWISLPFLG HQGEHSGMA
14013	44381	A	14095	897	2111	PPLLQSSPNFFLICYLPWHNSHE NTHRTGRRGAGGGARRGGSGR TGAHGVGGRLRHGGLQVPSPA PWEGS*GPARNRAQRRYHCSCP GLQSGLPHYSGYHT*PDEKEKN GREGQKLER
14014	44382	A	14096	1304	1922	KLNIGVIYSSEIPDSGAQLASPS GSGTRAAGGAVCQSCALRSHSS ALGWSMG/PGRRGAGGGARW GGLGRTGAHGVGGRLRHGGLQ VPSPAPREGS*GSVRNPAQRRW AGTAGGPSTPSAATGPGAKSLI TRGQQGWPAAPSEGPAKPTPTR NSSWPASAARSPGSRSR/RLPPH LPAS*GSGLQPWPAHYFEFFLPI GQNAQTEVSY
14015	44383	A	14097	318	533	MVCFDGADCPWVVDGTGRRG AGGGAHRRGSGRTGAREAGGR LRHGGLQVPSPARREGS*GPAS PAGCLAHL
14016	44384	A	14098	346	957	ARYTLHIPTRLGSPAGFTQWIPH RGCRWSCLPVPRRALAFLSPW VVCSFPVDGTGRRGAGGGARR GGSGRTGAHGVGGR\PGMAGC RSRALPRGKAAKARREIERSAG G/TGTAAGPSTPSAAAGPGAKS PFARG/LAGPAAPSARPAKPTST RNSSWPASAARSPGSRSWKMS LYMKKSASGQSQAQWIAKMW KSPRFKPLWLTS
14017	44385	A	14099	124	663	SCLPVLRRALTFLSPWVVNGTG RRGVGGGARRGGSGRTGAHGV GGR\PGMAGCRSRALPRGKAA KARREIEHSAGG/TGTAGGPGT PSAATGPGAKSPIAPGQQGWLA ALGINGAGERLFMKVAFSLKTC SLSCSYLRLTLSRGGSVHVLRG NLTVCKPQPALLRVVFHHQRQ ADCGALPVP
14018	44386	C	14100	1	672	

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14019	44387	A	14101	3	1759	RPLRGWRRTRDARAPRRCRCG SHGARRCLRKTAATSRCGGAP GP\RSRPPSTGQAAEAGDW/PAG CNP*GGLRAADGPGSRPPRGSI GLLCGQGGQGGSSPWVVHGTG RCGAGGGAPWGGSGRTGAHG VGGRLRHGGLQVPSPAPQEGS* GSARNRAQPRWAGTAGGPSTP SAATGPGRDGEGG\ETGAHVSA LKGTPGTEWPAHGLVPYSIGDQ TCLIFKVTFKAVVLKCGPQTTS STSISCPGSAN/SPPSPAG*/GSSG CGSSSLCSAHSVQEDSQPQ*KR TGLQS\TYGRSGSSSNEPRYHSD LPTSRSKLRNEDTFFGRRKKLS EVQRTGQDPA*SHHTSSYTLPG L*TAEGKDRVENAA*KGSPNFQ RSGTFNPKGGARKTRQAWHPR APNCQAGTPPREGSSGPRTSLS AAFRIPQEVVNFLISGPITRAQR HGEPESPRGQTGSPPLGKTGSE GTDRKSTGADKKSTGDRQEVR EPTESPQGLDRKPTGMDRRSTG NRQKVRRQIGSPLGLNRKPNGT DKKSTRNRQEVRRRQSAGARQ ERAGSSTFLRLSALCGLLVDVN REQVAKQKWDLYSSRFTSGNR
14020	44388	A	14102	1879	2607	GKPSLSLHPGHKCGISRCNGNV SSRLRSPAGFTQWIPHRGCRWS CLPAPRCALALLSPWVVDGTG RHGAGGGARRGGSGRTGAHG VGGRLRHGGLQVPSPAPREGS* GPARNRAQRRWAGTAGGLSTP SAATGPGAKSPIARGQQGWPA APS\GGPPSPSPPGTPAGPQAPH AAPVPAR\PLPPHLPAS*GSGLQ PWPAQKGAPTVQGGG*RAPQM PPKWEPRQGRRIVAFTIEVGVL
14021	44389	A	14103	2	272	GHWGMVNSPCRASATVSRGSP LPGVLPTSPPSATSTCRMRCHPR RCPLPFRRLSPPSLTPP/PGKPPL LPRPHSMPGLGLPLGGLPVFHP

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14022	44390	A	14104	101	1815	QSARQLRPCPGAPSLAGVENRR KKTTNLTSLAAPDTQSTCGQSC GCLHSMGSSCMQHSYYTGFLR SLWPCRCHRSAFSGQRRSEEKD SKSVRERSGRSQNVPARPALTS PLTQSPGPLAPGAGSWSRSQLG TGTGVLWWQRESATGDFRTES ARSSDPSRRDWPGAKRKREEG AATVLWACATASTAIICQDNAI SPLKSGNSPSNHLWRPQGQLPP VLGLAQPKRWRPNRLTTSPSPS RMMARPVDPQRSPDPTFRSSTR HSGKLEPMEATAHLLRKQCPSR LNSPAWEASGLHWSSLDSPVG\ PCRP*GLRPSTHGAR\TFSGARP GLGGYSPPPEEAMPFEFDQPAQ RGCSQLLLQVPDLAPGGPGAA GVPGAPPEEPQALRPAKAGSRG GYSPPPEETMPFELDGEGFGDD SPPPGLSRVIAQVDGSSQFAAV AASSHQCLSHHIPMSPSVGRNG LLTKPPSTSRRGKLTKRDDMYY FVPFRSLNDMMHMLPFIEDSR WTHNLDINREQKTNPLAGPKG RPISRTQAAASTSNSKTESQIQE KTEEAPFSLRYININNRSMDPLN
14023	44391	A	14105	39	877	AGPGPPRPLPPRSSEGPPGASISL CSEVPGPSCQGRFRGGRDAMS MPWREEERSLLAGE*PS*GG*S GRGVSRKCS*PGPRGVPRPRPL RSRPRAASSE\DQNSPLDQSLHR TRKTIPSSGGSTAIMPRRGSSSE TFFSAPSKTWVLGIPGETFISGP AAFP\APGGPRAAPRPSPSLNSL *SGGNGGPGPPRLHFSSCGKGP PRPSNSRN\GGQSACQGGSHLV C*SHRGSLGEGHAYQGDPCSPG HPAKAPSRAHAQARRSAHAAS LTSGPCDASCQAW
14024	44392	A	14106	358	546	CFPSRIRLALSRAPKWPAKRSPS EPEMS/PPVWSPHPDPNNTAPPK EQPPSSPGRVGRHGNWSV
14025	44393	A	14107	22	549	DHCLCSVVRNKRDSVYPLPIPP CCKTSTISPP/LVDAVRP*DISVS KRVTSCAPLEPQPHPCLPTINAG R/TLARPQGAPTPNKEEGQAPG RATASGQAAPATTVLGDTTK/G PQGRHRGTSASAAGPAPFAVA DQLPPEDRAASAEGRK*AAAFP FCHRLVQDGGPPPPAAGVPGA GES

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14026	44394	A	14108	146	2616	LAAVGMASHCFRQRRQSQSPA\ GLRGAGSAYSPA\EGARSSHGQ/ PPWRGRRRGPGDPVRGAARCR RPRAAAQPARPAARPPARPRPA P*AACCE/VPSAANSVAPSAAM *SSAGRDGASSQRSRRPHAAPP RSSALPANGK/PPSPVTRAARTC GARSSNTGA*SAARPKHSAASS RHPPPAA/MPLPARHA/PGGTSG RPLPTPQGSAPTSSASPRGPATP PPAGPRAPPPSPRRAAAPRPPGR QLSPAPGTPAAGGGGPPFPALR *SGSVFGRQLVGDGERGRACG ARGSAAVPALRTFVVSPSTVVA GAACPLAVALPAPDPLPCSE*A PLRSG*VPQPASLFCSQFRPQA WQHP*LLRAPCPRLGAAVPCV WCHSRALDSATPRWM*G*RLP AVWL\PAFPSPPFNQAFVPPCQQ NCSLQNRQTLSASAKIGTEEWD IAIKIPENVEVTLELGNEQRLEE FGGLRRRQEDEGKFGTPTDWL NGCDQNADSNMDSEGQGEDG GCSFGGAGLRGSGWGDQTRET FLALKANLRWPFRSSAQSQTSQ EGAAGARSGLKGGKKNPLKLP KKQAKKMNKAFKQKQEKERK KHKELKAKASWKGLRPQVEFK NLAERRGEAAVPGCPVVAGHS WRLLSLARGCAKRARQLLFPSE KLLAALREGSTRGGGAASQPQ RKLRVCMRVLDSSVEDFHMDG
14027	44395	A	14109	1	885	MIISIDTEKALDKILHPFILKTLN KLGIDGTYLKIIRALYDKPTANI IMNEQKLEAFPLKSNTKQGCPF LPLLFNIVLEVLARAIKQEKEIK SIQIGREEVKLSLFADDMIVYLE NPIISAPNLLKLISNFSKVSGYKI NVQKSQAFLYTSNRQTEIQMM SELPFTIATKGIKYLGI\HPLTRD VKDLFKENSKPLL/KELEKTTLN FIWNQKRAHIAKTMLSKKNKA GGVMLPDFKLYYKAAVTKTA WLGDDQVFLIPRGHISDYHMG KNLGQYPAFQDRGPCGFPQCIV PLVYRD

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14028	44396	A	14110	453	891	LIHLSTDALRVSGWGTVRSFSS HEAIFQTIAWGETLDNTLLSRA EVPAAFHGALCPWFIETREWQ* LLQSILLVNIWLTRHVLHSPRSL KP*FYTT*VFVCSKLGQSGWGK VAGAKLQMNNISAKQLFKVQV LFKIESLMSSLST
14029	44397	A	14111	452	2922	KMGLAREWILRFLVLILQEIRS MRQKENKDIQDLNSALHQADL IDIYRTLHPKSTEYTFFSAPHCI/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKLTQ\NRS ATWKLNS/YLNDYWVHNEMK AEIKMFFETNENKDTTYQNLW DTFKAVCRGKFIALNAHKRKQ ERSKIDTLMSQLKELEKQEQTH SKVSRRPITG\SEIEAIINSFTNPK RVPGPDGFDEPNFYQRYKQEL VPFLLKLFQSIEKDGILPN*FYE ASIILIPKPGRGTTKK/EENFRPIS LMNIDAKILNKILANRIQQHIKK LLHHDQVGFIPGMQGWFNICKS INVIQHINRTSDKNHTIISIDAEK AFNKIQQLFMLKTLNKLGTNG MYLKIVRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIRQEKEIQGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINLQ KSQAFLYTNNRQTESQIMSELP FTTASKRIKYLGIQLTRDVKDLF KENYKPLLNEIKEDTNKWRNIP CSWVGRINIVKMAILPKVTYRF NAIPIKLPMTFFTELEKTILKFR WNQKRAHIAKTILSQKNKAGGI RLPDFKLFYKATVTKTARYWY ENRDIDQWNRTEPLEIMPHIYN HLIFDKPDKNKQWGKDSLFNK WCWENWLAICRKLKLDPFLTS
14030	44398	A	14112	3	3349	

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14031	44399	A	14113	294	1107	RRHRLENYIPRTAQSPHPRKAL ARSESKRDGGFKNNWSFDHEE ESEGDTDKEPGPLDAPPRP/ESG PRAPGKGL*RRSRSPGPSERGSA ARLTAEPEARNPAASTLLRRGP SSRRARRRCGPWIKKEAAWEE EDGGRQERRLGQDLRTRTLNK SKGGIDSRIISLGQHSHPTHAKL WLDQSLREMEVLKIIGALIMKK KVKEIQIKSRARSTPLHDQIGTT SPRERTIASKRHPYYITPKGIRY EQDTLSRTPITTIRSRQRPLGPLT ASPPPSFPTLAPPTQAIKPSLHLR EGKPTPTPGERSTRPHHPEPPRK EYALSSLYPPTYLLAPTSTDLG NAHPTQEPQFNVDATHPRQNR FIPVAGNSPKRSSQFPIVFAPKK NTTPPYLDFAAILGLHRRPPRSR FRTSYPPKEFRSSPPERTAPRN
14032	44400	A	14114	2	297	VQKSVLCSFQAGTMEGVEEKK VPAVPETLKKKRRNFADAIQFL QTVFLAF*YTLLKGRQ\VYWLV EE*HQFYKISYRKKMVQRIRQH PQSCTVQKSWWP
14033	44401	A	14115	3	754	GTMEGVEEKKKEVPAVPETLK KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRTEIRMARMARKAGNF YVPAEPKLAFVIRIRGINGVSPK VRKVLQLLRLRQIFN\GTF\VKL NKASINMLRIVEPYIA*EYPNLK SVNELIYKHGYGKINKK*VALT DNTLIARPLGKYGITCMEDL/IH EIYTVGKCFKEANNFLWPFKLS SALSGMK/KKTTHFVEGGDGG NRVDQINTLNRRMN
14034	44402	A	14116	1	388	

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14035	44403	A	14117	1	1145	MTRNYEWLLEAESSPQPIAFQK MEPQPYNSKELNSANNQCLLE KPKLRQRLKDKEYDQGHTAVQ CQSWVYVLTPDSFCQQLILLPS TENFHECSRSDTAGHLRTGHVA SNWLSEHSPQTMPAAMQWDK KMQNTSSWFPQKAPEKVKPMS KLWQTPSQNDTLYKAVKALTL SSPERNSINTNKKDVHTETSSK GHQHQRPKVDKSMKMRKNQH KKAENSQNQNASSPPRNHNSSP ARERNWSENEFDELTEVVFRR WVITNSSELKEHVLTQCKEAKN LEKRLEELLTRITGLEINQAEERI SETEDQLNEIKHEDKIREKRMK RNEQILQEIWAYVK\RPKLRLIG VPENDRENGNKLENTLQDTIQE NFPELAR*ANIQIQ
14036	44404	C	14118	291	551	
14037	44405	B	14119	1	1308	
14038	44406	A	14120	82	367	ITLSSPPHSFIGHKTPASGPPQKI PPQPSQ/CKQWGDPTPVEAC/CV SCPTQGFISPTRGGPPCKHESLV VPLVGTPRRNQPGGHIQHSQR WAPVLT
14039	44407	A	14121	999	2661	VHLTGCGGPGQPVPEPAPPRGL RSMRC/GP*GFSPGAEA*TEP/C HYGGRGFPCGPFSLGCLAT\NSP WLPGPRPPCSPWAGP\CGLCPLP AAAAERQPALSVPGASPSCRLL PLVVLCHGSHLNGGRVLLRPG GSPCGHCHNCAGARRGLGHVL QGGAQARQREQLQR
14040	44408	B	14122	164	1042	
14041	44409	B	14123	320	566	
14042	44410	B	14124	1539	1674	
14043	44411	A	14125	185	780	QKAKKGKLKRSKQNSFPGLKK TVPSQLVQYCPSF*ISWKPMVY QKVPA*PRPPRTPDHHPDPGPA PHPRQHHPPPRSPDAEP/SPTTPT RRRPPTQPPDPHPKRPPPHSKPH PPQQPPTPPTATPTEQQRHTAPP TPRPPTTHPPSTPKHPA\PHTAPP PTKNTKPPTPQRTTQDKGRQKK PRRQPHHSEPNKKSPKAHI
14044	44412	C	14126	1	1128	
14045	44413	A	14127	319	536	
14046	44414	C	14128	231	425	
14047	44415	B	14129	1	1431	
14048	44416	A	14130	75	393	
14049	44417	C	14131	174	371	

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14050	44418	A	14132	79	164	
14051	44419	A	14133	343	775	
14052	44420	A	14134	554	724	SEGPSKEPTHRRMKFSHHDDLI FLDLSN*QPPNSPEPHPPQSP*KP WPQNPSSRQM
14053	44421	A	14135	20	242	VSFLSMGSGHCIRSTRGSKMVS WSVIAKIQEI*CEEDERKMARES \LAESMSTYVMMNHTYDS*GK THILIMKK
14054	44422	A	14136	229	366	
14055	44423	A	14137	131	505	
14056	44424	A	14138	1	1317	AGCSCGSRAMAEEQGRERDSV PKPSVLFLHPDLGVGGAERLVL DAALALQARGCSVKIWTAHYD PGHCFAESRELPVRCAGDWLPR GLGWGGRGAAV\CAYVRMVFL ALYVLFLADEEFDVVVCDQVS ACIPVFRLARRRKKILF\YCHFA DLLLTKRDSFLKRLYRAPIDWI EEYTTGMADCILVNSQFTAAVF KETFKSLSH\KDPDVLYP\SLNV TSFDFSCS*KAGMT*SPRGKNS WLLSINRY\EREGKIWTLGTGK ALVQLRGRLTSQDWERVHLIV AGGYDERVLENVEHYQELKK MVQQSDLGQYVTFLRSFSDKQ KISLL/RQLARVCFYTPRQ*GTL GIVPLGRPCYMAVPQFICCLIRV GPFGSSI*PQCSQGFCVEPDPVH FSEAIEKFIREPSLKATMGLGWE EPE*REKFSPGSILQEQLYRYVY
14057	44425	A	14139	1	648	MESKEEQGGVADHQKATRGIP TPQPREVVSERATQRGNRAFST KLCNPKTNRKQQQQYQQQQK GRTKTLPKGQHPQRSKLDKLTE MRKHQQKNTKNPKGQSPCSPP NDCNVSPARVHNWTGDEMEEL TEVGFKKWVRKNCAELKEHVL TQCKEAKNLDKRLEELLTRKTS LERNINDLMELKT/RA*ELCKA YTSINS*IDQAEERISEFEDHLAE

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14058	44426	A	14140	1	1365	MPVKGGTKCIKYLLFGFNFIFW VSERDCRALLSGPTCSRAPDTG RGRECRQLALPAPGRHRAGRES ALRLPAGSKAGSRAGRDGRDG RIRVGVSGTLFGSTTGLFNQSL AETGFTPYTQKSNDFLVKSLKI WHTYFKNFHQEARLYIRTSPGS NWNWFCTLGIESPEQPGVYEG QRPRVVTKSFASLTLKRVGTVL LLAARINADVLYVLQLAGIAVL AIGLWLRFDSQTKSIFEQETNN NNSSFYTGVYILIGAGALMMLV GFLGCCGAVQESQCMLGLFFG FLLVIFAIEIAAAIWGYSHKDEV IKEVQEFYKDTYNKLKTKDEPQ RETLKAIHYAVCRLGKDTLLRF LRIVSAHRLNCCGLAGGVEQFI SDICPKKDVLETFTVKSCPDAIK EVFDNKFHIIGAVGIGIAVVMPS FRSNHPDPHVSSYLL\IFGMIFS MILCCAIRRNREMV
14059	44427	B	14141	98	1064	
14060	44428	A	14142	560	964	KRLPRILGIRGKPCCPDTSRAGR RVRGRAAAPCREAARGRGQRR FLPPTWRCETGAATMFPSPALT PTPFSVKDILNITVRPRS/LGQAA LTKRLSASL\SPQSCARCRRRWS CVILSAVRGN*YAGSRAHRDCT Q
14061	44429	C	14143	189	452	
14062	44430	A	14144	1	647	

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14063	44431	A	14145	890	2905	LRLSLKFPMSQWTPEYNELYTL KVDMKSEIPSDAPKTQESLKGI LLHPEPIGAAKSFPAGVEMINSK VGNEFSHLCDDSQKQEKEMNG NQQEQEKSLVVRKKRKSQQAG PSYVQNCVKENQGILGLRQHL GTPSDEDNDSSFSDCLSSPSSSL HFGDSDTVTSDEDKEVSVRHSQ TILNAKSRSHSARSHKWPRTET ESVSGLLMKRPCLHGSSLRRLP CRKRFVKNNSSQRTQKQKERIL MQRKKREVLARRKYALLPSSSS SSENDLSSESSSSSSTEGEEDLF VSASENHQNNPAVPSVTYGQP WSKNIKEKTLEINSSQALTAYE CLHSAHVINLISPFYHHFPSSQE RSYLSTLSTLSNKKTGSVWFTR SPKVTQFFPGGAITGTLSQRPER EILRPLALPGKGNTPPYFCSPSM GCTHCPTSPNEMNQGISEDTAA APVRDIYIKPPSPWDRAPGGRG GCGHSFSRLKSPYLRALKSAAD FPAQHSSSDKGQAASSSGSLTP VYPVWVTPPSRGRQTPHRGEL WLASDGCPSGRKLPEEGTGSNL CCSAASAGDTQANRDHNSSPA REQTWTENKFDKLTEAGLRRW VINSSELKEPVLTQCKEAKNLE KRLDESPTRITSSEKNINDLMEL KNTAQELHEEHTSINSQ/DQAE*
14064	44432	A	14146	1	737	LNRGEQRAVRYYSHMKLNMA EEEDYMSGFLH*CPRRYQTRIA NAKANPRSPSKR\EKQQEANLK NRQKSLKEEEQERRDIGLKNAL GCENKGFALLQKMGYKSGQAL GKSGKSGIGHEASLKRKAEEKL ESYRKKIHMKNQAEEKAAEQF RMRLKNKQDEMKLEGDLRRSQ RACQQLDVQKNIQVPREAWY WLRLEEETEEDEEEKEQDEDEY KSEDLSIKKTYLQIVQDQLLQI MTKIIPNKVET
14065	44433	A	14147	1	1860	
14066	44434	A	14148	1	1203	
14067	44435	B	14149	1	1119	
14068	44436	A	14150	1	1407	

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14069	44437	A	14151	1	1731	ERSSSPATEQSWMENDFDELRE EGFRRSNFSELKEKVRTHHKQD KNLEKRSWFFEKINKIDRPLAR LIKKKREKSQINAIKNDKGDITA DPTEIQTTITEYYKHLYANKLE NLEAMDKFLDTYTLPRINQEEV ESLNR/LNNRL*N*GNN**LTNQ K/NVQDQMD*QLNSTRGTRRS WY/RFLLKLFQSIEKERILPNSFY EGIILLIPKPGRDNTKKDNFKPIS LMNMDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIISTDA GKAFDKIQQPFMLKTLNKLGID GMNLKIIRAIYDKPTANIILNRQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKISVQ KSQAFLYTNNRQTESQIMSEIPF PIASKRIKYLGIQLTRDVKDLFK ENCKPLLKEIKENTNKWKNIPC SWIERINIVKMAILPKVIYSFNAI PIKHPMTFFTELEKTTLKFIWNQ KRARITKSILRQKNKAGGITLPE FKLYYKTTVTKIAWYG
14070	44438	B	14152	1	906	
14071	44439	A	14153	3	553	EHSSSPATEQSWMENDFDELRE EGFRRSNYSELKEEVRTHGKEV KNLEKKLDEWLTRITNAEKSLK DLMELKTTAREICDECTSLSSR CDQLPRPDGFTAEFYERYKEEM VPFLLKLFQSIEKE/VNPP*LTL* GQHHPDTKAWQRHNKKREF*T NIPDEH*CKNPQ*NTGKPNPAA HQKAYPP
14072	44440	A	14154	1	909	MKAEIKMFFETNENKDTTYQN LWDTFKAVCRGKFIAVNVHKR KQERSKIDTLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QNTLQKINASRSWFFERTNKID RPLARLIKKKREKNQIDAIKND KGDITTDPTEIQTTIREYYKHLY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGAEIEAIINSL PTKKSPGPDGFTAEFYQRYKEE LECSSSPAMEQSWTENDFDDLR EEGFRRSNFSELKEEVQTHRKE AKNLEKRLEKWLTRITNVEKS LNYLRELKTMARELC
14073	44441	A	14155	1	969	

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14074	44442	A	14156	377	687	LLEGKLTNRKDIHTKTPSV/SPP SSKTKEHSSSPAMEQSWMEND FHELREEGFRRSNFSKLKEEVR THRKEVENLEKRLDEWLTRITK VEKALNDLMELKTMARE
14075	44443	A	14157	1	711	
14076	44444	A	14158	1	831	
14077	44445	A	14159	1	744	
14078	44446	B	14160	1	1479	
14079	44447	A	14161	1	810	
14080	44448	A	14162	3	651	
14081	44449	A	14163	2	1067	
14082	44450	A	14164	2	2063	
14083	44451	A	14165	1328	1639	PTNAHETSGRYIAGSSEKRTSA RTCGGTSAAARPAGTSMQTRC RQPPPSS*HAVPRVAQSSDSGL KATHPQAYQPCGHTPTRLPQES NCIEHERGLGKKKKKKK
14084	44452	A	14166	1	620	MTLGYGQRGANKDLRTGFDPD LCTMDNFAEGDFTVADYALLE DCPHVDDCVFAAEFMSNDYVR VTQLYCDGVNDSFLIGGLLRIG CKIENERSSSPAMEQSWTENDF DELREEGFRRSNYSELKEEVR\T NGKEVRNFEKKLDEWITRITNA EKSLKDLMELKTTARELCDKC TNLSNRCDQLEERVSAMEDEM NEMKHEDKFREKE
14085	44453	A	14167	1	514	MGKKQNRKTENSKNQRTSSSP KERSSSPAAEQSWMENDFDEL REEGFRRSNFSELKEEVRTHGK EVKNLEKRLDKWLTRITNTQKS LKDLMELKTTARELHDECTSLT NQFDQLEERINNI\EDH*QD**R RKERRIK*MQ*KMIKGISPLIPQ KYKLPSENTINTSMQIN
14086	44454	A	14168	1	366	MDTFLQAERKDYMEAYELIEQ EEQGEREPVAVNNILSTEALMA NAKSTLMFYAVGFLWQPGGGR GHKAASNPGVTRDVVGSLSSLT FLRGERSSSPAMEQSWTDNDFD EL\REEGFR*SNFS
14087	44455	A	14169	1	1026	
14088	44456	A	14170	1	3906	

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14089	44457	A	14171	1643	2721	IKPTKMGKKQSRKTGNSEKQST SPPPKERSSSPAMEQSWMENDF DELTGAGFRRLVITDFSELKED VQTHHKEAKNLEKRLDKCRTN G*LEWMNG/ITRITNAEKSLKDL MELKTKARELHDECTSLRSRFD QLEERVSVMEDQKK\MNEMKR EGKFREKRVKRNEQSLQEIWD YVKRPNLRLIGVPESDGENGTK LENTLQDIIQENFPNLARQANV QIQEIQRTPQRYSSRRATPRHIIV RFTKVEMKEKMLRAAREKGQ VTLKGKHIRLTVDLSAETLQAR REWGPIFNILKEKNFQPRISYPG KLSFISEGEIKYFTDKQMLRDFV TTRPALKELLKEVLNMERNNR YQPLQNHAKM
14090	44458	A	14172	351	898	SGVTAPWRPNGTLLITAATASH PVLAIPAHLCSPRCPSFLTTVTC SGPQHHAARGRVPFHC/SECGK SFRYRSDLRRHF/ARHTALKPH ACPRCG/KGFKHSFNLANHLRS HTG/ERPYRCSACPKGFRDST/G LLHHQVKTITT*PD/CGGCLVSN IVGSYSRPPWPCTRGPRRPLGSP SPAPGSVCLC
14091	44459	A	14173	1	551	
14092	44460	A	14174	3031	3207	TIHGCWWDPLSSIF*PFWGRGFI SHKICQAQISFRVISGTVLSLDK LLIMFHKAIFASP
14093	44461	A	14175	3555	3957	ENGQKTWTGTSQRRYTGDRM AQIQNPDTKCW*ECKATGTRIH CWWECKMVQPLWKS\WQFLT KLSILLPYNLAIILLGNYPNALK MYAHTKGFTCMFIAASFIIAKT WKQPRRPSVGEW/INNL*LVQT MEYYSAL
14094	44462	A	14176	3	883	CQPYPRPRPRTGTHGSCQPPSQ GSAEP*G*CLPTLLRMALKAQP TKVNPRTLLDSDPDVC/S*AAHS RVLITSPSRAPWRLPSP*RRCPA GTCMPSTATSAR*CSQRPGSSW *T*TGSSLGSQACGPSSSTAPPSS SWSACTCGCAAAARCSCAASS TRSGPTCGSSPPASSCASSTPAP GTTPSSTLTSWASSPWSTPCPGS AGPSSWSSSSSATPSASASTRTL SPGSPAAP*PWPTALSRLTEQEA VWGAWGISHGNSWDKETKLV RLPHPCSKSPCFRPSLQPYRAHR AP

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14095	44463	A	14177	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL\GILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14096	44464	A	14178	2	1044	AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLLRLASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALSSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNG\GGLA GMGGIQNEKETMQSLRDRLAS YLDRVRGLETENWKLESKIQEH LNVTRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEGKQV

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14097	44465	A	14179	1	2040	MPVPQLPPPVSRLAATAAASVT EPGPNPEAVRSASAEPEVKEGF PSQNHSVGHSNLIPSGGSVAPSS GRSHYGYASEDGTCSKLRVRPR LAAAPAAPFAFVADLASCCQG LSFFEGILLVRGPYRRLRATVV RDLVAVRMAEEQEFTQLCKLP AQPSHPHCVNNTYRSAQHSQA LLRGLLALRDSGILFDVVLVVE GRHIEAHRILLAASCDYFSMSFT TRSTFSTNYWSLGSVLATTYGA RLVSSTARVYAGAGGSGSRISV SRSTSFQGGLESGGLAAGMAG GLAGMGGIQNEKETMQSLNDR LASYLDRVRSLETENRRLESKIR EHLEKKGPQVRDWSHYFKIIED LRAQIFANTVDNARIVLQIDNA RLAADDFRVKYETELAMRQSV ENDIHGLRKVIDDTNITRLQLET EIEALK*ELLFMKKTPEEEVKG LQAQIASSG\LTVEV\DAPKSQD LAKIMADIR\AQYDELARK\NRE ELDKYWSQQIEESTTVVTTQSA EVGAAET\TLTELRRTVQVFGD STWTSMRNLKA\NLENSL\GEV EARYAL\QMEQL\NGILLHLESQ LGQTPRTEAQRQAQE\YEALL\N IKVKL\EAEICHLTRPPSWKIGE DFNL\GDS\LDERNSMQTIQKTT TRRISWIGQSGVLRPIDTKVLEA LSQQEASGTLLGKQEANKKFQS
14098	44466	A	14180	275	550	
14099	44467	B	14181	729	909	

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14100	44468	A	14182	1	1415	MGTQCDLLAKSLEDCPVDEVE DAFQGLGKEDEEIEQFSDKTFG SGAIDDDWREAHECLAELEVK QPVAVIEQTGNGERDEMDLLD DHEENLAERLSKMVIENELEDP AIMRAVQTRPVLQPQPGSLNSSI WDGS/VSSEANPRTTACSGNAY SVCIRICFASEA/SPRVQKMIGTF LNEHYQGGQLHLSLAVLLLELS P*APHLNRWLYPASPNRFCVRS LSMFGP/QMPPRYPAPYGERMS PNQLCSVPNSSLLGHPFPPSVPP VLSPLQRAQLLGGAQLQPGRM SPSQFARVPGFVGSPLAAMNPK SQAPMFRPDTTHLHPQHRRLLH QRQQQNRSQHRNLNGAGDRGS HRSSHQDHLRKDP\YANLMLQ REKDWVSKIQMMQLQSTDPYL DDFYYQNYFEKLEKLSAAEEIQ GDGPKKERTKLITPQVAKLEHA YKPETIICQALCRALHINYLTKA FQQAFEVSASIITIYR
14101	44469	A	14183	204	560	QGYWRGCTSSGGDGGCRGCW SPGKRR*GLSRTASGPPAAVAS PGRPRSPPSARTG*S*PGA*ARP CSRTW/PPPRCPLRPPSAARASA SRV/APL/GEPAPANTNIYCAAL THRATKSSTREF

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14102	44470	A	14184	59	1695	DMPWWPVLPWIKDSSPSSLEM NPDNTSGLRQKSVEAEPCSLW MVHRYTPQSTGEACTMAKAA GPSSP\GSCPPRPLGADPWPMSR LSH*EC*KTGTTASGYRRHQET APPESSGSPVGLSAGLWLSWA WPVSPACLHPGPPLCP/GPPALG LGPRSPAAS/C/PPLPEAPPACSP FCP*GEISSSGPLEPVPQV*LPGD LSEPPLGTSPLGRAPGLCSLLRA P/RPGAACPPASPSRPAMLLS*E APRRPGPSGETSPSPSLAPSEASP G\PPR\HHNGRDSEGAGTRTPGA SGSSKG/LGGQPAPHGPGGR*G GGRYRGSAAGSVHSAPGGCSP HAPGCA/CDVRG/AKPSHFHSG CQSG*GHQTSGGCPHLGLSPCS TCLCAGQLQQQK/PGSSSGNL* GQGHSSGDLGSAPPHLVPG\PG PLTAGGHG/SLVGDSEWGSPAP GAVLGQNSSGPDPQRAGRWLC SRAEKSGCYTAPPLG*LSAQFQ EEKASWVPPGSGQLEDSHPDPY TALPLAAPPWGTGTGCPPAWP RL/EPDDCGPRHLSPPTCSTLPS WGGCAGS
14103	44471	A	14185	264	643	RCLRPGEGRSRQGRRSRTGRGK AEEGGARTRQQRRAALLPERS ASQPGPRDSPRWRRRRQTTRGR ARPASSGGT*GSSWLTLAWPPR EP*RLRSASAQG/CRRQRLQQR RRGLYQPHRPATCGPRAAD
14104	44472	A	14186	114	1039	QSQRLRPLADTPRRSNRPCSAA GLLFPQSFWSQELSQGAFLLPPS SPCLHCLPGTAAASRHQRSPRT RPSVQERRETHGLCAHRCEWR AGSPAHGP*AHRFVSRAGSPAH GP*AHRCISRAGTPARGPYSRR* VSEAGSPA/AVVSAPCSLSS*AC VTG\CSPAHSP*AHRCASRAASP EHTSREDAEQAP*MQGLCPVH QEQPPSRKSVVTSPHIPPETDCR LLPKNPCANKHQPTATGGRAV PPEVQHVPPRSGMTLGSHQPLA LQFQMQATDAARLGLSPQGQG SPPGPRSTLLLGCLSLFQLSLLR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14105	44473	A	14187	1	1629	MIIYVENPKQSTSKCVRAYTFS KVAGHKAIEKRLEKLAVDPHR DRAQMLKVENVQQAWQQWIN KLPPARREDEDVKEIRWMIEEL RVSYFAQQLDHTGVDRGQPGA STWSASLMCSVTQPKLKTRKP GFLLGLGERNCFSVYGAGRSW GRGLGSCGFWLPPRTRIRAADV CLARWGWRAHRVRVLAGKNS RAESMLWSFHKAAIEAARTNII QAQTRVEAAQATERRIAADIDD SELKAPRDGRVQYRVAKPGEV LAAGGRVLNMVDLSDVYMTFF LPTEQAGTLKLGGEARLILDAA PDLRIPATISFVASVAQFTPKTV ETSDERLKLMFRVKARIPPELL QQHLEYVKTGLPGVAWSFLYSI NQTICLRLDSIEAKLQALEATC KSLEEKLDLVTNKQHSPIQVPM VAGSPLRTTQMCNKVR/CVNP* ATVVPPPVPQPTTQQYQGLDA GATTRVPRSLLRSEGSQTQKSP SCGSHSQDNSGGRKAVGARRD RWWLGAGKGPDCRGAKCGLP LSGQKCPTLDPYQVVGCTSKTG
14106	44474	A	14188	3	1010	GLQTQLVPLSSPVASLDNFSNL FGADLHVEKGQVPSSDQHLSQ RCHFPKAPPWSVCKALLPRSNP ATSLSGTSKPNSGGDFNSVTKS QPHCELNSFVLTGHSPVLWMM SEHDLADVVQIAVEDLSPDHP\ VQSCGTVVVLENHVVTDEDEP ALKRQRLEINCQDPSIKSFLYSI NQTICLRLDSIEAKLQALEATC KSLEEKLDLVTNKQHSPIQVPM VAGSPLGATQTCNKVRCVVPQ TTVILNNDRQN/DHCSQDGRPL EQQGTGFPGKMSLASQ*HGTNP TFPCHCAESHENKSTSLSQGTV QHTLHLCGHRVEPGRHRPSSLR SGRAGWAMLNA
14107	44475	A	14189	1	1710	
14108	44476	A	14190	52	457	
14109	44477	C	14191	1	838	
14110	44478	A	14192	92	514	
14111	44479	B	14193	1	531	
14112	44480	A	14194	1628	2008	

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14113	44481	A	14195	2	1616	CPPPRRPRPRAPPHHRPPAAGA RTAAAGDRSRHGPASRVGTGP GQQMRKTYCRNSEPSDLDQGG GSRGGPRRQSKCVRNWWVLGL TDFKNEAADPHDSGAQLASPSG FRTRAAGGAACQSRAMRSYSS ALGWSMGLGAVEQGVVLVGE AQAAQEPMEWVGGSGMVGCR SRAPPAGRQLRPDKKLSTAPVG RHRWRPSTPSAATGLGAKSLIA RGQQGRLAAPNKTDFKARAVK KDKEGHYIMIKGLVQKESITIINI YAPNTGAPKFTKQLPLDLRNKT DSNTIIVGYFSTPLTALNRSSRQ KVNKETMDLNYTLEQMDLTDI YRTFYPTTAEYIFYSSEHGTFSK TDRMIGHKTSLNKFKKIEIIPSTL PDHSGIKLEINSKKNLQNQTNT WKLNNLLLSDHWVNNEIKMEI LKFFKPNDNSDTTYQNLWDTA KAVLTGKFIALNAYIKKSERAQ VDNLRSHLKELEK*EQTKPKPS RRKEIMKIRAELNEIKT/QKIQKI NKSQSWFCEKINKIGRPLARLS KKGREKIQISSIRKK
14114	44482	A	14196	1097	1686	APRPLALRFGPLPSNSGAQLASP SGSCTGLQVELPANSCTVRWQ VSALGWSMGPG/GPGAGGSAD QGGSGGTGAHGGVGRFRHGG AAGPEPCPMGEVAKAPARNRA QRQWAGTAGGPCASS/NSC*PG C*APYCPGWWGQPAAPSAGPP SPRPPRTRAGPQAPWAAPVPAH ASP\PHLPAS*GSPLRPGIQGSKT YQKSH
14115	44483	A	14197	647	1496	FLNLLSWQNLMLCGLKKKRKQ FKDYEKKVKELNEERDKYRKG SVYIYTFGKEPTLNKVLDACDG KFQAIDFITPGTQYFMGCRWSC LPVLHCALAGLSPWVVDGTRR PGAVGSAGRGGSGGTGAHGGV GRFRHGGLQVRSPAHGEVLRPS EKSSAAQWAGTAGGPCASSTA ADLGAKPLTARGGGPAG\PPSA GPPSPRPPRTRAGP/PSTVGSPG/ SPPTPLPPHLPAS*GSP\SGLGQP RKGLPQCSGGLKGWLLKHRQS GCPGRGGAQSERGLRGLPARC

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14116	44484	A	14198	1	560	MAALLLVGASWL/LLLLVGAS WLLARVLAW/TYAFYDNCHRL QCFQQ/PPKRNCF*GHLSLCGA/ TEEDMRLMEDL/VPLFRDVQL WWLGSFYPVL/SLVHPTFTAPV LQASGG*PGFTTTMGLSFKRAK WQRLA/SEGSVRLEMFEHISLM TLDSLQKCIFSFDSHCQMVSPG SCTTSRGPRIPGALPTGGARAPE NGDPKEIE
14117	44485	A	14199	175	2225	RWSSVSFASGMPSAPCCWGHP QCPSAAQPTGPSWAGCRGLTM PNGQASPAS*VPPGAFPFLCIKQ PLWENLMTGVGKFSREAATLE GPTLPTR/GVGPQCRQIADLPLE RTEGWRGD\GNPVRGVRQKRK QLVAGETAASLLPCQASGESCS VP*QARGPPVLFLPQ\WGRRWA KGCASRSCF*PDFRPSHAVPGA REGAGLAAAPKRVARLSPAVPP ACC\GLQGGSSSAAQAL*PQLS GPRLPREK*GA/PCWRGGPRCC PQNSAPETLEYVEPRGTGAPGT THTGLPSPSQGCRGAEGW/WGL PGLPGPRAGSSPQPRGRAWRPR ARTPPPASWAAKGRGRPLAAG GLARPRDPGPGSGVAPAGSLRP HSSGRGWGRRRLRARPTGGNR GSEWPR/RPPGYPGARPGAPSVP RPQP/PAA*TRPLPVGCGARPFH PVPATV\VPHAGPP/SGMGRRRG RYPRPASARPAGRCGAGSAEPG RGTDKGGDGGEGKTKRGGG/L GGGAGAPKAAPGAAEPMGGR GAGAGGGGA\R*GGGGGGGSG TTGSGSSSRPRPPRTRAPPETDP APRPRPGLVRAAGGGAASGSG TGRGAEGCGVRAARGVPASLR AALARGAQARVLVSGPAPGWA EPRPAGGARGVGVWGPVLAGP GRGPRGGAGRGPRALSRGCAA *AWTPGRGAGQRGPGSGRGSG

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14118	44486	A	14200	1	2850	MHPQERTAAATNAAIIITDGAA TQMGVTSTPAPGHPRDGYYQG KDVSLLAHTHSFKISAAIEAKTT WVGMCRWGCKVALDVTFDVH QGKPEGAGRNKQIPFIQDFPFAL RSEKRPSLPATISGKTLPLNTKT CPQLLQCKREGHSLQCLIWLQ MVPQLGRLAVGGCHSNAWFPS KKAVIWEKFKHNLSGLVSDKG GKRTGKGLGECLLMMRKMSP ALEALTTFDSSLQHHFPRTFPVS ALEALNPGKPRQLVTPA
14119	44487	A	14201	1	1570	MQSATSDAGSAPKKQKKVMTL QEKSGIAWYFFTAAQEWPNTPP KLRTCTESMGCCLLDCCCTGQ GDWTRVTLYCRYPFILFGTNA WVANFERPRMNANSLLASPTG LSPYLRFGCLSCRLFYFKLTDL YKKTTLGSLPDAAMAFVNCHG AGGTVAVRTSRGHSRCHFGFG VSGTRYYHLTPQVVWERQQQK VDSLLGTQQMLEAQGREF/PGP CIPLPVPTNAPAAKTTPQPPSPD L*PPNYLFLCVDGHRPIC*EPKQ NKSDSFTSQA*SQDG*YCGCS/C RAPRPHGTSATIPMSSSCKRFQP SSPF/CKGPYHFRFLEERPLASRP SIHPSCGSYWLRLGCVAVGRTG /SRLNLQLHSASGLQALSKQR*R YCQSAGAGSPEPPRGGTR*CCR EAAPGCRAGTCPSPAANLPSLR RK/PGTC*PQNPPGRCGSCGASA AVLAETPARIRRSFPRARQSCPR TWMAAGAPGSSRRQGTKHVT* *SSTLEKQLDNPTATYFSVPTRK PVH*NQQKDL*VTG*LQIFHL
14120	44488	A	14202	11	356	VSGPPR*APWCPCLAAPTGSTS HGSTARDSSTACKVS/GGATCV/ SGCGPGLGVLGRGLSSTRSCCM PAG*CPSSKDTCEKSGGRTQPV PPFEWAAQDASLVRRCRILAHR PCRGTS
14121	44489	C	14204	333	473	

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14122	44490	A	14205	344	1035	QSAAQWFWWPGRSASLGGAK GMQPPSLASWPHPRSIRCLRAP AP*QFTNATDPRFRSAPRRSGQ QQPRGSSGPAALASPSPRQPNR AGALRTGGAGWATALDTWSC PRTRRRAPMGSCL*AAAQQCV TGATWPPPSAIA*QSAAQWFW WPGRSASLGGAKGMQPPSLAS WPHPRSIRCLRAPAPCSGPSASS AAVQVACCCSLACCGPSRPASQ GHLDGTPITSPETCTTSLWSPQR RRAAGPPKVVDIPD*RGSRELPS GRGAPNTTCIPYGGSPGAKWIE GCPAQ/RPSPPGLHPAMRASAL LLMPFLQRRHRSATRLLLRPGS DCTGKK/GKGFLAGPETKRQKR LCPSPKTLGRALGQQEALPANV RC
14123	44491	A	14206	41	292	
14124	44492	C	14207	480	1637	
14125	44493	A	14208	3	410	SPPCGAPPPPVFCAPAPRAPAPP RAPPLAEAALPGFASAAGSAPA RSGPAGAG*GSRSRPRARASAS LAPASAGDHLGYPSATAAAAP ASRPWLWRPSLNAARLGDPAC GWQASQWAAGSA*RAGSQWA AGEARA
14126	44494	A	14209	1	1274	FFFFHPLRSLLGDLGLHSQERSA PEIKPGALESTWSQARGAALRL AEAR*RAAPAAGTACSAGGAA SSPR*GSRATRRRRRGPTAPSRA ATAPGRGAAASAAPAARPART ALMASARGPP\TAASPAQALTR SAPGHLPPMSELGAVTALCESC PVT/AAPRSGGGEAGGTLASEW GRTCRNYG/PAPGIWPRPPLSAA RPAAASPPARRIWSPPAPVHSA ASPIGLRVAAPCSSGSAVPLRSR RASPPCGAPPPPVFCAPAARAP APPRAPPLAEAALPGFASAAAC RGKLRLALQGGLGRSGSRSRQE GPAAGS*LRTGKSWPSPPPGSA PLPLAQVLQALVEAGSRSRPRA RASASLAPASAGDHLGYPSATA AAAPASRPWLWRPSLNAARLG DPACGWQASQWAAGSA*RAGS QWAAGEARG
14127	44495	A	14210	2	335	

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14128	44496	A	14211	344	1062	TRAEVTQQKLSRFASPPPVLRL RSYVSPPAAPTADPRWRPSWST SLRWVVKPNVSAYRIPPRASNR GYRASDWKLDYA*\WTGRLRIT SKGKTAYIKLEDKVSGELFAQA PVEQYPGIAVETVTDSSRYFVI\ RISDGTGRSAFIGIGFTDRGDAF DFNVSLQDHFKWVKQESEISKE SQEMDARPKLDLGFKEGQTIKL CIGLCSKPGTTAIQLGPVLNGIG RTLRTDLRNKNDLEGTNL
14129	44497	A	14212	573	1017	TDQGVGSPHCPRFQQGPPRSPR FQQRSPHSPDSSRG/PPHSPRFQ QGSPHTPDSSSG/PPYSPDYSSG HPTP/HTSQQGIPC*DGHGWLPC GPVFLWSEAPHLNPGLGVWGQ PRAPALPGNSAESKLWPHDRPA RPETPGAGTAWAHQALRV
14130	44498	A	14213	707	836	
14131	44499	A	14214	724	927	SFMDFRFVLLFFHLVPNPK*RP VS/SPPGSKLLVPPWGPKT\PVPP HPSPPPPAHGEPGLPPPPPPPLPH
14132	44500	A	14215	29	157	
14133	44501	A	14216	1	363	
14134	44502	A	14217	770	952	
14135	44503	A	14218	1053	1995	KSSEPDLSHSFIFCSPNFPPSSSL KRPH\FQSSILACVFCITADSSRA PCVLRVCDGFAGLTRSSAPSSK EKPCGFSLPEFTPLAVSFPQAAL CSLGTVSCLRPRPQLTPSWECP VLLAGAVCPGLPCAAIGCPWA GEEGCPGATSQLDQVSWPSLQE APEVLWPCLDSWGWFWAPSTV IPLMASPRFGFMGRSQQPVLIN HLIKEPKAKFSNKNHSIRCCQG QRKWRRGNAAGMCCQPQIPGK GEVKTEFQPVSNRSVNYGCTM HFQETLWTPRLGLGDGDSNNN NNNNNNNRITANPGKEAEKPE HPHLLVKM
14136	44504	A	14219	482	833	THQGARGCTHARVSVREMRTR RGRWATGMRVPAPCSSVHTTA VQRQQVADQLQTTAELSME/IL N/KWDQDPEAFVRKVATSYET WIS*YYPEDKAQSKQWLPRSGS GATLYSATNQYP
14137	44505	A	14220	195	367	

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14138	44506	A	14221	989	2210	LLVSCAILLSVSFLHSSSFVRSRS NRDSPACVDATYRGCSCQGEG VCGEACSCFPDLNQPQGVHAG EGVLPCSGWEDTFGKNTCLVS YQQIPNKRRPCTCEECGKAFGQ RSHLVQHTSEKLYACQECGCTF SNNSSLVKHWHVHTGEKPYMC GHCGKCFRESSSLAKHQRVHT GEKPYVC/GESTHLVQHW*FHT GEKPFAC/HR/CSKAFADFSALL ACHGTYTGERPYECRVCCKAFS PSLSLAEHIRCHTGEKLYACQE CGKAFSHSSSLSKHQQVHTECG KAFSQGSYLTQHLKIHSGEKPYI RGEHPYACGKCGKTFSHSKFLT QHEQVRMGEKPFMCGDCGRAF MQTSSLALHQRTHNGEKPYKW NECGKSCIQMSHLTEYYQNLPE KGSKDPHTDATVHSPVMD
14139	44507	A	14222	1	245	PPFRKQQAQHRNKTVLVSRSQP VPVTVPE/PSA*RSTPEGPRRAG CDPRP*PCPAGPELPAQMKVLA IEQLLSLHFKKALLF
14140	44508	A	14223	477	947	LCSLSSLPPPPPPPFPPPPPPPP PFPPPSPVPLPPSPRSPPVSPPPH SFQGRSPPSELGSSAEPWLRPGT WV*/PPPLTFSQQEAASSAQK*N CPGES\PQPVPVTVPERQPDAAP NHSLLLPGQQCFWCQGPHPPY WMGPVDASSSGFLSQSFY
14141	44509	B	14224	438	1437	

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14142	44510	A	14225	584	2866	WHFAKLSRNTQDHTRPTLGAA QAVPATGQPAAPGPAGAGPEW VPFLAVYKEQLVRNDSVLKVFF FPPIFYREGWVCCSVVESHLQE GFVWLFSLQL*PPKLRSLFSLSY CLSP\SDIEISRGQTPKAVDVLA KEIGLLADEIEIYGKILVSSAGF A*VVWEIL*NSLSPPELRITPTPL GEGKSTVTIGLVQAVSLGLCPS WQLYLVTPALQPGQQSETLFLK INK*KDILFL*FNLHLTGDIHVVI SCELSKFMDN*LLCGLIFVLCFF RGIILVTLCFLFLLKLLTFFLLNH *KLGINKTDPIRTMPDTHQVAG PYLST\DD*SVLFQ*SPAPCGNG HPTGTVADHYLCLGW/YQAQF DIAVASEIMAVLALTDSLGREV PRG*PLPG*YFVRNLMFFSHLPQ IDLGFHASVCLLGF*FAFSLL*G TPVFVHAGPFAADRDLCPYQFL LCQTHIYKIHVIMAEYFQRYKL MMYAKQTSPLCDLEQAISLSGC VPCRHSHLKNEKFSCTGC*QYL PKLSLPNSDPLTLPFSADYGFKF ESNHANHSGDCQNLPLFLEDNS TYSTCFPTVTEAGFGADIGMEK FFNIKCRDVVLSFRSVV*AFLLL AV*LGRFGGRQYTGVWVLLFS FLQNIQLVADGV*MVSLSLKT* LNGYRCKTTNIFFTRTDTRAEID LVCELAKRAGAFDAVPCYHWS VGGKGSVDLARAVREAASKRS
14143	44511	A	14226	3	587	YPASAGLMLQNFGVIGLRYHF AIHSPAAGGLLDGLHAVAAIQG ITKIETTPNHQRAPAHWTLLTQ QAHLQPSPLHFNLPLTLCLMHC PTAIPHCFADARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVG\AYGAQLL

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14144	44512	A	14227	2	1256	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL\PIYRV SRKAANFEWSPEQEKALQQVQ AAVQAAWPLGPYDPADPMVLE VSVADRDADWSCWQASI/GHK VGHAQQHSIIKWKWYIRDWAR ADPEGTTKGQGQRRWWQLAE RQDSRDREAAIGERQETAVGKT ARDGEAVCD
14145	44513	A	14228	155	531	GNLWSVDLRPGTPLRQNFRGTI RQQHSRFTKNHCSQTPLLIPRQ TGSGVDLSKLQQTCS*GSCLVC TIDLANAFFSIPVHKA/HQKQFA FSWQ\YTFTVLPRLTWLQPC*V PNLPAAETNTEPSNGT
14146	44514	A	14229	1	518	MTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIGSTIKWVVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG
14147	44515	A	14230	281	1140	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLTAMGVI GSHGARGQVVALNRQRQGDL QPFTRVTVHWGKG/NMQIFGGL LDTGSELTLIPGDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGIMVGKAKWKQ LELPLPRKIVNQKPYCIPGGTVE ISATIKDLKDAGVVIFTTSLFNS PIWPVQKTDGSWRMTVGYRRL NQVVTPIAAAVPDVVSLLEQIN TSPGTWYAAIDMANAFFSIPVH
14148	44516	B	14231	1	1521	
14149	44517	A	14232	3	202	
14150	44518	A	14233	2	367	

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14151	44519	A	14234	1	553	MTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIG\PRQLLACY/WALVETEHL TISHQVTMRPELPIMNWVLFDP SSHKVGCAQQHSIIKWKWYVH DWARAGPEGT
14152	44520	A	14235	3	728	
14153	44521	A	14236	1	635	
14154	44522	A	14237	3	266	
14155	44523	A	14238	1	1245	
14156	44524	A	14239	2	837	CHCGPP/VKVEAYGSQVLKGVL AQVQLTVGPVGPRTHPVVIFPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSWRMTVGYCKLNQVVTPI AAAVPDVVSLLEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL
14157	44525	A	14240	1	533	
14158	44526	A	14241	1	1043	MTVDYHKLNQVVTPIAAAVPD VVSFIEQINTSPGIWYAAIDLAN VFFSIPVHKAHQKQSVFCWQG QEYTFTVLPQVHINCPALCHNPI LRDFDHFSLPQDITLVHYIDDIM LIG\PV*NMLLHLVPPTTKKETQ HLEVLFGFWRQHIPHLATPSSP NGPMNKVTMMA/ANVGYAWD QKHGLPLTKANLVMAIGECSV/ SPAAETNTEPSIWHHSSGQDSQ VQESKGGNGSGTTHHHP**STS KIFASCSHDITFCWPRGLSSRGR NAATRRHNNNFIKPEVKIAFWT LWDPPTFKSTG*ERS*SVGWW D*HELPR*NQSTTPQGSVSIIPH GQPPHQLFGVAKARTFGIT
14159	44527	A	14242	1	336	
14160	44528	A	14243	3	1885	
14161	44529	B	14244	1	1423	

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14162	44530	A	14245	1	1361	MIISIDAEKAFDKIQQPFMLKTL SKLEETASPSPVVATYTPQPML PSAFPPLSEEINPVLPETTVMAS PEAVTRQDNVDSPQKPPPTPMF ASRPITRLKPRRAPSEEGIQRLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGKAKWKPLEQPP PRKIVIQKQYHIPGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSWRMTVNYHKLNQVET PIAAAVPDVVSLLEQINTSPGT WYAAIDLVNVFFSIPVYKAHQK QFAFSWQGQQYTFTFLPQGYIN SPDITLVHYIDDIMLIGSSEQEV ANTLDLLPARVASWGVPYDQL T/GGRED*GLLHRWSCRICRHH PQGSWIQES
14163	44531	A	14246	1	1795	MRKCGKPQFKLGQTNKANSRI QEELIHSKSLIEQEGEKPVQFSA FHRMWQPADSQCDIIDSADIWA DPLVRHREIITGSGGINRRRTRG GRGRGGEAAGGAENCGSREER ERAGVGTAVTQLQNLNTIGIIGS RGGRGQVAAINHQRQGGHSYC KGQQKQNSNQNSVTHVELWH WLINHSVPRSEIDRKPTTFLLNL YKQKTSRDLWPFTRVTLHRGK RNDQTFQGLLDTGSELMLIPED TKHHCGPPVKVEAYGGQVING VLAQIQLTVGPVGSGTHPVVIY PVPECIIGIGILSSWQNPHIGSLT SRKTDGSWRMTVHYHKLNQM VTPIAAAIPDVVSLLEQVNTSPG SWYAAIDLANAFFFIPVHKAHQ KQFAFSWQGQQYTFTVLPQGE TLVNFSLPQDITLFHYIDDIMQI GSSDQEVANTLDLLPRKSTTPS G/LYGFWRQHIS/HLGLLLTPIY* VTQKAA/SFEWGLEQEKALQQ VQATVQASLPLGVYDPADPMV IEM/SLSDPSSHKVGCAQQHSII KWKRYVCDQA*ASPEGTS*LY CTSFIMEKEEVC/LSLEQTLTLD MGLPILHAMLLWIHLWIHGLPY PSSWYSTQQCL

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14164	44532	A	14247	55	1241	NRFVRAAPASLKRSAGIGLLCM PDLTVGIVVTQLKNLNAMGITG SELTLIPGDPK*HFGPPVKVGAF GGEIVNKYLAQLGLTDDPVGPR THPVAIFPVPECIIGIDILSSLQNP HIGSLTGRVRAIMKGKAIMKGY YEGKGKAKWKILELPLPRKIIN QKQYRIPGGIVEMSATIEELKY AGVVIPIPTTFPLNSPIWPVRKT DGCWRMTVDYCELNQVVTPT AATVPDVVSLLEQINTSPGTWY ADIDLANAVFSIPVHKAHQKQF AFSWQGQQYTFTVLPQG\WTV NSPALGHNLIGRDLDRFSFPRDI TLLVHYVDDIMLIGSSEQEVAN ALDLLVFSDHLAIKWVMHSSIA SSSGSGICVIRLKKVLKAQPAP MASWGVLYDQLTEEEKIRA
14165	44533	B	14248	1	346	
14166	44534	A	14249	485	717	
14167	44535	A	14250	1	345	
14168	44536	A	14251	300	689	TKRAPCSPAAGSRGRARSLALL TLYHGHYPALPPGPTPAQQPGR GLAEAAEPRGSEGGNGSNPCG RA*DGRSRREGRGRLGGWRPC CEPQPWRQAHDPAGPDRVDGG ERRGAGVLRGQDGQDEKKKPK

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14169	44537	A	14252	1	2430	MAVLQPSRHRLRPQLGLEPDN WHSQQDEVSSVATARAVVPSG RGAAWMGPSGNIGGSGLVSHE CGEGTGAAGSTQLQEGMHFCR QSRWAFLTALCEVYTQSLQDT VQWLQLCQWSAQGQDDHTLIE WLMGATWTVWNDAREIPETG TGQDAWLCGSWGVDDQRPHV ELAIHCSPTNVQRVLALVDTGA DCSLVFGNPVRKPDGTWQMTV DDWELNKVTPPLHAAVPSIMD LTDHLTMELGQYHFVDYVHSP TICRGLVAMELAAWKCPKGVL LFHYIDDIMLTSDSLADLKVAV PLLWQHLAACGWAINKSKVQ WPGLSAKFLGVIWLSKTKAIPE AIIEKIQAYPRPTTMKQLQTFVG LLEYWRPFVPHLAQMIKPLYGL SKKGATWDWDNEAGTDLLAA KWAIQQTQALQVIDQGCPFELD VHVTTDGFGWVLWQRMECFR TPVGFWSQLWKGAELQYSLIQ KELAAAYAALQAYETVTDWA TVIVQMSYPIVGWTGTAQTTTL AKRGAYLEQQSMLTTTPLAAE LQEALGPIVLMEDKAMGPEAPL DPEPSLLKKGYPLVPDGAWYT DGSSQGAAAAWTAVAIQP/ITD TI*FDTGCGQSTQWAELRVVE\ MDILEACQKCPACAQAYLRQR QLPNVTQQVTVGQMPLTRWQI DYAEPLPKLQGYTYALMAADI
14170	44538	A	14253	2	239	
14171	44539	A	14254	3	211	VVYYSPNEVKVVAEGFDSANG INISPDDKYGPL*NIFIFLQLWC WPNSLLCFLCQCENSFLDIYGIL
14172	44540	B	14255	13	87	
14173	44541	A	14256	42	854	VLVFLTAALFILPTFSNSMMILQ VSGGPWT/VILRRGVLLGVAPP PSLPAL\PENSVYQERQECYAFN GTQRVVDGLIYNREEYVHFDS AVGEFLAVMELGRPIGEYFNSQ KDFMERKRADQLPDCRDPLMP D*GVWISPLGQQVPNLTAQKTL QHLPSKKEPQQHHDLLVYHVT DFYPDSIQVRCFLNGQEETAGV VSTNLIRNGDWTFQILEMLEMT PQQDRT*AGVQLLEVTLNLSLF FLEAQSDSVQSKMLTGARGLFI NYLQLNLCTP

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14174	44542	A	14257	3	571	QGRATPENYLFQGRQECYAFN GTQRFLERYIYNREEFARFDSD VGEFRAVTELGRPAAEYWNSQ KDILEEKRAVPDRMCRHNYEL GGPMTLQRRVQPRVNVSPSKK GPLQHHNLLVCHVTDFYPGSIQ VRWFLNGQEETAG\VVSTNLIL NGDWTFQIVVMLEMTPQ/QGE DVYTCQVEHTSLDSPVTVEW
14175	44543	A	14258	1	1677	
14176	44544	A	14259	2	430	
14177	44545	A	14260	821	1428	QVTDVQDFPLKCKIQWRRTVR GDLQ/PFTRVTVHWGKGNDQT FQGLLDTGSELTLIPGDPKRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQ/NSHIGSLTGRVRA TMVGKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT G\VIPTSPFNSPI*PMQKTDGSW RMTVDYL
14178	44546	A	14261	507	910	
14179	44547	A	14262	1	2898	
14180	44548	A	14263	1	2580	
14181	44549	B	14264	159	2657	
14182	44550	A	14265	142	377	NHLLRRQQWQTPFPPPSWS/SPR SSSDCCGSSENFKPVDLSLLGSV GVGPTEPDHLDPWLQPPFQGSE RFCLAGVPGATG
14183	44551	A	14266	363	638	EVWKESSGWHLAGAPLGQSFQ RKEQAVIFAVLQPLLVIPKQTGS GVDLQQTPAHLQQRGLSGCLQ SLCSLTSS*PQRHPQNSSLVSNC VVS
14184	44552	B	14267	1	2424	
14185	44553	B	14268	446	623	
14186	44554	A	14269	245	690	APSRSTWGSSSTAARRNLKTTR KLRTPRTPPHQKPRNPHHGPPR TPSG*TPRNPDHRPPPG\PQVGQ PGCWAPSQGPRGWGQLGC*RE EVPGGGHAGRHSTPVGG/DFFL QAGPWPPDASLPTNPFVLRGAS TPPHPLSENNKDKFLLQK
14187	44555	A	14270	223	365	

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14188	44556	A	14271	1	687	MSEYIRVTEDENDEPIEIPSEDD GTVLLSTVTAQFPGACGLRCRN PVSQCMRGVRLVEGILHAPDA GWRNPVYVVNYPKDNKRKMV LGLPWKTTEQDLKEYCSTFGD VLMVRQSQDEPLRSRKVFVGR RTEDMTEDELWEFFSQYGDVM DVFVPKPFRAFAFVPFADDQIA RSLCGEDSMKGISVHISNAEPK RNSNRQ/LRSGRFGGNPGGFGN QGGFESYQRCERKAV
14189	44557	A	14272	1	833	
14190	44558	A	14273	3	447	RGTAGGQPGNGPALAQSP*WC RLGSGGT*GKSPGTSQGRALPW CSC/SVSTWATAAPGSQQRASP CSWAQPGPLASLRLLMPPRLR* GHLGHLAWLQLFAAPCPVIHV AVMWSLLGIALRKVHGDWAPL AILSLVVCASNKLNLKKKKK
14191	44559	A	14274	988	1803	RAARVPRAPLEAVAHRWASAS EDDGTVLLSTVTAQFPGACGLR CRNPVSQCMRGVRLVEGILHAP DAGWRNPVYVVNFGDVLMVR QSQDEPLRSRKVFVGRRTEDM TEDELWEFFSQYGDVMDVFVP KPFRAFAFVPFADDQIARSLCG EDSMKGISVHISNAEPKRNSNR Q/LRSGRFGGNPGGRLQGTRYS PAPAPGSPGRAQGLG\AG*SRPS GSWLSGHLQRPEQSVGRAPAA PRHAVRRSLRRLAALCRRTRAR CRRAQLHVSPQRRRH
14192	44560	A	14275	3	184	
14193	44561	A	14276	1	352	KAAMVRFKHRYLLCELVSDDP RCRLSLDDRVLSSLVRDTIARV HGTFGAAAC\SIGFAGTIRTCQK FLIQYNRRQLLILLQNCTDEGER EAIQKSVTRSCLL*EEEESCEEA AKAME
14194	44562	A	14277	1	456	PTRAVEAAMVRFMHRYLLCEQ VCDDLRCRLSLDDRVLSSLVRD TIARVHGTFCAIACSIALALARA LNEEGNPEGWRDVAGASAGGR KKGHECPSPCTVFCTL/RYPNA YTVIGLLRCKKELYQVVWSVL YLMTYLENKGHRYPCFFNTLH
14195	44563	B	14278	34	267	

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14196	44564	A	14279	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL\GILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14197	44565	A	14280	2	1044	SSQMPSPQEGMCGKACTPALS QADSLCPLLRLASEVEGYWQM ACAEPYVQSEMNDHLSVWSLQ HGSTTLASMSFTTCSAFTNYWS PGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTSF\GGLA GMGGIQNEKETMQSLRDRLAS YLDRVRGLETENWKLESKIQEH LEKNRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEGKQV
14198	44566	B	14281	247	857	

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14199	44567	A	14282	1	2104	LRGSELAGGVAAPDPSSRARAP GRGQGSEPPRRS*GRGRAPPRA HTPLDDFPPGRAALSPGRGLSS RRPDPGSAGRPLLLCLRPPLHSP PPPRGCQAPAFQSLPSFHLALRL RSSGEEKLWGPRRAPAAP*SQR RKPDPARPGLAAAVPLRPV*AS D*GAAQVPPPSPLRDGGQPGGR EGVGRRTPHRAAAWLLGE*AA DAAAFHWDGGRPPAAPARLLP GAPHHREDRVHHQPRGHPLQH QSPGDPTPAGEQHASRH*LCRN PETQKLRH*TSERRDGHREEEH TGTAGVPRSRPATQRPHAVPAG GLQPHRMLPALSSGAASGGEA EHGQLSGRGREEDGPVWPQLP AGLQGHFRGESPRWPPCLGDGS EN*PGPVQAEFSGG*DPAVSESE DNQPRSRQFLRLQREEKAKP\D QRFTYLPANVPIIKTEPTDDYEP APTCG/RGEPGVKSSPKTILQPA ARDATRPQLLPRGRLPALSAEK HPDASSPWREPQAPRPFSRCLH QGRCQPGPLSPRTPAAGRRGPR RPG\VPRPVATHPGSPGQPPPAL LPQQ*MK*YEMTSPARAPTPSC HIGALSSAGVC*LQQTKTFE*IN *THTWYHSEPPTD*MPGAEH*Y VQRLALQQEGKQGGRETTVSP GGEVIS*QQKGGGRAEHGRPTV QGP/SHGNGPHAV*PHAQPFWH PWGSILEVPYLTRPSGHHRIEH
14200	44568	B	14283	41	4224	
14201	44569	B	14284	1	1332	
14202	44570	B	14285	140	215	
14203	44571	A	14286	234	657	VQQPGRGLDLSTDGPGGRSQV GLIWSCCCLH*AASGEPGGRCP GS/GAPGPAGSALEFRARDGVP\ GVGGPSWESHSPAAATPPPAEC RGPGPTPSPAPGEAAPEDREDG AAAPGRAEPASIVAPADGSQGQ VLATQAGALGA

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14204	44572	A	14287	134	789	PDSSQAPSRNSTRPAASTRKSSS PPAARS\AGNELGSSRGDADPPP QNPTGPAPQSAEVPRCD/SSSA WASNGSSISPSFFSLRPWPSST/S KVPGAGHHTPPEGAGGASAR\S SSLAPSAGAPVPS\A*RSQLGTW LSVLRPRSL*QSRVRSPSSHVSS PGSMQAPNSPSSFQPGMNGAWI WWL*THIPLARWPGPPGILVITC PTVTWIKWSFICSFHPT
14205	44573	A	14288	465	1541	GPPKRKLISNFSKVSGYKINVQ KS*AFLYSKK/QTESQIMSELPF TIASKRIKYLGIQLTRDMKDLF KENYKPLLNEIKEDTNIWKNIP CSWIGRINIVKIAILPKVIYRFNA IPIKLPMTSFTELEKTTLKFIWN QKRAHIAKSILSQKNKAGGITLP DLNLYYKATVTKTAWYWYQN RDIDQWNRTEPSEIIPHIYNHLIF DKPDKNKQWGNDSLFNKWCW ENWLSICRRLKLDPFLTPYKKIN SRWIKDLNVRPKTIKTLEENLG NTIEDIGMGKDFMTKTPKAMK TKAKIEKWDLIKLKSFCTAKET TIRSFGSEQKSHTLVRATRLVSD HSQSFEAWLQFLGDTRFGTQKL RDSD
14206	44574	A	14289	1921	3199	GYLAAGQVTSRIHTGRRHFSGP ARCPCVSCCRRPGC*PQPAVRP SG*HCRKTAPSHGPSIWQTR**P GSWPNLRPG*GWRWLRAQPRG RGIPVGCRSNLQLHPTKNPGSH *GSGSPWQCPGVLL*ASGRQPG SPSGGCT*SSGKAGLEPQWHPA IPGHCRNKPAAPASWERAPRPR AHALACGWWRYSSC*SWRS*S SPETPGPAQV*CHRPCPAAWW RCHS**TAQFL*D*FS*FLQTIGE PCICPKPISVPH*PMKQSH\RGIG GCLQYSSHPGIESSLGMSRGF/D RRDL*TLQIGS*RHPRAGPEGA AL*CLAGESSLRTPSAPCPGSPH TPGSSASGNTSPV**ETGCGSRQ GSARLVLESLLSR**CLSGPSRP SCLLRGISWQCGTAGRLSSSGPP AASGAGADAAPGGFPRLPCLEF GTV
14207	44575	A	14290	3	626	

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14208	44576	A	14291	1	1065	MRGSCERSGEDEEQKEEAMVA CGRLSGVPEAEQGPEANWDSD LETEGTDGLGELVRDTLYLRSC RAHSVVPISCFLRQGSAQELNL RHRGLGPQGARALASSLSSNPY VKRLDLRDNGLCGAGAEALAG AL/QQKQQHP*CGPVGEPAGSG RSPGP/RVPPSQ/CNQAMRKMQ LSGNGLEEQAAQHLAELLLAH TDLKSLDLSYNQLNDQAGPAPS LRAFPQANIFLKVLDISYNGFG DPGASAVGEALKANNVLEELN MSNNRISAMGALSLGLGLRVN QTLRILVLCVRVSQVSRNPMRS EGCFGLLKSVQDNPASALELLD FSDIQVNAEFDGLASSVRGILPG LGIKDWRLQSGV
14209	44577	A	14292	1	416	
14210	44578	A	14293	2	384	ELWVVTSFMAYGSAKDLICTH FMDGMNELAIAYILQGVLKAL DYIHHMGYVHR/DLQGYDAKS DIYSVGITACELANGHVPFKDM PATQMLLEKLNGTVPCLLDTST IPAEELTMSPSRSVANSGLMTA
14211	44579	C	14294	142	474	
14212	44580	A	14295	1	1470	
14213	44581	C	14296	91	471	
14214	44582	C	14297	195	480	
14215	44583	A	14298	121	1130	SRSTQYELMSFLTNDASSESIAS FSKQEVMSSFLPEGGWYELLTV IGKGFEDLMTVNLARYKPTGE YVTVRRINLEACSNEMVTFLQG ELHVYKLFNHPNIVPYRATFIA DNELWVVTSFMAYGSAKDLIC THFMDGMNELAIAYILQGVLK ALDYIHHMGYVHRSVKASHILI SVDGKVYLSGLRSNLSMISHGQ RQRVVHDFPKYSVKVLPWLSP EVLQQNLQGYDAKSDIYSVGIT ACELANGHVPFKDMPATQP/M VLVLSSPDAARETERHSALPVG YQHHPR*GADHEPFALSGQLW PE*QPDHQHPPALQR*LALPPLP PNLLPPLPPLC
14216	44584	A	14299	304	412	
14217	44585	A	14300	2	350	
14218	44586	A	14301	191	299	HRPATAVLHVPTRSPPSPGSRPS *PPPAAALLWTPA

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14219	44587	A	14302	537	5523	LARYYKFMHQDRQGVARNLL CQKEKRR*YTTKCEDNTCHWT GRTSS*PRSV/SNLNSQCGPRLW PPVTIIRQANIKTGEKAH*TSKL LPPVQLKFPARDDTLPWPGYIP* QLRRPSPR*SILSMLPRKVVPCL *QKP*TVCWKF*EPLSYIHHSLV LKMMIPMPMTLLGA*CLTQAL K*SRMERKKGRAAQRSSTLGC QSPRGSPGGGPGPPGPPGAGKQ QSNSVQTSRLLARTLI*SFSSST VKDKELARNTAP
14220	44588	A	14303	2868	3095	PGWAGGLFGPSAGMRAWATK PSLTPPAPAGQRCPQGHRG*SG PGIYAVQPPSVPAWAAHATTQ ARLCHPRSPPLR
14221	44589	A	14304	693	821	SDRQT*RQEKRLTRRQSCCLPC N*SFQPETTLFHGPDTFHDN
14222	44590	A	14305	338	645	
14223	44591	B	14306	181	480	
14224	44592	A	14307	155	543	
14225	44593	B	14308	1	1260	

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14226	44594	A	14309	1	2025	VINIINAAQESSPMPVTEALDRV LEILRTTELYSPQFGAKDDDPH ANDLVGGLMSDTGLEIIKDGEE EGESRTAQQYPGLSESTRQPWR RSRTPRTTWGWKATEQQCPDF PPPGPHPHLELLIFHCEGQGTGQ KHSTSYPCTLMSEKRGLMNVFF AKYTGPAMRKSSGLTPSLLHLY CADPLHSKPLFNCPPPTTSKTEI LGSCNCSPSESVRGAEKGDQEL LANIKQAEKHEKNHPEVTVAM ALTDIDLQLQFSMSQPEALLLL AAGPADHLLLQLYSGHLQSAT GIYGEGRASSATLEDLESQYQE LAVALDSSSTIISQLTENINSLVH TLKEEKHEIHQVQKLGRNLFKL KNQTAEPLAPEPPARPSKVEQL QDETNHLRKELESVGRQLQAE VENNQMLSLLNRRQEERLQEQ EGWQEEQERLLDKNNENKSAL QLEQQVKELKL\ENLEATSQ*K QQL/TAQLSLMALPGEGDGGG HLDSEQEAPRPMPNIPGDLESR EAMVAFFNSAGANAQEEQRVC CQPLAHPVASSQKKPEVAAPAP ETGGESVCGETHQALQGAMEK LQESTSARGQCQRRSTGRGGHR QAGPGPGGDEEMLCTCTQVSS AGRGMGMLTVVLVVSLMMLS ASFSTWCMRSISSCHCAYSAHS SISVFWFPREYILASGSEMMNS
14227	44595	A	14310	3	564	SLRVSLLKAVVDRAGSRILSYIA GLGVDLGFGGGSRVAGGIADL GRSGGGKATRSRRGSRAGGGR LRSRHHEEALQLRETPGPGAPE\ PMDQEYAGPGYDIRDWELRKI HRAAIKGDAAG/VWSAAMTRR FRDLDARDRKDRTVLHLTCAH GRVEVVTLLLSRRCQI\DICD\N* NRTPLMKAVHCQEEA
14228	44596	A	14311	515	778	GQAQGTGDREGAVLFTARAPD QCRP*SCSSSRPTASSCPLGHSC SPGPLCTHLPLQGPPQAPTVPG ATATCWFSWNQCRCRAVSSYP
14229	44597	A	14312	411	608	EAEIP*TGLPGHSRPPGPLCTHL PLQGPLGAAAWVPEAGLGQVP TEAAGAARAGCSAHKPWKRRK
14230	44598	A	14313	2	338	
14231	44599	A	14314	1	390	

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14232	44600	A	14315	237	488	PWKTLDSSEAEILRGVSESSAV TLHCMEGQAVGPRQVKRIVHC *ASSA*NPHAMLLLQNR*LALC TSVPQGAAVLCGGWDPGN
14233	44601	A	14316	358	616	
14234	44602	A	14317	13	1155	IKLPPPGCRRRGGRHRRHRYRG RAEPLAPRRRRLPPAPEQPRARP PASRFLKNTMSNGYEDHMAED CRGDIGRTNLIVNYLPQNMTQD ELRSLFSSIGEVESAKLIRDKVP GHSLGYGFVNYVTAKDAERAI NTLNG\LRLQSKTIKVSYARPSS EVIKDANLYISGLPRTMTQKDV EDMF\SRFG\RIINSRVLVDQTTG LSRGVAFIRFDKRSEAEEAITSF NGHKPPGSSEPITVKFAANPNQ NKNVALLSQLYHSPARRFGGP VHHQAQRFRFSPMGVDHMSGL SGVNVPGNASSGWCIFIYNLGQ DADEGILWQMFGPFGAVTNVK VIRDFNTNKCKGFGFVTMTNY EEAAMAIASLNGYRLGDKILQV SFKTNKSHK

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14235	44603	A	14318	1	2340	MFVWRNVEGHSAAVFSWYSIP FLTPPCSHTRPSNLPVTQWPPTR ENNLPSWQPLLMSVHQAQSLS ALRKEQDSSSEKDGRSPNKSDK DHIRWPMSGAHDLQQAAPGPG GAHQGHPNQDNRTVSQMLSER WYTLGPNEMQKYNLAFQNVE ARIRYVIVRGNEQGFFRMHHLR GVSSLQLGRRRPGPGTYRLEVV DMITIDARYRCSGLRSPPDPDH LKSVDLHRNEHFFLQKARWEIH LVLQATPSQIQLLHVAFVLAKQ PLRCRKQTLFLISVVGTKEKNV ASEGRNPVRPLRGHRWLPASPP AAEHFAGGADRKSRLSRAPRSA ATATPANEQRAVADVGQWAR ARGGRVRAAGRSGSCALRRSR CRRRRRRHRRHRYRGRAEPLA PRRAASGQPGKLRARRGINCNA SSIPMLQVVRIKSISKHCQMAR VAGEGSLPLSHAQLTHCVFGN KQVQRTIAYLPPQQQGVQGFL KNTMSNGYEDHMAEDCRGDIG RTNLIVNYLPQNMTQDELRSLF SSIGEVESAKLIRDKVAVGLLSL CVPIRNVEIVASTSWWSLPLAP YVPRGIRRSQPSTLMDDLSCRS HQAAAPFTASVLLYISGRVKAH TAAQGFNHIPEEGVSQEAGSG WSQAWKDGWLTNVFMFSCTG HSLGYGFVNYVTAKDAERAIN TLNGLR/PPVKNH*GRPLQLGFL
14236	44604	A	14319	701	1050	LIVHFCLQVGCGVGNTVFPILQ TN/NTNSEYDPSRCFAFVHDLC DEEKSYPVPKSSLDIIILIFVLSAI VPDKMQKAINRLSRLLKPGGM MLLRDYGRYDMAQLRFKKGIL KVLNPNH
14237	44605	A	14320	701	1519	LIVHFCLQVGCGVGNTVFPILQ TNNDPGLFVYCCDFSSTAIELV QTNSEYDPSRCFAFVHDLCDEE KSYPVPKGSLDIIILIFVLSAIVP DKMQKAINRLSRLLKPGGMVL LRDYGRYDMAQLRFKKGQCLS GNFYVRGDGTRVYLCHTRCNW TRFSPTAGLEKPQKP\VDRRLQ VNRGKTTDNVPGLDSVQILQAP SVQHQLRGYLLPTRCKPVVVS GLFLKKKIVALGVV/RCL*SQPL RRLRRGGSIE/HQQSNLGKIVRD PVSESNDKIKRI

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14238	44606	A	14321	756	1334	PGKFVLMSFLDPQPPTRILEVGC GVGNTVFPIFTNRTMTQDSLVY CCDFSSTA\ELVQTNSEYDPSS VF\AFVQGPV**RESVTQCPRAV LDIIILIFVLSAIVPDKMQKAINR LSRLLKPGGMMLLRDYGRYD MAQLRFKKEELDTLFTTAGLEK VQNLVDRRLQVNRGKQLTMY RVWIQCKYCKPLLSSTS
14239	44607	A	14322	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
14240	44608	A	14323	1	5796	
14241	44609	A	14324	1	2721	
14242	44610	A	14325	1	3438	
14243	44611	A	14326	1	3306	
14244	44612	A	14327	1	2364	
14245	44613	A	14328	1	2091	
14246	44614	A	14329	1	2334	
14247	44615	A	14330	1	1986	
14248	44616	B	14331	1	2559	
14249	44617	A	14332	1	1671	
14250	44618	A	14333	1	1845	
14251	44619	B	14334	1	2055	
14252	44620	B	14335	1	1554	
14253	44621	A	14336	1	2559	
14254	44622	A	14337	1	1714	
14255	44623	A	14338	1537	2204	

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14256	44624	A	14339	2004	3751	YQSLAETQQQQKKNFRPISLMN IDAKILNKILANRIQQHIQKLIH HDQEGFIPGMQGWFNIHKSINV IQHINRTKDKNHMIISVDAEKA FDKVQQHFMLKTLNKLDIDGL EVLARAIRQEKEIKGIQSGKEEV KLSLFADDMIAYLENPIVSAQN LLKLISNFNKVSGYKINVQKS\Q AFLYTNNRQTESQIMSELP\FTI ASKRIKYLGI\KLTRGVKDLFRE NYKL\PLIKEIREDTNKWKNIPC SWIGRMNIMKMAIL\PKVN\YRF NAIPIKLPMTFFIGLGKILLLSSY GTKKRAHIAKTILRQKNKAGGI TLPDFKLYYKATVAKTAWYW YQNRDIDQWNRTEPSEIMPHIY NYLIFDKPEKNKQWGKDSLFN KWCWENWLAICRKLKLDPFLT PYRKINSRWIKDLNVRPKTIKTL EENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLKSFCT AKETTIRVNRQPTKWENIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWVKDMNRHFSKEDIYA AKKYMKKCSSSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRC WRGCGEIGTL
14257	44625	A	14340	519	1286	LNLEERAFRHKSSEHLPHLKVH FRHSSCGIKTKSLLHVSPPTTLIF PYPPLWGNPSN*ARPPCSVHSG PYPQGLASIIAHGSPGNVRGVH V*INDSEGGISRPSTASHKETPR PPTPARHADLAATRPRSLTTSPS \GAGPRA/PSRAGPSVGGLGLRP SGRAPRAEVALPAGLSPAGLAG PPPSGRSTGALPPAAAPTTSGP/P ASTPPNAPAPGHTLSSRSPHRA ARPPPHCGAEEWTGFTMRPSW RISQSFIVKDS
14258	44626	A	14341	482	700	

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14259	44627	A	14342	1368	2416	SSMTQSSCPMTSYLKSKFGEPL MPSYTNPTETGVSKLVNKTQVF TYAHKGPVSIYFDACQAAHLSK LNNIWT\SVKI*DKKESASRATK AITEESKKECPDCDNQWTTHEF NQHLYTGRAALFASQEEKIGYT TGTCYPLNLTILKPNMTFWTKG HKGLLTFDQAGALLGLGIPLVI TKKTQRTQVQLSPIQQFRFYKS FNEHFNSEVSKIQIPPISTENLFV QLAKSIANNLGVTSCYVCGGA NMRDQWPWEARELMLQDNFT LPEFVTKFNANPSVWLLRNPIIG KYCIACWGKSFQNQIGETTCLG QQYFEESENRTQWRSFIDDSS\G HFNPFLQFPTLNQSWYQLE
14260	44628	B	14343	1	1071	
14261	44629	C	14344	89	283	
14262	44630	A	14345	244	315	NPKGQKDREAPLSRSVFVLKIKI KRAFALLLHGRF*PSTPAASASP ASKSPRGSGKALASALFYIVQL TK
14263	44631	A	14346	1228	1656	QVYRPSQTPHLALSPERVAPGR RAAGRLAPEARAPRGSP/LPPHR VSEKTIRVVVFHPGARRAGGTP PRAPRGDTGGAPGA\PTYSTPL MSLHRARLESSPTGSSFPADSA KPVPLAVVSLDSR*GQWESRSS IHA\VTN*MTRH
14264	44632	A	14347	2	705	GSWPGLDDGSATRILACPWPGL GDGPAAPKANLPLVRWKPQCF RGEGL*GSSCFSATLLTGLDLW ACCSSRSTASARLSTYPSAFTSG WCSSLGPTEEAPGSWINCPLAG ILGAATSPKPSAIPQASPEVSLD AEDTGMKP*DSA\GPPGPARGL CGRGCGLSPACMGLRP/PSPPA QSPSTALTSLT\PSPFHPPRKKW SPPSAPAPSAPSPAPASLTPSPAP PAPSPAPTPAPAP

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14265	44633	A	14348	367	1174	WVRGQPSQSQLDLLACSTPTS* WPPGRAPPPPLP/PPPPLPP\PTP ASPPLLHPPRRAPPPPPVP\SFTP ASPPPDPVPRPTKALTGLP/LCP LPCMGR/PFVPYLGGLLPCLGP DFSSL**SPGGWDRPVRPLGISQ IPE\PPLTMGL*MQ*IPP*PRFQG HYAPLPPLQTLCISVKTPGRNPR GLPMHKILQPQNPSQPPCELPQ AHCPTTPPPKQCP\PAAFSILPVT FADKDPGAAPEGTVKAPMPTQ *EL*PLRPREHRVLSGPTAGQT
14266	44634	A	14349	332	988	RRAGTPASWGHNGARAKTPSR ACACLGLYPIHQPTARRAPAAR SHGPGPPALPRKGAAHGPRSVS HHPLRPCSRSSCLAWPCLHHPQ PLHCHPHRHWPKWHPHPLAPH PLLGLHPRSRPQTPPWTSCGPSR RLPTPSGSWPAPFDRDWPN*AR PSALCCPFCQEPQLTPCLHLCPH PHPHRHLPGLSCPHRPPRWRSP QSPCPWWLLWWTGQWWQPGE
14267	44635	A	14350	190	718	FVLQLPPAPKSGLGRWGSPPPG QFSSSQRTGTVRGRGRCAEPRG SLPHPT*GNNK*HGNWMGLGS QGL\GRQPGEDKHCYQR/IGVG GAHLLRPPHQRIRSLTSTGSGCS HPWSRELGCSWDGQRASAPLA LRQAWGEGLAGRNHTIVPFHG DISIAPRLLPCRETLFSALCGGES
14268	44636	A	14351	1	486	MKGEVSCKQHQDALQQVLWA MLQDADKQVRRAPGPVENENH CDFVKLREMLICTNMEDLREQT HTRHYELYRRCKLEEMGFTDV GPENKPVRVLLFKSLSDSKRVK YDEEWIRLPVE/MKY/MLERKV TQKQP*VPLVFVSWRSR*ESLR REEEENQQCHVLEL

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14269	44637	A	14352	1	2380	MMWSVLLQPVVLAAVERQGE ALEFLIGVPESDGENGTKLENT LQDIIQEDFPNLARQAHVQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKGRVTLK GKPIRLTADLSAETLQARRDRG PIFNILKEKNFQPRISYPAKLSFT SEGEIKYFTDKQMLRDFVTTRP ALKELLKEALNMERNNRNFFG VTFAFFVGGQSLGKALQETSIPF LREEDLEKTSILETGNGDWEAT RGLPEECAGMRERDCQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLGLIPTYDISSNIYLISKSCLW QANFRLNSALAQSPAITNFQFR GHSLKTLDLLTMKNLDSKVNII PVIAKADTVSKTELHKFKIKFM SELVSNGVQIYQFPTDDDTIAK VNAAMNGQLPFAVVGSMDEIK VGNKMVKARQYPWGVVQVEN ENHCDFVKLREMFICTNMEDL REQTHTRHYELYR\RLQLEEMG FTD\VAPKNKPASVQETYEAKR HEFHGERQRKEEEMKQMFVQR
14270	44638	A	14353	105	328	
14271	44639	A	14354	107	676	IRPDSLPSASPAQDFYAASSNTF PA/DRWSALTKIYEDQTSHNIPL SQ/TLIQSKALTLFNSVKAEKDE EAAEEKFEVTRVVHIRGLIDGV VEADIVEALQEFGLISYVMVMS KKRQALVEFEDVLEACNAVNY TADNQIHIAGHPAFVNYSTSQKI SRPGNSDDPEREQCASLYHPEP HLFDHHGCSLHYR
14272	44640	A	14355	221	648	LDWLRRVVGIPSLRWTCATLV GTRRAARHRCVNVWECGGLKE ITY*SVEGLCRA/EKPKPLALLE ETCKLPERQVVNAKEKFLEE\IK SATPVNT*MIRKRNCIITDMEK V*AVWIEDQTSHNLPLSQSLIES RALTLFNYVMA
14273	44641	A	14356	122	317	

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14274	44642	A	14357	338	489	WLGQN*RHGKQPGPGVGHVGT TVWS*PHSPACWAPAPQGPAPT GEEGCHF
14275	44643	A	14358	1	459	RPVWRNSQPPTAAYRWASGSR MWSTSFSRWNKTPSGKACSSS DKGPPMAQVPIPQRNVPPPTK/ QPLVLCHGEAPDFSRPPQHRPS LQKHPSTGG/PSHSPLPTSAPSSR AGLPPLAMTLDLTSGWRLWTPI QPFRLPPGSCREGTILLCSVMD
14276	44644	A	14359	609	2077	GLKAQPSSSRGHSRGPGACAAA PASRVHLPVTFCPEPNSSPCPHC TGGWGGRGQ/PACAGNPTASSP CQIECPALRSCLHALMDLGSPQ\ LRGAPRTGVPDPRLHLLPQPAL SSPPVLLRGPLLRGTCPLAARQ GQSPPAPGLLGHPGSHRGRLPP AQGGHRLPQPPGPGRRHRAPQP DPRRPGLRAAAASGPGLAAWG AVRAAERPGSGGLPGGAGPHH ARAQPGPRAAPPAAAAPGVAP AGGGAVPGGHPHRPGGEAALP AHGLPAPAAERTAPR\QPCPAC GLIARSDVHHPPVLPP/LSGPAP APGRLVGQLGVRGAPSSPVPHP ALHFPRAQP/PPGKGITTTSQTQ PAGSPPSPCMPPAATPGARHPP GSA\GHRAGV*GHTGPCDPHGP GHHGHAQLL*/DQAAVGVRGP GPWALSGMSQPPT\LPTAGHPA PACGVRAFQDGTRPPRAKPAL/ LSDKGPPMAQVPIPQRNVPPPT KHPCPGPQSSTWMRQ

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14277	44645	A	14363	47	1250	EPRPSRSSGGPQLGQGLPRPMK KIPGSSAKTAGPLATRPEVPRAP *SAGRQPWFQRPWGKRKGRKT *NHGSPGVKP/TPGPLNKDKGE KEERPRQQDPQRKALLHMFSG KPPEKPLPNGKGSTESSDYLRA SVTPGPWSFSP\QVASGPMPVH TTKKPA*APPQVL/EPKERQTGA AADMPQPAVRHQGREPLLVVK PTHSRPEGGCREVPQAA/SQNPR PAPGLQTPGTRQTS\SVTPQPCP PAATHSLGLGSNLSFGPGAKRP AQAPIQACLNFPKKPRLGPFQIP ESAIQGGELGAPENLQPPPAAT ELGPSTSPQMGRRTPAQVPSVD RQPPHSRPCLPTAQACTMSHHS AAGHDG/DPASQSALPETGKRT LELQPPGGPLISLS*EAGSLSRSE PSCVREV
14278	44646	A	14364	23	714	EAPEIPRQNRRMTMKERPVWL PHK*IHPNVAKWSRVPVQVQK NPQFQE\PTPEFIPVPGTSPEAAG FWH*GAHDSPGTRDRSEVEPGR GHPHLGPRDSAAADPGEHSPCD CP*ACPEVRRWPA\APVQIQYIIP SVDDFSLEFHAQDGDISDMRRE NVPFSPAEEGKAAPLYQQPLMI PQANHMAGISPS/SPTAAEFQHR DVHHRGPGTRDRTHTETGRVC PHPVPTDSPAL

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14279	44647	A	14365	3	1869	ITTVAPSRPASSDCESDGS*EQD AGPGSRMGPEK*AGPRPTRRVG RWSQTHSQTDDTSGAVVPEYP SDR*YAGGRGPG/PGGPTVHP* KRRS*NPQETKMMARRDPKSW AKRLSPV*PRLAALLTSASPSCP LEPRVLPFRVPPSHGLCEGTSYP NSPGT*RPPCRSSAKTAGPLATR PEVPGAP*SAGRQPWFQRPWG KRKG\GKPETMEAPG*SQPGAL EQG*GREGRETKATRPAEEGSP PHVFRETSREAAAEWKRIHGVF *SSEGHPG*FPFSFPSAGGNRGT PLSCLLGVRDSTILPGCKRANA GPHNQ*EAARGPCPR*S\SAAE MSGRGSVLASLSPLRKASLSSSS SLGPKERQTGAAA/AHPSACSQ APGPRASPRGEADTQPPRG*LP RSSPGCLQNPRPAPGRQTPGTR QTSCGDL/SSPARQPPHTAWA* APISASGQEPRDLP\SSDSGLPEL PQETETGSLPDPRKRHPGR*AG GPGKSPTSASRNRTWTKYVAP DGQEDTGPGAQRRPAASAQQT LPAYCPGLHHVPSLSGQP*WGP ASQS/GSSGDWKTDAGAPASW RPPHFTLLRSREPSSLRALMCQR SLRLPVFVSHRASSMRTFRFPPP QRTAILTWS
14280	44648	B	14366	1	1519	
14281	44649	A	14367	312	1326	TTKTGQDKDRLEEFSMQQLSGS KRKMSTQPRTEL\PPNRHTTTTS TTPATNTTCTATVPPQPQYSYH DINVYSLAGLAPHITLNPTAHP QLKQCVRQAIERAVQELVHPV VDRSIKIAMTTCEQIVRKDFAL DSEESRMRIAAHHMMRNLTAG MAMITCREPLLMSISTNLKNSF ASALR/PDGSSAIQL*SND*SCS WRPKLYDAFWDLSSLRV**PSR PEGEGRVSSEGMGESLPFSSSW PRQYQSFLCICWTDAPARNTED R*SHNKVLSSVY*NVC*NQLPC SG*AAAQSCCQSHHDPSQVLSQ PGCLCSTHCTARETLRGGHQHC HKD*SAEQGL

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14282	44650	A	14368	2	1120	PEPEPGARGGEQLNEDFEG*VA VPTCLHCPALSRTQSRAIQALT VRRGEATIRPPPCDDTKGGHRF LNELIKVVSPKVGAPSPSSDLPC RMWGEERGWTVGLPEEVKIAE AYQMLKKQGEAHRGWGATRA CLPLPHHERPKNVIFEDEEKSK VRLQGGTYGDSEPRWGSVGSI KEMVQE/DSGRAQSTGRRRDG GIELGH\NVKLLTEMVMSHSQG GAAAGSSEDLMKVHLPPCLPHS LPTPQPTRTLRMRPTLFRLASDT EDNDEALGEPRAGAEVRSPPLP PPPAPVRGEEVNGDATAGSIPG EEVAGELGGHPSGWRGTESYP AMPTRPGEQASPEQPSASVSLL DDELMSLGEEGARPGGGRAQQ
14283	44651	A	14369	1	432	GTRQEVTAGVEPAREWQRRLM EVQWGLERAPYCIQHAPR*RRS PARPGTQSCGLGACWIQ*GALS SPHCTSISRRCHSLAGSTPAVTS CLV
14284	44652	A	14370	16	471	
14285	44653	B	14371	66	206	
14286	44654	B	14372	234	390	
14287	44655	B	14373	207	427	
14288	44656	A	14374	2	572	FLLERAPYGVGFSLLPGLWLGS RAGVGRHHDKRVGLGRAPTWS LEGAVSSM/TPRPQLCVP/WPC WGPSSPGG*QQLGQLSCSYSLV DR*VALLWFWMLVGSPLVKGH CPTPWSRFVDFSVPLATPPGIVY WGLFAVFLFSHLLPARPGEQMS ACCRHLHAPSSPLLTLDSLIKVY SCNSQGKLVRVFPPGD
14289	44657	A	14375	175	499	KQNKSMGRKSQGFVASFGNHL YCTASCGMPASSTSTQTWPRVL PLHSQ/ESSHGGCSWRGRR*GP RPRPHKTPVPMVMDSTARNRA RRELVLAWCKSPLATALLVSW DK
14290	44658	A	14376	408	625	VFGEQEVFGYMNKFSSGDF*DF GAPTTLSSEHCTQCVVFYPSAP SFPFPPVPKVHCVIPHSLVPTYE WEHTM

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14291	44659	A	14377	1263	1812	AGDAAPEDPAGRGQEDLYDEE LPGWGLCIPHPACLQPCHA*VT KAG/ARVKVILPS*DTQRTKDIL KAGGG/PSSIHFINSAHGKPAVI VRPRGIWVLNTTPLSGQWGPYI GVYTAATVDMKSLGSGSLGLQ LALPLAASWLGVLTEAARVFG EQVVFGYMNSFFSGDFWDFGA PITRAVYTVPNV
14292	44660	A	14378	1	693	
14293	44661	A	14379	2	1299	WDYV/KRPNLRLIGVTESDGEN GTKLENTLQDIILENFPNLARQA NIQIQEIQRTPQRYSSRRATPRHI IVTFAKVEMNEKMLRAAREKG RVTHKGKPIRLTADLSAETLQA RREWGPIFNILKEKNFQPRISYP AKLSFISEGEIKSFTDKQMLRDF VTTRPALKELLKEALNMERKN RQINETENQQGYPGIELGSAPSG PNPLFCRHLQMSVDGRHLQNSP PQINRIYIFLAPHHTYSKIDHILG SKTLLKKCKRTEIITNYLSDHSA IKLELRIKKLTQNCSTTWKLNH LLLNDYWVHNEMKAEMKMFF ETNENKDTTYQNLWDTFKAVY RGKFLALNAHKRKQERSKMDT LTSQLKELEKQEQTHSKASRRQ EITKIKEELKEIETQKTLQEINES KSWFFERINKIDRPLARLTKKK REKNQIDAIKN
14294	44662	A	14380	2	383	
14295	44663	A	14381	1	1536	
14296	44664	A	14382	2	1118	REHLAEGMAVGTASADLNISA CWLRREQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQRK EQAAIFAVLQPPLVIPRKTGSGV DLEQTPADLQKRGLTVTRKTN KQKAIASTSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSSPAR EQNWTENEFDELTEVGFRRWV ITNSSKLKEHVLTQCKETKKLD KRLEELLTIITSLEKNINDLMEL KNTAGELRDAYTSINS*IDQAEE RISEIGDQLNEIKCEDKMREK\R MKRNEQSLQEIWDYVKRPNLR LIGVPESDGENGTKLENTLQDII\ QENFPNLARQANIQIQEIQRTPQ RYSSRRATPRHIIVRFTKV

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14297	44665	A	14383	1	1154	MLPILGSRHPSSLGQARKLDYR PSKSQCLEPGTPRACLVLYTLV AKLIYNDYFIHYFAPRGLPPME KNVVFVIDISGFMFGTKMKQD HNFSLAREQNWTENEFDKLME VDFRRWVITNSSELKEHVLTQC KEANNLEKRLDELLTRITSVEK NINDLMELKNTAGELREAYTSF NSCNDQAEEKISEIEDQLNEIKP NLRLIGVPESDGENGTKLENTL QDIIQENFSNLAKQAN\VQIQEI\ QRTPQRY\SSR\RATPRTH/IIVRF TKVGNGREKMFKGQPGGKGR\ VTLKGKPITLT\ADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKYFTDKQMLRDF\ VTTRPALQELLKEALNMERNN RYQPLQNHAKM
14298	44666	B	14384	1	1554	
14299	44667	A	14385	1	909	
14300	44668	A	14386	2	207	DIMSCILQNYNRPPVMALAIPIA VKFLHRGNKELCRNMSNYLSL AAITKAD\LLADHTEVIVKSILQ
14301	44669	A	14387	496	1207	PLITGTHDSGSVESQLIKLILTM HQLFRLVLGQKDLSRAGDLF\S *NNSEIEDSLTEALEQIKIISSSSD YQTNNNDQAVVEICITRITTAIR ETESIEKHAKALVGLWDSCLEH NLRPFGKDEDTPHAKIASDIMS CILPELQPTPQSMALAIPIAVKF LHRGNKELCRNMSNYLSLAAIT KADLLADHTEVIVKSILQGMVR KLSLGTCFGRYLKVFSSSIYGL WEARPRVLEAN
14302	44670	A	14388	219	448	VSLELCLKTTGPDCGCQTSQTP PAAAYHHL/PGAGLPCGPRLPA LCCSCPMGARPL*HHKR/DPSRF QEKTHLYLPSSH
14303	44671	A	14389	542	1365	GTEGVMANRSQEGNGGGSWR AKQVVVTVPF*EQSLVIMLWR RGGNT*QRPSEGTSRSHICSFH MSRHCQ*CKCLLKEP/VSAEAR DALDTKTHFPLAMIPSYLLLNG NIGELPEGPAGGCAQNPGLWAS /RGPARR*RSQASSSPEVRWPPG QCGLRGRPCKKE\PRPHPWSRP CASPYRGAGGQRLRRACSAAG RKTPDRRPLPEPTRGPVSQRAV LGKLRAAAGHRIPIGDLGDGLS LGAPPAGRHLHTVLPLRREFSP CEDALGIGEQQGKKRVT

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14304	44672	A	14390	3	723	PVLRGGIQEFAYIKALYERKFL VPKPIDYNRHAVDMELINGYPL C*IHHVEDPASVYDEAMELIVE LANHGLIHGDFNEFNLILDESD HITMIDFPQMDSTSHPNAEWYF DRDVKCIIDFFMKRFSYESELFP TFKDIRREDTLDVEVSASGYTK EMQADDELLHPLGPDDKNIETK EGSEFSFSDGEVAEKAEVYGSE NESERNCLEESEGCY\SDHLETL NK*RKTVYQKRVLMHGVLK
14305	44673	A	14391	1	1889	MGSKVKEVEDDSQMSDLVRG MNAFSKTGSGGVEQGRTGQGG TNGHIKKAKARDRDRRFKKTP QRKVGNDNLQLPLRWTEQHAE THIMNFCSKNYNRNIPGKPRESI DTLNEAACRGRLSKTARKLWS EAQDQRSFQATEMQAFLFSAK RIAAEKKTIIRRRDLCSIWGKLL PRPGSQSVPAQIPENLQEQEERA KWLLNGRSKFFPQTTSTLGKVT SNKTGVKEPELESRQPNLLKVE MGMKNHEIVPGSLIASIASLKH GGCNKVLRELVKHKLIAWERT KTVQGYRLTNAGYDYLALKTL SSRQVVESVG\NQMGVGK\ESYI YIVANEEGQQFALKLHRLGRTS FRNLKNKRDYHKHRHNVSWL YLSRLSAMKEFAYMKFRTLEIR DYFYWVKINVLTGPCSPKRGSS GEFVPCLLQLLLGFGDCWHSFG LWHITPVSVSMLTLLPSLLLVK QKKPTLDSRMGQFDFVVELQL YLCVLEREVIREYPPDGQIFGRY FDRDVKCIKDFFMKRFSYESEL FPTFKDIRREDTLDVEVSASGY TKEMQADDELLHPLGPDDKNIE TKEGSEFSFSDGEVPEKAEVYG SENESERNCLEESEGCY\SDHLE TLNK*RKTVYQKRVLMHGVLK

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14306	44674	A	14392	150	1910	STPPGGPSVLM*STEEPGAGRS QPLCDDLSTRPLSCLGAGCCLW PAKRISAKEEPWYSSRSKDKKE KN\YSSPETTTSGGCHSPGDSQY QELAVALESSSVTINQLNENIES LKQQKKQVEHQLEEAKKTNNE IHKAQMEQLETINILTLEKADL KTTLYHTKRAARHFEEESKDLA GRLQYSLQRIQELERALCAVST QQQEEDRGHCLSSPDQNFSLFTI QSSSCREAVLHRRLQQTIKERA LLNAHVTQVTESLKQVQLERD EYAKHIKGERARWQERMWKM SVEARTLKEEKKRDIHRIQELER SLSELKNQMAEPPSLAPPAVTS VVEQLQDEAKHLRQEVEGLEG KLQSQVENNQALSLLSKEQKQ RLQEQEEMLREQEAQRVREQE RLCEQNERLREQQKMLQEQGE RLRKQEQRLRKQEERLRKEEER L/TKAGKEAVGPGGEAVEEGGE ATKAGGEARALPEPQARQAAG RATVQLRGSEQREKERTAVGA ASKGAAGEARRGEGDAVHGHL SAADL*EGGAAQAVTAADPVR GPAAAAGSLGQSGAPRSCQPPE PTARDPAKPRGSPWRRRWRTT
14307	44675	B	14393	463	3755	
14308	44676	B	14394	175	1835	
14309	44677	A	14395	102	465	RAYCWAYIRLSCLTVILIAWCS QESALSEEEEDTTRPLETVTFKD VAVDLTQEEWEQMKPAQRNL YRDVMLENYSNLVTVGCQVTK PDVI\SSWSKKRSPG*WRKKCL GGTVQNPEEERTAV
14310	44678	A	14396	1	330	
14311	44679	A	14397	1	531	MLLNIPQHTRQSPRAKNYLAQ NVNSVKAWCSQESALSEEEED TTRPLVRLKHLFVSCIILQCSYV LLPLTPEYQLNKFLYVVITMPN FDDFKLISIMFLQETVTFKDVA VDLTQEEWEQMKPAQRNLYR DVMLENYSNLVTVGCQVTKPD VI\SSWSKKRSPG*WRKKCLGG

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14312	44680	A	14398	1	539	MPTTTTREMTQNSSETIKNKNG KKQRKQRKNSKKNRRKQKDE DKTRRQNKRHHKKNDINPEEE RTAVRLKDGGAPAPQAVQEHD AGICSASGGAQETYILVEGKGE ASTSPGQSKGSREGGVGANETC SKKLYRDVMLENYSNLVT/VG CQVTKPDVYSSWSKKRSPG*W RKKFWEALSR
14313	44681	A	14399	322	1227	FDLKMSKCRKTPLQQLASPASF SPDILADIFELFAKNFSYW\KPL NNEWQLPDPSEIFTCDHTEFNA FPWI*RTP*NEVKKPTGVIRTW DEWHEHTCFH**SGE/ISFPHGR KSVNAELWTQAWCKFHEILCS FPLIPQEAFQNGKLNSLHLCEAP GAFIASLNHYLKSHRFPCHWSW VANTLNPYHEANDDLMMIMD DRLIANTLHWWYFGPDNTGDI MTLKFLTGLQNFISSMGTVHLV TANGSFDCQ*NPAGDQRMVKG HCYFPSWNWLHLSKHTQCGNE FIFMTKKKQSLTAKSLPDTFS
14314	44682	A	14400	3	183	KRKEITNSLDAAASRGTVPAAL AGVQYLEPRAGAAGRLGGAG WGRVPRPGSS/SSLSLVGR*GW CPVLRTQGRCCRPPGGCWVGA RPKAWELLSLSLVGR
14315	44683	A	14401	21	399	IWNSAPTASRRPWSLAPGSPRS TWCVASTPPCAPGKAREPRDRS EVPPATAPAVLQSHWPCPRSSR SGSAGNCVGPPHSWAPGHSQH LTPGPGHGGPRGP\CWHLLMQT AWPALTPPGAMPGEAEGQ
14316	44684	A	14402	59	478	RCSQPWHCPAALAGVQYLEPR AGAAGRLGGAGWGRVPRPREL LSLSLVGR*GWRPQEQDQLFPH LRRPVGTRSESTWGNRAGAAT W/RAATPSPWRT*NGTKSKQW TASGLWQKGDGWD*GSGKPPL PLSVPAGQRLVPVC
14317	44685	A	14403	1150	1319	PRRLPTACTP*RS/CSRYWMVP KSPRMTMMMWTKLARMGAQ W*PRKSNACLSRAASS
14318	44686	A	14404	34	304	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPRRAPPPAPRRPVPST TQ/EARRSAASLLSPARPRAHRD GTNNSRRATLRAVTLTARVRG F

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14319	44687	A	14405	1	360	SSSLSYLPAGQGSGPAARHA*A SHPLHGLLCGPSLPNEHRPLLQ GAQSH*PPKG*GVRAHGVGLA GRSTCSP/ECGIH*VKPAGLLSFL GPRCFYEL*QSPRRSAAASLLSP ARSRAHRE
14320	44688	B	14406	80	1166	
14321	44689	C	14407	1	543	
14322	44690	B	14408	1	930	
14323	44691	B	14409	1	1473	
14324	44692	A	14410	388	606	
14325	44693	A	14411	1	798	
14326	44694	A	14412	687	832	
14327	44695	B	14413	1	1218	
14328	44696	B	14414	1	642	
14329	44697	B	14415	1	807	
14330	44698	A	14416	554	724	
14331	44699	A	14417	216	494	
14332	44700	A	14418	1	3408	
14333	44701	A	14419	330	858	VPSLDGQRGLELDTECRLVYLQ SLS*T*RFSTSSPEQLDTECRLV HSQTLC*TQGADWCIYKP*VGL QVELPASPAP\WLAFLSPWVVN GTGRHGAGGGARRGGSGCTGA HGVGGRLRHGRLQVPSPAPWE GSCSLPSPIGPPFKRAHSVLQKG SSTLMVGTCASSPKVVPFHLLS
14334	44702	B	14420	182	1513	
14335	44703	B	14421	1	1608	
14336	44704	C	14422	1	1830	
14337	44705	A	14423	167	433	LPSRGAGLGTCSPPCLSLPPTPW APVRSEPPRRAPPP/GSTVPSPIN HPRAEECERMARDWQAAPPAA PVRDPLGEASWAPEFFGSMLPL
14338	44706	B	14424	32	352	
14339	44707	B	14425	103	451	
14340	44708	A	14426	158	921	LPSRWAGLGTCSPPCLSLPPTP WAPVRPEPPRRAPPSAPRRPVP\ RPPKG*GVPAHGAGLAGSSTCS PDICRVCRSEGTPEKPLYHPCVC TGSIKFIHQEC\YSPDMPSRLPIQ DIFAGLVTSIGTAIRYWFHYTLV AFAWLGVVPLTAWHQLLDLGS TLNPGCSHLVILKLTTSTKTLFP NKATFILVVLSQDKTLMEDPR MEDKWKEDRFSPFNSEALEITL GERHRPQTASVIPWFCSSRHVL NLGKINFEVD

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14341	44709	A	14427	242	515	IQSVHWCIHKP*ARHRVLIGVFT IPELDIKVLHVPTRLRNPAGFTH WILHRDCRCSCMPVLRHAPALL SPWVVNGTGRSRAGDSTHRGG SG
14342	44710	A	14428	759	988	TWPRKPLFPPRPLGL*WEGMLQ RSLTCPGDIFPIILVISIWLLVTY ANFGSWL*FLPRKWVFPFFIPVP NKFLIFI
14343	44711	A	14429	130	788	VLQLIKAVWTPRTQEPSWLPPV NPARELQVELPASPAPCARTPQ LLGGRWDWAPWSRGWRSFGE ARAAQKPMEGVGGSGMAGCR SRALPHGKAAKARRAIEHSTGG LALLGDPVHSPQPLARVLSPSLP RASRAGWLLRVRGPPSPRPPGT PAGRQAPHAAPVPARASPSTPP/ CRAERVGSSPGQPRKGLPQCRG EAEGLLKCHQSGSPGRGEELW HSR
14344	44712	A	14430	108	1686	ANRCPLPHPGTGAGRCLGASA GRAEEAGV*GPLHEGLGYRPA GLFLRADTGHRTPGWGGGGGG AGGRGGAAPGPGVGATRRFAG RRGCARHGAAVPAAVR\CCERL VLNVAGLRFETRARTLGRFPDT LLGDPARRGRFYDDARREYFFD RHRPSFDAVLYYYQSGGRLRRP AHVPLDVFLEEVAFYGLGAAA LARLREDEGCPVPPERPLPRRAF ARQLWLLFEFPESSQAARVLAV VSVLVILVSIVVFCLETLPDFRD DRDGTGLAAAAAAGPFPAPLN GSSQMPGNPPRLPFNDPFFVVE TLCICWFSFELLVRLLVCPSKAI FFKNVMNLIDFVAILPYFVALG TELARQRGVGQQAMSLAILRVI RLVRVFRIFKLSRHSKGLQILGQ TLRASMRELGLLIFFLFIGVVLF SSAVYFAEVDRVDSHFTSIPESF WWAVVTMTTVGYGDMAPVT VGGKIVGSLCAIAGVLTISLPVP VIVSNFSYFYHRETEGEEAGMF SHVDMQPCGPLEGKANGGLVD
14345	44713	A	14431	1	427	
14346	44714	B	14432	8	323	

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14347	44715	A	14433	20	1050	FNLVYMSHVSDEGALSESASAT AASWPPHGFLQHFVPGRPQVPI CLYLLGQKTG*HMAPLLRQVT GSPIPPKTPGRGIRNMKRNEKR RYKTLMADGWELHQELSLGRT SSLPPYKGPGPWSPGFQKVSKG ANPVEIKRGVMLAVDAVIAEL KKQSKPVTKPEEIAQVATISAN GDKEIGNIISDAMKKCGRKGIIT KISSVQSIVTALEIANAYCKPLV IIAGDIDGEALTTLILNRLKVGL QVVAVKAPGFGDNRKNQLKDT VIATGGEVGEVTVIKDYAMLL KGKGNKSQIEKCVQEIIDQSDV TTSEYEKEKLS\EKLSDGVAVL KSHPWSFCTKIYPLT
14348	44716	A	14434	3	764	TTATVLARSIAKEGFEKISKGA NPVEIRRGVMLAVDAVIAELKK QSKPVTTPEEIAQVATISANGD KEIGNIISDAMKKVGRKGVITV KDGKTLNDELEIIEGMKFDRG\ YISHPFINTSKGQKCGISRDAYV LLSEKKIS\SIQSIVPA\LEIAHAH RKPLVIIAEDVDGEALSTLVLN RLKVGLQVVAVKA\PGFGDNR KNQLKDMAIATGGAVFGEEGL TLNLEDVQPHDLGKVGEVIVTK DDAMLLKGKGDK
14349	44717	A	14435	1	3288	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVC
14350	44718	A	14436	2	422	

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14351	44719	A	14437	529	2484	WGINIIKKNKKAAPRAFGVRLE ECQPATENQRWQDLNVISSLLK SFFRKLPEPLFTDEELPLAPSFCP EEENGGRGGGPSPRYRLEPMDT IFVKNVKEDGPAHRAGLRTGD RLVKVNGESVIGKTYSQVIALI QNSDDTLELSIMPKDEDILQLPA ERESGGEASEPPRVVRPEPSTRA LEPPAEDRGDEVVLRQKPPTGR KVQLTPARQMNLGFGDESPEPE ASGRGERLGRKVAPLATTEDSL ASIPFIDICVRPCAWLHALLDW MAQQRVLDMQGQSIGMGVSW DRELEEKGSEKGYDEPTSPSIDL QAKHVPASAVVSSAMNSAPVL GTSPSSPTFTFTLGRHYSQDCST SAHLNIFAGIFDISNDHLQVSTL ESNFTRIHLTHYTGGNFPAWLA WDAVPFSSDLLNLGVHVLETG AGTPFLGSACSSDGIASQMNTA GLPQIRDLPGHYYETLKFLVGH\ LKTIADHSEKNKMEPRNL\ALV FGPTLVRTSEDNMTDMVTPHA *PLTRSWETLIQALQTGSSVTKR YKGKENPCGLTRSLRQCPTLST FLPNIWQDSAPWRPGVSGPVGD LKDSTTCSSAKSKGSWAPKKEP YAREMLAISFISAVKPQAQEAA GDAGAGQQHRRRLGAGGAQS LGRGPQRRGHQERS
14352	44720	B	14438	1	1473	
14353	44721	A	14439	5	694	VPDKWGWCLFMSRYLETAIRT AACAASPRYLNPGRCSAARGPS SQSPRPPWSGHKKRTASPGWG GQSAASPMPPSRSWPASVGGPE FRLSETPSRPFTLSGMK*GWQV HSWAPALFCSVMSFSPDTCCLC K*AHSQPCSPSPSTVILLRETSSN WDWQPEDLGAPKASASPPPSTT RITRLRSSELQLRRLNPSDSCHR GFCFSFRCLLTPEHVLPKTVLRI QPGCKVA
14354	44722	A	14440	303	757	MAWKVSLRGRKVAGRAPSQLR WASPPSSGQSVKSLLLPPARRL CPGPGVPARCHRRI*GLGPGRG WRGEWRRDTNPWEPPQPRSPS/ G/PNCAWSDGCPRGAPRRPRAL *AGAARRAAPARI*VPWRGSAG GCSNRRLQVPAHE*TPTPFIRYL

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14355	44723	A	14441	1	534	RHEDHSEPTFLISPSLLCFLLPSA PPLPRLTPI\PAALLVPAVQRME PVLFLPAPGAAACRVWHPALPP PRQAAVSSSRPCY\PCVARSAPA GRVRAAGVP\PAPPSSSPRLGRV GGRSRSPNVVFRVRGAAPG/PG L*ISPWTP/PLNEAS*RQRGCPAS FAVYGGQEWRPPQWPGPPRGP
14356	44724	B	14442	157	2143	
14357	44725	A	14443	258	4089	QLITCLSRPETGGKFEVDTQRP VCPPSRARAARASAAAVAAAA TLTPPTMDSFDLALLQEWDLES LCVYEPDRNALRRKERERRNQ ETQQDDGTFNSSYSLFSEPYKT NKGDELSNRIQNTLGNYDEMK DFLTDRTNQSHLVGVPKPGVPQ TPVNKIDEHFVADSRAQNQPSSI CSTTTSTPAAVPVQQSKRGTMG WQKAGHPPSDGQQRATQQGSL RTLLGDGVGRQQ/HSGQTSVQC GGGPSDPGEATCHGGQ
14358	44726	B	14444	1	1326	
14359	44727	A	14445	453	710	SQHFGKPRQVDHLRPGV*DQP GQHGETPSLLKIQKLTGRGGAC LW/QSQLLRRLRQENRLNLGGG GCSEPGSCHCPPAWATERDSVS
14360	44728	B	14446	32	290	
14361	44729	A	14447	244	426	
14362	44730	A	14448	69	221	QWRFCGIERGERWGKD*EIGW LPCLCGKK*IWETF\ILFCTKKN SSALGSC
14363	44731	A	14449	27	220	AVILTAKICSFTPEPSKTTSPPGG TNNSRRATLRAVTLTVKVCSFT P*GSAASFLKSVRPRTHQ
14364	44732	A	14450	115	732	EPETRIDPLSWNSSQLPVAALH LPGMSSVGAGQAICNLCCLGDL VSPSSLPALERTGPPPWNRGPK GRGRLPSL/TVSQPSLVIPPGTG KSEVNADRSRPPAYCSNLGRYS GPGPPSLVIPPGTGKSEVNADRS GPPAYCSNHFPSALP**RSSMRS LSLQQTSAWTCRHFHTS\LKSR WRFPNLNSCLLCTCRPNTTWKP CLGACTL
14365	44733	A	14451	528	875	EHGYFQGTLGQKGCKSGKPPG GTLKTLLVTLREPGRLQSP*TSL WVSERLP*YP*GDTGENCPKLS FHLRNLGPS*AG*RERPPQGGL YLPPQAYRLMQGSAFWPLFGY APSPQR

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14366	44734	A	14452	2788	3414	ACFSYIAFWRINTTSTANLSKES LTSTTSRSWVINVNIVIFCTDWL FYKWLLKNFPIYFYMIFPFNQIT FHSMGSCAARASPTSTTPCSTA PSPIDHPRAEE\SSTRRVTGRQL HLQPAKICSFTPEPSKTTSPPGG TNNS\SALP*EL*HSPRRSAASL QFRTR*YPYRYQSQGPGSHF*L PLPLPSSIHDHF*LFHLQHTFQS HALLP
14367	44735	A	14453	662	1338	VLQLIKAVWTQRPLGGRWDW APWSRRWCSSGRLRPHRNQWS GWEAQAWGLQVPEPCPAGRQL RPGEKSSTAPVCTSCCRTRSTA GPTGCPSTRRDPTLSASPS*TST TSLATATASASMWAGSCTSIST RGSASLVHQALTWPGSGPASPR KR\TGSHPVA*AGVRWRAHRSL QPQTPGLK*SSHFSLPSGWNYR HSNHPISQSFPHLSPLSIPQNHH CHHGPFSM
14368	44736	A	14454	3	415	DFLLFSEILPASQSASAILPALPA SHRCPCCLDVPLPPEVPGPARLP VAAASVWRPVQHLSLLGRWA GPT*DRTESRETNAEVEADLPP LYAHGRLEPTAGPSGASAVLST SSEYCPGPHPKMGHRRVTSCLS TCQS
14369	44737	A	14455	659	818	
14370	44738	A	14456	2	710	
14371	44739	A	14457	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGGLHDLKIVVL
14372	44740	B	14458	1	1338	
14373	44741	A	14459	83	426	
14374	44742	A	14460	93	345	APALCLQILLDCKSVRNRTSRF RPREVGIQQYKKGGGAAGKGG TGNAPGFLLFSKDS*KDPTPLPP PLLL*GQRDH*IQLHQE
14375	44743	A	14461	1	1302	
14376	44744	A	14462	1	1174	
14377	44745	A	14463	274	1428	
14378	44746	A	14464	411	627	HCLSHFQNTGPRGDVDFQQEL\ FPVLMADIRKEERSHLCRSSRR TWTILDKS*IQGSRLSSKEQGW GWGTSRK
14379	44747	B	14465	1	1553	
14380	44748	A	14466	226	449	SLQPDI*CSGLRGSLLLV*PKSD
14381	44749	B	14467	1	2061	
14382	44750	B	14468	10	1099	

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14383	44751	A	14469	34	406	GGGFISLDTGSHHKSHPGGS*H ALGWVRPHTLNSP\PSQQPGNC GNPAWEC*GPHG/APSRWSCST PCRPSHPKVPAVRVAGPAGGCT PYRT/PTRRTPR*RPGPCAACDR P\LHPHCGPRGPGAYPR
14384	44752	A	14470	623	1671	VLRSVSSWLPTSMAMTVLAPM LRAMSAGRLLM*PPSMSRCPSL GSHSGGR*PDS/GHAGAHVPPQ GAIFVDSHG*GGDICGHVEVRQ P/QGPQSAYPGRPDGCCG*RQT Q*TWR*LGT*GPTQVPAPKSCS WPTPGPAASCGWRCAPPRTTLR *KSQWTCRPPGPRGPPPPLMPL VLRCASSPWPRPRLAQGQWCS P*APSPSGRSRCAGPRAWRKPS RRAHAAWQGCGAKRGGADSA GAGAPSTSCAYLATPRCAWGP HPPLGGAGLAA*GRAQPCSPAS APAGRG*APGPPGPQ*GCSRPV AGSARSRASARRPSGRVRYGV HPPAGPATLTAGTLGCYPVRRP PGVPG
14385	44753	A	14471	32	972	QSGTFSTKNEGRTTRDVYDGR GPRVGRCGTCVYVRYVHDRPH APPHERARRNDGNTQRTGNAR PGTAMPTATTDQPKGRSTRHK ETKRGRTARNGKQQNNPRK/RP RKDKRKQGSAGEGERGAGGKE KGQPRDTEAKGDRRTDFPPPNG \P*GQSKRGANIGGWFPPPRLGT PNPPLPGPQSAQVSGP*TPQMW MPTGTGCCGGSQ\SGSPPPWCV SP*PVAEALFHSST/PAPRHPSPP SSSPKHSHQPSTPPP*ISLGQGPC RPPKRRPAPDQPQVPRCPEPSC AYLATPRPTMRMQSACRGSAR SRASARRPSG
14386	44754	A	14472	1	3128	
14387	44755	B	14473	239	5474	
14388	44756	A	14474	542	781	PASIIMTGSISHITILTLRVNRLN ASIKRHRLTDWQIR/IKSQDLSV CYIQETHFTCKDPHKLKIKGWR KIYQVN*KQKKK

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14389	44757	A	14475	724	1340	QLTLQGRRVAPR*PSRVALEQE/CGYNALLRYEGFENDSGLDFWCNICGSDIHPVGWCAASGKPLVPPRTIQHKYTNWKAFLVKRLTGAKTLPPDFSQKVSESMQYPFKPCMRVEVVDKRHLCRTRVAVVESVIGGRLRLVYEESEDRTDDFWCHMHSPLIHHIGWSRSIGHRFKRSDITKKQDGHFDTPPHLFAKVRSFYKNPHL
14390	44758	A	14476	1822	2226	KRLFTNRTRITPFVAINSHHHHHHHITIINTIITTTSTINSHHHHHYYHHHHHHHHHHQHTTTTNTTTTNTTTTNNNTTTTITITTTTNTTTTSTINSHHHHHNQHCHHHHHHHHH/HHHHHQYHHHHH*HYQ\HHHHHHYYHHHHHHHHHHQ/HHHHHQHHHNQHHHHQQQHHDHHHHYHHHQHHHHQHYQ\HHHHHHNQHCHHHHHHHHHQHHHDPPHHHQH*HSHQHH
14391	44759	A	14477	232	625	EGCCCIAIMVQKYQSPVRVYKYPFELIMALRK\RYPRCCVTCS*TGGAQQVGFRFLDLPLSLCTP*CLWRTSSSNF*RKAAGCSGSRLQSHHFGLIPQPTAPKPWSSPLHITKPQTLGQRDPGPRTRKRSK
14392	44760	A	14478	1	808	MPKTTACNVHTVTWASCENADSDSTGLRHHDSCEDPASPGRSDLCLVPHPTRPAVRGGRPAGGRCPAVPAEGPWRHLQQAQEGLKRLAGGLERLLENPVRRALPQGAQGHRAEPTEARPHPAPEHRRAGAAAERAERLESQPVGASAAAASAASARIPYLVAVPAAGPPRHRCRRHRRGPGTSSGPRTALIRPATARARAGIVSEPRTAPGATRARPWRQGSHNPVAPSAP*LLRGPSIPWQIRPMPCPTSHQTCSERRPSGRWQMPGSACRRSLETSSAGAGRAQEAGGRLGETSGESG/RAGLYLKELRAIVLNQQRLVRTQRQSIDELERRLNELSA*NRSLWEHPQLPQAQPPPGFLTS*PSPLPALLGTAAAATAGAQEHLQDHGQRSSARPLPAPELASFQNHEQLLAQPEPDPGGRAHTTQSPHQHPGTLGVKANKEKKGPPGCCAAPGTPLQQESPAPSARES

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14393	44761	A	14479	1	831	MIRYFGDYWTQALLTLIPGDPK HPRGPPVKVGVYGGQGYINSL ALCHNFIWRELNRFSLLQDVPL VRYIDNIMLIGSIKFLGVQWCG ACRDIPSKDPADPMVLEVSVAD RDAVWSIWQALIDESQQRPLGF WSKSLPSSADNYSPFERQLLAY YWALVETERSTMGHQVTMLPE LPVMNWVLSDPSSHK/ANGLA GWSGTGKKHDWKIGDKEIWRR GMWMDLSEWSK/D/VKIFVSHV SAHQRVTSAEEEFNNQVDRMT RSMDTTQPLYPTTPVIAQWAHE
14394	44762	B	14480	56	3476	
14395	44763	A	14481	3	591	DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLTM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWTA VALQPLSGTSLQDSSEEKSSQW
14396	44764	A	14482	1	1275	MEKNDIDQSRRRKVVEMNENV QLVRYGEQASDLKTATKFKSPS EVKHIRFIQQAFIGSKLLMRPW TTVTKQILSLKSAKIALSESLIPC RKRAEFVEKQTQAFIMQVSDL QQKVHAQPSQVSTVKVKALIG KEWDPATWNGDVWEGPDEAG DTEFVNSDEAFLPEATAFPSPEV GNDQTVWGLLDTGSELMLIPG DPKYYRGPPVKVGAYGGQVIN RGLAQIQLSMDPVGHRTRPVVS SPLPECIIGTDILSSRQNPHIGSLT DITLVHYIDDIMLIGSSEQEVTIT LDLLVQAVAQAALPVGPYDPA DPMELKVSVADRDAVWSLWQ APIVTMRPERPIMNWVLSDPSS HKVGCAQQHSIIKWKWYIRDW ARSGPEGTNHSRRVCS/LPQVQ APSAR*ATARRGGQAASGCCLF WSCTCFSNFDV
14397	44765	A	14483	604	1760	NSWCRWFNFRY*YPTFYWES* NT*IPLREWFG*NHDASCP*TLD SKSFSFETRTGSPCSSSLQTAYC GTLWIVQGV
14398	44766	A	14484	2710	3060	
14399	44767	A	14485	3	227	
14400	44768	A	14486	3	266	
14401	44769	A	14487	2	564	

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14402	44770	A	14488	2	503	FFFFLPIGFWRQHIPRLSVLLQHI Y*VT*NAASFEWGPEQEKAL*Q VQAVVQVALPLGPYDPADPML LEVSVADKDAGCTRL\QAPIGE SQWRSLGFRSKALRSSAENYSS FERQLLACYWALVETECLTLG HQVTI*PELPIMNWVLSDPSSHK VGHEQQHSIIKWK
14403	44771	A	14489	2	469	
14404	44772	A	14490	1	633	MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAF\LPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPSS GDIKEYFPNAFVLLTTASLQGQ DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
14405	44773	A	14491	1	518	MTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIGSTIKWVVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG
14406	44774	C	14492	33	932	
14407	44775	B	14493	27	2457	

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14408	44776	A	14494	332	2158	RGYVFCSWKKTDGS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQGQQYTF TVLPQWYINSPALCHNLIRRDL DCFSLPLDITLVHYIDDIMLIG\P RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVLFDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTTPVISQWPHEQCGHG GRDGGYAWAQQCRLPLTKAD LNTATAKRPICQQQRPTLSPQY GTIPQGDQPATWWWVDYMGS LPSWKGQRFVLTGIDTYSGYGF AYPACNASAKTAICGLTECLIH HHDIPHSIASDQGTHFMAKEVR QWAHDHGIHWSYHVSHHPEA AGLIEWWNGLLKSQLQCQLGD NTWQGWGKVLQKVVYALNQH PIYGTVSPIAKIHRSRNQGLEVA PLTITPRDPLAKFLLPFPATLQS AGLEVLVPEEGTLPPGDTMIPL NWKLRLPPRHFGLLLPLNQQA KKGVTVLAGVTDLDYKDEITL LLHNGGKEEYAWNTGDPLGLL LILPCPMIKVNGKLQQLKPEAL VPKGVVFPPGDTTMLSLSWKL RLPSGHVGLLMPLSQQVQKGV
14409	44777	A	14495	1	3187	MAEGKEEQVLSYTDGSRQREN EEDAKAETPDKTIRSHETYSLPR EWYEGNRPHDSITSQWVPPTTR GNYGSTIQDEIWVGDHSGYVRP VPVPRSLNSDISYFGVGGKQAV FFVGQSARMISKPADSQDVHEL VLSKEDFEKKEKNKEAIYSGYI RNRKDDYDNHTGIDLVGTIIATI KGSNEEDTDTPLFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTDE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP
14410	44778	A	14496	266	467	
14411	44779	B	14497	152	1245	

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14412	44780	A	14498	1	1445	MLRAAAGGQGLAAAGMGLCA RPAGGSQLPRERMKGNRACLP LPPAVALTKGREKPDAGHQGR STQMMRESERGPCTHWTEERP GRQLKILLQKQMRQNTLMAFQ VSWDGRNKEIGRTFPHATAPHT QQLIFAMKIKRTGVTVEPWGLF ETGQRIRPIQAAGL*LSSSSTTC VALAPLLTMHVKSLALLSAP/Q MGALSTITSITTTRRQTPAESHF PAARFHLLAPHSPTLPPCCPGEP SESAVTVLCFAKGKTAQDAAV\ PTTSLTAAGHLAPRS*SSWSRM PVKVRRAPDSLPETSAHALPLT H*SWLPSASWGPASRALPGSEW VLKPVWQ/AITGPVSQITSSPGIP KP\GPLQA*GSAHPQALGFSVL QIPLSNSPTSPMTPPLPRPKISNS SLPSQ/PPQALFPNRWTNSSSPV HVITSAAQ\PRTPREWPAVSFYR TTATTASLIPHLWAPPQEN*QTS PAQNGSTLPCMSQATFHFPSP
14413	44781	A	14499	44	455	HLRNRTR/PSQITPHIYNHLIFDK /PLFNIWWWENWLAICRKLKLD PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/TGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP
14414	44782	A	14500	1	346	
14415	44783	A	14501	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL\DPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP

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14416	44784	A	14502	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
14417	44785	A	14503	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL

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14418	44786	A	14504	1	2877	MENDFDELREEGFRQSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERVSAME DEMNEMKGEGKFREKRIKRNE QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLYTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPITGAE
14419	44787	A	14505	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQHFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSL*RRI/W KRLQRTLSIPVLDAV*PPMF*AS
14420	44788	B	14506	1	2265	
14421	44789	A	14507	1	2832	
14422	44790	A	14508	1	2109	
14423	44791	A	14509	1	2757	
14424	44792	A	14510	1	2304	

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14425	44793	A	14511	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD
14426	44794	B	14512	1	2337	

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14427	44795	A	14513	1	1544	HINRAKDKNHMIISIDAEKAFD KIQQHFMLKTLNKLGIDGTYFR KSINVIQHINRAKDKNHMIISID AEKAFDKIQQHFMLKTLNKLGI DGTYFRKSIN/DNPAYKQSQRQ KP\LIISIDAEKAFDKIQQPFMLK TLNKLDNIIVYLENPIVSAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNSQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTKKWKNIPCSWVG RINIVKMAILRKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA PVAKAILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI GQWNRTEPSEITPHVYNYLIFD KPEKTKQWGKDSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIKLKSFCTAKETT IRVNRQPTEWEKTFATYSSDKG LISRIYNELKLIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSSSLAIREMQIKTTVRYH LTPVRMAIIKKSGNN
14428	44796	B	14514	110	2153	
14429	44797	A	14515	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
14430	44798	A	14516	3	2820	ENKDTTYQNL\WDAFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKREK NQIDTIKNDKGDITTDPTEIQTTI REYYKHLYANKLKNLEEMDKF LDTYTLPRLNQEEVESLNRPITG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFR

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14431	44799	A	14517	687	2274	LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARMAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDVDQWNRTEP SEITPHIYNYLIFDKPDKNKQW GKDSLFNKWGWENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKTLEENLDITIQDIGMGK DFMSKTPKAMATKAKIDKWDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKRCSSSLAIRE IQIKTTMRYHLTPVRMAIIKKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCQMRKNTK TLI
14432	44800	B	14518	1	3192	
14433	44801	A	14519	1	2814	
14434	44802	A	14520	1	3144	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK

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14435	44803	A	14521	1	2616	TTYQNLWDAFKAVCRGKFIAL NVHKRKQERSKIDTLTSQLKEL EKQEQTHSKASRRQEITKIRAEL KEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDAI KNDKGDITTNPTEIQTTIREYYK HLYANKLENLEEMHKFLDTYT LPRLNQEEVESLNRPITGAEIVA IINSLPTKKSPGPDGFTGEFYQR YKEELVPFL/LKLFQSIEKEGI\M NIDAKILNKILANRIQQHIKKLI HHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGIDGTY FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSEITPHIYNYLIFD KPDKNKQWGKGSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGMDFMSKTPKAMAT KDKIDKWDLIKLKSFCTAKETT

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14436	44804	A	14522	782	3024	SKTVPTGNSLEPTQNCWLQQW LPQDIEIEKQEQT/HSKASRRQEI TKIGAELEEIETQKTLQKINESR SWFFEKINKSDRPLARLIKKKR EKNQIDAIKNDKGDITTDPTEIQ TTIREYCKHLYANKLENLEEMN KFLDTYTLPRLNQEEVESLNRPI TGSEIEAIINSLPTKKSPGPDGFT AEFYQRYKEELHINRTKDKNH MIISIDAEKAFDKIQQRFMLKTL NKLVLEVLARAIRQEKEIKGVQ LGKEEVKLSLFADDMIVYLENP IVSAQNLLNLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNERKEDTNKWK NIPCSWVERINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKSILSQKNKAG GITLPDFKLYYKATVTKTAWYS YQNRDIDQWNRTEPSEILPRIYN YLIFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDPFLKP YTKIKSGWIKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLKSFC TAKETTIRVNRQPTEREKIFATY SSDKGLISRIYKELKQIYKKRTN NLIKKWVKDMNRHFSKEDVYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRITI VLLPGSLIVRSFHVTLNAILLHP
14437	44805	A	14523	1	1701	
14438	44806	A	14524	1	4434	
14439	44807	A	14525	1	2913	MGGPAALCIAVVPGDLVVALC LEEGLGSGIATWACSPWRISQG THLTFRSSLAVAAIPEGLPIVVM VTLVLGVLRMAKKRVIVKKLPI VETLGCCSVLCSDKTGTLTANE MTVTQLVTSDGLRAEVSGVGY DGQGTVCLLPSKEVIKEFSNVS VGKLVEAGCVANNAVIRKNAV MGQPTEGALMALALKDQEDIY FMKGALEEVIRYCTMYNNGGIP LPLTPQQRGAGPGDTALPSAAS AFARMSAAERNDAFQG

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14440	44808	A	14526	1	3009	MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDGS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVPNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14441	44809	A	14527	1	4800	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVNNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14442	44810	B	14528	1	2901	
14443	44811	A	14529	569	3443	RKH*TWKRTSSTSHHKNMPN* LEKQEQTHSKASRRQEITKIRAE LKEIETQKTVQKINESRSWFFER SNKIYRPLSRLIKKKREKNQIDT IKNDKGDTTTDPTEIQTTIREYY KHLYANKLENLEEMDKFLDTY TLPRLNQEEIESLNRPITGTEIVT IINSLPTKKSPGPDGFTAEFYQR YKEELVPFLLKLFQSIEKEGILP NSFYEASIILIAKPGRDTTKKEN FRPISLMNIDAKILNKILAKRIQ
14444	44812	A	14530	3591	8157	TGTSQKKTFMQPKKHMKKCST ITGHQSNANQNHNEIPSHTKLE WRSLKRSGNNRDVGNVVEAM YGDLPPPIMLIGHSMGGAIAVH TASSNLVPSLLGLCMIDVVEGT AMDALNSMQNFLRGRPKTFKS LENAIEWRNIKDLSWADSIKNV AAASLACISGALPASAVTTSPD NKRMARNVLKYERLLAESPNH VVAEAVIQRPNIPHLQTRDTYE GLCQTLGSQPTLYQIPSLYCSYE TNSNAYLLLQPIRKEVI

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14445	44813	A	14531	172	328	AVKTEPEMKSQATKLSVVHEK KSQEGKPKEHTEPKSLPKQASD TGSNDAHNIKAVSR*SHRQPSC LWFMRKNPKKESRKNTQSQKA YPSRHQIQEVTMLTI
14446	44814	A	14532	3	660	TSPDCWEEGRSVDWPRPGPALS LHNCKLDLGIEGGTLQPPTPSF* PTGTRAV/PTRRRSRQETQLNSE RTVSPGSR**EKRTSRAW/RSPL QGPGPGHAGQVAGGTGPRTGS TRGD/TLQKCGKIQSVPLNCELI PI*/PSILKPKVLPCSCPGIGASSS\ CPSD*VFFCTS*PWPYLLSYPLS MNFYRYHDHILKLLVQYTLYL LLQFLQVLLKYLLSHPKQHS
14447	44815	A	14533	1	1086	MVDNDVPWPLVVAQEKGQPD LCLSSKGYRPLALVQLDFHQVS VTSKIFILSGALRSLTGAATAD WTCRVLVIYPHDIMADSECNSL LVPSTTRKIMKHMLASEKIKTQ NFNYNVDECVSLLYHHKANKL EAAEARQECELLRVASVSRHC W/RDPAHPHSCWPRC*APHCLG PARAPNARPAKPATTWNLRSSR APCAAPVPTQSWAGAPSGTAG AEPS*ECRPPENQARTAGSGVH AEACAPATCPACPGPGPCSGLP SSGRALFLL/CATLAIPCV*V*LC FLATPPPCR*HVTAPSAGKCIW* PDA*VTK/PRDLCGPVQVARDN GPRQVAQKKESSSYVSWFGTFI SRVGDRSPPPRRAATL
14448	44816	A	14534	23	506	PDIDNIFSEFGAKSKPYLTVDQ MMDFINLKQRDPRLNEILYPPL KQEQVQVLIEKYEPNNSLARKG QISVDGFMRYLSGEENGVVSPE KLDLNEDMSHPLSHYFINSSHN TYLTGMNFLVLCYFSQSHQISP TSTFCCSEAEV/WFSSISCEVPLR TLGFHH

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14449	44817	A	14535	341	1248	KNAFTSFLTSFPPGQISVDGFMR YLSGEENGVVSPEKLDLNEDM SQPLCFMGIWGLFCWCFIAGQL AGNSSVEMYRQVLLSGCRCVE LDCWKGRTAEEEPVKILAY*IY MCSHF*EVIEAIAECAFKTLSLP TFLLLFLFSLSPKQQAKMAEYC RLIGSSIFKEYAFHFY*LESGVPL PSPMDLMYKILVKNKKKSHKS SEGSGKKKLSEQASNTYC*NGD MMICY*NLTGEADTESD\DADS GNV/CLFYSYFQGTAGSEAMAT EEMSNLVNFLTFPFFVLLLLNSE RNKSFEMSSFVETKGL
14450	44818	A	14536	574	647	C*PGNM/HISGQHLVAGEKEAE SEDEEEEDMKLLGTPEGGSKFT QKKVKLAADEDDD/DDDADDD DDDDDDDDFDDEETEEKAPV
14451	44819	A	14537	3	630	PGATHASAPPGVLRLKCGSGPV HIIGQHLVAVEEDAQSQDEEEE DVKLLSISGKRSAPGGGSKVPQ KKVKLAADEDDDDDDEEDDD EDDDDDDFDDEEAEQQAPVKK SI\RDTPAKNAQKSNQNGKDSK PSSTPRSKGQESFKKQEKTPKTP KGPSSVEDIKAKMQASI/EKKG GSLPKVEAKFINYVKN\CSRMT DQEAI\QDLWRWRRSL
14452	44820	A	14538	1	1971	
14453	44821	A	14539	316	1169	RVGGQSHGTQRISLCRHSVCSP LARQSPSNMK*VRTEEIQMAVS CYLKRWQYVDSDG\PLKQGLR LPQTAEELAANLTVHRESHCAD IVSAVP\CQAEPQQYEV\QFGRL RNFLIDSDSPHSHEVMPLLYPLF VCLHLSLVQNSPKSTVESFYSR FHGMFLQKAS\QKGVIEQLQTT QTIQDILSNFKLRAFLDNNYVV HLQEDSYNYLIHYLQSDSYTAL CKMFILLIHLDVQPAKTTD*QL YASGSSSRSENNYLEAPDMPSPI LQNDAALEVLQERIKQVKDGC PSLTTVCFYNT*QLLNTAEISPD SKLLAAGFDNSCIKLWSLQSRK LKSESCQVDMSRIHLACDILEE
14454	44822	A	14540	1	297	

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14455	44823	A	14541	2	1089	APLLGECRSGRGLASSRSRRRT TMTQSVVVQGKLRRAGRDLVA AESSGHVSCLMSYSLSFLSSGRS RLALREHAAVNQVPARRREPPR LSARSSSPYSFHLQSE*L*KKIH* LYFIFLSQAVLIDMEEGVVNEIL L*IRTNQIKK*MQGIFKIHILIFR AVGHKVFGSLYQDQILEKFQIL HNYILNHLC*FLKTL*SSGTGSG LGTFLLKVLEDEFPEVYRFVTSI YPSGEDDVITSPFLVEYHLHPLF LIASLPMFFPQKSLFDIISKIDLM \VNSGKV/GGTTVKPKSL\VTSSS GALKIELHLKCIILKLKIFSF*C* LFSSARFEGSLNMDLNEISMNL VPFPPSS*EIVSLKYVLYFN
14456	44824	A	14542	129	461	TCISGWHLFRASVTCPGIQTSPH NWHISDNSSLPNNIFIVCWNLL GMTRNYIIFIEQPLKMNLWKIA TSKIRGKAFSDGIS\GNPQCNTR FHVVEKRTGQLLPGRYYSKPF
14457	44825	A	14543	1	522	
14458	44826	A	14544	1	927	MEDLLTEARSPYWGRARAKIQ DSCWSVTSDPNAGSVDILAPLL LPSPSSYLPNFTCTVSVVTSHLH EAFLDLGFRGTGGSNCKTSRQV QLNNQKRKKKKSKSLPFHMSL QIQNYKTQEEPHAKPSSQQHQH SEHESIQTKLVFRSSMTYMHTL KLIREKGSIMLSSTQGECPNSTC RWPAEEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNLWKIATSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQT T*INPDKISIQKQHDIHAYIEAD KRKRKHNAVIHTG*M/YQI/GTC RWPAEEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNLWKIATSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQ\I LNVKTMRMKTFMMIYYHLMN

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14459	44827	A	14545	1	882	MAEILTQVPDDMLKKKTPRVK SVWRSQRGSCTPLIGTTELTLD TSHMSIRNMDRSHINVHTVRKP SADLPYFRTHEWAHTGGKPYD CEECGKSFISRSSIRRHRIMHSG DGPYKCNFCGKALMCLSLYLIH KRTHTGEKPYECKQCGKAFSH SGSLRIHERTHTGEKPYECSECG KAFHSSTCLHAHKITHTGEKPY ECKQCGKAFVSFNSVRYHERT HTGEKPYECKQCGKAFRSASH LRTHGRTHTGEKPYECKQCGK AF*PRFQMTC*RRKLPE*NQCG EVSVGH\HSLNRHHRADTGHKP YEYQEYGQKPYKCTYCKKAFS\ YLPYFRTHEWAHTGGKPYDCE ECGKSFISRSSIRRHRIMHSGDG PYKCNFCGKALMCLSLYLIHKR THTGEKPYECKQCGKAFSHSGS LRIHERTHTGEKPYECSECGKA FHSSTCLHAHKITHTGEKPYEC KQCGKAFVSFNSVRYHERTHT GEKPYECKQCGKAFRSASHLRT HGRTHTGEKPYECKQCGKAFG CASSVKIHERTHTGEKPCSSNTS
14460	44828	A	14546	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL\GILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14461	44829	A	14547	2	1044	AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLLRLASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALSSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNG\GGLA GMGGIQNEKETMQSLRDRLAS YLDRVRGLETENWKLESKIQEH LNVTRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEGKQV

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14462	44830	A	14548	1	1212	GPGTGIAGGLAGMGGIQNEKET MQSLNDRLASYLDRVRSLETE NRRLESKIREHLEKKGPQVRD WSHYFKIIEDLRAQIFANTVDN ARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKVIDD TNITRLQLETEIEALK*ELLFMK KTPEEEVKGLQAQIASSG\LTVE V\DAPKSQDLAKIMADIR\AQY DELARK\NREELDKYWSQQIEE STTVVTTQSAEVGAAET\TLTEL RRTVQVFGDSTWTSMRNLKA\ NLENSL\GEVEARYAL\QMEQL\ NGILLHLESQLGQTPRTEAQRQ AQE\YEALL\NIKVKL\EAEICHL TRPPSWKIGEDFNL\GDS\LDER NSMQTIQKTTTRRISWIGQSGV LRPIDTKVLEALSQQEASGTLL GKQEANKKFQSFK
14463	44831	A	14549	1	2382	
14464	44832	A	14550	2	173	
14465	44833	C	14551	1	732	
14466	44834	A	14552	455	682	AWKRAVALGKSRPMGAVAFK RRMQPVAGPRAMQEKPFPSSSS SLSIPPAF*YRLALSLAEPSRRW RARTGALMQL
14467	44835	A	14553	158	368	
14468	44836	A	14554	87	251	
14469	44837	A	14555	1	1026	
14470	44838	A	14556	201	578	
14471	44839	A	14557	336	767	AFVRAGSRFGGTPGARPDPAPA TRAPNPVGQSRHLRAASSRGRL FLRRTRDRKFPRRPRLSRRLLG AI/GCRWNQPRAAEKSFSAGAV LDFSPGLSCLPAVQGSGPAARH A*ASHPLHGLLCCPSIPDEHHPL LHGAQSHRPPKG
14472	44840	A	14558	6	535	ARHRVLIGVFTIPELDILSTSPPD SGAQLASPS\DPAPGLQVELPAS PARCARIPQPLGGRWDWAQTQ EPSWLHLVEPAPGLQVELPASP TPCACIPQPLGDRWDWAPWSR GWCSLGRLGPHRSPWSGWEAE AWRAAGPEPCPTGRQLRLGEK SSAAPVGWHCWGTQYTLRSH WPGC
14473	44841	A	14559	375	638	
14474	44842	A	14560	92	514	

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14475	44843	A	14561	54	380	SCHHYCRIHRRCARFLAGP*LPS RGARLGTCSPPCVSLPPAPWAP VRPEPPRRAPPPAPQRPVPSTTQ GLRSAGARRGTGRQLHLQLRG SAASFLKSVRPRTHQFRTH
14476	44844	A	14562	531	773	
14477	44845	B	14563	92	1774	
14478	44846	A	14564	1	390	LHDLQLSKPLSDDTALTDGG/Q PLPARWWAQPGRLQRCARFLA GP*LPSR/WGRARDLQPAMPEP PTPSVGSCAAQASPTSAAPCSM APSPIDHPRAWPVLCSFCMLLS LFVASISSCSQHQPMQVGTMVC L
14479	44847	A	14565	165	545	SLHSKLCWWLQQLWVTDTCPR CSVQDCRQRWASAGNQS*RLL VDPAPGLQVELPANPVPCARIP QPLGGRWD*APWSRGWCSSGR LGLHRSPWSGWEAQAWRAAG PEPRPAGRQLGAMSCKVETGT
14480	44848	A	14566	1	309	SACLAGRPIRGEGRPRDLQPAM PEPPTPSMGSCAARASPTSATPC STAPSPIHHSRAEECGHTALG/H GRQLHLQPRNLPQTINWRTTYS SFPATLNRLDGGG
14481	44849	B	14567	1	843	
14482	44850	A	14568	143	535	
14483	44851	A	14569	375	571	
14484	44852	B	14570	289	972	
14485	44853	A	14571	27	363	
14486	44854	A	14572	2	490	
14487	44855	A	14573	574	961	RLTLPDRLGSPPDTHQAQQITW ALLPQGFADSPHYFSQAQISSSS ITYLGIILHENTRALPADHV*LIS QTPISSTKQQLLSFLGMVRYFC LWIPSFTILTKPLY*FTKANLAD PTDPKSFPHSSFRSL
14488	44856	B	14574	182	1513	
14489	44857	A	14575	894	1305	QTQEPSWLHLVDPALGLQVELP ASPVPCARIPQPLGG*WDWAP WSRGWCSSGRLGPHRSPWSGW EAQAWRAAGPEPCPAGRQLRP GQHPL/RHMNKSQALSLLIAQP LGINLLSWWPPKYNRPVPLIGL SGLLIPATF
14490	44858	A	14576	531	801	

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14491	44859	A	14577	441	783	RAPPPAPWRPVPSTTQGLRSAG EQRGTGRQLHLSAAPVRDPRG EAIWAPESGRSAASILKPARPPA HREERTTPDAPP*EL*HSPRRSA ASLREDPWLHS*SQ*DQEPTNS GHTVSQDQSYYS*LEVSETKNP PIPDTL
14492	44860	A	14578	344	1632	FLAGPYLPSHGAGLGTCSLPCL SLPPTPWAPVRPEP/PPMSTTPCS TAPSPIDHPRAEECERTAQDWQ AAPPAAPVWDPLGEASWAPES GTNISITPGNATFVTRVQGQAW FASCITGHDMSSLKTSSVVVLR RQSEALLPANLTCNWQDSSAL ATLESALSQVRHKRFTFTLMVF TGSAIDIMATVSIAVVSITESVQ TTAFVDNLAKNICDELLLQDM DEAGNQHSQQNNTRTENQTPH VLTHKWELNNENIRIQGGEHYI LGPVGGRDEKTLLLRTYCLKSQ EGADTKCRNKHNKETQKQSKS LVYSSTLNPEKLLVCKRLSLEL TRPENTLRCTNIGKLKAVAGG MSAASGIYLETDTQPYPLKQEL KEIKECVGKNSVVVVFLVRKK LSVSQYAFARCLDAKHSTSENV EIAGKLRIQSFEVGKQL

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14493	44861	A	14579	3	2233	NWLPSVSRCQETHKIAANQSLT QRQMPLTSLYCDVVILPVSVGL ESLQSPYYRTSPCDPVSQFCLIK ISASSLPVLSLWKTLKNAQSYQ RDYRHDNKAHYFQKLVTMQE NLYVLLCDEELDAVSLEAVHQ QKMKNRQAHSSSGCCQKVAN APRNEESSGQFRVIGNEKFEKG PCGVRQQIFEKVLLPNRTCEFV TPRFNRNFEDLIKDLKAAETLID FLVYEPKNQRRLVNRFRLPCKL LHNLGHPLKTDAAQSPRKPPGP SWMPSFGSKPPSHPPLVSPHLNP QVWDTSSPSLATEHASLTISLKP NHPYPAQSQYSIPQHALKGSKP VITRLLEHGLLKPINSPYNSPILP VQKLDKSYRLVQHLCLIYQIVL PIHPMVPNPYTLLSSIPFTTHYS VLDLKHAFFTIPLYPSSQPLFAF TWTDPDTHQAQQITLAVLPQCF IDSPHYFSQAQISSSSVTYLGIIL MKTHIGLGAVEQGVVLVGEAR AAQEPMEWVGGSGM/CGLQVP SPAPWEGS*GPARNRAQ\PVTIV PVLDFNPAFHIIPDTTPDHHDCI SLIHLTFTPFPHISFFPVPHLEHT WFIDGSSTRPNCHSPAKAGYAI VSSTSIIEATALPRSTTSQQAKLI AYTDSKCAFHILHHHAVIWEER NFLTMQGASIINAFLIKTLLKDI LLPKEAGVIHCKGHQKASDPIT QDNAYADKVAKKQLAFQLLSL
14494	44862	A	14580	1	642	SGTVPPTFVRTVIQAQGARTVI QQSLIGSLYIFRHCVRCQGIESV FVIIIWSRVGYDEKGFCLFTSVL GVWGHVRTKPCLLITWRTLKS RSGLE*PAGFSSSPGTSPQIIRKQ KRGVPQHPVCDLPGRFRPRAGT PLAAQIQVPGLPPCGHQE*NRR WAGSSALCPPYLCARAGTGAV CRACEPAGV/AGWAWAWWAP HSEHAASPAGPRQWGT
14495	44863	B	14581	393	549	
14496	44864	B	14582	1	591	
14497	44865	C	14583	226	828	
14498	44866	A	14584	1	1362	

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14499	44867	A	14585	1	585	MANVHQTMPMRLRKLPDSFKP PEPKSNSQRVSTEAGTAGALTP QHVRAHSSPASLQLGAVSPGTL TPTGVVSGPAATPTAQHFQQSS FEIPDDVPLPAAREMAKTSSGQ RYFLNHIDQKTTQQDP\RKTML SQMNVIANPPVQQNMMNS\PQS PQGGV/MGGSNSNQQRQMRPQ QLQMEERLQLKQQ*LLQQELA LR
14500	44868	A	14586	345	1053	RWRLQNLSFCSSCSGSGSEGAT CFARGRQQSNLQSKIKFPSNTD SRSTGYNSFDRQPNICFYKRQE TPHTGPHPVPEGRPYPMPG*CG A*SPGPFASRN*SEKN*SYKCSL HTAFNVIFSSVI**RYCTRQW\HI VKCLDSFCDPFLISDELRRASTD AGTAGALTPQHVRAHSSPASLQ LGAVSPGTLTPTGVVSGPAATP TAQHLRQSSFEIPDDVPLPTSW GEAKTSSGSKIPF
14501	44869	B	14587	607	1185	

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14502	44870	A	14588	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
14503	44871	B	14589	1	1647	
14504	44872	B	14590	1	2025	
14505	44873	B	14591	4	2121	
14506	44874	A	14592	2	1879	
14507	44875	A	14593	1	2130	
14508	44876	A	14594	1	3018	
14509	44877	B	14595	1	3171	

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14510	44878	A	14596	1	2700	MEKKQSRKTGNSKNQSASPPP KECSSLQATEHSWMENDFDEL REQGFRRSNYSELKEEVRTHGK EVKNLEKRLDEWLTRITNAEKS LKDLMELKTMARELLDECINLS SQFDQLEERVSVMENQMNEMK PNLRLIGVPESDGENGTKLENT LQDIIQENFPNLARQANIQIQEIQ RMSQRYSSRRAIPRHIIVRFTKV EMKEKMLRAAREKGRVTLKG KPIRLKADLSVETLQARREWGP IFNILKEKNFQPRTSYPGKLSFIS EGEMKSFTDKQKLRYFVTTRP ALKELLKEALNMERNNRYQPL EKQIQTTIREYYKHLYANELEN LEEMDKFFDTYTLPRLNQEEVE SLNRPITGFEIEAIINSLP/TKKSP EPGGFTAEFYQ\RIEKEGILPNSF YEASIILMLKPGRDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHQDQVGFIPGMQGWFNIR KSINIIQHINRTNDKNHKIISIDA EKAFYKIQQPFMLKTLNKLGID GSYLKIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NLVLEVLARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIA SAQNLLKLKGNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSEL PFTIASKRIKYLGIQLTRDMKDL FKENYKPLLNEIKEDTNKWKNI PCSWEGRISILQMAILPEVIYRF
14511	44879	A	14597	1	2310	
14512	44880	A	14598	1	1305	
14513	44881	A	14599	1	2148	
14514	44882	B	14600	1	777	
14515	44883	A	14601	2	2971	
14516	44884	A	14602	1	3810	

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14517	44885	A	14603	1	1773	MNIGAKIINKILANQIQQHIRKLI HHDQVGFIPGMQGWFNICKSIN VIQHINRTKDKNHMIISIDAEKA CDKIQQRFMLKTLNKLGIDGKY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKDIQLGKEEV KLSLCADKMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLQIHQTRDVKDLFKEN YKPLLKEIKEDTNK\NIPCSCVG RINIVKMAILP/KELEKTTLKFIW NQKRARITKSILSQKNKAGSIM LPDFNLYYKATVSKTAWYWY QNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDPLLTL YTKINSRWIKDLNVSPKTIKTLE ENLDITIQDIGMGKDFMSKTAK AMAAKAMSTKAKFGKWDLIK LKSFCTAKETTIRVNRISSYASS STSLQAFSRKILNCSKRFFKIAQ MCKLVELRPQDMHTSRGSGNC SEARTLLCDFSAGRTSVNHGRI WRQIREAGAADPEIGLEVCNKN PTSFTLFYFLSYTTG
14518	44886	B	14604	1	2070	
14519	44887	B	14605	1	3190	
14520	44888	A	14606	1	3370	

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14521	44889	A	14607	569	3030	RKH*TWKRTSSTSHHKNMPN* LEKQEQTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKKREKNQI DTIKNDEGDITTHPTEIHTIIREY YKHLYANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLKLFQSIEKEGILPNSF YEASIILIPKPGRDTTKKENFRPI SLLNINAKILNKILANRIQQHIK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIISID AEKAFDKIQQPFMLKTLNKLGI DGTYHKIIRANYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLARAIRQEKETEGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQVFLYTDNRQTESQIISEL P\FTIASKRIKYLGIQLTRYVKDL FKER/YNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIWNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPDKNKQWGNDSLFNKWC WENWLAICKKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLEEN LGNNIQDIGMGKDFTSKTPKA MATKDKIDKWDLMKLKSFCTA
14522	44890	A	14608	1	2742	
14523	44891	A	14609	1	3828	
14524	44892	A	14610	1	2667	
14525	44893	A	14611	1	2325	
14526	44894	A	14612	1	3057	

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14527	44895	A	14613	603	2973	DNTARGTIRQQHLLFTNIRCSA ASAADTQANRVWSGPPANSNR PAA\RVLTVRRKTNKQKGHPH QNPICTSPSSKTKETQTTIREYY KHLYANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRITESDIE AIINSLPTKKSPGPDGFTAEFYQ RYKEELVPFLLKLFQSIEKEGIL PNSFYEASIILIPKLGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKHIHGQVGFIPGMQGW FNIRKSINVIQHINRTNDKNHMI VSIDAEKAFDKIQQPFMLKTLN KLGIDGPYLKIIRAIYDKLTANII LNGQKLEAFPLKTGTRQGCLLS PLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLCLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTGDV KDFFKENYKPLLNEIKEDTDKW KNIPCSRVGRINIMKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKSILSQKNKA GGITLPDFKLYYKATVTKTACH RVGRAQQHSISKWKWYIHDWS QVGPEGTNDSARYPDTTQKWT AAALQPLSRTSLKDSHEGKSSQ WAELRAVHLVLRFAWKEKWP DVQLYTDSWAVASGLAGWSG TWKKHDWKIGDKEIWGRATPV IAQWAHEQRGHGGRDGDYAW
14528	44896	B	14614	1	3105	
14529	44897	A	14615	1	3654	

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14530	44898	A	14616	735	2839	RSFPRSRPSPFLLLSRYLRIHMV FSVLPFGLQNPKYLLSGSLQEK FRTPGINSHKTLDPNRVIIKVRR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITTDATEIQTTIREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPITGSEIEAIINSL PTKRSPGPDGFTAEFYQTYKEE LVPFPLKLFQSTEKEGILPNSFY EASIILIPKPGRDTTKKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHYDQVGFIPGMQGWFNKRK SINVIQHINRTNDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCPLSPLLFNI VLEVLARAVRQEKEIEGIQLGK EEVKLSLFADDMIVYLENPIVS AQNLLKLISNFSKVSGYKINIQK SQAFLYTNNRQTESQIMSELPFT TASKKIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPC SWVGRINIMKMAILPKVICRFN AIPIKLPMPFFTELETTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITPHIYNYLI FDKPEKMSIIDTGGWYEAPVSS FFKEGLCRTGTENQVNRQPPAA SPFKVYVSCTGSLHPRPHYFLE
14531	44899	A	14617	1	2250	
14532	44900	A	14618	1	2870	MKAEIKVFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITKIRAELKEIQTQ KTLQKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITTDPTEIQTTIREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGAEIVAIINSLPT KKSPGPDGFTAEFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK

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14533	44901	A	14619	248	2623	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMLLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAEFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASIILI PKRGRDTTKKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIPGMQGWFNICKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLGIDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWYWYQNRDIDQ WNRTEPSEITPHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKLKLDPFLTPYTKIHPRWI KDLNVRPKTIKTLEENLGNTIQ DIGMGKDFMSKTPKAMAAKA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKK\TNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPSLAIREMQIKTTMRYHL
14534	44902	A	14620	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14535	44903	B	14621	1	2758	
14536	44904	A	14622	1	5178	

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14537	44905	A	14623	1	3382	MGDFNTPLSTLDRSTRQKVNK DTQEFNSALYQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCERTEIITNYLSDHS AMKLELRIKNLTQNCSTTWKL NNLLLNDYWVHNEMKAEIKM FFETNENKDTTNQNLWDAFKA VCRGKFIALNAHKRKQERSKID TLTSQLKELEKQEQTHSKASRR QEITKIRAELKEIETQKTLQKIN ESRSWFFERINKIDRPLARLIKK KREKNQIDTIKNDK
14538	44906	A	14624	965	4091	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID
14539	44907	A	14625	3	3229	
14540	44908	B	14626	1	2791	
14541	44909	A	14627	1	3158	MVKGSIQQEELTILNIYAPNTG APRFIKQLLSDLQRDLDSHTLIM GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDIYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNYLSDHSAI KLELRIKNLTQSRSTTWKLNNL LLNDYWRKQERSKTDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKKEKNQID TIKNDKGD
14542	44910	B	14628	1	7849	
14543	44911	A	14629	1	3985	MENDFDELREEGFRRSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRSLRSRCDQLEERVSAM EDEMNEMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLARQANVQIQEIQRMPQRYSS RRATPRHIIVRFTKVEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKID

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14544	44912	B	14630	64	5735	
14545	44913	B	14631	891	6894	
14546	44914	A	14632	33	476	
14547	44915	A	14633	1	360	GQGEPKQLGRHPGVLRPHVVS AKTGDAC/IWTQVRNLFPERPK VQWKEGCA\LQSGNSQESVTEQ GSKVSAYSLSSPLTLSKADYEK HKLYACEVTHQGLSSPVTKSFN RGEIIEGEVPPCI
14548	44916	A	14634	40	508	LPGECHRAGQQGQRLQPQLLG LLMLWVPGSGGEIVMTQTPLSS SVTLGQPASISCRSSQSLVHSDG NTYLTWLQQRPGQPPRPLIYHV FKRFSGVPDRFSGSGAGTDFTL E/ISGRVEA*\DVGVYYCMQG\T QFPCSFGQGTKLETKRTVAAPS
14549	44917	A	14635	3	652	AWWNSETPAQLLFLLLLWLPY TSGEIVLTQAPGTLSLSPGERAT LSCRASQTIGSTYLAWYQQRPG QAPRFLIYGASSRATGIPDSSSSS SSSSSSSSSSSSSSSSSSSSSQQ YNNWPPGGTFGP\GTKVEIKRT VGCTHLFFIFPAHLMSQLKIWE LPSACVPVCNNF\YPREVQSYSG KVDN/VPSNRVTPRESVTEQD\S KDSTLQPSAATLDA
14550	44918	A	14636	3	440	
14551	44919	A	14637	457	1270	SRRVSFPPSA*QAVSDPSRQQLP SLRLRWGPEGRSFPAENLGRGV RWVGGRDPLAA\LP*SSGPLNA GRLFARPQESGAPRIGNVRDVP RAREDVGTQAGRREREFPRLFG PAAVVGCERHLSPFPRAAGAG GRAGAAGRRSAPPGGLGSCRSC RISAGPHGNDVPTLGGRGW/PL *NSGAEKL*EQ*G*/TGTGSWSL AAILGGVPREP\GFRGAGRETLG PRGWLVMLSRAVLLHSVLLCT CHSSWVLLHSDLACHADNNPD IQSCLFPMSKY
14552	44920	C	14638	90	465	
14553	44921	A	14639	116	439	
14554	44922	C	14640	278	364	

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14555	44923	A	14641	116	687	EIKDAALQLPLWRAQDRERAM KERREKRREREKERDREKKRK EKMFCKRSCHTIMEPTPELSCV LPCLAPIVLAPPPLPL\PVLPLPY ATR*LPQQNRQSTLTEAHGL\TR GPITLATNRCMPSTTRDRRRLT PPSTLPNTTNLSWGVREGPNQD PEPSLSPCVPHDPFDYNAESLFS YWLVSVTPMTAHTP
14556	44924	A	14642	474	1166	HPNRQGLRAPATAPGHPGREQ ALCEAPQGPGQKCGPPRAQEA Q/GTEPRRASRAAGACRHHWP QVA\RPGAGAPAGAARLGGV*E PGRAA/APRLPLPSQCCHR*GTS PAHLSASRSSSATCPWRRTAGR SGPSPCMTL\KQRQGHPRDGWI RAPSCDVTNRGLSSLLNLGGSA QQLLLASRPLGSGSGALEALEH GKSRAPWEPWLHGTHNPVHGK DPAGSTSHWPRPPAPRT
14557	44925	A	14643	283	806	PRGSFSSTGRTRNAAGSTSNCSL RSLSARIEERKVSRVCGVPNHR HLRLGALTTTRPSWNGAIPTLA KLPAKRC*RRSGRRSKTWSFPG ST*LGNFAEEMICAASARPAGV PGPAL\PTPLRAPLPGVPWTSSR GRMCARLSCC/HAGRPVPARPG AARARRAAAGERHRPPALRV
14558	44926	A	14644	1	338	
14559	44927	A	14645	1	1091	MSNDGRSRNRDRRYDEVPSDL PYQDTTIRTHPTLHDSERAVSA DPLPPPPLPLQPPFGPDFYSSDT EEPAIAPDLKPVRRFVPDSWKN FFRGKKKDPEWDKPVSDIRYIS DGVECSPPASPARPNHRSPLNS CKDPYGGSEGTFSSRKEADAVF PRDPYGSLDRHTQTVRTYSEKV EEYNLRYSYMKSWAGLLRILG VVELLLGAGVFACVTAYIHKDS EWYNLFGYSQPYGMGGVGGL GSMYGGYYYTGPKTPFVLVVA GLAWITTIIILVLGMSMYYRTIL LDSNWWPLTEFGINVALFILYM AAAISLM*MIPTRGGLCYYPLF NTPVNA\GSAG*KEDR*LQ*SSC LSP**FISLVLWFA

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14560	44928	A	14646	398	1107	SPGLVCGLLIFCKVTVPICAGPY RCPFGGLRH*SAR*QPPSGLREN GARPPGGEWLCPC*FPP*PLNSR WKLPPRLVT*GEPWAAGEKFP RLGAGTGPAAGEGLPRARDWE PGRAGPERWAPGRGPAGTPAK TAAVKRSAPLPGS\GDYANGER KPPPSPFCQVKSGNL*VLCG*RL SLPAA*KPKKA*RRGRRQSPGK TGYQVQQTRPKNDPKSS\GPSP KNRQSLCLQPLWSFLIQ
14561	44929	A	14647	1	540	MGVRDPLEEAVCALAELQHCA GRFAALFRASRQERLSLLKLCP QLPLPPRALSQGYKPLIG\LLAF FQRCTAQRGGI*RGSLATVTL\S CGGLCPV*TSQRRCL\PVRGKLP TQASVMANAPPRTRLQHLRSTS DCCAGSENFKPVDLSLLGSVGV GSTELDHLAPWLQPAFQGSEW FYLTF
14562	44930	A	14648	169	487	EVCYYPPSETYFCQFVKLILCPV LFPCWQGVVIQPKLSCMRCLST \LLRGVSQ*GYMGVRDPLEEAV CPLAELEHCAGRSAALFRAGRQ ERLSLLKLRPQLPLSPSA
14563	44931	A	14649	1	210	
14564	44932	B	14650	1	1683	
14565	44933	A	14651	1	529	MDSEVQADDEVSDENGELIGN WGKGGMGVSDPLEEAVCPLAE LERSAGRSAALFRASRQECLSL LKLT/LTAAPSPRGTAFRSPFKS PAQRRSIIC*Q/LYSCKTFRSTVA PMPRLCLPQASGKVQ*EN*SWA IPA*QGTSPMCSLCSGAPHQPG APLVLPLPPPVNRLRRELQCWL
14566	44934	C	14652	295	430	
14567	44935	A	14653	452	637	
14568	44936	A	14654	151	446	MVLSHWHSRCHWGMKKNYLQ LARCLPKWLPSFVFETQGPCDV STQGTLLVYGLQRPWEKHSI*A R*HHPSQHGPSQLPLARGGSSP TPCASRMRQHPT
14569	44937	A	14655	2	335	EDRSAFRPRQPHTLHPLHARSL APRSPTPPSPPSPDTQLGLSGPTS GPESAPTA/PGNPSWRSSRWGSS SPCAASST*KSPYP*/CSPT/CAFP SPRLPFCRSAYQPAAGAGRGK
14570	44938	B	14656	373	502	

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14571	44939	A	14657	1	400	GSPAPAAMDEERALYIVRAGE AGAIERVLRDYSDKVKSPGPGR AVSHPRAALRACTSHPSPPPSFR GCAL\PPPKTFPAWACVFVPPAF SIHAS/SHPTTPTVAPTPLIPGPA A*PPVLLSSVQVTPPESVDVHL
14572	44940	A	14658	659	1177	ARKGSALLRLYLSNAWCVCVK VLRIFSTASAYITRRDSSLGPVW TFLNFSFGSPGEIPTPFFFFPVFP LPLVAWFCPASFCLPQCP\LVPS EPSPPPHSGDAHCSPPKTFPAW ACVFVPPAFSIHAS/SHPTTPTV APTPLIPGPAA*PPVLLSSVQVT PPESVDVHLCPVPHS
14573	44941	B	14659	1	318	
14574	44942	A	14660	2	131	
14575	44943	A	14661	354	762	CPEIRPPS*THGTK/SHFPPTASG THSVLEAL/PDTQRQPSPRVHQ DPSPAI/PALLPSPHEHGPQHLL QLPSHRCHPDTAPFNCDAVKAC PGHATAALEHPYLSGRQSPPSP THLPKLPAGRGYTVCALPKGPG ERSAV
14576	44944	A	14662	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL
14577	44945	A	14663	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL\DPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
14578	44946	A	14664	1	1584	
14579	44947	A	14665	1	4729	
14580	44948	A	14666	1	1566	
14581	44949	A	14667	1	1424	
14582	44950	A	14668	1	576	
14583	44951	A	14669	1	3325	
14584	44952	A	14670	1	2195	
14585	44953	A	14671	1	3162	
14586	44954	B	14672	287	2018	
14587	44955	A	14673	1	1073	

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14588	44956	A	14674	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
14589	44957	A	14675	1	1838	MIIPIDAEKAFDKIQQPFMLKTL NKLGIHGMYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LPPLLFNIVLEILARAIRQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGKDSLF NKWCWENWLAICGKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNLIELKSFC TAKETTISVNRQPTEWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPIKKWAKDMNRHFSKEDIY AANRHMKKCSSSLAIREMPIKT TMRYHLTPVRMAIIKKSGNNRC WRGCGEIGTLSHCWWDCNLVQ PLWKAVWRFLKDLELEIPFDPA ISLLG/IYPKDYKSCCYKDTCTQ STFTCRQHLPL

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14590	44958	A	14676	1	2354	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKTSRRQEITKIRAELKEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKREKNQIDAIKN DKGDIITDPTEIQTTIREYYKHL YGNKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITGSEIEAIIN SLPTKKSPGPDGFTAEFYQRYK EELRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMLHIYNHL IFDKPDKNKQWGKDSLFNKWC WENWLAICRKLKLDPFLIPYTK INSRWIKDLNVRPKTIKSLEEDL GNTIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTIRVNRQPTEWEKFFAIYSSDK GLISRRYNELKQIYKKKTNSPIK KWTKDMNRHFSKEDIYAAKRH MKKCSSSLAIREMQIKTTMRYH
14591	44959	A	14677	1	3144	
14592	44960	A	14678	1	2745	
14593	44961	A	14679	1	2742	
14594	44962	A	14680	1	3264	
14595	44963	A	14681	1	2982	
14596	44964	A	14682	1	3102	
14597	44965	A	14683	1	1443	
14598	44966	A	14684	1	3723	
14599	44967	A	14685	2	1841	
14600	44968	A	14686	572	744	DLLTTIRMPTDVKKCSSSLAIRE MQIKTT\M*YHLTPVRMPIIKKS GNNRCWRGCGEI
14601	44969	A	14687	1	3588	
14602	44970	A	14688	1	5569	
14603	44971	A	14689	1	3992	

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14604	44972	A	14690	755	2415	QELRVSGWSPASAPANT*CPPA QPCPTRRSGGQRAPARTRSRPG SRPRTASALPRPAAQKAASRSA RASRTNPYTAPKPLPSVESALQ EAAIGEAHAQQRVSCTCAAPA APPSPAWPWSAARSAAPPPRT* ASAPA*SPL/PVRLKKSPGSSNC EARGEGWKT/PALPVQLGAHGP PQPAAVPCASPGSGAGPRWSRS ARRTPRGPLQRGRTWVSPDPGR EATPSGTQWPQKTRGSLPGS*C APETPCSAA*SSGTSPPRGAGGC CPGTVPPALEGHN*PQRWGSHS AGRVE\TRAEGPQCQQGAPAGC SLGVGGQRGPPGLPPIPVPGLC* TCRSS*MEAATGSVEKCKRMA SLMQASRWSFLRVAPVSGQVK YTPGTARWAEPSSLGSDTTLVP GAS/RAPADGGFGLKFLSHLVS DGVLRCGGPRPGTASAPAGLR AAAA\PSVPSLVGPWRGGLGAG WLGFSLWAFSPTDSLSF*PGPA LLNLMSALNS*KNFFMVAARS CGGGTRGRGGTGPSRGRGRRR PATGRK*KKKKKKKKFTSPPEV PPSPGLPRDNRL
14605	44973	B	14691	1	822	
14606	44974	A	14692	1	2789	MAAVRKQLPRGVLGYGGSGAL LSTAAADTSLLLGSLQERKSAS AGPGYLRSSVAAWSGLWLTGA SEAHSVVLACFSRKDVEASLSV GLPVHPDASCARRLDAADGVA GGSPRLPQSTDGWRLTAHSLPQ STDGWRLTAHSLPPPTDGWRL TAHSLPQSTDGWRLTAHSLPPP TDGWRLTTHSLPQSTDGWRLT AHSLPQSTDGWRLTAHSLPQST DGWRLTIHSLPQSTDAWRLTA HSLPQPMDGWSCRSAQWCV
14607	44975	A	14693	176	440	
14608	44976	A	14694	114	253	

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14609	44977	A	14695	124	890	GSRAWRDPRLEVAAATTTLFY GYGFVSAELKKASKRMTCHKR YKIQK\KAPEHHRKIRGEAKKR GHNKPRKDPGVPNSAP\FKEAL L\REAELRKQRLEELKQQQKLD RQKELEKKRKLET*SWIFKPSN V\DPMEK\EFGLCKTE\NKA\RSG KQNSKKLYCQELKKVIEASDV VLEVLDARDPLGCRCPQV\EEAI V\QSGQKKLVL/IYLNKSDL\VP KEDL\ESWLKLF*RKDLPNSGCF RASTKTQRVKGKITKVSFIS
14610	44978	A	14696	553	997	EVTACWQSSQPSLTLGASSAW APTLAALEEPFSPPLHCGSPFLG WPRLEPAPSAPPWAPVRPEPPQ QGPPSAPGRPIPSTTQGLRSADA GRRTGTQLHRQPAKVCSF/IS*S QRDHEPTRRNEQLQTRRLKSCN THREDLQLHSRRKKL
14611	44979	A	14697	1410	2036	
14612	44980	A	14698	3	630	RYKGSPRPHQTQEPSWLHLVDP APGLQVELPASPAPCARIRQPL GGRWDWAPWSRGWCSSGRLG QHRSPWSGWEAQAWRAAGPK PCPAGRQLRPGEKSSTAPVGRH CWGIQYTLRSHWPGC*VPHSSG PAGLAGCSGTPAGPQAPHAAP VPARA/CSLHTSLQAEGVGSSL GQPRKGLPQCRWGLKGSSNAA KVGAQAGEVQARALRTAS
14613	44981	A	14699	190	383	ASHPLRGLRSGRSLPDERHRLL HSAQSHRPPKG*GVRAQGAGL T/WQLHL*PQCGIHWVKPAGLL
14614	44982	A	14700	1	1095	
14615	44983	A	14701	1	777	
14616	44984	A	14702	1	933	
14617	44985	B	14703	1	996	
14618	44986	A	14704	978	1207	ASLPLRGLLCCPSLPEERRPLLH GAQSHRPPKG*GVRAHGAGLA/ WQLHLRPRCGIHWVKPAGLLS LGPHQQSSKSA
14619	44987	A	14705	111	558	

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14620	44988	A	14706	1	1103	MKPWALKVSVTALKVARLEFV PPDVRMCSEFLPCGVKLQTFAV SVTALKAARLELFVSPGGLVVS LASGVKLQTFPVSVTAHKSSVD PRSEQQQDLLQRAKEQTFHTVE GDRSGSPPDSGAQLASPSGSRT RAAGGAACQSRALRPHSSALG WSMGLGAVEQGAVLIREARAA HEPMERVGGSGMAGCRSRALP REKAAKARRETEGSAAVSGWL SGIAQWPKIDHEGFRAVKMPQ AAWLLKAVTFIDLTTLSGDDTS SNIQRLCYKAKYPIREDLLKAL NMHDKVAAGFPAGQTHLKTRL EEIRLAVEDGATEIDVVINRSLV LTGQWEG/LYSPVVYSALPCNI* HSRLFLPSGNALLLWLWCLHS
14621	44989	A	14707	2	2300	
14622	44990	A	14708	2	1058	ARSNIRMVTAFRSLPAGSSGAA RA\MSAHNRGTELDLSWISKIQ VNHPAVL\RRAEQIQARRT\VK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGIT\TAAVCV\YP ARV\CDAVKGTSRPAG/CVNIPV GISRAAGF\PAG\QTH\LKTRLEE I\RLAVEDGSLQKIDV\VINRSLG A*QAQWE\ALYDEIRQF\RKAC GEA\HLKTILA\TGELGTLTNVY KASMIAMMAGSDF\IKTSTGKE TVNATFPVAIVMLRAIRDFFWK TGNKIGFIPAGGIRSAKDSLAW LSLVKEELGDEWLKPELFRIGA STLLSDIERQIYHHVTGRYAAY HDLPMS
14623	44991	A	14709	576	998	VLQFLKAACPEFVPSGVPMCSE YLPSGGFVVSLASGVKLQTFPV SVTALNALRLELFVPPGGLMVS LASG\GSCRSSR*VLQLIKAVWT QRPLGGRWDWAPWSRGRRSFG EARAAQKPMEGVGGSGMAGC RSRSPAPREGS
14624	44992	A	14710	2	589	RHHPRHAVQARPFPAGPLAGA QRGSGAE*RGPQGS\PGPAGLS GGESL/PGETDRGADKEERGRQ RWQRALGRLSAGADPLPAELR GRRQRRGR*AGQRAAQEAACE APIQGSGARNGRRG*GRRL*GC YQ*V*FPGLTRGWGRGSRPSAV HCGWEPP*AGKPSGQTPRHSG* PAG\VDGLPPKVTGPPPGTPQPR

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14625	44993	A	14711	1	1596	MRLTRCQAALAAAITLNLLVLF YVSWLQHQPRNSRARGPRRAS AAGPRVSLPPHPLTCVWRCSRP AMDRPPAASRPETTVATEFVAL VLDGARAEAHALLERMVEALR AVSARLVAAPVATANPARCLA LNVSLREWTARYGAAPAAPRC DALDGDAVVLLRARDLFNLSA PLARPVGTSLFLQTALRGWAV QLLDLTFAAARQPPLATAHAR WKAEREGRARRSALLRALGIRI VSWEGGRLEWFACNKKNQRC
14626	44994	A	14712	225	980	VPSRTWAEYRTRFVPHSLGQPR SSHIPQSPQTDQTAQGQQALAP PAGRSGQ*GRPGRRARLGPGER HS*APPPLSQLLLQTFPHLQALP SAHARPSGQPHADRGHSRSPSG /DLSTSSVLKVVRPQAGGPKQA RCPQAGRVCHCPRGGRRGPE/Q Q/GG*RPEAPQASPEKGSTGLRP SAKDSKNQGTGIFLRCQVAPRP EALCCPPPRGADTPVSPCLWVA GAGIPLQPPEGAEGAVLGSLCT LCPGSPDSPPTS
14627	44995	B	14713	405	893	
14628	44996	A	14714	178	499	
14629	44997	A	14715	231	436	
14630	44998	A	14716	141	393	
14631	44999	C	14717	97	351	
14632	45000	A	14718	119	358	
14633	45001	A	14719	21	614	PPCTSLRPLHAFSGKMTHLNRG TLSLLDSQLHNLIALQMTCFKD VEIPNFFWEPSVTPSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGFGGYLSSDVSSSP RKAAVASVMYTVITSMLNPFIY SLRNRDIKGVLRQPHGSTVQFQ YLLICSIPFVVWVKKGSKVK
14634	45002	B	14720	162	1263	

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14635	45003	A	14721	696	1791	VWIALKSENITCELLLFKMQTQ CQVLVYLFPIFQPSFLGKRCPIS TDPQNLTDVSIFLLLEVSGDPEL QPSPCWAVPCPCAWVTVLGNL LIILAISPDSHLHTPMYFFLSNLS LA\DIGFTSTTVPK\MIVDI\QSHS RVISYAGCLTQMSLFAIFGGME E\DMLLSVMAYDWFVAICHPL YHSAIMNLCSVGFLVLLSFFFF\ LSLSDSQLHNLIALQMTCFKDV EIPNFFWEPSQLSHLACCDTFTN NIIMYFPTAIFGFLPISGTLFSYY KIVSSILRVSSSGGKYKAFSTCG SHLSVVC*FYGRGVGGYLSSDD VSSSPRKGAVASVMYTVVTPM LNPFIYSLRNRDIKSVLRRPTEH CLISKK
14636	45004	A	14722	1	1971	MTRKVTLLLRTWRGGCGRLA MGMEATPQGSLHPLFQEHWIR AEDFGVLSPMHPNSVQGVDDM IRLGDLNEAGMVHNLLIRYQQ HKIYVSLPSPVSTGEPLTGANLL DREKKMMHRGHCPIALTEGVS GPDNPEGRARAKAKAKARAEL PLPGAEGTDHLLPSQTYTGSILV AVNPFQVLPLYTLEQVQLYYSR HMGELPPHVFAIANNCYFSMK RNKRDQCCIISPQNRVGAQTDT VLKVFQHLLISLICKTTLQACCI PSHPYLSSAPGPPPLTTQCRSYS DSLLGPQLFGDVCYNCSHVIEG DGEALCSLPHPTCSPGAWVLQL VSPLNKAWCVSCFSCSTCNSKL TLKNKFVEFDMKPVCKRCYEK FPLELKKRLKKLSELTSRKAQP KATDLNSAEGPLAQLGAVGA/V TGITHEPHIPQVENGSQQLDDV PALGV\ENWRIFMAERMEAQG GQRLLLSTMHEEYEFVSPSSVAI AELVALFLEGLKERSIFAMALQ DRKATEGGPVGLTKKQGLLAS ENWTLGQNDRTGKTGLVPWH CLYTIHTVTKHSDSCCTAVPTL LEASSGCIFMSYKKHITLTPKSA DSNKRPSTLGSQFKQSLDQLMK ILTNCQPYFIRCIKPNEYKKPLG FSDSFMLIKLIRIDKVQYDSFSYI

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14637	45005	A	14723	1	1197	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSRKTLMTHQSTCPKH RASRVGPSNSLQNKQTVKKGD QTSVRRKRNDLKVEERHKNHH LARELTSSAAAASPTGHAAATA QAPQRHVEVGRAAAPAGDLGE GIVGEQVLGAERLVGPDASRAR ALCVLGDRREAGHTAEMTAAP PAQVPGPGGPTALRRPSSYLGL GVDEQNPMSVDGDEDDVRVQ HQELRDCLIKHTILIRGEFVTRS LNIAQAADRRDAFVKGIYGALF LWIVKKINAAIFTPPAQDPKNV RRAI/GLLDIFGFENFENNRIIRT LCWRYREARC
14638	45006	C	14724	1	1032	
14639	45007	A	14725	1	4960	MSTTSIFQQLNLLLSHSHKQKQ QIQLPNGRSRYSCLMAAFRMQ YFLSLPMKSLILVGFERLQAIAR SQPLARQYQAMRQRTVQLQAL CRGYLVRQQVQAKRRAVVVIQ AHGQGMAARRNFQQRKANAP LVIPAEGQKSQGALPAKKRRSI YDTVTDTEMVEKVFGFLPAMI GGQEGQASPHFEDLESKTQKLL EVDLDTVPMAEEPEEDVDGLA EYTFPKFAVTYFQKSASHTHIR RPLRYPLLYHEDDTDCLAA
14640	45008	A	14726	86	370	RTWMTHVWRRRRVQAAPTAY SSFRPGTSPCPAQPRAGARA*TR SGTSIMPTGFSSHTSCLTVP\PFT ASSAGQHRQRHRKTTAAGHPT TTGAASF
14641	45009	A	14727	3	455	MQSVLPAHGVSSTRASSRSVTL SSPSTSTNCRGRKSSRVT\SPVG SGPGGGGGGPGSGRFGIDPPRK FAAAGSFSTGAPSSVMVVRVSG MPSLSW*QYP*SCSTLGCRSRSS STISLSSLWA/VQPIAAPPYPELA TQLPISCR*SPSPCAPS

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14642	45010	A	14728	338	1782	NQLSK*KAHSIRT*TALQQSSGR SQICIVQSSADALPSSRCTNPSST FTPTPLPPRPHPRTCSTLGCRSR SSSTISLSSLWAASR*QPLRTPN SRTQLPRSWPLKSTALSPPPPGQ ATRLCWWMVSSK*RTWMTHV WRRRRVQAAPTAYSSFRPGTSP CPAQPRAGARA*TRSGTSIMPT GFSSHTSCLTVPRLHCVLCWTA SSTPQESSPGGWTRPWPSWRRC CTCTGAGRYLQNSTAS/T/PVPS TSVSQTAPSPKEDYRCWPSYHH GSLPPFSVQPG*GCGMSVRAMP SVGPLWSPTRPPGQIKRQNYLL NYWSCWKMTLLAGIIPSST/GS RPADLDYFLGSSQCPRDERTLK GHVSCDPTSSISITGEKLKQKLE S/SSTLADTKSAFLQDSWT/SSLP TLGASAI\RTTSAS*TDQCPPAP GPLHVSF/SLNSTYPSRLCSSTCS TVDSFQIIPMPN*MPFSTCGAFC WCLWFSAITALYFVM
14643	45011	A	14729	148	1040	WCTGSQFSKGTWEILLRKKPSL GNVGALPCVATACLTTVEKRA PRGHPLAPVLGDICPKVGSMSS STSEL/CTWGNFEFWGRNKYNH WF*WGWALLHQFKMGKGAQG LQEASFYRKDTY*A\TMP*NPIG ISEFGT\LALPGPCKNVFERFMS RFELPGKAAAMTDNTNVNYVR YKGDYYLCTETNFMNKVDIET LEKTEKMWKPRFRGICPQLQG CSVTEQGFEFSDDAKSWALQH PKRPAQQDWAMSRGNQGWAN LGLKIIRGEAVTTRAKEVSVVL KVLEVTDGKVWAREKKLRDSR
14644	45012	A	14730	189	507	AAGADTSQGPGGGPPPSQSQR\ PKSPSAGRKGSQLSPQPQKKGL PSPQGTRKSAPSSKATPQASEPV TTQLLGQPPTQEEGSKAQGMR* PPQRLGASTQQQTNQEAA
14645	45013	A	14731	2	356	DGVSLCHPGWSAVARSQLTAT SASWAVCWQGCGETGILLPCW WECEKVQPLWKQYGRLSCEDH LNS*VQVILTTQPPILFPKWLHL FTFPPTGQKDSSFSTTLPTHCPG GRGCSELRSRHCTPAWVTE

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14646	45014	A	14732	1	408	FFFFFYTTFFLFFYFYFFEMESH SVTQAGVQWYNLSSLQPPPPRF RRFSCLSLPSS*DYRCPPPHPAN FLCF**RQGFTLLAKMVSIS*PH DPPTSASQSAGHVLTSKWELNI EYTWVIKMGTADTGEHKNGEG WE
14647	45015	C	14733	262	536	
14648	45016	A	14734	179	745	TDCLHNRCHRSPRSPPPGPPG*R SRADWWRRGRCWGSWCASSR RVC*RCPAPSASFSCCRSPRGRQ GRTFPPSPCPAPD*TQ\PVSPGDS TRPCPPPSSPPAHRAT/GCCGRR RLPGNASYLASPGKEAGEFPAS QGDS*PGQYGYIGDSSS/RPTRG TWMAKASTPRHPIAPQICGA*G FGEHQEVPVREK
14649	45017	B	14735	1	1164	
14650	45018	A	14736	35	542	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGAL PLDTVTFY/KDYGDKLNMELSE KYKLDKESYPVFYLFRDGDFEN PVPYTGAVKVGAIQRWLKGQG V\YLGMPGCLPVYDALPGEF\IR ASGVEARQALLKQGQDN
14651	45019	A	14737	11	908	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSG\LHTKGA LPLDTVTFYKVIPKSKFVLVKF DTQYPYGEKQDEFKRLAENSA SS\DDLL\VAEVGISDYGDKLNM \ELS\EKYKL\DKESYPVF\YLFR EGDF\EEPSSHYTGGS*RLGAIQ RWLKGGKGVYLGDGLELVCT V*LTPWSGEFIRA\SGVKARQAL LKQGQDNLSSVKETQKKWAEQ YLKIMGKILDQGEDFPASEMTR IARLIEKNKMSDGKKEELQKSL NILTAFQKKG\AEKEEL
14652	45020	A	14738	3	227	
14653	45021	A	14739	1	424	
14654	45022	A	14740	1	207	
14655	45023	A	14741	2	352	
14656	45024	A	14742	1	441	

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14657	45025	A	14743	1	461	MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAF\LPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVP
14658	45026	A	14744	1	928	
14659	45027	A	14745	283	1074	
14660	45028	A	14746	450	1970	VRVLSPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLTAMGVI GSHGARGQVVALNRQRQGDL QPFTRVTVHWGKGYDRTFWGL LDTGSELTLTPGDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGIMVGKAKWKQ LELPLPRKIVNQKPYCIPGGTVE ISATIKDLKDAGVVIFTTSLFNS PIWPVQKTDGSWRMTVGYRRL NQVVTTPTAAAAPDV/VVSLLE QINTSPGTWYAAIDLANAFFSIP VHKPHQKQFAFSWQGQQYAFT VLPQGYINNPALCHNLIQRNLD HFPLLQDITLVHYLNDIVLIGSA IKWVMHSS/DSIIKWKWHVHDR AQADPEGTS*PGYGHF\WCPIC QQQRPTLSSQYDTIPWAISQLPG DRLIIGPLPLWKGQKFVFTGIDT YSGYGFAYPACNASAKTTIMES QNTLSTLMVFHTALPLTKALTS WLKKCSSGLMLMEFTGLTMFSI

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14661	45029	A	14747	1	2589	MGPPYKPPTTWPPQTLSYHSTT PVKLQSLSLPPTAARGATEPCH LQAPASSVQQMTPPAPGLKHL GGKSQMCLEQDGRSGSVRGSP CHAGHWVAGAGFGKGTTRTW GHVNLIVPPNCPTASSSAARDS APNQPLLGVVTAQIVPPTCPPA MTVQELIAPLTLPPAAGCRRGV RPFQTRVWLLAQLLRARLGGP GEGVVTCHSWRLERVAPRLAS LWWALAAETAARLDWAAKRP SAWGSIKAAEFSSKATPRLEGA SSRTLWVSYIQAKETTTGKNGP VEPSHLWEAYCRATAPHPAVH SPSAEVTYTCGIVNLLLQGLVP KSHLETHTGCHVVVELIICSVV LPLISRLSDPDWIHLVLMVIFSK ARDPTPCPASGPEQPSVPTSLPL IAEVQQLPEGRAPSPVAAPGFLS KQIQDALCALEGSQALEPKGGE GSEGVEAEGPGTETETVLPVST LNFCPEIQIDIADKEIEQGEVTTS VTALLEGLEKTCSSRPSCLEKD LTNDVTYLDPTIFSFEPLSSPDG PVVIQNLHITGTITAQELSGTGL QPCTRYTVKCETSLDGENSSLQ QLAYHTVNHRYWEFLNLQ/SH QEKKPDL*KFIKN\IEKMVVSAI VDNLKTAFPCSESQGPTEELSE AETESKSQTEGKKARKSRLRFS SSKISPALSVTEAQDTILYCLQE GNVESKTLSMSGMESFIEKQTK
14662	45030	A	14748	478	3507	SKILRAVIWGSHLVRSAMKTET VPPFQETPAGSSCHLNNLLSSR KLMAVGVLLGWLLVIHLLVNV WLLCLLSALLVVLGGWLGSSL AGVASGRLHLERFIPLATCPPCP EAERQLEREINRTIQMIIRDFVL SWYRSVSQEPAFEEEMEAAMK GLVQELRRRMSVMDSHAVAQS VLTLCGCHLQSYIQAKEATAGK NGPVEPSHLWEAYCRATAPHP AVHSPSAEVTYTRGVVNLLLQ GLVPKPHLETRTGRHVV
14663	45031	A	14749	1	417	
14664	45032	A	14750	34	350	RERGQEGGVAGRVEMDVSVVE RGAYADQIWGRPKGGESRGEK RKGRWVQRVRALRARVTPAGL GECKWGRGRGD*VRRVKPRAL RERWGDGSTVSDSTPMKPGLE

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14665	45033	A	14751	1	1604	MASKRCIRDFRSRGGKLKSFQL YATFRKEGCGPVLANGNPGGG RGQEVSATQDLRRGWGIASSAS RFPWRQSWPGRPRLGNYDSGA PGEAKMPSKGKDKKKGKSKGK DTKKLIKTDESVVDRAKANASL WEARLEVTELSRIKYRDTSRIL AKSNEDLKKKQCKMEKDIMSV LSYLKKQDQEKDNMIEKLKQQ LNETKEKAQEEKDKLEQKYTR QINELEGQFHQKAKEIGMIHTE LKAVRQFQKRKIQVERELDDEI NDLLVKEKIMQLVQQRSQIQTL QKKVVNLETALSYMTKEFESE VLKLQQHAMIENQAGQVEIDK LQHLLQMKDREMNRVKKLAK NILDERTEVERFFLDALHQVKQ QILISRKHYKQIAQAAFNLKMR\ EHVQEEQNIPKSEHLMAESTAPI V*IRIFWRPKNGHILKEMWILEI *PGSRRKKYCDCSLQK*MAVLL GNTTQSSRPSSSRTMLFLDSGET KEFGDESKLQDKIFITQQIAISD VFW*SGATHYSKRTSGV*HSGK SESLQPRGQRLI
14666	45034	A	14752	95	473	
14667	45035	A	14753	168	449	

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14668	45036	A	14754	1	2000	MAFEQAKQVVKLALDLWPIGD GPVELQVTVLDQHANWSLRQE QHGKRGPLQFTDVAIEFSLEEW HCLDTAQRNLYRNVMLENYRH LVFLGIVLSKPELITCLEQGKKP LTVKRHEMIAKPPGQKNWEKQ ALPLTGCLTKYPSWAKNIDIIVT CSHFARDLWPEQSIKDSFQKVT LRRYENYGHDNLQFKKGCESV DECKVHKRGYNGLNQYLTTTQ SKIFQCDKYVKVIHKFSNSNRH KIRHTGKKPFKCIECGKAFNQS STLTTHKKIHTGEKPFKCEECG KAFNWSSHLTTHKRIHTGEKRY KCEDCGKAFSRFSYLTAHKIIHS GEKPYKCEECGKAFKRSSNLTT HKIIHTGEKPYKCEECGKAFKR SSILTAHKIIHSGEKPYKCEECG KAFKHPSVLTTHKRIHTGEKPY KCEECGRAFKYFSSLTTHKIIHS GEKPYKCEECGKAFNWSSHLT THKRIHTGEKPYKCEECG\KGF KYSSSLTTHKIIHTGQQPFKCEE CGKAFKCFSILTTHKRIHTGEKP YKCEECGKAFNSSSHLTAHKRI HTGEKPYKCERCGKAFKRSFIL TRHKRIHTGEKPYKCEECGKGF KCPSTLTTHKTL\EIHAGKKPNK *E/ECSKAFKDTSALTRHKIIRTG EKPCEFDECRKAFNQLSTFTKY
14669	45037	B	14755	269	1131	
14670	45038	A	14756	2	149	ALFRAGRQECLSLLKLCPQPPL SPTCFVPGR*GFYLHFFQRCAA QRGGI
14671	45039	A	14757	2	175	

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14672	45040	A	14758	1523	2667	PLLVIHRQTGSGEDLQQTPADL QQRDLLERKLTNRNE*HQHQQ KRHPLKNPTQMSP/CIKDQRYIN PRSTIKLELGIKKLTENCTTTWK LNNLLLNDCWEKQERSKTDTL TSQLKELEKPEKTNSKASRRQEI TKIRAELKEIGTRKTLQKINKCG SWFFEKINKIDRSLARLIKKKRE KNQIDTIKNDEADITTDPMEIQT TNREYYKHLYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TSSEIEAVINSLPT/KKRSPGSDR FTAEFYQRYKEEL\VPFLLKLFQ TIEKEGLLPNSFYEDSIILIPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHNQIDFIP GMQG\WFNIHKSINVIRHLNR
14673	45041	A	14759	640	1771	APVARMTA/PLFYTALLVFSAL GNILALCLTCQ\KRRKINCTGIY LVHLAVSDLLFTVALPGRVVC YVLGSSWPFGKGLCRLTAFVL YTDTYGGVYLMACVSVDHYPT \VVCAHWGPCLRTAGRARLVC VAIWTLVLLQTMPLLLMPMTK PLVGKLACMEYSSMESVLGLPL MVLVAFAIGFCGPVGIILSCYM KITWKLCSTAGRTQ*PAGKDTT GGASPGGPSDQPEKTPPAGAAQ EDPVTPRERTPPAGQPERTQ*PA GKDATGGTAREDPVTSRKGRH WRGCLLTLLMLVAVVVCFSPY HLNIKQFMARGMLHLPSCAER RAFLLSLQATVALMNMNCGI/D PIIYFFASTHYRKWLLGILKLKG SSSSSSSSSTLY
14674	45042	A	14760	1	401	MVLVQWLTAITSAFWETQNKG SLQFEDKWDFMRPIVLKLLRQE SVTKQQWFDLFSLGATLQDSSG PLLTGKLKKKRKVSGTKY/IEAS SATSLKATTDTHHLLLYNPFWI PLTLI*HLCWLQRFA*SCDTDPH P
14675	45043	A	14761	184	2720	
14676	45044	A	14762	34	251	
14677	45045	A	14763	2	452	LQIEII*ALEELAAKEKANEDAV PVCLAADFPSAGMGSSCDGQE DELDIKSRAAYNVTLL/NFMDP PKIPHLKEKPYFGMRKMAVRW HHAENLVDRPQ\EESEDDSHLE GRDLDTWHVGVKISWDVKTPG LATPQGDCYFMLGNLWRTKIIL

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14678	45046	A	14764	1	1701	MPFKCKKQHTFNKTSPKEGAII FTHGCLCTSPFNSELSEHLGNL KLSSWEHLHHRSQQTLSVRLH VPTPQPVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPLWQL KYPKLILREASSVSEELHKEVQ EAFLTLHKHGCLFRDLVRIQGK DLLTPVSRILIGNPGCTYKYLNT QLFTGP\FPVKGSNIKHTEA*I\A AVCETFLKLNDYLQIETIQALEE LAAKEKANEDAVPLCMSADFP RVGMGSSYNGQDEVDIKSRAA YNVTLLNFMDPQKMPYLKEEP YFGMGKMAVS\WHHDENLVD RIQLQLWDPVDGTTASSAVPKQ GRDKRREVPNTLSQPNSQEGLI SAFHSRCVHAVFYKLTSAPKTT SLPDVPSDLLAEGLAASRAGQA LWRCDKKSLLTLVRKINLQGK RDGGRSATNQQSQPHLDNTGL ERQLEQKVGRCRSPWRGLGHL EGNAQKGHLLHGVNKNGQHL LRRHGVSIRAGRAPHLAAADT APGRISCLGHSEALKPRIQAGGL GAESIWQVLWEGGSNSSVFCR HDEEPAAELPLPGKQASGGHM
14679	45047	B	14765	16	1462	
14680	45048	A	14766	89	566	MEQGSIITQAWREDALVLTKQ GLVSK\SSPKRPHVCHILK\APFC CSCTQHVGQSSSPR*ANPHIRRE STPIAMSDQLQRLQYQFYQIPG TCLLPEVTEKNQGRICMVTDLD ETLVHSSFKPISNADCLVPVELE GTMHQIHVLMRPYMDEFLT*M EEMF
14681	45049	A	14767	1	305	LSGLEMFQAGAGAPSSPGY*GS CWAISWSGPPDKHSNRGASCG LETWAGAAATDTAGPHPAAGR C*A*AGSGGDQGTGSTAPLPAT P*PLQSLV*AAALPA

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14682	45050	A	14768	1070	2653	SLKPCMACL*HS*EKTLSDSSG RSWICAVSF\GSPGPAAAPLPEL SFPLRPGYTKLLPHATEEVSPFG SGAGRKLGPMLPSTAELCPGTR ARWSEGYRDLGRQAQDLQAG RKSVVTWALEGHPREEERAAA KVQQCQRMWEGCSDPQELIPR PGRNPDPVPDSAVALLPWGPSR VPDLGPDSEHR/PAHSRVQYWL HKAPAPPSPSPQLAEPATPPTRP SSPGSRSPSSWHRLRSWSLNAD PW\RPRPADLPPGNPAPPSRGGA HGTWGKDVRPLGRGSRLFSVV CGRREVQRAARRVGTTGPGWR APGREREAASR*QPPGTG/PASP MGRASSSGSRVSPGPIRRTAPW EGCSCRSRHHWGKGLGPPDGE PG\PGSS*VAQPTVGGRRSLGPG GAAPARDAAAATPPGDAAARE GSGRHLRAPASRPQHQPRSPRS HPPASATTASLQKFRSASSEPPS EDRPFDFSPTAPPQCPRVAPSAG AR*R/AGGRLPE/PR/RPGPWGG GSRTNLTIPTSLHGPTPAAARTS PHRKSR
14683	45051	A	14769	748	1073	SQHFGRPRWVDRLRSGVRDQP GQHDKTPSLLEMQK\IAGRAGG CL*SQLLRRLRQENPLNPGGGG CSELRSGLCTSVWATGRDSI*K KKKKKKKRKPWSLLSLIVLVQF
14684	45052	B	14770	59	466	
14685	45053	A	14771	2	3184	HRTGIPGSTISSPGGETVPE\MTA AMRERFDRFLHEKNCMSDLLA KLEAKTGVNRSFIAL\GVIGLVA LVLVV\GYG\ASLPLQPLLGFCY PA\YISIKAIGE/SPNKEDDTQW/ V*TYWVV\YGVFS\IAE\FFSDI\F LSW\FPF*LHG*KCGFLVGWCN GPEAPSKWGLKLL*QAASSGPF LSLEATKSQIGQVLVKD\LKDQ GPKETADAIH*KKPKKSLP*ILL G*KKKKK
14686	45054	A	14772	14	455	PQFPCRRFRALSEEELDNEDYY SLLNVRREASSEELKAAYRRLC MLYHPDKHRVPELKSQAERLF NLVHQAYE\VVERRRTPAEIRE EFERLQREREERRLQQRTNPKG TISVGVDATDLFDRYDEEYEDV SGSSFPQIEINKMHISQ
14687	45055	A	14773	328	479	

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14688	45056	A	14774	15	1095	KVAKMATALSEEELDNEDYYS LLNVRREASSEELKAAYRRLC MLYHPDKHRDPELKSQAERLF NLVHQAYEVLSDPQTRAIYDIY GKRGLEMEGWEVVERRRTPA\ EIREEFERLLREREERRLQQRTN PKGTISVGVDATDLFDRYDEEY EDVSGSSFPQIEINKMHISQSIEA PLTATDTAILSGSLSTQNGNGG GSINFALRRVTSAKGWGELEFG AGDLQGPLFGLKLFRNLTPRCF VTTNCALQFSSRGIRPGLTTVL ARNLDKNTVGYLQWHCSSPLL QVQRPHRNTRACAPEPSFRPFL HVPTWDAECSGARTPSTAWTS AAVKLREACLSGPGSGSHQLLL LTPRSKRRTGGG
14689	45057	B	14775	508	1765	
14690	45058	A	14776	2	639	GRRRHRRRHRDCSRGDCYLPT GTNTQQPLPPPREPLPELPARTP DLSMQNSEGGADSPASVALRPS AAAPPVPASPQRVLVQAASSNP KGAQMQPISLPRVQQVPQQVQ PVQHVYPAQVQYVEGGDAVY TNGAIRTAYTYNPEPQMYAPSS TASYFEAPGGAQVTVAAS/SPP AVPFHSMVGITMDVGGSPIVFS AGAYLIHGGMDRPELLANL

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14691	45059	A	14777	1	2091	MKPDDNSTQNEGGQSFEERHE TLQRVKFRGGPKTAPGRKLIAF LGQMNSGTSGGQRVPGEEELM AGGATCLPNTEAHQPIRMKNL HTPAFRLCPLTLQDNEADAFW HQAFVDWGMPTGKKPQTLGLT YKTTHDLSMQNS/EGGADSPAS VALRPSAA/APPVPASPQMLPLE LVILGVV/PLDKCIPAQWSKEG QTNSYTYNPEPQMYAPSST/AS YFEAPGGAQ\MVGITMDV/GGS PIVSSAGAYLIHGG/MDSTRHSL AHTSRSSPARSFRSNSKAPSSRK FCC*LPTLSSKTL/SLFSKNLLRK LPLGKHSPDSVQWPWIYGLLV AGSESLASLLFPKASSSGETLGF ATGQLAGESRLPSLLAFILVPID VAWGKEQLVTQTTVYRVQGS GQHLNKAWQEPALVNICGMGE KVDVQVGLCQHRAHLDGWNS SRAASVWPGETLTHHQDQCQA NLPPGIETSILGTKGARYPSPQE QGGGRVWLERLDPRG/AVSGT DL*CLPQSDVPPGRA*SGGTGD KSISTHDKSGRGNSKYHY/YGIR LKPDSPLNRLQED/TQYMAMR QQPMHQKPRWCRAELGGAGSP L\GMEDVSHVFPEFPAPD/LGSF LLQDGVTLHDVKAL/QLVYRR HC/EDVV/MNLQFHYIEKLWLS FWN/SKASSSDGPTSLPASDEDP EGAVLP/KDKLISLCQCDPILRW
14692	45060	A	14778	94	3006	RTRSLTRKAMAEHAPRRCCLG WDFSTQQVKVVAVDAELNVFY EESVHFDRDLPEFGHVLDVHG VHVHKDGLTVTSPVLMWVQA LDIILEKMKASGFEFSQVLALSG AGQQHGSIYWKAGAQQALTSL SPDLRLHQQLQDCFSISDCPVW MDSSTTAQCRQLEAAVGGAQA LSCLTGSRAYEFNLVCDRKHLK DTTQSVFMAGLLVGTLMFGPL CDRIGRKATILAQLLLFTLIGLA TAFVPSFELYMALRFA\GL

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14693	45061	A	14779	1	710	MGPAAGAPTSRASRGPRAPALR AAVGRRCPRPEMPCQCHPLAR CGLDPAWTQLPQETAGAPRQD PRCTNQLICEHLPLEGLGFGYL GNKDSLRHVKVVAVDAELNVF YEESVHFDRDLPEFGGLASSAV TQSSS/DDLQQVP*SLQSLHAA* SLQTNASPFTFEHSFLGKRHPK GAGQKRAESPTRPPLRLQEAAP GELQRPLPYGTQVPAGLCPSVS GLRLRARALLPYRTHSLSV
14694	45062	B	14780	1	252	
14695	45063	A	14781	73	198	
14696	45064	A	14782	762	1080	AGRAEMQQERESHEEAKDPSP LSPREGSQKQQQNVNTSTPSHC PR/PPLRMPPPAPRRPVP/CDHPR AEECERKAQHWQAAPPAAPVR DPLGEASWAPESGGDVESLYI
14697	45065	A	14783	1	309	MTKTEREQNEQLDGGGYGERL GEYSLFLLCVPSELNQGKCERV SSYFGMNLSGVLKKLPFPPTRE SWPPPHFTGTPHNHHGGVSNG ALGCAQRCSLHHATNAGGWER GGVSNSRLFFFLLSASFSDAKIK PAPSPIDHLRAEEC*/PPPLSQPP ALVAWCREHLWAHPKAPLLTP
14698	45066	B	14784	1	471	
14699	45067	B	14785	1	1143	
14700	45068	A	14786	1992	2205	WRSMSGLRKRQLASQISYCPC WS\CP*EESHCRRVSPAPLA*LL SPCPAPQQRSHTDPPPFPFKHFP LPFSG
14701	45069	B	14787	389	973	
14702	45070	A	14788	287	525	TNPFNLLQH*KKP*CYTYISITD PTDACHKNKAFSSPAVSQLT/CI FSSTAGSFFVLSGHSCGHLAVFS LWPRSPQLPGTR
14703	45071	A	14789	475	616	
14704	45072	A	14790	1	704	MTKWKSNPQIHMELQRTLSNP NNLEKSNVKTYYKAKIFDDNLI QLTFQQHRQDRDTEQEKKKEE EREKRKQQQEPLRKKAKMQTV RPGFDLTQGPNCLTPHGKTWSR LPPKNHRRPYTSRPEGPRVKA* NHGPEGRRGTRLPPEAAKRAQ AEEAAQ*WPTRSTLRLEVTPRA MPP\SPSEDPRVAGVHPAPPRGP RSDS/APLRPQLRPPRSLFSLASE PAAAGNARGRHSVLALY

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14705	45073	A	14791	200	408	SPHLMSINLITFANFLFPCE*RNS QFLKS/SIFVMWMIHNGMKCRQ LDTCHCRHGTCKDSICPGLEES PLP
14706	45074	A	14792	240	771	GRGMQSPAQVDPAAKRGNIAG HTAHLWPKGGTLPLCF/YHLLI MQIREQP*SSLEYPTF/RILSLVS GTKLNKILANRIRQHIKKLIHHN QVGFIPGMQGGLPTPGSEQGHL RVSPSSPSSTVTLKLFNFMEPFE NLNLSKGKASVHTITQENTDSL KVQGSQFSQGHEKRTLDLKVS
14707	45075	B	14793	1	1557	
14708	45076	A	14794	150	1668	ESDARQGPFPLENTRPHPSCMQ NHGICRSLHPGLCGCPPTARDA APATAGGVPAY/GPLTGAPPG* LPGAGIGSKQSSTMGPSGAGSC LGL*APSQPAD/PGSIQGVLVIA DTE*PLVGGDGGLEAEHQWQ* EAGP/GGLIPKHMNPQSRQQSLF GRRGYRDSSLRSVLGRTGQQT* HAELGAGVMGPGGNGR*GH/G PRGLPCLVQGRRGPGVAAVAA GVSVAVPSGMLSENGPGCSK/P HSGDAGQRRGLRENL*GVRALI WGAASSFLLTEQDLQELADCL HSGRKTCFFYFQGRGDVAPGPV APAHHRLAGISTVVPEGPGLCV GEDRQLPG/GNQRAEPPP*LVRS VSSLTGLPALGPRQMPNAGAG NGSGK*RGVRGSGPDWDCTGT HGGAGTGKLLWAGLSLFPLSG KSEAHQQRAAGHGYGRGLGSP GRPPRSRKGRVLGSESAPA*GSP QPLRSARQKPESSCPRQGQPVG RGPGAPLEAGHCSFPRPLGPAR SLHPDFPQGLQA
14709	45077	A	14795	3	374	RRPPSWG*RGCSQLPECAADGS LEDHGPLPPMVSCFSRHPAGRF LRVFPPSPLLAVDCCWHNNSYV VAVDCCSATSCSLLLYPSQEFPP HKFLVYLVLSWHQLLGGLELIC TQQPVNPVVSDG

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14710	45078	A	14796	73	890	MSLVRTDGKVSFPHSRAASSPP PRFAGSLPWTPKGHGFTSFPRL EGYCPS/REGPSDWGRNSFRVSS WAWRPSQGVSHHTPGQGP/PSP GNRDK*VATRKSPGQPGSSPEP GWSLQSTSSPGATRTKGNLNTL KG*KQVVD*WVGVGTGWEGS GAPQSPQPSREWRLSPRGVGVV KETWPSPWSGR*APPCPGQPQG QQTHMERGGR*G*QVGACGLG P*GQWSSVTNGKDTRAPWSPPP RQRNGRWPAPPPFTFHYYYYY YYYYYYYYFFFFGE
14711	45079	A	14797	273	678	TEESTSVLSVPNQTGAGAARIGI VSLRLCGLYVTSPPRAARMHIR PHGPWPGGSHHENGEAGPES/E GAPASASGRGAPEGQAWPPRD AVLSSLMLALFRTKSARHLVLG TRQTAASPFPFFSQPSWYCSLG VDGG
14712	45080	A	14798	551	743	PTRITRSAGSSSWGSCRPRAPAP FSWSRPCLQGPRG*CRGLHSRF YAAP*VQGHPVHILPYSKF\RRG RAALRPRGQWGLDSVLGTAVC GCGP/RSESDICSGR*GPE/WYIS PPVPPHVHRGFQQL\NCARQVG KGGGGPGCPMLGNH\SSQVGL GLGGQDQDSLESPGRVSSPSGP SAASDPGG*GFQGNPDPVHPAP APPDW

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14713	45081	A	14799	705	2299	KREWRPRHHPLGPPPRCAGRSA PLSGPASPFS*WLPPGHGPCGR MCSRAARGGDVTYRTHNTRAP SCPSLHWVGERG*DAHTRTPSC PSLHWVGERG*DAHTRTPSCPS LHWVGERG*/GCPHSGLQLSFP PRSAGCCKALFEAEKSKGDTGL GKRGWAGGGAGGAARPCICNP TVPCPQSTQSPPV/PPGTR*QLG SSASHSRAASSPPPRFAGSLPWT PKGHGFTSFPR/RGGVLPFPEGP SDWGRNSFR\GPAGPSMW*PAP PSDAQVGHGPGRAGLQRCRGR GGHTPFVLAAAAIDSAYFS**/D P*VFGSNFPHLSCFPG\GCGEGN Q*ARRRPLAGAAALPGPNLES WVCELSVAGPAVWDPVPSP/GD PTTGPESP/RNSAGACGAQGSM R*T*GTPATWSL/GPPPELPGSR HQRQCECGPAHVQRERMPGW ACMLKSVAQRGFQRR*QLSKA QAAAWRV\PGGR\GAGKD*GW RRWGVSRGGGGLCCARGGGGS SVRRGEVEGS/GCARGGGGCAG WRALSPSSLPISGAQELGS
14714	45082	A	14800	1	267	CSAGGPWRAPQPRRFHRRRRP AQLPPPLPLPPLPASPRIHNRTF\ PRPSQRTPPPAALGCPEPGS/RS QGRGHARPPGSGEGDPTVSSPG
14715	45083	A	14801	218	430	
14716	45084	A	14802	9	201	
14717	45085	A	14803	1453	1936	EVEKHLCQG*ELLRAQHN*AA ACRRPRPPAPGPQCSAGGPMAR APAPQVPPPPPPCSA\PPPLPLPP LPAS/HAHPQPHFRHGRRSALLP RPPWAVRSRGALAGPRTRAAA GLRGGAGAAPAPADARFPASSP AE*PKFPQNSARALTGFPRCTD PTVSSPGY
14718	45086	A	14804	1	580	TSGCSHSLHKPAGVSTRPPTVA SICAPRPRTSPLRRGSLTLWPFP GGHLTLLETP\GFDSCPEEVEGP RFSTFKTS*ARGGRRQRCAPRG RREVGPPSAAESGRARGEPPRC RLLCRGGK/DPQPRAGEGEAAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR CVWGEPGGRRTRLFPDE

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14719	45087	A	14805	279	1148	ALHEFAMSRSLHASLH*S**STC P*QQPAPAPAGEPRARFPGKSSS ASSGPG/WPRNHGKQLHLPAQP Q/QQGRISSPRVAGGSGCTGRA LLLAAGLQNSTRSLNPRDPPTIL SHRPLQGM/PDAP/RGCSHSLHK P/SRS/TPLSGQL*PPSAPHAPAQ APSVAGPLPCGLSPGDT*RYWR LLRFDSCPEEVEGPRFSTFKTS* ARGGWRQSRVWASARGASTL QASVQGR*NPQPRAGEGEAAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR FLGGCLL
14720	45088	A	14806	765	4270	SQDTPGDLQCHGDLL*DGAVLS EAPGGERVPRDD*GGVCPEGVP HVSLLRDSVAEALQPRGEAGG DQVPEAHARPPSAQR*PAGAGL RLHPPAAGGVPGQSGGHLPKIQ DDLTSKS*TNSITKTLFPNKVTL SDSGRA*ILEGHRSTQGSLGLEA DPGTVSHHQHPCPPNAATHHF HRTARPGVQQGPGPASVQQPES DGDGALLRSPCSLLPQGADEVL LQPDGDKQGGRPRGDSESD*G YSERR*AQDEYQGH
14721	45089	B	14807	133	2943	
14722	45090	A	14808	1	814	MEEELLRELLYSENWWSIPYND TIQELCCWAVLKRTFINGNTSR KPGMKMVTGLKKQERRSKQW GCEKEAKFVPDMWIVLEVGRP EERGIDGKRWGKSCSVEQSVW AFQNPIWSKAQTLLNSMK/AYE KGKEGVEEKFEARRSWFMRKK AISHLHNMEMQGEAASADVEA AVSYPEDLAKIIDESDYTKQWIS NVDKTVFYWKKMPSRTFIATE EKSMPGFKASKDSLTPLLGTNA AGGF*LKPLLTYHSQTSRALKN YAKLTLLMLYKWNK
14723	45091	A	14809	123	515	PKQSAKTIWTSTARPEDVVTCS FKEEFLPGNTHHDFSIKNRSDPE LEVSRPLARPENFPANRSHSLLE L/RPCRGRWAAHWTGCSSLLD ASSAPRTDQPSLWRNLPTASLG GPWSHNQPGIVFQNTYLMKWP

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14724	45092	A	14810	279	1136	VDVDLACVRGLLCSCDEFLSW LALNRTVLATPALPSCLSQMAS SLPGLCARTRRGERADSQRGTC AFFSPARTASQAPLVASSVRKQ RVWAPNPLNCHTLPPSRGSQRG GYIGEEGVFGSRVVGIWVPGPN GSPWPLGVQR/PECVLLGVGSG S/SSHELFSEADFISRLLAPSPSP APAS/MGNAIEEEAPELGPLGRV FVDDFHYDYNFIHLHEDLCYGP LEGPDLDLAGTGDRTPPLHSRP RASLSPSALRCP*ALGF/WSTLA WGSPNSSSRVPEAQPPAPSLAE
14725	45093	A	14811	1	1597	GGRKAAVGVETRPQGSAQPTW LPVHGDTCTTLLLPCRAWWRL GGLPWAASVVGAKCVWTPPER GLLMLHKPMPGWSSGYRVVLP AVAFFRLRAQVTKLGEEVSLRF LKREAKLCGFLQKSFLALEKR MKASESSRLKLEGSLRGELESR WEKLRGLMEERLRALQGQHEE SHLLEQCQGLDAAVAQLTKFV QQNQASLNRVLLAEEKAWDA KGRLEESRAGELAAYVQENLE AAQLAGELARQEMHGELVLLR
14726	45094	A	14812	150	1625	CLGKAFSCRELNAYLRLPTFFIV FSLRQPSLRMHSRAWVKTCGA MPCSCCRIRHCSSVTDMAVRSL ALLQLVNRTPLRRRQISAACQR MSTFLFFRACTF*PRNRSSSGRH /DLTARPRQAILRQNFLK/RAQS RNLTAPNSPR**LLVKTYRQTS RPVSAAH*CPR*RGRAALAAAC HSGSPGARRQTAGPAEGPAR*T RRDFL**RAACLRRRWKWPE*L *RSRSSSP*SQGSCPPALPAPPRR CSAGSRTGPAARWCRAGAGSR RHAGSSSA***SRR*GRSASGRR PRHGGTAGSGRWLWWARCPA *AGIPWPSWPCHSSWP/PQSVRV VSSG*RASLHSPGLDSSGGGLQ SFLLVQLPAQGKTSSQP\RHAA APSAAACPHAE*CTLGSCPRSA TLSPTPPRASPPAG\RSAVSPCPP GHEGVLVISKHHLLLLSRSGRG LGGNVVRPCSVQPMDGVGQEL AVADRDQLPCLVCQDGECPLK ASGRPVLGCP

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14727	45095	A	14813	921	1446	ACCISHGNLWHHLDQKHGLQS *GEKSRLFSRPNLQVPVHTGLD HRARYLTGPRKQGHLWPTGPS SVFDNENFCKLSVGM*TGRASA RQQIQSPFAESGKAFSDICSVSL RLCVLPHPWNSRLRSPALRNSL KYSVTSSAAARRKLLPLASGPL RLGPRSLPTRLQVLRWEKVASA
14728	45096	A	14814	1	675	
14729	45097	A	14815	1	2341	MASDLVNRCEACDLPQGPISVH QFPRLSNEVTTTVGRNSESPNQ RSVSGPWTPREVRRGVAAAAH GFSGQNAKWAAHIPATAMSFA LPYSVLHSPHALTTHPLNPGDA VTMPSWTSTVSAANASKGRSFS QCFQSTEEGQERRRPRTSQAKV QQGSTAGKVNELITLAGHIKSQ APHGKRKPPPRDSHVICSMLRK RKPDETPSPSSDAQFSGMLAVA VSSLLCPRSSPSQQWHCHSPSTT ILGSSDVSDTSFQPSTKLGPVHG FPPQSRDCILDFELIRKVTGAWS SLTAGSWETKIQEFSEEDILAPH RITPGPHSSKSPVHFLASLWGR KTKLYHHTIQDKEPRSVPEAGS SGRRDGGGAAHSMLCMAPEPD HPGSNPNCRSPATLHADADGN LQREAAKCQGDGTQVSTHVDH TSAPRQAETGPATGENEKMESH GRSKRGLVGADQCPAETLDSY TLLVGHKKRDKDRQTPGPAPQ VNSFVPENYLLRGPLAPLGSAIS MKTAGAVHIRPSGDLGRAPAP AVRPRPRPPRRPRRLLPGPAHLP GAPRPPAPAPLSRRAARQSPAA AAAPPPGCE/RRG/PAGPASGAG PPAPAHGARPGGKPAANPPRAP QP*P/RRRRSRRRAQPRPGPAPL SRMRAEGPARALRPPPHYQPEL GPPSETVGPVTELLAPIPTARFP TRSHPYPVTASPARSS*TSGLD*
14730	45098	A	14816	44	455	HLRNRTR/PSQITPHIYNHLIFDK /PLFNIWWWENWLAICRKLKLD PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP

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14731	45099	A	14817	1	279	IQDIGMGKDFMTKTPKAMATK AEIDKWDLIQLKSFCTLKEITIR VNRQTTEN\YPSDKGLISRMLP NF*RLFPAS*KKPPLFDIGKTEK TNYS
14732	45100	B	14818	1	2025	
14733	45101	B	14819	1	3570	
14734	45102	B	14820	1	1380	
14735	45103	A	14821	1391	2742	KKRESSLTHVMRPASF*YQSQA ETQQKKRILDQYP**TLMQKSSI K/YLAKRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLELEETTVKFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSLFNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKTLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLKSFCTAKET TIRVNRQPTKWEKIFTTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYAAKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRHAPFSIH THIMFGSLYLQIQKDLSILGFW YPRGILEPIY

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14736	45104	A	14822	1	1698	MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIQIQEIQRMPQRYSS RRATPRHIIVRFTKVEMKEKMS RAAREKEIQTTIREYYKHLYAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAEFYQRQSESQI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTFFTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNIRPKTIE TLEENLGITIQDIGMGKDFMSK TSKAMSTKAKIDKWDLIKLKSF CTAKETTIKVNRQPTKWEKIFA TYSSDKGLISRIYNELKQIYKKK \TNNPIKKWVKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLTPV
14737	45105	B	14823	91	1596	
14738	45106	A	14824	1	2757	

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14739	45107	A	14825	1	2677	MGKKQSGKTGNSKKQSASPPP KEHSSSPAMEQSWMENDFDEI NKIDRLLARLIKKKGEKNQIDT TKNDIGDITTNPTEIQTTIREYY KHLYTNKLENLEEMDKFLDTY TLPTINQEEIESLNRTITGSEILAI INSLPTKKSPGPDGFTAEFYQRY KEELVPFLLKLFQSIEKEGILLN SFYEASIILIPKPGRDTTKKENFR PISLMNIDAKIFNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIR KSINVIQHVNRTKDKNRMIISID AEKAFDKIQQPFMLKTLNKLGI DGTYLKIIRAIYDKHTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIIYLENPIV SAQNLLKLISNFSKVSRYKISVQ IPQAFLYTNNRQTESQIMSELPF TIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTKKWKNIPC SWAGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATATKTA WYWYQNRDLDQWNRTEPSEIT PHIYNYLIFDKPDKNKQWGKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIKQE SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYSELKQIYKK
14740	45108	B	14826	1	1186	
14741	45109	A	14827	1	2304	
14742	45110	B	14828	1	2995	
14743	45111	A	14829	1	3095	
14744	45112	A	14830	1	3654	
14745	45113	A	14831	1	3189	
14746	45114	A	14832	1	2064	
14747	45115	B	14833	1	3031	
14748	45116	A	14834	1	3192	

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14749	45117	A	14835	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
14750	45118	A	14836	1	3144	
14751	45119	A	14837	113	1336	PTLAGTGNQETSHLGFNAIPIKL RMTFFTEL/EKTTLKFIWNQKR ARITKSILSQKNKAGGITLPDFK LYYKAIVTKTVWYWYQNRDID QWNRTEPSEIMPHIYNYLIFDKP DKNKKWGKDSLFNKWCWEN WLAIYRKLKLDPFLTSYTKINS RWIKDLNVRPKTIKTLEENLGN TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIELKSFCTAKETTI RVNRQPTEWEKIFATYSSDKGL ISRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYAAKRHMK KRSSSLAIREMQIKATMRYHLT PVRMAIIKKSGNSSRSNIVHSVT QANALESSWIPLFLIPHIQYISKP QASSFKMYHVTDPILPPSSQHL DQAAIINLCLQWPLLWFECMCP SKIHMLKLTPQ
14752	45120	B	14838	1	3127	
14753	45121	A	14839	1	2742	
14754	45122	A	14840	1	1998	
14755	45123	A	14841	1	3030	
14756	45124	B	14842	1	2558	
14757	45125	A	14843	1	3828	
14758	45126	A	14844	1	4134	MRKKQSRKTGNSKKQSTSPPPK ERSSSPAMEQSWTENDFDELRE EGFRRSNYSKLQEEIETKGQEV ENLEKNLDKCITRITNIEKCLKE LMELKAKARELHEECRSLRSRC DQLEERVSVMEDEMNEMKQE GKFREKRIKRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLARQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
14759	45127	B	14845	1	3555	

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14760	45128	A	14846	1	3345	
14761	45129	A	14847	1	3451	HTKNPSVHHHRQRPKVDKTTK MGKKQNRKTGKSKTQSAFPPP KERSSSPAMEQSWMENDFDEL REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRN WIKSQDPSLCCIQETHLMCRDT HRLKIKGRRKIYQANGKQKKA GVAILVSDKTDFKPTKIKRDKE GHYIMVKGSIQQEELTILKIYAP NTGSPRFMKQVLSDLQRDLDS HTLIMGDFNTPLSTLD
14762	45130	A	14848	1	2606	MVASRSSRVGVFYGGQNSVDG VSRRSDGSLNELCLYRPPTGAY LAYDTLDVLPSGQFTVNTPPID VNGKSLLALLWEHTSLLTSMG GGRWAMQPLGQLGQLEHLGD RRDQVLDRSGRSRRLDAAQHL RHRPDRRPQGMVGVLTNQKEP RTRWIHSRILPEVQGGTGTVPSE TIPIDRKEGILPNLFDEASIILIPK RGRDTTKKENFRPISLMNIDAKI LNKILANRNQQHIKKLIHHDQV GFIPGMQGWFNICKSINVIQHIN RTKDKNHMIISIDAEKAFDKIQ QPFMLKTLNKLGIDGTYLKIIRA IYDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSAYKINVQKSQAFLYTN NRQTESQIMSVFPFTIASKRIKY LGIQLARNAKDLFKENYKPLLN EIKEDTKKWKNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLHY KITVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKIHPRWIK DLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMAAKAKI DKWDLIQLKSFCTAKETTIRVN
14763	45131	A	14849	1	2862	

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14764	45132	A	14850	1	3724	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14765	45133	A	14851	2	2375	
14766	45134	A	14852	1	2376	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKGREIITNCLSDHS AIKLELRIKNLTQNRSTTWKLS NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLTRLIKKKRE TNQIDAIKNDKGDITADPTDRQ TTIREYYKHLYANKLENLEEM DIFLDTYTLPRLNQEEFESLNRP ITRSEIVAIINSLPTKKSPGPDGF TAEFYQRYKEELRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWYRTEP LEITPHIYNYLIFDKPEKNKQW GKDSLFNLWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEENLGITIQDIGMGK DFMSKTPKAMATKDKIDKWDL IKLKSFCTAKETTIRVNRQPTK WEKIFTTYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKKHMKKCSSSLAI REMQIKTTMRYHLTPVRMAIIK

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14767	45135	A	14853	1	1576	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNYLIFDKPEKNKQW GKDSLFNKWCWENWLAICRKL KLDPFLTPYTRINSRWIKDLHV RRKTIKTLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLKSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAAKKHMKKCSSSLA IREMQIKTTMRYHLTPVRMAII KKSGNN/R/CAPGTPERQNHSLS WKGS*SQEPSGLAQWIPLPWSP AS*DPLA*NSCCQHSCLKSTWD AQACARKLRTLIKGYRNCQLE
14768	45136	B	14854	328	1467	
14769	45137	A	14855	3	3412	
14770	45138	A	14856	1	2907	MDKFLNTNTLPRLNQEEVDSL NRPITGSEIVAIVNSLPTKKSPGP DGFTAEFYQRYKEELRIKYLGI QLTKDVKDLFKENYKPLLKEIK EDKNKWKNIPCSWVGRINIMK MAILPKVIYRFNAIPIKLPMTFFI ELEKTTLKFIWNQKRALIAKSIL SQMNRAGGIMLPDFKLYYMAT VTKTAWYWYQNRDIDQWNRT EPSEITPHIYNYLIFDKPEKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14771	45139	A	14857	1402	3004	TEPKTKTT*LSA*MQKGPLTKF NNPSC*KLLIN/IVLEVLARAIRQ EKEIKGIQVGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNILCSWVGRINIVK MAILPKVIYRFNAIPIKLPMPFFT ELEETTLKFIWNQKRARIAKAIL SQKKKAGGITLPDFKLYYKATV TKTAWYWYQNTDIEQWNRTEP SEIMLHIYNYLIFDQPEKNKQW GKDSLFNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEENLGITIQDISMGK DFMSKTPKAKATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELK QIYKIKTNNPIEKWVKDMNRHF SKEDIYAAKKHMKKCSSSLAIR EMQIKTTMRYHLTAVRMAIIKK SGNNSLIVGASMDTSLLSGPIPY DIQHFDRFGSVTVRRGCAIEFY

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14772	45140	A	14858	884	2925	GIKYLGIQLTRDVKDLFKERS/Y EPLLNEIKEDTNKWKNIPCSWV GRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR ALIAKSILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI DQWNRTEPSEITLHIYNYLIFDK PEKNKQWGKDSLFNKWCWEN WLAICRKLKLDPFLTPYTKINSR WIKDLNVRPKTIKTLEENLGITI QDIGMGKDYMSKTPKAMATK AKIDKWDLIKLKSFCTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYAAKKHM KKCSPSLAIREMQIKTTMRYHL TPVRMAIIKKSGNNSPTCVSQD WKLTQAVGLWSAEAEAPKSAQ RRPLAEGHRAAVQRDGSGLQL LCTVKLQVLPCIIAQGNGGRKA TSSLEAELTSWRPLCLEDGTGF RGEDTLETVNAEGRENRRKAG HRAAGSSASRRCRNTGRSVQRL RPQKTQAFPTHCHFCLILVVKA TQLNPKSRVRKVPFAPMKHGK ALAGPWANICAGKSSNEIRTCD RHGCGQYSAQRSQRPHQGVDI LCSAGSTVYAPFTGMIVGQEKP YQNKNAINNGVRISGRGFCVK MFYIKPIKYKGPIKKGEKLGTLL PLQKVYPGIQSHVHIENCDSSDP
14773	45141	A	14859	1	2577	

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14774	45142	A	14860	3019	5574	RETRGEVKNSKNQSTSAPPKDC SSLADPKKIQTTIREYYKHLYPN KLENQEEMDKFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLKLFQSIEKEGILPNSFYE ASIILIPKLGRDTTKKENFRPISV MNIDVKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIHKSI NVIQHINRTKDKNHMIISIHAEK AFDKIQQHFMLKTLNKLGIDGT YLKIIRAIYDKPTANIILNGQKL EAFPLKIGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEV VKLSLFADDMIVYLENPIVSAQ NLLKLISNFGKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WVGRINIVKMAVLPKLPMTFFT ELEK\TTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKAT ATKTAWYWYQNRDLDQWNRT EPSEITPHIYNYLIFDKPDKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NIRPKTIKTLEENLGITIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKQESFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYSEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAAKKHMKKCPSSLA
14775	45143	A	14861	1895	6140	
14776	45144	A	14862	1	2875	MKAEIKVFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITKIRAELKEIQTQ KTLQKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITTDPTEIQTTIREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGAEIVAIINSLPT KKSPGPDGFTAEFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK

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14777	45145	A	14863	2843	4460	HQHQQKPHPHRNPIQKSPTSKT KVLEVLARAIRQEKQS/GIQIGS QEVKLSLLEDDMIVHLENPIISA KNLLQLISNFTKVSGYKINVQK SQAFPYTNKTQIENQIMSELPFT IATKRIKYLGIKLTRDVKDLFK NNYKPLFKEIREDTNKWKNIPC SWVGRINIVKMAILPKVIYRFN AIPIKLPMTFFTELEETTLKFIW NQKRARIAKSILSQKNKAGGIT LPDFKLYYKATVTKTAWYWY QNRDRDQWNRTEPSEIMPHIYN YLIFDKPEKNKQWGKDS\LFNK WC*ENWLTICKRLKLDPFLTPY TKINSRWIKDLNVRPKTIKTLEE NLGITIQDIGIGKDFMCKTPKA MATKAKIDKWDLIKLKSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRC WRRCGEIGTLLHCWWDCKPVQ PLWKSVWRFLRDLELEIPFDPAI PLLGIYPKGYKSC
14778	45146	A	14864	1	8335	MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSAMEDEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIYRTLHPKSIEYTFFS APHHTYSKIDHIVGS
14779	45147	A	14865	1	3166	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDISRTLHP KSTEYTFFSAPHHTYSKIDHIVG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQSRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDAFKAVCR EKFIALNAYKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQ
14780	45148	A	14866	1	3912	
14781	45149	B	14867	1	2832	

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14782	45150	A	14868	1944	3531	LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARMAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDVDQWNRTEP SEITPHIYNYLIFDKPDKNKQW GKDSLFNKWGWENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKTLEENLDITIQDIGMGK DFMSKTPKAMATKAKIDKWDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKRCSSSLAIRE IQIKTTMRYHLTPVRMAIIKKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCQMRKNTK TLI
14783	45151	A	14869	1182	3891	KMIKGISTTDLTEIQTTIREYYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPITGAEIVA IINSLPTKRSAGPDGFTAEFYQR YKEELVPFLLKLFQSIEKEGILP NSFCEASIILIPKPGRDTTKKENF RPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFN IRKSINVIQHINRAKDKNHMIISI DAEKAFDKIQQPFMLKTLNRL GIDGTYFKIIRAIYDKPTANIILN GQKL
14784	45152	A	14870	997	1161	CTSTVIMSICTKLQNKEHVIEAL RRAKFKFPGHPK\IHISKK*DFT KFNADEFED
14785	45153	A	14871	1	1458	
14786	45154	B	14872	53	1468	
14787	45155	A	14873	1819	2235	

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14788	45156	A	14874	707	1613	VRARAGERARVVRENGKAELP VALVLPSRALSHTFTCTDLKVQ FHQRLRLQEKGSKFIGSNMSQE SDNNKRLVALVPMPSDPPFNTR RAYTSEDEAWKSYLENPLTAA TKAMMSINGDEDSAAA/HRPAL *LLQENQSEPIPREGVGWG*GE ER\ERMTEEEQEGEGGGGGRGG GEGEEEEEEEEDVEEEEEEEEE EKEEEEKGGEKEEENEEKEKQR EGRRGKETSNGQMVRPRLLPP HQEHSRNYLVFIMDSNMIEICF REASISPKAQAYVLIPDFKNCIY GWEEDSIEILWGLPGSHVL
14789	45157	A	14875	3	346	QRSKSCKVPGLGKPLTLPPKPE K\PQGQKDRRPTGFKP*N*RRRR SEKSLRFFPPGS/PQAVPIPVGFS FDTNL*HFL*KPLIFIMGGTVSL PHPRSPSAPPGTPQRPMTFCHLK Q
14790	45158	A	14876	1868	2666	GLLLSPFQGLQGVAPRKTRSNL HPGSLAHLSHQPPAPWPPRGLW PPGQETSCHCASGRALGTGSPR PPHAPWLHLEPQRAPHSGAPSP GSSPSAPLHIPVAPENLQSLGHR SPPNPSGPDCYPSPSGP/PPSSLD SPGLQTAPGAMFLSPRSGVQSA CPTPRSLDLRNSPASTPDQSVCP TPLSLAWLWPPPSPTSAKSLLFT LTSEVQSFSPTPIPPGSSDPPLSK QP\SGSCLSSSGHLTSPSVPRHSP WPRSSPQNPHSWTLPSS
14791	45159	A	14877	762	1528	AIPGGAAWPFRAEGAQGPGKR LTFKPLGAQRQSVSGGSEVPPL PLHLKMAPEMPVAL*SPGTGV HPSLLPPT/GPKVPPGRIDRGPVP TLAPQVGTAPIQWHCRGSRCPS G/SRPPGGWR/RPCQAPAPPLGQ HLPRLLPPPTGPQGPRPLTPSEP PPWSCWLPASPPAGPGSRRVGG GPGTCQGLLRS*GLLLSPFQGL QGVAPRKTRSNLHPGSLAHLSH QPPAPWPPRGLWPPGQETSCHC ASGRAVGTGSRRPRA

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14792	45160	A	14878	1	963	MARKDCCSPPGDSSPGRLPLVL PAQCLVLLRLQITAFSSIHVAAN DMMSFFLMAKQDSIAYKYRIFF IHSSVDGHARPLSPSLVVENGC GKQVFLLCSDNASPEVSTVALA SCPGTFPRHCGAAESTHICATG LGELTPQGHGHIPNKLCACCAT GLEELVPRDHGKLGISWFGFIA GAYLNLARVVGECQGSYGYLS LHHYCYCHYYHYCHYHYH\AA TY*NHYYHYYH/HHNNSYHHH SYYHYSYHFYHYYYNCYHHH YHCRHYYHPHDYYHYHA/RHY SLYYCHYLCHYYYRCYHDHSS HQHNHHECLP*VRHSAEHLQY
14793	45161	A	14879	105	1448	CHQPPASPFSRREPGGSEKPPER GCPAWEPAAQGPVQPLGEDGP RLCQPPPPSPDHALG\PYGHQRS GRPTLPGPRK\PAKKRGR*PSSS TGQ*SHRPTTGTPGGQAGGSG* VTAGGQ*PPQNL*AKISCPEMP GPSPGMQQGVKHPSLFSHQTV AKGFTTRWNCRQVCPHRGERK WISSVRPCGGALAPSCA/DGLR GRRTLSGSQPLW/PPAAVSAVG QLQPPCHTLTPHPLQNSTQHAE PQRGSVYSL*EGTSP\LAAVPFA PHIEKRPFSTFPAGDA*PSEAHA/ PGPACCHSPGGLEGPVSRAGPG TSAGR\PGNGRERAWPPHSGPS TPPDTSCG/SPGPQLARAGSRRA NGSTLPPTRQGFLPGRKDSAGA CGQP*AEGAAAGPSRSPAAER AVLPLPR\GRRKCRGGGPGVET GVSGARRGGDRSGCSPAALDA EAPASLAGVSIREG
14794	45162	A	14880	1	2421	

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14795	45163	A	14881	1080	2571	VHCRFWILALCQMSRLQKSPLL FNIVLEVLAKAIKQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI V/SAQNLLNLISNFSRVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTKKWK NIPCSWVGGRINIMKMAILPKVI YRFNAIPIKLPLTFFTDLERTTL NFICNQKRAPTLPQVQSLS\QKN KAG\GIT\LPDFKLYLQGLQ*PK TAWYWY\QNRDIDQWNRTEPS EIMPHIYNYLIFDKPWEK/HKQ WGKDSLFNKWCWE\NWLAICR KLKLDPFLTPYTKINSRWINDL NVR\PKTIK\TLEENLGIT\IQD\IG MGKDFMSNKTPKA\MA\TKAKI DKWDLI\KLKSF\CTAKETTIRV NR\QPTKWKKIFTTYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCST\SLAIREMQIKTTMRYHLT PVRMAIIKKSENSRCWR
14796	45164	A	14882	136	420	RESRNLSRGEESEDPAEPS\RNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPPSPAPPPETHTGSPRPPSGRSR IRAYLH
14797	45165	B	14883	1	1197	
14798	45166	A	14884	3	538	GAGTDGGRTPAPRAFPDPLGEA RTSAPTGPARPGGSASAARPAA VRPAEPAAEETQEQPRAGKRAI HEYRYVYVQQRRKTDPQPAVA VFGIPADGD*VSRTAYHAHQPL AWSGR/E*MCLSMAMWNT*ST MKK*ISIRVISRCSGPVHRTN*QI PEPVRAWRFLICRCICFSPGRWI KT

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14799	45167	A	14885	1208	2765	KMAPTWDKMVSSAQMGFNLQ ALLEQLSQDELSKFKYLITTFSL AHELQKIPHKEVDKADGKQLV EILTTHCDSYWVEMASLQVFEK MHRMDLSERAKDEVREAALKS FNKRKPLSLGITRKERPPLDVDE MLERFKTEAQAFTETKGNVICL GKEVFKGKKPDKDNRCRYILK TKFREMWKSWPGDSKEV/RGY G*EIQDADPIQQPQGASRAL\PY TVVLYGPAGLGKTTLAQKLML DWAEDNLIHKFKYAFYLSCREL SRLGPCSFAELVFRDWPELQDD IPHILAQARKILFVIDGFDELGA APGALIEDICGDWEKKKPVPVL LGSLLNRVPLCIENKLGVGGED WGDQLRVYWWNPSKREGGSG WSHGSEDANQSLKHLRLSANV LLDEGAMLLYKTMTRPKHFLQ MLSPWETTLAQIIMLDWAEETS SDKLKYAFYCSCRELSRLCPCN FEELVFRDWPELQDDIPHILAQ ARKILFVIDGFDPLGGRTLWTL TRGHLRELGNRRKRCPSSWGV
14800	45168	A	14886	213	625	EPGIDTSCLCAGRCSRPGKGRA CGGSSPCSWPGQPPAPPAAAAV PACPSGGRGAGPIQSGTCCSRS ADSRCTSWTAW/WPPGLGAAT VQTVMS*TV/WPMPHVPQAGW LALGQGAAAAKHPLTSATTRS WCLGVGPGPWM
14801	45169	A	14887	1	375	MCNAQVLEYMGKSSSLLTSDL QLVRDALRSLRNSFSGHDPQHH TIDSLEQGISSLMERLHVMETQ KKQERKPPLVIPRQT/WVWSGP PANSNRPAAEGPDC*KEN*RDA LRSLRNSFSGHDPQHHTIDSLEQ GISSLMERLHVMETQKKQERKP PLVIPRQTGSGVDLQQTPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL

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14802	45170	A	14888	1	750	MGELNQGSWRQGHLPLDAAN GIAIRVPRRRKDESRKNPTRKPH SWKPTKNFEDDVEVMKRSMSI RIEDTHSGPSAAGVLEFAGGPL QTLFAWVSPAEAAEQQRLLPVP /CLWKLCPRGAPARC\RQNSPSK LPSGFVYTVRGKLPTQASVVVD APPATKLECPRSTSDCCAGSKN FKPVDLSLLASVGPRVNLQQES SHYGKISVTVAGHCPTHATGRI LGKQALRWSPMCSMFIGRALG LVPVEGGLLQIA
14803	45171	A	14889	81	164	VGKQGLEWTPANSSRPAAEGP DC*KEN
14804	45172	A	14890	1	674	MVVYACSPSYLEAEVGGSLSLE VEATNPKNSSKKFLDLISEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFKYFGI YLTKEEERLKPSRKKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTPPLVIPRQ T/WVWSGPPANSNRPAAEGPDC QKEN*QTERNSINIKKKDIHTKT PLCI
14805	45173	A	14891	619	931	YLLMDFPLLHSWLVSLGDKVP HEFWRGCPSCSFGPRFWVAGV LVL*APKL*LRQVRSAGKRCGQ KW*IK*/SDRLCVD*NK/WSDSD LKPATSCSLIVTCHSLLGF
14806	45174	B	14892	1	658	
14807	45175	A	14893	48	288	LCSIKKPEKSLLCW*YPGNRVW SGPPAKSNRPAAEGPDC*KEN* QTERNSININKKDIHTKTPSEGH QHQRPKTKPGRI
14808	45176	A	14894	801	1157	QSGPSAAGLLDFAGGPLQTLFA RVSPAEAAEQQRLLPFPSSGKL RPRGAPARCQPELSCMRC\R*SL LGGVSQSGYMGVRDPFEEAAC PLSELECSAGRSAALLRMVRQG HLGLLKLRP

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14809	45177	A	14895	1	1891	MPVWVTVVKSWNTQIGRPGH VSALGFELTKNPWPLTYESGDG RSLGKPGAVSRRGGRHGPHPQ QAECDLPAGRIAGPCERGLERQ EKLPPAPQGGAWHLRLSRERFK SEDAPKIHVALGGSLFLLNLAF LVNVGSGSKGSDAACWARGA VFHYFLLCAFTWMGLEAFHLY LLAVRVFNTYFGHYFLKLSLVG WGLPALMVIGTGSANSYGLYTI RDRENRTSLELCWFREGTTMY ALYITVHGYFLITFLFGMVVLA LVVWKIFTLSRATAVKERGKN RKKVLTLLGLSSLVGVTWGLAI FTPLGLSTVYIFALFNSLQAHKQ LKDRKVGPHFMQGAVFLEGKF WGVDIASFEPQEQFWWTNLGK EDEDKSFDMPHSWVEQIEISPEE EAMGSAQMVRGVSGPERGSKK RPQLTVSTAFETRCPNGKKVIQ YKRAKLEKWAPYLNSNGLVSR LTTYEDLQCTNILEIKEWYQNR EDMLELKHINKTTDLKTDYFKP GHPQALRVHSYKSMQPEMDRV IEFYETARVDGLMKREETPRTM TEYYQGRPDFLSYRHASFG/RPS QEAHSEQCRVKPPAHCAKPAE DDV/RKSACFWSRRSASSCATT AVRTTSRPPSASSCGAPRWTAK
14810	45178	A	14897	1	425	HVQQTEISRTVSTGSPIILSCSVP VTLPNGPVLWFKGN/AGPNRKL IYNFKQGNFPRVKEIGDTTKPG NTDFSTRIREISLADAGTYYCV KFIKGRAIKEYQSGRGTQVFVT VSYSSRSQKSEICISGLKSRHQQ NCSFWRF
14811	45179	A	14898	1	393	RQGNFPRAKQIGDTTKPGNTDF STRIREISLADVGTYYCVKFIKG RAIKEYQ\SGRGTQVFVTEQNP RPPKNRPAGRAGSRAHHDAHT CLSALPERNSTNYFVQPCCCLR LLGLTGFAVKIIQTGKERTSK

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14812	45180	A	14899	1	753	MGSSLSPVLYVALPVRQPLLRS VVEERSTKMRVGSPGFQAKFRF YSQGLSWSARGEEGLVPAFWL QPYPRPLNFKAEMTEQKENQT YVDGGFRPYIHRRKNLTEGHK AEKEMEPWDGFSDESCRTHCQ VHDYAKGHGEVQRERVDEQK EHLGGRRQDCQQQHLNRRLHC /TVSGEAPSEASGSVRGHGRAH GLAGSERHGHDHAAPEHQLLQ SVDADHVVPVAWYQFWDDEG RGILSPGDHKPDRRGAALY
14813	45181	A	14900	6	726	VEGISRTGIQAEQAPGFTTMPIP VSVNPGDVLTLACNMSALSPE GPVLWFKSIGPGQQLIFSCNGS HFPRVTPVENTMVDQTDYSIILS CSVPNTLPNGPVLWFKGTGPNR KLIYNFKQGNFPRVKEIGDTTK PGNTDFSTRIREISLADAGTYYC VKFIKGRAIKEYQSGRGTQVFV TGEYVSYTPYPLVYNS\PLWDE ASRGRSRQQSLLFCSLHW*YPR KQDLEWTSSKLQQTCRRVA
14814	45182	A	14901	760	978	KKLLLLLLCGIEWHGFSSDSGS GGWVPEG*K*GCEHELLPEDVP SCFGWAECWLVRRTLPLFHYV ELCYSFHG
14815	45183	B	14902	772	1165	
14816	45184	A	14903	1	2133	
14817	45185	A	14904	1	1311	MATTPGRALGSLLPTLLLGLTA GQPFISLTGPSHRTSPGDSVPFN CTAVPFNSQDFSRDFNVTWLK DSDEHPASAQRLVPDNGGNDFI TSKAWVTLTRQDVSSEITCEVT HRALAEPLKTTMNLSQATRNP DGTYSLEHTWQAEATLEEREF ACWVVHDEQPPLKANVTLQAQ VRRQGKGQSVQPYKLQGPLQR SEPGTRIRLTYASSGFSTHQVTV TWLKNKHELPNPQTSVQYSGH TYNVTSSVLVPLMDDDVFSHV VCHVEHKLTWFFQKTTGLDQY L/QG/DP*QLCGGHLTLPSSPRAP PQLPGLQHP/VVFHSQVLLFSCL VAVTCLVQRFYPQNVHLAWLE DCHTLKGTEQPTLKKNNDRSY TLEKLLLVNASVQGPERVLTC MMEHEGQPPKRANLVLSTAAH TAYKPIGSTESIMVTMIITISQM

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14818	45186	A	14905	3	341	RRATRPGN*GGRHNAGRSSARL ETGRPAMAPQGRPRPLGCRTPQ HPGHWPSAPGLLPPAPGPVAG MTQAQRWCPEPDAHFLQYTLY FVRHIPQLPKQTPHHYIATRLPC ATQ
14819	45187	A	14906	154	679	GVCCPLLGGVSS*ATWGSGTT* GGNTHLI
14820	45188	B	14907	1	2554	
14821	45189	A	14908	387	826	ARAACLPRGSARGTAGAGEEPP DPAPLHLRGEGPAP/HRPRSPRG MGWPAAPSTRSPPST*RRCPLPP RPRWSP*SHPGPRASARRLP*LS *RASRSSEAPSPGSLGSVAGQD CSRTGTGFSPPAFPSDGQQTPPP APSSVPTLNSLG
14822	45190	A	14909	86	2223	GQEPQVREQKACHHLGSSPPPS WEL*EQRPAGP*N**PSTLTTGT GSTTT*QIRMKVN*MGN/DSPQ GKNTPKMYSGEFSPVRVHVPFS LSDLKQIKIDLGKFSDDPDGYID VLQGEDILAKAGAIRHLNIGEG THVCCPLLEEGINPEVWATEGK YGRAKNAHPIQVKLKDSASFPY QRQYPLRPEAQQGLQKIVKDL KAQGLVKPCSSPCNTPILGVQK PNGQWRLVQDLRIINEAIVPLY PAVPNPYTPLSQILEEAEWFTVL DLRDAFFCIPVHPDSQFLFAFED PLNPMSQLTWTVLPQGFRDSPY LFGQALAQDLSQFSYLDTHVL WYMDDLLLAARSETLCHQATQ ALLNFLATCGYKVSKPKAQLC LQQVKHLRLKLSKGTRALSEER IQPISAYPHPKTLKQLRMFLGIT GFCQIWINRYGKIARPLYTLIKE TQKANTHLVRRTSLQPVAYLS KETGTSLQPVAYLSKEIDVVAK RWPHCLRVVAAIAVLVSKAVK MIQGRALTVWTSHDVNSILTAK GDLWLSDNHNEEKIEHNWQQV IAQTYAAQGDLLEVPLTDPDLN LYTDGSSFVEKGLRKAAYAVFS DNGILESNPLTPGTSTQLAELIA VTQALELEGKREPENPADNASY SCEPLEDLRLLFRRQPIEAVKLQ MVLQMEPQMQSMTKIYRGPLD WPASPCSNVDDIEGTPPKEISTA

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14823	45191	A	14910	929	1324	RRYQVQRPSEGTLVYLFWPV*/PVVGVDPWLPTGPD\YSLLVPIPPPRARTPRWA*A*MKGCRRSATA*WCMC*SCRVPCPSCTPMFHSPCSAMTAVTPSLARP*THGSPPKAQGAPQGVKGPSSGLEAPPWA
14824	45192	A	14911	2	286	
14825	45193	A	14912	220	249	P*N**PSTLTTGTGSTTT*QIRMKVN*MGN/DSPQGKNTPKMYSGEFSPVRVHVPFSLSDLKQIKIDLGKFSDDPDGYIDVLQ
14826	45194	A	14913	1	163	EPENPADNASYSCEPLEDLRLLFRRQPIEAVKLQMVLQMEPQMQSMTKIYRGPLDWPASPCS*DFLGRGAFNVINIGAWASRPVQGSAVDLSHGLHLGLHLKNHL
14827	45195	A	14914	1	287	
14828	45196	A	14915	2498	2788	
14829	45197	A	14916	112	333	
14830	45198	A	14917	329	1666	
14831	45199	A	14918	1	756	
14832	45200	A	14919	1256	1651	RRYQVQRPSEGTLVYLFWPV*/PVVGVDPWLPTGPD\YSLLVPIPPPRARTPRWA*A*MKGCRRSATA*WCMC*SCRVPCPSCTPMFHSPCSAMTAVTPSLARP*THGSPPKAQGAPQGVKGPSSGLEAPPWA
14833	45201	A	14920	1	987	MLVLGYNRKNTEGTQKQKGTNASDFHFLSQVLEQVVSPKGSKEAQCCVLRHLGCESSESAPGIPPNLGIQLLTWAVMWDPFPTTLARAPSLALELMTQYFNNWNWVYNNITDQGESKMSKLKGKERRQREGERRERKRREKRERESQRKERKREKKGKKRREKDRSDLKQIKIDLGKFSDTPDGYIDVLQGLGQPYYLTWRDIMLLLDQTLTPNERSAAITAVREFGDLWYLSQVNDRKITEEREQFPTGQQAVPSVDPHWDTESEHGDWCHRYLLTDVLEGLRKTRKKP\IN*SMISTITQGKEENPTAFLERLREALRKH
14834	45202	A	14921	473	1015	
14835	45203	A	14922	3	937	
14836	45204	A	14923	530	612	LQAKVFFLLRWPAILRG*NYGPRGVPH
14837	45205	A	14924	101	430	

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14838	45206	A	14925	1	1587	MAALTLRGVRELLKRVDLATV PRRHRYKKKWAATEPKFPAVR LALQNFDMTYSVQFGDLWPSIR VSLLSEQKYGALVNNFAAWDH PGDIVLDLCAAPGGKTLALLQT GCCLTWSRKRCAALSMFSRPA RCLCRARTTAPRAVRRPDQRR ATAAATKQQARATPEAPGSAA HSSYCTMIPSACCCLPRQLKPPH AQPARSAAKPGLDQPGSHARL RGRGGEARQSLEAIRGGPSGIA PSDIPLPAKPSRRVIAQTYAARG NLLEVPLTDPDLNLYIDGSSFVE KRLRKAGIKAVKLQIVLQMEPQ MQPMTKIYCGPLDQPASPRSNV DDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYYLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKP\IN*SMISTI TQGKEENPTAFLERLREALRKH
14839	45207	B	14926	1	939	
14840	45208	A	14927	1	4317	MQSMTKMYCGPLDQPASPCSN VDDIEVKLEIMLLTERDDGKEV LDVGEERRYEIEEYDSKWTRK YNCLAVLRVHSGSQITTMKLIL WYLVVALWCFFKDGKIAASRS GGFSYGSSSSGDLDRKKPLFSL EFGSPGETEDKSRQRQDAGSPK SEDTPAGGFFNSSSSSGDSDRTK PFFSLGLGAPGKAEDKSGDSQD AGGSKSEDTPPGGFFYGSSSSG DSDKKKPLFSFEFGATGEDEDK SRERWDAGNSRSEDS
14841	45209	B	14928	110	269	
14842	45210	A	14929	1	561	EVFPACSQLVYWGKPITIYPLCE NNVYMLSPNASVCLYSP\LAEQ FSHQFPSHDLPSVLAKFSLPVSL SEFRNPLAPAVQETQLIQMVV WMLQRRLLIQLHT\YVCLMASP SEEEPRPREDDVPFTARVGGRS LSTPNALSFGSPTSSDDMTLTSP SMDNSSAELLPSGDSPLNQRMT ENLLASLSEH

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14843	45211	A	14930	1891	2522	GLSNQNQQPGRCIPDAHPVQDL VQDLVHTWCRVPCTSYVPCV* VPGAYLVHTRCIPGAGPGAYPV HTWCRTWCIPGAGFPAL/RPYH ALLLLSDEKSLLGELPIDCSPAL VRVIKTTSAVKNLQQLAQDAD LALLQAMGSAVA\LVMWAWP RATGPLKYCLRVGAGGACGWR PRLVAVSRALLLVWRCGSPWG PALAWQKSPEYSTKVLEKQ
14844	45212	C	14931	113	274	
14845	45213	A	14932	1	1634	MEIPAVILTVAPILHLTSCGFPV TGDGLKQAEGKCAPEEWNPTK FIKLTDNQACFACGLWPLSEIQ RRTSRTVTIISRISALREKGNGR KPTSISGSVNEMRQVLVKDQVS MPRVLPTIIFVPDEAGFSAGAV WPCAAPLWGSSWTPLKVENCS FYIRLSFAISVGGDELKIAKLVS AFPERAYDLVGHQHQRPKVDK TTKMGRNQSRKAENSKNQNMS SPPKEHNSSPAREQNWMENEF DELREVGFRRSVITNFSELKEH VLTHHKEAKNLEKRLDEWLTR INSVEKSLNDLMELKTTLRELR EAYISFNSQFDQAEERVSVIEDQ ISEIKQEVKFREKRVKRNEQSL QEIWDYVKRP\NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANIQI/QGKLQRTPTKVASSRT ATPRHIISVGSPKLNMK\EKILR AAQRERSGLPTKGKPFRLTAAD LSAETSTSQKTEWGPIFNILKEK NF\QPR\ISYPAK\LSFISEGEIKYF TDQAKCLRDF\VTTRAFSCLP*K STRPALKELLKGST

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14846	45214	A	14933	1	1429	MVLAAGDPVEKGITWARENAG IYISCTMMKLSMIPIGDQSYRNL IPLKFVACILIEGNAKCWPLPEF DPSQIRLIVYQDCERRGRNVLF DSSVKRRNEDISVSRIKYLGIQL TRDVKDLFKENYKPLLNEIKED TNKWKNIPCSWIERINIVKIAILP KKLGSDAQVKVFGKCCQLKPG GDSSSSLDSSVTSSSDIKDQCLK YQRTVDLSAQLSSSGKGQTTSS SGSLTPMTPHWEIPPSGGQQTS HTGELRLASGRGSSGMKLPEEG TDRNLCCSAASSGDTQANRDW SGPPANTSRPAAEGPDCDRENG TKLENTLKDIIHENFPNIARQAN IKIQEIQRTQQRYCSRRATPRHII VRFTKVEMKEKMLRAAGEKH WVIHKGKSIRLTVDLSAETLQA RREWG\PIFNVLKEKNFQLRISY PAKLSFISEGEMKSFPEKQMLR DFVTIRLALQELLKEALNMARE /NR*QPLQKHM
14847	45215	A	14934	2320	2811	ESKLTRGVKDLFRENYKPLLNE IKRGHKQMEEHSMLMGRKNQ YREKWPYLPKVNL*IQCHPHQA TNDCFHRIGKKLL*SSYGTKKE PALPSQS*DKRTKLEASHYLTS NYTTRLQ*PKQHRYWYQNRDI DQWNRTEASEIMPHIYTILILWT NLRKTSMGERHP
14848	45216	A	14935	2	872	
14849	45217	A	14936	769	828	
14850	45218	B	14937	1	669	
14851	45219	A	14938	1	807	
14852	45220	B	14939	35	212	
14853	45221	A	14940	235	837	QQAHKTPQRRHSAFTEYVRNN RLPETVIRVKQPALAIFSPDIAPL FVHFRADDDVTARVIHAIIMIF WCDRVEKRVSDAVACFTLESEI AEVGVLCRTHIRQ*RQVTPARM *ALSRILHACRSEDVRHNRPPYP VIRVKQPA\RRDLAPT*PHCSSIS AQTITSLPGCMREVT/ELRPEFF K*RKTVLRPTPIMRARAERRCK
14854	45222	C	14941	1	1755	
14855	45223	A	14942	1	747	
14856	45224	B	14943	1	2466	

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14857	45225	A	14944	1	333	LNLVLFQQRAELMIS*PQ*FSRA LLVIFPLLQTELQQLFFLLHVNP AAVEAPPSVPIGLYSENVRNNR LPETVIRVKQPALARFSPDIAPL FVHFRADDDVTARRVEKRCK
14858	45226	B	14945	1	1794	
14859	45227	A	14946	1183	1899	LNRRDSYVEYLADKVADREED AEEYLEAIMEARVTVAGMGLV MEVQDYFDGEADRLAKAWLA EYTPQIKSLKDERKEAYRQIVE MSTEPQDVDLVRPANKFEMTR VREGEKEADLPVWKHHL/SV*R KRELSGSVEPLGNQVFEIETKRE NS*EL**KSLKDERKEAYRQIVE MSTEPQDVDLVRPANKFEMTR VREGEKEADLPVWKHHLLCDE SGNYPALLNHWETRFLRSKPN VKIHRSSDKSPTYFVFFISQYDL PAFYPINGHFLVERVVKVRIVFI EEFADHHHLAIFQFNNRLQRHA FVVTLANVTNQPFSVVVVVNL
14860	45228	B	14947	1	3099	
14861	45229	A	14948	1174	1545	
14862	45230	A	14949	1	945	
14863	45231	A	14950	62	576	
14864	45232	A	14951	1	1642	MLANIGFYNSNVIHRSKGAIGE GPPDPRGIVEQNLGGDISIPCYN GPRPRRSAQKTTLGPLNQPRIPS AQCAGAFPRVAAAGAGGGGG GGSGGSGFCLGWRLRRRRQRR RRWRRGEGEGDGDAGHMRPR PAGRAEARRRRRLRGNPPPGAR LPNREGNGSGVSWAAEVSGDG RGARTEAARTRRRPGGADNYP GAVPPVQLLTGWCVTAKAPPDI SAISALTAVKHGNCSSLTPLLNP PGSDVIVCAEMDEQWGYVGAK SRQRWLFYAYDSLRKTVVAHV FGERTMATLGRLMSLLSPFDVV IWMTDGWPLYESRLKGKLHVI SKRYTQRIERHNLNLRQHLARL GRKSLSFSKSVELHDKEELAAL FSELKQEQKKVDELIAKLVKNR TRIVNESDVFSWVIRREFQELR HPVDEEKARCLEGIGGHTRGLV ASLDMQLEQAQGTRERLAQAE\ LCWNSSEMRTTMSSSGSSTPWP PVSRRRPWTERRLGSVRGDRLR ERSRPAVNRTPRMSRVPSGAPR GTPSRRWWMMKCWDHQMRG LVEEEVG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14865	45233	A	14952	1	1513	MIIALQKESLMSLQAQLDKALQ KEKHYLQTTITKEAYDALSRKS AACQDDLTQALEKRTGRDWNP PPFRTQQRGSKSLTAIRPLCLFR KLNHVTSETKSLQQSLTQTQEK KAQLEEEIIAYEERMKKLNTEL RKLRGFHQESELEVILYEEEMG NHNENTGEKLHLAQEQLALAG DKITSLERSLNLYRDKYQSSLS NIELLECQVKMLQGELGGIMG QLSKTSSDLSKM/RCY/TTW*M WTKLQFIHSILTSVIFHLLSFSSM GSI*KWIMALSGSSFLLDAHYIS QFGPRQLPSVCAEPEKEKATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQPAGQ*RHRL RG\MDEQWGYVGAKSRQRWLF YAYDSLRKTVVAHHREQGSIK CKLEEDLQEATKLLEDKREQLK KSKEHEKLMEGELEALRQEFK KKDKTLKENSRKLEEENENLR AELQCCSTQLESSLNKYNTSQQ VIQDLNKSPMEIRFQLYIFTPDQ
14866	45234	A	14953	125	363	INVSVWSQPFPGG*QPEKGLKE HPADARPGSC\PPAGRPVQGRA EVASAAPPRGSSPAAAPGQSHP PSCLRAPLYWSFSR
14867	45235	A	14954	306	583	TCSTRRRKNDLSVKYVSVWSQ PFPGG*QPEKGLKEHPADARPG SC\PPAGRPVQGRAEVASAAPP RGSSPAAAPGQSHPPSCLRAPL YWSFSS
14868	45236	A	14955	225	407	LRGMVTFSPFSSILNGQFEPNSG CPL/CPVCWVCLREPGDPEKLG EFLQKDNISVHYFCLVS
14869	45237	A	14956	484	722	NTCRCGHNRSPEVNSRRGGLRS IPRMPDAGSCS/PPAGRPSAGPG RRSPPPLLPRGSSPAAAPGQSHP PSSSQGAAVLEL

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14870	45238	A	14957	434	1790	GNFFRKTISACIISVLSYLVSCLR GASPTEASMDFCLKTSKREAAR ASRKICFVCKKKGAAINCQKDQ CLRNFHLPCGQERGLPFTIFWR VQIIL*QTSP/EHRTSNMGHVGE ESCILCCEDLSPTECLRTFQSPC CSQAIYHRKCIQ/TNMPTHQSK HFFKCPQCNNRKEFPQEM/REN GNSYSRQRCCLGTRARGFLRLI SALSAL*CPHLVCMNKAETALR MKGGGASFCVLHADPTEPTGT APLLDLTVRNGSVRSVHL/PAA TDYIPENSGDIPCCSSTFHPEEHF CRDNTLEENPGLSWTDWPEPSL LEKPESSRGRRS/VLLEVQGCQ NH*QLQKIQVTPSE*LLVPHNR V*TCAPPSGLGREHSGTVRQGS RASSETMS/LSKEKSQWSMRRE QSRCQQGNAFMATRVPLLSPPL LPPRILPP*SCFHMPLLTSPMFV VMQIKVFSPKKKKK
14871	45239	A	14958	146	484	
14872	45240	A	14959	228	353	
14873	45241	A	14960	214	722	TARELPGRVLKEMYIQQK*EGA ALGRPTRPGRQGQRVRRAECR RLFRGVLRPCNRC
14874	45242	B	14961	1	951	
14875	45243	A	14962	241	517	QSCGQRLPTVLR/PLRTPWILPM YPQPLPAGGPTPCLRSRPYINITI LKGDKGDPGPMGLPGYMGRE GPQGEPGP*GSKGDKGEMGRP RRPVP
14876	45244	A	14963	748	1055	DRKQTSPGDAYHTIPGSLSSSSD HVLSEPD*GEGSHL**SVQHDD VPPTA**RLQY\RAVVLFPTATL PAILIM*GMRCPLVPRNCSRTW TAQIRAYIEVQQT

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14877	45245	A	14964	1	832	MPHVCAQRRLPVAAVLPPDGA QNCILLAGLSAGTFCHHGGVHI LLSNPVATSLLVAIDRVGQIPIPP PPPPALPYDCCCPPPSRHTEDRE HVPIPLHWKLMVNRWFLPVPT EWIATLSNSSRSSRTCSMQGLSF LDSQVHLKAMIEDLRGNVSKES SPCLADNADVGQFPMEGGQKD PKQRIIPFCQGVTNLSGPHGPGA VCGGSHYQKQESSEISLSVGQV WTSSRRMSQVGGSSHCRGARL GPCNVPRRPDGVQDEFSLQPEE DAG*QTSVDPMVLEQYVVVA/ NYQKQESSEISLSVGQ/VVDIIE KNESGWWFV/STAEEQGWVPA TCLEGQMGCRMSFLCSLKKML DWIQRRVSL
14878	45246	A	14965	1	346	
14879	45247	A	14966	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL
14880	45248	A	14967	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
14881	45249	A	14968	1	2235	
14882	45250	A	14969	1	2148	
14883	45251	A	14970	1	1821	
14884	45252	A	14971	1	1248	
14885	45253	B	14972	4	2121	
14886	45254	A	14973	1	1137	

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14887	45255	A	14974	1	1240	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNICKSI NVIQHINRAKDKNHMIISIDAEK AFDKIQQPFMLKTLNKLGIDGM YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFSIVL EVLARAIRQEKEIKGIQLGKKE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRLKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMPFFTELEKTTLKFIWNE KRARIAKSIPSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEITPHIYNYLIF DKPEKNKQIQKAFILH\KEPWV MWNMGTNVR
14888	45256	A	14975	1	2241	
14889	45257	A	14976	1	2802	MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIQGCDFSGTCRQ TLSILTQPLRQWGLEGIKKPNS WIISEESVSNGGPPLLIPRQTAS GVDLQQTPTDLQLRVLTVRRK TNKQKGIASTSTKRTSTPKPHL YVTIIKDQSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWDYVKRPDLRLIGVPD SDGENGTRLENTLQDI
14890	45258	A	14977	1	2739	
14891	45259	A	14978	1	2478	
14892	45260	A	14979	590	727	
14893	45261	A	14980	1	3255	
14894	45262	A	14981	1	3810	
14895	45263	B	14982	1	3127	
14896	45264	A	14983	1	3325	
14897	45265	B	14984	1	1734	

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14898	45266	A	14985	1	2067	MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLHLIGVPETDGENGTKLEN TLQDIIQENFPNLARQANVQIQE IQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTTIR EYYKHLHANKLENLEEMDKFL DTYTLPRLNQEKVESLNRPITG AEIVAIIN/SLPTKKSPGPDGFTA EFYQRG\ILPNSFYEASIILIPKLG RDTAKKENFRPISLMNIDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHVNRT KDKNHMIISIDEEKAFDKIQQPF MLKTLNKLGIDGMYFIIIRAIYD KPTAHIILNGKKLEAFPLKTGM RQGCPLSPLLFNIVFKVLARAIR QEKEIKGIQLGKEEFKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQTFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKVPMTFF TELEKTTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITPHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKD
14899	45267	A	14986	1	1293	
14900	45268	A	14987	1	3229	
14901	45269	A	14988	1	3352	
14902	45270	A	14989	1	1419	

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14903	45271	A	14990	1	1716	MKAEIKMFFETNENKDTTYQN LWDTFKAVCRGKFIALNAHNR KQERSKIDTLTSQLKELEKQEQ TYSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKRQKNQMDTIKND KGDITTDPTEIQTTVREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEVESLNRPITGAEIVAIINS LPTKKSPGPDGFTAEFYQRYKE ELPGRDTTKEENFRPISLMNIDA KILNKILANQIQQHIKKIIHHDQ VGFIPGMQGWFNIRKSINVIQHI NRAKDKNHMIMSIDAEKAFDKI QQPFMLKTLNKLVLEVLARAIR REKEIKGIQLGKEEVKLSLFAD HMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFRENYKPLLKEIK EDTNKWKNIPCSWVGRINIVKV AILPKVIYSFNAIPIKIPMPFFTEL EKTTLKFIWNQKRARIAKSILSQ KNKAGAITLPDFKLYYKPTVTK TAWYSYQNRD\IDQWNRTEPSE ITPHIYNYLIF
14904	45272	A	14991	1	702	

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14905	45273	A	14992	473	2385	HSFLSFIVLMYLTMDLTRSQKH GWASSPSHGTSPWPVRLRTSLA KPCKWQVSLCWWLSASPGSSF SLVRSSLLIIVPHAESVSRRPSLL SRVGLFPARY*HRVWQRSPSPQ TRDHLIKRNPSQDV*RRQQPRG TRVSN\KCSLHTSALGIGRQPSC DATL*GQQGLP/VK*KRQQPAP/ MSQQQTGAALEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPTVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRITYLGIQ LTRDAKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKEPGWARSLVFGARGLQG QGRCGQSRGGGGSCLGGGGST ENWQHREPSARKTGSTENRRH REPAAPRTGSTENQHREPAAPR TGTENRHREPSARKTGSTENRR HREPAAPRTGSTENQHREPAAP RTGTENRHQEPAAPRTGGTENR QHREPAAPRTGTENRQHREPAP RTGSTENRQHREPAPRTGSTEN RQHRESAAPRTGSTENRHQEPA APRTGTENRHREPSAPRTVGTE NRRHRELVAPRTGGTENRPREP PAGTRPRHTPMRGGSEGALFH QRRFLEPTPDREQLEGIRYPPVA

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14906	45274	A	14993	687	2274	LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARMAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDVDQWNRTEP SEITPHIYNYLIFDKPDKNKQW GKDSLFNKWGWENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKTLEENLDITIQDIGMGK DFMSKTPKAMATKAKIDKWDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKRCSSSLAIRE IQIKTTMRYHLTPVRMAIIKKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCQMRKNTK TLI
14907	45275	A	14994	1	3189	
14908	45276	A	14995	1	3351	MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSAMEDEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIYRTLHPKSIEYTFFS APHHTYSKIDHIVGS
14909	45277	A	14996	1	3192	
14910	45278	A	14997	1	2742	
14911	45279	B	14998	1	2313	
14912	45280	A	14999	1	1542	
14913	45281	A	15000	1	3300	
14914	45282	A	15001	1	1824	
14915	45283	A	15002	1	2982	

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14916	45284	A	15003	1	2375	MSGFLISPKHKHGTNSGIVSWA DVQSQLRHIEAAFDQEAAAVL MARLGVFRAESEEGPDVLRWL DRQLIRLHSLLTTLDIVPAGKGE VVKGPMSISQQAKGCQKFGQY NKEDPTSFRLSDSFSLYPQFMF HLRRSPFLQVFNNSPDESSYYR HHFARQDLTQSLIMIQPILYSYS FHGPPEPVLLDSSSILADRILLM DTFFQIVIYLGETIAQWRKAGY QDMPEYENFKHLLQAPLDDAQ EILQARFPMPRYINTEHGGSQK KREKNQIDAIKNDKGDITTEPTE IQTTIREYYKHLYANKLESLEE MNKFLDTYTLPRLNQEEVESLN RQITGSEIEAIINSLPTKKSPGPD RFTAKFYQRTNDQKHMIISIDA EKAFDKIQQPFMLKTLNKLGID GTYFKIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSLLLF NIMLEVLARAIRQEKEIKGIQFG KEEVKLSLFADDMIVYLENPIV LAQNLLKLISNFSKVSGYKINV QKSQAFLYTSNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRF NAIPIKLSMTFFTELEKTTLEFI WNQKRARITKSILSQKNKAEGI TLPDFKLQYKATVTKTAWYSY QNRDIDQWNRTEPSEIVPCIYN YLIFDKPDKNKKWGKDSLFNK
14917	45285	A	15004	1	1428	
14918	45286	A	15005	2	1975	

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14919	45287	A	15006	1	3891	MKPEIKMFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKINTLTSQFKELEKQEQT NSKASRRQEITKIRAELKEIETQ KPLQKINESRSWFFEKINKIDRP LARLIKKKREKNQIDAIKNDKG DITTDPTEIQTTIREYYKHLYAN KLENLEEMDKFLDMYTLPRLN QEEVESLNRPITGSEIEAIINSLP TKKSPGPDGFTAEFYQRYKEEL VSFLLKLFQSIKKEGILLNLFYE DSIILKPKPGRDTTKKENFRPISL MNIDAKILIKILANRIQQHIKKLI HHDQVGFIPGMQGWFNIRKSIN VIQHINRTKDKNHMIISIDAEKA FDKIQQPFMLKTLNKLGIHGTY LKIIRAIYDKPTANIILNGQKLK AFPLKTGTRQGCPLSPLVFNIVL EVLAWAIRQEKEIKGIQLGKEE VKLSLFADDMTVYLENPIISAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNGQTESLIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKED\TNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTDLEKTTLNFIWNQ KRARITKSILSQKNKAGGITLPD FKLYYTATVTKTAWYWYQNS MVLVPKQRYRSMEQNRALRN NAACLQLSDL
14920	45288	A	15007	1	4215	MHSCLPDATGEGELYNSLGSLT WSFLSMIGVLLWVDFSGDSIDL CSPLWNRTNLEALQKKLEELEL DEQQRKRLEAFLTQKQKVGEL KDDDFEKISELGAGNGGVVFK VSHKPSGLVMARKLIHLEIKPAI RNQIIRELQVLHECNSPYIVGFY GAFYSDGEISICMEHMVLLQER PCPGFLWMENSDYGLLLPLDLL LCLSFSFSKVLSDLVSDILIHGM KARNRSIHGDVVVVELLPKNE WKGRTVALCENDC
14921	45289	A	15008	1	2823	

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14922	45290	A	15009	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14923	45291	A	15010	1	2816	MEDEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFTTCICDDAEDLQSPSTA GPWFGVLYTKGGPYPQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPNQCH IGEVLLDGFTAEFYRRYKEELV PFLLKLFQSIEKEG
14924	45292	A	15011	1	3347	MGDFNIPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNCSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDAIKNDK
14925	45293	A	15012	1	3855	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14926	45294	A	15013	1	2559	
14927	45295	A	15014	1	2956	

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14928	45296	A	15015	1	1853	MGRNQSRKAENSKNQSASSPP KDCSSSPAMEQSWTENDFDELT EVGFRRSVITNFSELKEHVETNL KEAKHLEKRLDKWLTRIKSVE KILNDLMELKTMAQELHDTCR SFNSQFNQVEERVSVIEDQINE MNIDGTYLKIIRAIYDK\PPRNII LNQQKLEAFPLKTGTRQGCPLS PLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKSILSQKNKS GGITLPDFKLYYKATVTKTA/W L/YHTPLSCLPP*WNRTEPSEIIP HIMAVAQIQQVKLLLLQGQHA SSRLQPTSSTKCGGWTASSASP RSMGLSSWKGNLASAIHYFPCK PLTLPSRISTSSSSWGCRQAHAV LEVLRWPPGLGWPGWHHLTLL HVPPVRITKSNGPRACTRASAS HARHHQYNQEPSLSPLHSPLPP PEQVLVSTAERTEDRSYHRTLC RHSPYFKNEAADLRGEGYSS
14929	45297	B	15016	1	3276	
14930	45298	A	15017	1	2274	
14931	45299	B	15018	440	3383	
14932	45300	A	15019	1	2646	

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14933	45301	A	15020	1	2229	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VQNFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKEIQT TIREYYKHLYANKLENLEEMD TFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AEFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEASIILIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDKIQQPFML KTLNKLGIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRIKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPK\IGKTTLKFIWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWYWYQNRDIDQWNR
14934	45302	A	15021	1	960	
14935	45303	A	15022	1	2928	MEDEMNEMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSMRQKVNKDTQE LNSALHQADLIDIYRTLHPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDAF
14936	45304	A	15023	1	1782	
14937	45305	A	15024	1	4881	
14938	45306	B	15025	1	5962	

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14939	45307	A	15026	1	2053	MKAEIKMFFETNKNKDTTYQN LWDAFKAVCRGKFIALNAHKR KQERSKIDTLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLLKKKREKNQIDAIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGAEIVAIINSLP TKK\SPGPDGFTAELYQRYKEG AVLEVLARAIRQEKEIKGIQLG KEEVKLSLFAGDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYGF NAIPIKLPMTFFTELEK\TT*KFI WNQKRARIAK*ILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWSRTEPSEIMPHIY NYLIFDKPDKNKKWGKDSLFN KWCRENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTITTLE EKLSNTIQDIGMGKDSMSKTPK AMATNVKIQKWDLIKLKSFCT AKETTIRVNRQPTTWEKIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWVKDMNRHFSKEDIYA AKKHMKKCSPSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRC
14940	45308	A	15027	3	3229	
14941	45309	A	15028	1	3907	MGDFNTPLSTLDRATRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSITWKLSN LLLNDYWVHNEMKADIKMFFE TNENKDTTYQNLWDTFKAVCR GKFLALNAHKKKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIGAELKEIETQKTLQKINESR SWFFERINKIDKPLARLIKKKRE KNQIDAIKNDK
14942	45310	A	15029	1	4005	
14943	45311	A	15030	287	2708	
14944	45312	A	15031	1	4602	
14945	45313	A	15032	1	4806	

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14946	45314	A	15033	965	5928	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID
14947	45315	A	15034	383	8708	
14948	45316	A	15035	2	3257	WRKIYQANGKQKKAGVAILV/S DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLSTLDRLMRQKVNKDTQEL NSALHQVDLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQSRSTTWKLNNLLLN DYWVHNEMKAEIKMFFETNEN KDTTYQNLWDAFKAVCRGKFI ALNAYKRKQERS
14949	45317	A	15036	1	3508	MELKTKARELREECRSLRSPCN QLEERVSAMEDEMNEMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSDHSAIKLELRIKNLTQNHST TWKLNSLLLNDYWVHNEMKA EIKMFFETNENKDTTYQNLWD TFKAVCRGKFIALN
14950	45318	B	15037	1	4760	
14951	45319	A	15038	1	3110	
14952	45320	A	15039	1	5546	MELKTKARELREECRSLRSRRN QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSSRRATPRHIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE

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14953	45321	B	15040	1	4534	
14954	45322	B	15041	1	1826	
14955	45323	B	15042	1	1626	
14956	45324	A	15043	248	1212	NSKHYRSGQKKKLPTLPRAAN SRWRSLKI/GFTVSFDETLKPFV RDVSGSRLKDLPKPNKSDDETR ANDAVNRYKLLKKDARTIAAQ QVARLESAMCLRRRWSLENFQ LFLVEHPLVRHLTRRLIWGVYS AENQLLACFRVAEDNSSSTADD DLFTLPEGDISIGTPHVLEISPTD AAALLFADYELLPPFRQLDRNS YALTEAERNASELTRWAGRKC PSGRVMGLANKGWIKGEPQDG GWIGWMIKPLGRWSLIMEIDEG FAVGMSPAELSAEQLLSKLWL WEGKAERYGWGSNSTQEAQFS VIDAITASELINDIEALFE
14957	45325	A	15044	1	1788	
14958	45326	A	15045	1	3048	
14959	45327	A	15046	1	3546	
14960	45328	A	15047	969	1205	SPVRCCISAVHRTYHRRTSALL RLAELHRLLEKCASRQWMYEN I*SPFRQIA*CLPYSDHKNQRLH GLDSIFLARLLW
14961	45329	A	15048	877	1248	WPLTVPYCGVGYAS*A*VADN HRAVGYLSRWAGRKCPSGRV MG/LANKGWIKGEPQDGGWI/G WMIKPLGRWSLIMEI/DEGFAV GMSPAELSAEQ/LLSKLWLWEG KAERYG/WGSNSTQEAQFSVID
14962	45330	A	15049	854	1313	DHGVASAATCVYTNEGHRQSY VRVCEYASRTRVSHHCSV*RVL RCEAIRIVSPDRSC*RDPEFSYL\ ALPENYNRLFLPNSTNQTNNRI KTLNSIAIGKLLAAGGVYNGNI EGFRDTAEKLDGRTIDGYDQIL NEKTAVIAKATA\SILLTKRS
14963	45331	A	15050	1010	1396	KPFGKLTYKLFEGHAWLVKAE KVRVGYRILGRLTYPFDIRFPAL PFGLVL*KGAHFTVPRIWAGHA C*LMPMALPMFRWKVTGLLFIP ICLVKPSFLTLTIIIAIRRISTSTN CRKTPKQPSRWCKPR

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14964	45332	A	15051	361	837	DGQQLIALHRLALRELQQAVH AGLPQQAKILFDGGSEIGKIPSEI YFCQLVKLILCPVLFPCWRRVA ILWRRRDVLFFGSFSFSALVSPH LCG/SYLPFVFDVGDRL*LSVG WS\KEIWPCK*GFGHLMSVLNT PMKSLVEGFKHFPLAGFGYEYL SFFCR
14965	45333	A	15052	1563	1652	
14966	45334	A	15053	2756	2995	AMRSAHRCTVFSALLNCWQITP HLTPSVMICGQLLTLVNRC*PSS TIFSIIPLSKQVARMFRSAMSPL NRARCWKVPCN
14967	45335	A	15054	762	2184	WRAVPSEPISFILKADTEKYVY L*NSSSAQYSGSCTRAYYLDTQ HPTPRLCLIF\GGKDSGLMLHLT AELARQMGKKICVLFIDWEAQ FSCTINYVQSLRELYTDVIEEFY WDALPLTTQNSLSQYQPEWQC WEPDVEWVRQPPQDAITDPDFF CFYQPGMTFEQFVREFAEWFSQ KRPAAMMIGIRADESYNRFVAI ASLNKQRFADDKPWTTAAPGG HSWYIYPIYDWKVADIWTWYA NHQSLCNPLYNLMYQAGVPLR HMRICEPFGPEQRQGLWLYHVI EPDRWAAIGSPADREEDAEEYL EAIMEARVTVAGMGLVMEVQ DYFDGEADRLAKAWLAEYTPQ IKSLKDERKEAYRQIVEMSTEP QDVDLVRPANKFEMTRVREGE KEADLPVWKHHLLCDESGNYP ALLNHWETKVFEIETKREGFAF WYRNPQYTGQSSLGIAYVEAE QYKIVRPDFLFFAEQDGKMVV
14968	45336	A	15055	2069	2586	PWLENLPVGICWSAVKKMGGT RSLVSCL/AVTLVSPQLMNAYL LGQQLPEVWDFGMFSIAKVGY QAQVIPALYLVVVPVCSLILAV FLAHALIGPFGRMIGDGVAFAV RHLMTGSFAPIGAALFGFLYAP LVITGVHQTTLAIDLQMIQSIGC TPVLPVNALSNIDLWHISILV

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14969	45337	A	15056	356	1205	APASMTFEQFVREFA/VMVFTK RPAAMMIGIRADESYTVLSPSP V*INNVLPTITWTFPQTIYDFLW LIGEAIFF/YLPVGICWSAVKKM GGTRSLVSCL/AVTLVSPQL/MN AYLLGQQLPEVWDFG\VCSLIL/ AVFLAHALIGPFGRMI/GDGVA FAVRHLMTGSFA/PIGAALFGFL YAPLVIT/GVHQTTLAIDLLMM QSMGGTPVWPLIALSNIAQGSA VIGIIISSRKHNEREIPGEVFPRT GVGKGKSLG*PLH*LQPYRQHL GAGSYSQTLKKQIAESAVRLSIP
14970	45338	B	15057	1	435	
14971	45339	A	15058	2	1785	WLLYRAHVKGE/STEALLPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLLLGDKVIPATIL GIQSDRVIRGHRFMGEPEFTIDN ADQYPEILRDSGKVIADYEERK AKIKADAEEAARKIGGNADLSE TLLEEVASLVEWPVVL/TAKF/E EKF/LAISRTALVPYSADNMYQ LVNDVQSYPQFLPGCTGSRILES TPGQMTAAVDVSKAGISKTFTT RNQLTSNQSILMNLVDGPFKKL IGGWKFTPLSQEACRIEFHLDFE FTNKLIELAFGRVFKELAANMV QAFTVRAKEVYSASMRYIYVIV YISYRPPNLLDSHIIGFSSITTHC AVTSHHYNSCDMTMTIHSYVT PYISVRVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDDTRHIHTI ESRCRVCGAHDSRDAERLDRF AQTADEIRIADRGFSSRPECIRS LAFGEADYIVRVHWRGLRWLT AEGMRFDMMGFLRGLDCALIS KTRLLSENRRKGRVVQAETLE AAGHVLLLTSLPEDEYSAEQVA DCYRLRWQIELAFKRLKSLLHL DALRAKEPELAKVGIFANLLAA FLIDDIIQPSLDFPPRSAGSEKKN
14972	45340	A	15059	1	993	

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14973	45341	A	15060	1	5621	MSEKTFLVEIGTEELPPKALRSL AESFAANFTAELDNAGLAHGT VQWFAAPRRLALKVANLAEAQ PDREIEKRGPAIAQAFDAEGKPS KAAEGWARGCGITVDQAERLT TDKGEWLLYRAHVKG\EGTEA LLPNMVASSVAKLPIPKLMRW GASDVHFVRPVHTVTLLLGDK VIPATILGIQSDRVIRGHRFMGE PEFTIDNADQYPEILRERGKVIA DYEERKAKIKADAEEAARKIGA KAWGTNVEFHVQNQP
14974	45342	A	15061	82	732	
14975	45343	A	15062	1	3849	MDLGANGWQTFRYVVLPNLSS ALLAGGMLAFALSFDEIIVTTFT AEQVDAAVRAADAAFAEWGQ TTPKVRAECLLKLADVIEENGQ VFAELESSNNTAFARASSNGDL PTKADLQAQLDSLNKQKDLSA QDKLVQQDLTDTLATLDKIDRI KEETVQLRQKVAEAPEKMRQA TAALTALSDVDNDEETRKILST LSLRQLETRVAQALDDLQNAQ NDLASYNSQLVSLQTQPERVQ NAMYNASQQLQQIRSRLDG
14976	45344	A	15063	219	1186	PPKLGRKRGIFLPSHSNPNTNRI CPNCCMNGVSTANTTSKSSLVI CAWTKHALLNAILQPEQLWKS GSRWRINLALPRGYRESLLQPW QAERLTTDKGEWLLY/RAHVK GESTEALLPNMV/ATSLAKLPIP KLMRWG/ASDVHFVRPVHTVT LL/LGDKVIPATILGIQSDRVIAA TGKAKIKADAEEAAR/KIGGNA DLSESLLEEV/ASLVEWPVVLN AKFDEK/FLAVPAEALVYTMKG DQ/KYFPVYANDGK/LLPNFI/F/ VANIESKDP/Q/QIISGNEKSFVR LADAEFFF/NTT*KRLFLPHQKL PPSQILHQQTRNYASFCHRHRD NWTSA

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14977	45345	A	15064	1	1496	SGGCAGLHGGLCSKEPFQASV QQGVAGHACAPAALQVPVCGT LSDCGSRAASLCENPSFISLYGR LVATSLAKLPIPKLMRWGASD VHFVRPVHTVTLL\LGDKVIPAT ILGIQSDRVIRGHRFMGEPEFTI DNADQYPEILRERGKVIADYEE RKAKIKADAEEAARKIGGNAD AKFEEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIFVA NIESKDPQQI/DRIQALAGWIAE Q\IGADVNHATRAGLLSKCDLM TNMVFEFTDTQGVMGMHYAR HDGEAEDVAVALNEQYQPRFA GDDLPSNPVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRIIVEKNLNLDLQTLT EEAVRLYGDKLTNANVVDDVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPTRPADFDDWHALG RAGTGDVVVGVRGRLAIVPLT DGLDEAGHSTGVLQGEVPQRL ERAATVPGVTLQPQALQARGL
14978	45346	A	15065	134	384	VTPTGWRKRRIRQWCSDAGCG VNALSGLRFSHSLALFSAAMFI LGVVSGITMSISP*ILSCVRSKNP LLVSGSGPLSCNSTIH
14979	45347	A	15066	1	723	TKSPKIARSRHIPLCHFIFERRPI MTNSNRIKLTWISFLSYALTGA LVIVPGMVMENIADYFNLPVSS MSNTFTFLNAGILISIFLNAWLM EIVPLKTQLRFGFLLMVLPVAG LMFSHSLALFSAAMFILGVVSGI TMSIGTFLVTQMYEGRQRGYR LFLAASLFSMAG\MIFPMIAAFL LAPSS*W*WVYACLGLAYVTIF IMTFGCEFPALGKHAPKSYAPV EKVKWGILGGASSFRAV
14980	45348	A	15067	422	1045	LLEGKLTNRKQ*HQH*QKARPC KKPIQSAQN/WNREEYDELTEV GRRWVIITNSFELKEHVLTQWK EAKNLDKRLQEGLTRITSLEKKI NDLMVLKNTARELHEAYTSINS RIDQAEERISEIEDQLNEIKLED KIRGKRIK/RQTNKQSL*KMWD YVKRPNLRLIGVPESDEENVTE LENTLQDIIQENFPNLARQANIQ IQEIQTLLR
14981	45349	A	15068	1	1131	

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14982	45350	A	15069	383	756	LNPSNKLALINPAASPIIKGVDL TANQI/PCIADIPLYDADVQQE* CFPATVEALGEQIRQADGVVIV TPEYNYSVPGGLKNAIYWLSRL RQILVFLDAMVMNKPEFMGGV IQNKVDPQTGKVIDH
14983	45351	A	15070	343	924	
14984	45352	A	15071	223	308	
14985	45353	A	15072	57	5546	NKMARKKFSGLEISLIVLFVIVT IIAIALIVVLATKTPAVDEISDST STPATTRVTTNPSDSGKCPNVL NDPVNVRINCIPEQFPTEGICAQ RGCCWRPWNDSLIPWCFFVDN HGYNVQDMTTTSIGVEAKLNRI PSPTLFGNDINSVLFTTQNQTPN RFRFKITDPNNRRYEVPHQYVK EFTGPTVSDTLYDVKVAQNPFS IQVIRKSNGKTLFDTSIGPLVYS DQYLQISARLPSDYIYGIGEQVH KRFRHDL
14986	45354	C	15073	1	1818	
14987	45355	A	15074	493	576	
14988	45356	A	15075	381	498	
14989	45357	A	15076	48	514	LLLFLLLQSYDWSESGKRQSAL HGRQKGLPKSPTAARGGSDPW PSCRHP*GPNRKRRKS/R*PMET APRRPSVSPALTPARPPGLTATP RLHPRPP/RSPNPSANLLRRPTP DT*AHATFGPGRSRHHFPGQLS TE/RRRSAEGGRSRRNEASRRE GGE
14990	45358	B	15077	1	1116	
14991	45359	C	15078	249	332	
14992	45360	A	15079	710	1326	RAAGNCFPEPGFVKQLSAAAA VVAPAAAATEGSIPDTGKSPSSI SHWPNPQKNVICKRRGRVEQE QAWEKGR*RVVFGL*KSMRCP VDLLPQSCLCQRFLHQ/GKWIL TKDYIIHSAKSGRWLDATTYE WGYKIEKDSRYSPQMQSAPKR WREELKRTGAPGAFHRWKVVL LVRTDKRSDSLIRFSDNFGDCDI RMEEKTFRTLMES

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14993	45361	A	15080	602	1257	FGKRGRTITLCILAVGMLCCRK GHTKPRRRPGASPISTHLHSSPPI STHLHTSPPPHRREEAR\SGQ*R QSCGAAAAR*PWWWNCDGWG PKCQRFSKH*DIAQPDEVSWGQ *PWAVGALAGPHP\PQASEGPL GCTPASICGSTRKPSKPLSKKPP QAARTSSSRIVIFTPISTRPPTQG QPEKAKSATPTNDLEGPSAKVK FVNFLMDETFPEPSFFFI
14994	45362	C	15081	140	175	
14995	45363	A	15082	2295	3089	NLLGYQEINPPLQIFWDKLLAV SERDSSVKEESGDVESDDTML* MLPCP*ETTEFSS*PFRISS*LSS* STAQI\PAETCFAGGWYSIFCPQ RIEQETMCLL*SWQSEVAVSCE SPWPTALHHSHPNSRAPPPCY/S KSTSSSLSSPLENSG*QNRPPSLL ITSVLPLRITCLP*VSFIPPIMQLG GSFLSNDRL*QSFILPKNVSLEF VSFPLI*GAVSKPAISFNTSVSPL LVSDIFFALSLLP*GLGTWLIPSS SSLLLVRGF
14996	45364	B	15083	143	1727	
14997	45365	B	15084	307	1017	
14998	45366	A	15085	1	959	MSRMGLLGFGERKELPNHPAV SEWPLTLVTGCSSGTVAEGEGN LTTSGLFSIVPLHPDGVAAGQR HSSLPRWGSQAEALLTSQTVDG QAEMLLTPQTMGGQEEMLLTS QTTGEDFITRSTESGTHSKSHKG DEGEPRWMLGWMLWVCDIAE PLVKAKLLDCKHTCCSVCLQQ TRTSQKDVRCPWCSGVTKLPPD FSVSQLLDDPEVLAVITIPHASE HMPVFIRLPGSGCY\SCPCPSPRS TRCCPEI*AATCCPGTGRSPSL\C DHPCWTAASARQGSPGGGGGG AGQAGHGEKLHVVEGVHCHL GGLRLGLPPQHRAP
14999	45367	B	15086	112	672	
15000	45368	A	15087	2	530	SGRSAALLSARVNRSQSFAGVL GSHERGPRSFPVFSPPGPPRKPP ALSRVSRMFSVAHPAAKVPQPE RLDL\VYTALKRGPDGLLGAVH QQEQEKLQGQIRESKRNS/RLG EWREGFLYDLDKQVKSIERFLR RLEFHASKIDELYE\AYCVQ\RR LR\DGALHMG\RAYTTGSPGSR

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15001	45369	A	15088	216	1369	EPVLRRRPRQPRAGAQGFPVFS PPGPPRKPPALSRVSRMFSVAH PAAKVPQPERLDLVYTALKRG L/QAYLEVHQQEQ/DKLQGQIR ESKRNSRLVMAGGVLWTVV*E RGAVTSLSASAGVLLIPPKYLPL LPTPAGL\LYDLDKQVKSIERFL/ RRLEFHASKVRVQHVCRWD\D ELYEAYCVQRRLRDGAYNMV RAYTTGSPGSREARDSLAEATR GHREYTE/DEGWGPMRQRHRS MCLLES/ELEAQLGEFHLRMKG CAVDINDLGTIKLSLEVTGAAS SVNKASTVTKRSPPIARAHRTH PHFGNSFLSTRKPNTYTANHRR RPIEQHPDMRTPPPPHRARTNT GRKDKVRAHEGEKATPTRTRG APHGKAQRLRPLYQYVTIATLS
15002	45370	A	15089	1	940	MSYNSKNYVETITTMNSVKFG ETTPRNRTHYLSTNEKKIFLSGV FSNAYPAGLSRGWDSPWGSTP WVRHFCYLSSTQLCDQNCSLLS SLLPAGPSVCNRLLASAWQKSS SSASSEASETCQSVSECSSPTSD WSKVGSHEQPSGATLQRRKDR VE\PCETQSPGPASGGTLGPSGE EAPRPRMSPATIAAKHGEEVSP AASDLAMVLT\RGMSL*HQKSS RDSLQYSSGYSTQTTTPSCSEDT IPSQGRPAGLGPTKPVSIESTYL QSPQRLKQEWATEGKIQKLPPQ IQVVNFQVDSSPSLPLIMVPEH MHVS
15003	45371	B	15090	1	777	
15004	45372	A	15091	26	336	KISPMINVFCSESSPSGERRGA* TPPSPQSPPCGPKPSS\PPSCSPSR NYFLLFQGLCAEHPALAAPAAS VGTCPSPASGTHAAAPSGPWRG RCVHSGPGGRLW
15005	45373	C	15092	46	423	
15006	45374	A	15093	1773	2219	ELDYLYCSNSSAQCPGALLPSL ALPGPAGSARQAGSPARRLCAP VQPSGRWPAPGGPGFPGSSCPA SPTRQ*LLTSGSGCPRPCHHPSG PPQ*QSTQAWDWVILGPGAHG PSGQRCERCLPSRPSGPQTHSG VGSEPRAVRGPGVSFV
15007	45375	B	15094	1	7916	

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15008	45376	A	15095	16	545	GLPWRQHVRVEECGRS/PLRPC SPGTPSPS*PLPAATRGPATCQS LSGLQPEKTT/SPS/CAAVAHER PPGPVPQCPAQGTGLIF*EGWT QPQQIRQGPHPVAHE\CAHDLQ QAAPGPGGAHQG/PSQPG*PDR QPDAERAVVHPGAQ*DAEIQPG LPGEGGPLATRTERSPAQRPSP QARG
15009	45377	A	15096	320	1167	MDLKTAVFNPARDGKLRLLTK *\MASKSKEEVSSLISEKTNGAT PLLMAARYGHLDMVEFLLEQC SASIEVGGSVNFDGETIEGAPPL WAASAAGHLKVVQSLLNHGAS VNNTTLTNSTPLRAACFDGHLE IVKYLVEHKADLEVSNRHGHT CLMISCYKGHKEIAQYLLE\KG ADVNRKSVKGNTALHDCAESG SLDIMKMLLMYCAKMEKDGY GMTPLLSASVTGHTNIVDFLTH HAQTSKTERINALELLGATLFT QKEISCDESGRTRDLSPRRKPPH
15010	45378	A	15097	187	623	KLKTQKNNIGPQACNSQLASVS TRSPPPTLSVPIIMTDDSQASQL LLAAVTIRKLWSRMAPMLALP TGQSGQTGAEGQGKEGERGQS PCWKPRLDPKLC/EPRQPAQLL* ADVCTGP/CGVRGCPADCRLPC LSPSSAQQPKEASRSA
15011	45379	A	15098	789	1041	
15012	45380	A	15099	707	1373	SAWPSCHCCHLDILSR/PGDDA CSVQILVPGLKGDAGEKGDKG APGRPGRVGPTGEKGEKGDSG DIGPPGPNGEPGLPCECSQLRK AIGEMDNQVSQLTSELKFIKNA VAGVRETESKIYLLVKEEKPYA DPPLSWQGRGGTLSMAQDEAV HGLKGAYLGQARLGRGFIGIHR PWKRRAPLLLF*TLSPLRSF*KG DGGGNTQKGSRKKRELAGQIW GPCIRR
15013	45381	A	15100	79	420	WRRLFLLGVLFRGYLGCLRSRS VLGRLKVSDMRIFFFACGCGHL STLPSWPLRPSLWLRL*EEQELP SLSVPSSGRSASRLL*LGWRGF GPSPSPRLTVQFSGGRRAQGPS
15014	45382	A	15101	3	284	
15015	45383	C	15102	83	112	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15016	45384	A	15103	84	303	EEQELPSLSVPSCLWGPCPRAG WLHSLHWPVSHSFSATSTFGM AIWT*SLASGIKPQSSSKVSSRIQ VPPTM
15017	45385	B	15104	112	462	
15018	45386	A	15105	326	1323	DRKAINLQVKLEGAVAL*KP\G EAQLEFGKALGLFQ\STLGHHF VNNKEKILGDF\QEATLQAATK LTRGRSLVMENMEQLLSMRME DQSQRNMPLSVVLIREKAHSPF ENRKQEQGEGASPENFRAR\QG *FLAFKAAPPA*AASGPAAQER SVQEPSVNAPG*IPEGGLHTLA GVHHE*ALAWCSPLNKPRFLW KRLP/SRTFHFPVEDESAPGSKP SGDLLTLLLGGNAAGDFKLK\P CLVYPSENPCFLKGSFKPNLPL VWCSHKKAWVQPG*QSETPFQ KKKKKKKKAWVTMSLFQEWF LHFCSTVE/ARCTQYDLPYKGL PILDSTPGHPGC
15019	45387	A	15106	3	375	HASAHASGLQQSYQAVKEKSS EALEFMKRDLTEFTQVVQHDT ACTIAATASVVKEKLATEGSSG ATEKMKKGLSDFLGVISDTFAP SPDKT\STAMSSPYDGTKARLY SLQSDPATYCNEPDGPP
15020	45388	A	15107	184	377	YCTNNQKVN*TKEIITKRKTPSR QKKDSAFSPSHPLTEGLKW\ND LTLSVSLTHDGFVWRRGKGV
15021	45389	A	15108	3	816	SWEDVGWWRSWLQQSYQAVK EKSSEALEFMKRDLTEFTQVVQ HDTACTIAATASVVKEKLAIAA CSRGACFLCPFSIQTEGSSGATE KMKKGLSDFLGVISDTFAPSPD KTIDCDVITLMGTPSGPAEPYD GTKARLYSLQSDPATYCNEPDG PPELFDAWLSQFCLEEKKGEISE LLVGSPSIRALYTKMVPAAVSH SE/TFWHR\YFYKVHQLEQEQA RRDALKQRA/VSGDSCT*SGVL TNE*KGSWVRDTERVRSLPLQT FSEGVGWREC
15022	45390	A	15109	1	281	

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15023	45391	A	15110	1	1194	MGFLHLGQAGLEFLTSGSSTDI SEDWEKDFDLDMTEEEVQMAL SKVDASGEPFCFWKGYPGGEL ETLIRLLQKLFFLKTDPAFVLSP STLVKLHLWGNEGLQESLESLV LHDAALVILVPNLEKKGEISELL VGSPSIRALYTKMVPAAVSHSE FWHRYFYKVHQLEQEQARR\A RLKQRAEQSISEEPGWEEEEEE LMGISPISPKEAKVPVAKISTFPE GRTLAPQSPCEENLVTSVEPPA EVTPSESSESIPKSPLPTRALGTD
15024	45392	A	15111	213	1031	AGNKPDPWAGRNRTAVLPDVS VFHREDVGWWRSWLQQSYQA VKEKSSEALEFMKRDLTEFTQV VQHDTVCTIAATASVVKEKLA TEGSSGATEKMKKGLSDFLGVI SDTFAPSPDKTI*\RDVITLMGTP SGTAEPYDGTKARLYSLQADP ATLLY*P\DGPPELFDAWLSQFC LEEKKGEISELLVGSPSIRALYT KMVPAAVSHSEFWHRYFYKVH QLEQEQAP\RDALKQRAEQSIFE EPGWEEEEEELMGILPIFPKEAK FPLAKISYIP
15025	45393	C	15112	414	557	
15026	45394	A	15113	98	467	
15027	45395	A	15114	1	155	
15028	45396	A	15115	16	94	RCPIASEASWTITD*RCPIASEAS WTITDALGNSYSGGMAF
15029	45397	A	15116	95	115	IIRHLCND*TPREGCLPSP*PAW SDTFETWVNNQASLQ
15030	45398	A	15117	3	282	LKPVITCLLQLGLLKPINSPYNS PTLPVQKPDRPYSKPNSLP*LNP SLLQRNYTSIFLLTLNMPSISCT TMLLYGQKEISSLHKGPPSLMP
15031	45399	A	15118	548	1401	SCTPCWHLTGRLWGITAVRQK RHVLSVDPKLRHQSRTGKAAFP WCLIIAGTPL*LYTHVSRVSDH AGMPALVLHPLQQVPLFWGRG NTL*KD*SLLSLAC/VQHGLLKP INSPYNSPILPVVKPDKPYKLVQ NLRLINQIVLPIHPVGEAPVPLE TGGKSGKDCILWFECHLSHNTI EHQVSSSTFRIVVATGVLVSLH PQLYMAQNRERHAECLGESKG REQESLSGNPENSRFSLLTSRRY LYKSTRTIVLLGLAGPLKQKKL RSQHPSLYKYLQSFRNKDSYR

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15032	45400	A	15119	144	298	WQVPLFWQPFPEPLELWPKA/HLTDSFPDLLGLAAED*RCPIASEAPCTQVI
15033	45401	A	15120	449	667	
15034	45402	A	15121	2	111	
15035	45403	A	15122	323	401	LLLGLAAED*RCWIASEAL*TITDAK
15036	45404	A	15123	2	593	CTLPSH*NLITLTPLNANIPSHGML*KD*SLLSLACYSTAF*GL*TPLTIPPFYLFKNQTRLTG*FRICPLSTKLFCLSTPWCQTHILSYPQYLPPQPIFLFWISNMLSLLFLCTLYPSLSSLSLGLTLTPIRLSKLPGPYCRKPSQTAPTSNHPSSFSGSWYSVETSYPLSSSIFRKGRTDSWSLKDTPHQAQPPT
15037	45405	A	15124	354	630	
15038	45406	A	15125	29	354	RFLVSLMLPPAVVMLNHCYSLIFTNALVKRLFAWNMLSELATCAGNLATGPRNARSPGFLLSCVPSVRDPTGNQTVQLTWQPLPEPLELWPKA/HLTDSFPDLLGLAAE
15039	45407	C	15126	1	576	
15040	45408	A	15127	377	624	RDQLQCLQLWDAGACYTCWKSATGPRNAHSTVFLLSHVPSVWDPTENRTVHLTWQPLPEPLELWPKA/HLTDSFPDLLGLAAED
15041	45409	C	15128	1	462	
15042	45410	A	15129	44	340	PCQTTQGRLLTAGTPL*SFTHVSRVSDHAGTPALVLHP*RQVPLFWGRGNHISGTQELPNT*TAV/VQAF/LPEPPPTG/CLLHVPEIWPLGQGMPAGQDSS
15043	45411	A	15130	242	522	RLVWPTATQRAWSQSEAAAAKTVDLALSARNSATGPRNACSPGFLLSCAPSVWDFTGNRTVQLTRQPLPEPLELWPKA/HLTDSFPDLLGLVTED
15044	45412	B	15131	1	1080	
15045	45413	A	15132	1	642	

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15046	45414	A	15133	245	1033	TALLLTQSLFGGLFTQTRMKFG AVTRIGGPPLGDQSPVLLFFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPIS/ ASHSML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRFTG* FRICALSTKLFCLSTPWCQTHIL SYPQYLPPQSIILFWISNVLSLLF LCTLHPSLSSLSLGLTLTPFRLS KLPGLYCRKASQTAPITSVKPK FLPYLLPISA
15047	45415	B	15134	146	556	
15048	45416	A	15135	1	555	LTSFLHCCLSHHYHGAQIHPRH FLHLICRCHCHQYCHHAYLDPC PQDSHHLHWCWQPLPEPLELRP KA/HLTDSFPDLLGLAAED*HCP IASEAALPPCFPRPDMITSRLQL QRRRQTALGVRYRNATYRTRT ASTNSLRPRGSPFPLALVTNDR QVRSQLALWKRDRLLQLSPINR AISESSFT
15049	45417	B	15136	1	555	
15050	45418	B	15137	499	769	
15051	45419	A	15138	752	1111	MQPTIGNSQSVSRPTA*MPLAE SHPITQLVGTVTTPRVTPLSIRH PWRCRSANAGAMILTMKQLAI VMRVYQHQVRRSMRPGRNGA RSGMSAVGAYYSSCIRVMTAL QSCTGDDEAVLL
15052	45420	C	15139	1	632	
15053	45421	A	15140	1	375	PGVRGAQGGPSIPRQCEESAIGP KFAWIISSFHWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGFIWQPLPEPLELWPKA/HLTD SFPDLLGLAAED*HCPIASEAPA LVYTAGLHCFSKPSQ

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15054	45422	A	15141	1	1340	CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGDSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKKNGEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTDQPKKHLTNFKSKTKET GFIHGPKTPAPVTDWEGSLPLV FNH\SGTPL*LFTHVSRVSDHAG MPALVLHP*RQVPLFWRRGKI* LTSPSRCTIIEKSCNSLPPL*DKP QPHLQHTRTSKCLNRSGQAF/L PEPPPTG/CLLHVPEIWPLGQGM PAARDSS

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15055	45423	A	15142	2	2107	IDMIFTPGPPSTPKHKKSQKGSA FTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFVKVERQVQDMG KKLDFLVDMHMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTIICNYSETGPPEPPYSF HQVTIDKVSPYGFFAHDPVNLP RGGPSSGKVQATPPSSATTYVE RPTVLPILTLLDSRVSCHSQADL QGPYSDRISPRQRRSITRDSDTP LSLMSVNHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDTDTDPFTPSGSMPLSST GDGISDSTVPLFLSSEILQKQVG QSITSMLGFLSRGPSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFSLLSVTSYS SFAFHKFSVAVYNISNLKTVDP AKFPTRYCYCLNNRTNDLSDFT ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFICVMTGKSGR NLSDFWEIEEKYPIINYTFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIGGPPLGNQSPSSCSL LHEKDPPTTSGPQTDQPKKHLT NFKSAARPTFLGQGQVPLNPFS FTLS/EQVLLS*AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPLLCVSSLFSRLASFTM GAFTHGTQTPSPTKATAPRYPQ TGDLSAEWPFTAGEEPVLVPRP
15056	45424	B	15143	1	930	
15057	45425	B	15144	401	1093	
15058	45426	C	15145	1	843	
15059	45427	A	15146	1	498	
15060	45428	A	15147	112	669	SLQGRLSDYTPTFQGCQTTQGC LPWSFTLCSKSRFSGEGETRFKR IKACYHSPATAWPFKAYKLSLQ FPHFTCRKTRQALQVSSESAPY QPNCFAYPPRGAEPIHSPILNTS LHNPLFCSGSQTCFLY/SFLCTL HPSLSSLSLGLTLTPIRLSKLPGL YCLKSSQTAPITSVKPKFLPHLL PISA
15061	45429	A	15148	957	1100	

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15062	45430	A	15149	303	2028	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKEHLTNFKSD KGDMFYPWTQN/YQCRSRTGK AAFPWCLITAGTPL*LYTHVSR VSDHAGMPALVLHP*RQVPLF WGRGKLLLARPS*VPILPQPLLL HPIIFLSPPLLTPGPAYSFVL*LA LPHLPSNLLLKRWLEPKA*SSM/ TLKGLKPVITRLLQHGLLKPTN SPYNSPILPVLKPDKPYKLVQD LRLINQIVLPIHPVLGIIGLTSSV RRDAGQDLKRDRAEFLLGDEV HHPHRRRIAEARRLLLGQHFDP LHRLIGQVLELGEARYAPPVEQ HHRLAPARRTGQRLHPLEQFG QAGRAQRRNRLGIEHRDRLDRP DDGAGNALAGDGDFRRGCLFA GIGIRPRYCRYRQSQDDRRPSH AAPRPRALPIPHRPATPIADVM VMFSVAIMSQLRLVLRHIDGIS RWPPAVVFITDVKIWLVYPSDD CRIRSNDRDDMQGEAPAMSMN AAARVGDPIGHSFSQGLFGEAL DGLFFARRSEVDMRAGNLGRLI ARGLSGGRWTPADGQLTLGSR DVFINGPPATMTIRSTGQCRQH
15063	45431	A	15150	653	1076	RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCTPTPYFHDPTPFPLFW KELATSARNLATRPRNACSPGF LLSCVPSVRDPTGNRTVQLTW QPLPEPLELWPKA/HLTDSFPDL LGLAAED*CCPIASESP*TSDILG RDTLLLALKVQTVVLQTACGE GHVAGNCGRPLETEGSLQLTAT KKLRDSVLQPKSPEFCQQFTRA WNRTQVPDETEAPAGTYAAQS GDLPWEINPLSSCSLLHEKDPPT ASGPQTDQPKEHLTNFKSGFRG VRPRRDACLGPSPLAASPAFLG KGQVPQPLLSVSLPLLRLSGGQ ETPNPFSFTLSGKSAFLEEQVPQ PRISVPQSLISTPRPLISVAQSLIS APQPLISLCPNPLFPCPDLLSLHP NPLFPRPNPFPAFLEGACYKCQ KSGHQAKECLQPGIPPKLRPICA GPHWKSDCPTHLAATPRAPGT LAQGSLTDSFPDLLGLAAED
15064	45432	C	15151	234	449	

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15065	45433	A	15152	2095	2663	LGLGDLPWEINPPSSCSLLREKD PPTTSGPQTYQPKKHLTNFKSA CFERIKACYHSPAKAWPFKAYK LSLQFPHFTCLKTRHAI/PS*FSD LCLINQIVLPIHPMVPNPYTLLC SIPPYTMHYSVLQLIRAFFTIPLH P*\PSLY*VSLGLTLTPIRLSKLP GLHCRKASQTTPITSVKPKFHP HLLPIST
15066	45434	A	15153	678	1189	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSE TKETCFIHEPKTLAPVTD*GRQP SLGV*SLQGRPL*SFSHISRVSD HAGMPALVLHP*RQVPLFWGR GKYPNPFSPCLLPLLCFSGDRG KYPNPFSPCLYSFSAFLGTGQVP QPLLSLSLPLLCF
15067	45435	A	15154	649	1428	QCISELQFLLASTVRQTPATSPA HKNFQTPELQRPGVPPEPPPTG ACYTCRKSGHWAKECPQPGIPP KA/HLTDSFPDLLSLAA\ED*HC PIASEAPETITDAELPVTLTVEA HLHPGEINSHVAHTKPVWWSL HRDAHEIWCCDSDRGTSLRRPI PCPPALCSVTKIHLRPQVLRPTS PRNISPISNPAAPHQAELGPNPS/ SSLCSSTL*SFYHLPSSHLVWLT VSFRD
15068	45436	A	15155	240	1208	LRSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKEHLTNFKSC KQ/DLFLLSSPTSLTIPQPLSPFN LGATLQSLPSLNFNSFHFLVETK ETRFIRGPKTPAPVT/VLGRQPS LGV*SLQRCLSDYTPTFQGCQT TQGRLPWSFTLSGK/CPLFWGR GNTL*KD*SLLSLACYSMGLLN PINSPFPSSHFTCPKTRQAVTS* VQDLRLINHIVLLPIHPGGAQPH TLFCPQYRPVVLPIILFVYVKHA FFTIPLQPLIPSLSLPSLRLTLTPI RLNKLPGLCCCKAFRDSPHYLN QAQISSSSVTYLGIILIKAHVLSL PIVSDW
15069	45437	A	15156	1174	1623	KFGLVQLTLGKPLPEPLELWPK A/HLTDSFPDLLGLAAED*HCPI ASEAPYTI\TDAELRVTLTVEGK SVPFLINTEATHSTLPSFQGPLSL ASITVVGIDGQASKPLKTPQLW CQLRQYSFKHSFLVIPTCPVPLL G*DTLTKLSASLTIP

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15070	45438	A	15157	1	1610	MGLGKSLCILKDAVLALREIKG ISFQYAPNTNRLWGYRQAKQT QHLSGISTLDCPQRYNGDDTGS VWALEPSCMLWACPLVFPSEIY YFISEDVWKHLDAQEKFAAVM GPSRRTSVRAVWKGNVGLEPP HRVPTGALPRVAVKRGPLSSRP QNGRSTYGLHCLKDTPTQEDW LVSVLPEGSRVGVDPLIIPTALG HGRTTFLKVLDFQGPAPCPAA MGVRLMAGPQCVSSDYWKKM AKVLRSAGHHLIPVKENLVDKI WTDRPERPCKPLLTLGLDYTGI SW\KDKVAD\LRLKM\AERNVM W\FV\VTALDEIAWLFN\LRGSD VEHNPVFFSYAIIRD*ETFMLF\I DGD\RIDAPSV\KEHLLLDLGLE AEYRIQVHPYKSILSELKALCA DLSPREKVWVSDKASYA/V*SE TIPKDHRCCMPYTPICIAKA\VK NSA\ESEGMRISDEKSAGNLTED PFYVIDRTLITTGVVCNSTEKSS LMSVASADTAENLWHLFFHILP SERALTRKLRVLKLGPVNYSVQ NPTAQLHQQGPHLGVA
15071	45439	A	15158	1	756	
15072	45440	A	15159	1	1677	
15073	45441	A	15160	1220	2620	GPTEPHTGELWLESGGCPSGTK LPEEGTGSNLCCSTASAGDTQA NRVCSGPPTNHSRPAADRPVRR KINKQKTATSTSTKRTSTQRPH PKVTNDHSSSPAREQNWMEN\E FDELTEVGFRRWVITNSSELKK HVLTQCKEAKNLEKRHSLGTK EPAALKGRTQYWQDSSPADLR PWLCATLLKQYKPTVFSHSTVA VHPRAGFLNLSTVDQHPVLDEP IAEAVCIIADTNKWSVQVATSQ RKVPHNLKLGQDVLVSSQVSSL LQSILQLYKLHLPADFVGDILLD NNLKCVFQLGSILPVTFRSHDP YDGEGTDELRTAACSPDTEQLA RQSGTYPVSLGQATVLEDSKA ALPGLGPTLMAVTVVTTEAAV DMVVGDRGEERGGTLVAPGTR GLTEEIWFPVPSPSRWWSSHPV VAFITLAKYGPTSSPPVFHHGPN IIRHGAQGAASAGDSGSSSRCD RLPCRQNA

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15074	45442	A	15161	666	1536	FSSAGDTQANRVCSVPPTNHSR PAADRPVRRKVNKQKTATSTS TKRTSTQRPHPKVTNDHSSSPA REQNWMEN\EFDELTEVGFRR WVITNSSELKKHVLTQCKEAK NLEKRVRVNCLT\RIT*P*RRTI\ KTLMELKNTARE\LHEAYTSINS WINQAEERLSEIEDQLNEIKRED KITEKMKNSTTVRVAASMQSK LLQGVAEEGPLRLTRSASFSAEI SMCHQWLFSTFGNGKSRNRYH CEKAHIEGNQLVEETGRAFKSR HRYGTGPLHKFEIHEYTELHHV LMLQGKC
15075	45443	C	15162	104	364	
15076	45444	A	15163	162	467	
15077	45445	B	15164	1	1122	
15078	45446	A	15165	188	456	
15079	45447	A	15166	485	1580	GEGYKADLAAATVECPICQQQ RLTLSPQYSHIPQGDQPTTW*Q VDCIGPLLKGQRFVLTGIDTYS GYVFAYPVCNASAKTIISGLTE CLIHCHGIPHSIASDQGTHFMA KEVWQWAHVHGIH*SYHVAD YPEAAGLIEGWNGLLKSQLQC QLGDNTLQGWGKVLQKPMYA LNQHLIYGTVSPIATIHGSRNQD WNGSSLRGWTFTILFTAPRREP GTYIASDQRTHFMAKEVWQW AHAHGIHWSYHVADYPEAAGL IEGWNGLLKSQLQCQLGDNTL QGWGKVLQKPMYALNQHLIY GTVSPIATIHGSRNQGMEVEVA PLTITPGDPQAKFLLPVPMTLCS AGLEVLVPEGGTLPPGHTTIPLN
15080	45448	B	15167	10	2352	
15081	45449	A	15168	2	497	WKPIAMRKSRRRQEKLLPVQK EGQPKEGEREEGGPVQAQKVP NRLHLHWTT/HLPSFFQLPLLLD SLWRALKFVVLEAIVKMIRFNG VLGKCEAIRAQALHEGGPPLPL AVFHNRRLQIVACSRISARLRGS PPPKSNNEQSSLSTDLRTDSQRL PPLSRNAQQKG
15082	45450	B	15169	1	1911	

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15083	45451	A	15170	1	1569	MPIGKVGEYYIKGTLRATKESE QQSSALELSSDRVYLNEKEPGD QPWNAAFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSLTLIIQGCKQEGFYS PSMRPRVVPKRGSAPKVRAEEN AALPSRCPPGPLPVAQPRGLLM GAHVSSAPAVGVGAASCHRLC PGFPDRPRPTLRSCIMNAVVGG CDLRGQVYDPTGGWANEGTR DLSAVQGVPNHPGGRPCPTPQS SRQLPVVSRRPVVRPGGEAPPP LDILPAALALHQSLLTPQDPRE DRPSPADLWAQDSWVGQPQEL PVGSRVRTGTEPDTHSGSVCTS RQGKDGSGPLARESSVRVILQG PSSAWMMFPEYTPGPRARAGT AVVGAMARQTVNVCLTKVRL QHPEGIPGGGRGPLVPKPVCTC/ IVDVKGSRV\WHVHICMSMGC RHVCLCGRSVGSWRMCTAGQT PKLARQASIELPSMAASSTKSW WETGEVQAQSAAKTPSCKDIV AGDMSKKSLWEQKGGSKTSST IKMDSVTT
15084	45452	A	15171	328	641	LLMRSWSLPSAPRGFSCSCLQP QYPCRTESWPQTEPVPSPVSHR LLVLATAMLGSSME/RLAG*LG GPASGLDGLGVLFQPLINLGDG QVWLGFLHTVTLLYGAV
15085	45453	B	15172	120	1458	
15086	45454	A	15173	1	440	IQQDSQAPLYS\IKETQRANTYL VEWEPGAETAFKTLKQALVQA PALSLPTGQNFSLYITERAGIAF GVLTQTRGTTPQPVVYLKDGEP IEHDYQQIIAQTYATQDDLLEV PLANPDLNLYTDGSSFVVNGIR RAGYAIVSNVTVLE
15087	45455	A	15174	288	376	NHWLLLTMDPRIQQDSQAPLY S\IKETQRA

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15088	45456	A	15175	777	1548	SKIQRDSQAPLYS\IEETQRANT HLVEGEPEAEIAFKTLKQALVQ APALSLPTGQNFFLYITERAGIA LGILTQTRETTPQPVAYLSKEV DVVAKVWLHCLRDGEPIKHDC QQIIVQIYAARDDLLEVPLANP DLNLYIDGSSFVENGIRRAGYAI VSDVTVLENSLAAVTLQNRQG LDLLTAEKGGLCTFSGKECCFY TNQSGISSPLEDTTTAGPFLHPI QQEVARAIIGQFPTAFGVSCLE GRLRGEASWTSWVE
15089	45457	A	15176	1	1359	MGPEPKNTHPGSCTCPLACSSS HKGFECLAVEQGSYTPVASPIV GVKENQEILDLLELKYNQTRSA VTRCVLGAASTARIKQAEEGGR SRLAESSGLRLPFVLELPALEHQ TPSSSGFELLDLHQRLATWSQA FNYRLKDTLLASLLLRFWDSD WLPCSSVCSWPIVGLHLVIIERN YSYQQGTETVVSSWATGVSAA ASVSATIPINRVQGHCGFLGKR CFYCCIGECNHSDHQGPGTVAG SWARGVSATASQIQVDLGKFS DDPDRYIDVLHLTWRDVMLLL DQTLAFNENNVALAAAQEFGD TWYHRPVNDRMTAEQRDKFPT DIKTAAGIPWNHWLLLTMDPQ TQRDSQAPLYS\I*ETQRANTYL VEWEPEAE/TSFKTLKQALVQA PALSILTGQNFSLYVTERARLAL GVLTQTCGTTPLYQDELRKKTL RHRDSEGSGFNQLEASAD
15090	45458	A	15177	368	5192	AAPAPQLGLGPCKLASHLLSQS HLSQSVRSEAEQKAGASPASSI QREPLFKDQLKAPLPEQKRRSL LTVPLLTFRAQKCGPGSPLVAR GGATDSWLVSEEFRLSDSTAPP TELRGQEATGITKPPASLHPQPH AWDWARGRDPRRHLLGTPELQ EHSEKTTTETLPADMGKLRTW ERKEATAGQAAEGAAGGIHFE ATSLLRPSSYVPQTQGALSTTY KEAKMDRDLHLTPILAAQRAR GPRIHSFPSDEMIEPS

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15091	45459	A	15178	76	969	KKSTALVIDNGSCMCKAGFAG DDAPQAMFPSTVGFPGHQGVM VDMGQKDSYVGNEAQSKRSIL TLKYPIKHGIITNWDNMEKIWH HFYNELHGAPE*QPVLLTEDPL NPKDNREKMTQIMFETFNTPA MYVAIRDVLSLYAFGRTTGIVM DCGHRVTHTVPIYEGYSLPHAI LHLDLTGWDLTEYPCILLFSEK SYELPDGQVITIGNEWFWCPEV LFQPSFPCMESCRIHQTTINSIKK CDVDIRKD\NTVLSGGTTMYPG IADRMQKEITALAPSTMKIKIIA PPERKFSVWIGCS
15092	45460	A	15179	1	451	
15093	45461	A	15180	130	227	LMKMKKVM*RA*KEEERRTPP AEDDFEKDLEWLINENEKSDAS IIEVYIANSIHNNYITKCFAIL
15094	45462	A	15181	104	1715	KEEERRTPPAISVIPAAAFYTAY FLHKQKMNENKDTDSKKSEEY EDDFEKDLEWLINENEKSDASII EMACEKEENINQDLKENETVM EHTKRHSDPDKSLQDEVSPRRN DIISVPGIQPLDPISDSDSENSFQ ESKLESQKDLEEEEDEEVRRYI MEKIVQANKLLQNQEPVNDKR ERLLKFKDQLVDLEVPPLEDTT TSKNYFENERNMFGKLSQLCIS NDFGQEDVLLSLTNGSCEENKD RTILVERDGKFELLNLQDIASQ GFLPPINNANSTENDPQQLLPRS SNSSVSGTKKEDSTAKIHAVTH SSTGEPLAYIAQPPLNRKTCPSS AVNSDRSKGNGKSNHRTQSAH ISPVTSTYCLSPRQKELQKQLEE KREKLKREEERRKIEEEKEKKR ENDIVFKAWLQKKREQVLEMR RIQRAKEIEDMNSRENRDPQQA FRLWLKKKH\EEQMKERQTEEL RKQEECLFFLKGTEGRERAFKQ WLRRKRMEKMAEQQAVRERT RQLRLEAKRSKQLQHHLYMSE AKPFRFTDHYN

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15095	45463	A	15182	881	2040	MKAGWRQTQHLHDAGQLLHLI LPGEQGVARVQLRRDAAQAPH VNGHVVGVAQDHFWGSVEPA LDVRVYCGGKTGGKQRERREG RCGVEILMVGERKMNENKETD SKESEEYKDESEKDLEGLTNEN EKSDASIIEMACEKEENINQDLK ENETVIEHSKQLSDPDKSLQDE VSPRRNDFISVPSIQPLDPISDSD SENSFQESKLESQKDLEEEEDEE VLPRSSNSCVSGIKKEDSAAKID VVTHSSTGEPLAYI/ASTYKLAY IPPLNRKTCPSSAAISDRSKGNG KSN/HGQSAHISSVTSTYCLSP* QKEL/QKREQKREKLKREEEQQ KIEEEEEKKRENGIVFKAWLQK KREQVLEMRRIQRAKEIEDMNS RVSKTSLKNKFIQI
15096	45464	A	15183	873	4292	MVVSLGRVSSLSEDSDPTGRVG R*VDCKVDRSIWAGVWISEDAP SEA*EIGGLGRK*MLSGGPQSPS KHVHIL*DQDSSSIPEPMGPCCP\ PHAPGKEPGTSCSIDTDGKLSG VSGDDS*T/GTDGGESEEILLPQ *QLPVTLPSLPLPG*VRYTSRSR SRSRSTRDPGRKSRPISGLRGLC GDGATS/PLTPRHAPARDVQ/PG VSMAFAGDR\GDGGRRGGASQ/ PAPPGPAVPRPCAQYSARAMPA SGRRES
15097	45465	B	15184	1	2214	
15098	45466	A	15185	3	361	
15099	45467	A	15186	1	1035	MKIHKSGGLKATPQLYASQFSG VAILATWGPHRPRNSSTSFSTQS KLRRPDESSVDFQKLMLCKEAT KKSKEKEPGMAFPQGHLIFSDV AIKFSVEEWKCLNPEQRALYRE MMLENYRNLES/VG*LFKIHDG VLINRARQYRSVPHRDIGKT*FL LPRNQERYSGL*VSVARN*KK WP*STHDRNQRVN*VHTGEKP QKCNECGKTFSQKSYLQCHHR LHTGQKPYK*E*CDKVYSCRSQ LKTHRRIHTG\EKAYKCKVCEK AFWDNSCLSCQKRVHIGEKPYT ALVMHKAIHTGEKPYTCNECG KAFSRKANLALYHRLHTGEKP YKCEECDKVYSRRSHLERHK
15100	45468	B	15187	1	1347	

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15101	45469	A	15188	1	1446	MWRETKRYAAVLLLTPHYSAS LLPDW/PNLYLHQSGHHVPGVY LKFG\SSNPIYPCVDSAKTVFPN APLHDRVQSVRRMGPFKGVFR KVFSNLGFEYSLSTWATMGSPG SLGVSPFGKTLFVESASGSLDA LWPTVEKEISSHKNYQKHSEKQ IYDVRIELTGLNALPNISLNFYK NSVSKLLNRKKGLIHLLQPFILR LCVSLHKNREENLGITIQDVAM RLSALPNIVCRLYKKTASEVLK EWSTRWDEYTHHKEVSQKALP TLSVKIYKKNICQLLNQNNGPN SEMNALITKKSVKSASGYLESI AALVEKEISSYKNYTEAFYNLL CDVYSHVTEMKLSSIEQIGNTL FVESASGVWRALRPRGKEVNDI FIDQIANSVLVDSSKDICKRFEA CGAMVKKENLHIKTRQKISEKL HWPFGAPRLTSLTGPEKTGKGE HPGAKARGELSGAPPLIHTRKL SLMSNVETLLLEKLQGYTGAH
15102	45470	A	15189	1	966	
15103	45471	A	15190	157	531	GDHTTFLCLLMVNAEFKYNFK TIIS*DLLKKDSGQYGHFTIFFRS MSIGCFSIYLCIFNFFHQCFAVF LVEIFTFLVKCIPQVDSIEDTTFG HPEEATPHPFSFFMRLEQFSHIF SSWPVSFTAH
15104	45472	A	15191	9	494	PTDRPRPRALAGARGPPGRAPR VPPPAGGPRPSQYGHGGRPNPR HGWHDAFCPNNTPYR\ERPLDS RYLTPGPLDMRGDSGFRTGRGS DVGSLKPTDTRRNGKIYLNGS/ NVFYYQQRLHPVHRGDGARRG FSGRTCLHRMVC*YEQTGHQS DQT*KARSAYG
15105	45473	A	15192	1361	2038	
15106	45474	A	15193	1376	1906	LAFPDGMASLIMMSLPAMRTL AWAMAVSGNCIPEGQFSALSC ADFGISPKLIL*SSSAPN\YLAMG ISCPRADDLPEAGTAETDRACR SIPQYGTDLGWYPATAAGPQSE SVQGAV*PHRYEAG*ST/VWKP LKKK*KPLPRR*LARWQMIRFR KPSPLTTSLKLTCAWRFLDFRW LE

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15107	45475	A	15194	1	1388	MIEHPRRRDNYRQSGPPVADKP TTKGEPLISDIVSDAQQANLLIP VDETPPVINDEQSTSTPLTTAQT MALAAVADKNTTKDEKADDL NEDVTASLSALFAMLPGFDNTP KVTDAPSTVLPTEKPTLFTKLTS EQLTTAQPDDAPGTPAQPLTPL VAEAQSKAEVISTPSPPSISGVT RSKMRQREWLVLPPEDSLVIRR SNKTSQLPAFNVPLSAAKAAAS KPWRASNTACRNSRPSKVCSAE GEQWFSASGRGEIHSQSPARDM AQMCKLAAEGHFAEARVINQR LMPLHNKLFVEPNPIPVKWACK ELGLVATDTLRLPMTPITDSGR ETVSGDETYLEAAPLAELHAPA GMILPVTSGDYAIPVTNGSGAV GSYSAITEPGAGSDVGSLKTTY TRRNGKIYLNGS/NVFYYQQRL HPVHRGDGARRGFSGQTCLHR MVC*YEQTGHQSDQT*KARSA YG
15108	45476	C	15195	1	1905	
15109	45477	A	15196	285	1706	YARVHSGRSSIRRSIPVSICIRSSI RGCVPVVHCIRSSIRRSIPVDHL YQIIHTKKHTRCPFVSDHPYEE APDYSASLLPDWLPVPSSKVVI TYPGFTSICGYYTTSSKACFSVF AWCFVTSDVPGRFSDEDEDDSE MWSLTALMGVMGGWKTSARS EVSILCSTSSKVIHSSYPYADRA FQVWSLDARFAHINKPFGVDRF SGEAPSRAITTMYGVKVLNRPA TGTAHRLVPPDVPVHPHGGESN KPRVQTTVSSGISRLSIPISASAL QNVPDKTHDISNITDTVYHCPL SQSSRWYWRFVPVRSPPLSNGQ TAVRPGGSRAGAAGGPLSEYS GSGFGVMKWTKDQLTVTVKV HHLPEVVEFLYYKQGGWLSVL FGNDERKLNGHYAVYYVLSRE KGTKCWI/TDSMDYRQR/PAPT NDAETYEFINELGARKTTVVPI GPLHVTS/DEPGHLRLFVDGENI IEANNE*IHRTQC
15110	45478	A	15197	3	1396	
15111	45479	B	15198	1	1399	

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15112	45480	A	15199	283	796	FVGVKSAGNRLKTIDELANESR SSVGLTQAALKTLESSGAIRIER RGRNGSYLVEMDNKALLTHVD INNVVCAMPLPYTRLYEGLASG LKAQFDGIPFYYAHMRGADIRV ECLLNGVYDMAVVSRLAAESY LPQKGLCLAL*LGPPPYVGE\YQ L*QVKAKSEYVKRVGHV
15113	45481	A	15200	48	3376	
15114	45482	A	15201	49	681	DPGADRRGSVWGLSDLRNTYN ALYLTHSGRLSECPTPANEEKE PTNHNRTLTNQTQKEKKKTRT KDCTTRNKNSTRPGSGIIAGPSY YTVAGPPSAIDPRWLRPTPPAL DPQ*MPHTSKRGKRADQSQPN ANKPNTEREKKDKNEGLHHKE QEQ\QRPGSGIIAGPSYYTVAGP PSAIDPRWLRPTPPALDPQTEPL IFQQLEIDHYVAGLTHEVMSLS HLTLVMRWGSVSAAHLAHWA RCRWISTELTPNSITSTSSPLKD CSSSPAMEQSWLENDFDELTED KKTCLCDH
15115	45483	A	15202	3	587	
15116	45484	A	15203	3	774	MVLMAGFTAGNEKGELVVLG RNGSDYSAAVLAACLRADCCEI WTDVDGVYTCDPRQVPDARLL KSMSYQEAMELSYFGAKVLHP RTITPIAQFQIPCLIKNTGNPQAP GTLIGASRDEDELPVKGISNLN NMAMFSVSGPGMKGMVGMA ARVFAAMSRARISVVLITQSSSE YSISFCVPQSDCVRAERAMREE FYLELEESLLEPLAVT\ERLPII\S VGSDGNPPPCGGISPKFF\AALA PRPISKFVALCSGIPF

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15117	45485	A	15204	1474	1511	HS*VPANLYMELKACFTGA/NE KGELVVLGHNLAVSYFIALAAS LRADCCEIWTDVDGVYTCDPR QVPDARLLKSMSYQEAMELSY FGAKVLHPRTITPIAQFQIPCLIK NTGNPQAPGTLIGASRDEDELP VKGISNLNNMAMFSVSGPGMK GMVGMAARVFAAMSRARISV GLITQSSSEYSISFCVPQSDCVR AERAMQEEFYL\ELKEGLLEPL AVTERLAIISVVGDGMRTLRGIS AKFFAALARANINIVAIAQGSSE RSISVVVNNDDATTGVRVTHQ MLFNTDQVIEVFVIGVGGVGG ALLEQLKRQQSWLKNKHIDLR VCGVANSKALLTNVHGLNLEN WQEELAQAKEPFNLGRLIRLVK EYHLLNPVIVDCTSSQAVADQY ADFLREGFHVVTPNKKANTSS MDYYHQLRYAAEKSRRKFLYE HNTFVSPHIRPLIERRGRSSTRD KWCARPSTERQQDNSAARILSC QQGNTSFEHTSSIRVGTTNSLN
15118	45486	A	15205	198	462	

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15119	45487	A	15206	31	1981	RWLMRGMGIALPAAMASTVSP STIAETPEPPPLSDW/LRASG/DV WVHLLGLDPHLSSLLLSICLFSR SLIWIF*LQP*SV/ALAFQMGAS LFASNIGVIEGEGPQAKPL*CLT VSYFEMLNNLNAQGPKGKLSP CQCLSLQVMTMPEYLKKRWTL GQRSQWPQMHVSFSS*LFPF*A DIFAGAIFIKQPSGEGKYMRTH G*NALVLFFLSLGGLEVVIINIG CLRFQ*DISFYSDAFLAFNEVGG YESFTEKYVNATPSVVEGDNLT ISASCYTPRADSFHIFRDAVTGK GR*LPLKSSPGLFHECVTFSRQV IVQRCL\CGKDMSHVKAACIMF LFV*WLLVLPIWASLDSLLNSSP DMVACVVPSECVISTLSGLARQ CPATNQCLYPFPAPGLRGLMLS VMLASLMSSLTSIFNSASTRTK AQWK*L*CFCLMFKLCCFLLRI FVLLLTVVSIVWVPLVQVSQNG QLIHYTESI***LT*ISFSYFLNILI FFLLLLQGAFWGLMVGLAMGL IRMITEFAYGTGSCLAPSNCPKII CGVHYLYFSIKVPFYYTIANICL LLMHFCMVPVQLYRLCWVLR NTTLTRISSSFVI*IFCNHLLIFVP DYPEKSRGCLKKAYDLFCGLQ KGPKLTKEEEEALSKKLTDTSE
15120	45488	B	15207	1	1392	
15121	45489	A	15208	57	1523	
15122	45490	A	15209	473	589	LPRQLALSCVVHCQTLVPAIRCI DWGWLF*W*SVTPVM

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15123	45491	A	15210	1	1297	MGKIMSSYQHVDLIVDCDFEA YHRQPSSGTKSVVTGPSAQALI TEKIVTYHWDQHVGDVLVLNI YCVINVLDHTVKAVIDDRFMG GITTINLQLMAIIVRYFFASGSA YIVAMLPVFAMLANVSGAPLM LTALALLFSNSYGGMVTHYGG AAGPVIFGVGYNDIKSLCFDER TRIDVADTYASNWRSRCNQTIF NGECPNTRQHIAAVRRGIDTLL MNDYLRKQIIDISTRIAGTANN GDFTGQWITAANTVNFQIVAGT HNCHQYFIALRLIFGILKYIQDR AREGLKQRDLAEALSTSPQTVN NWIKRDALSREAAQQISEKFGY SLDWLLNGEGSPKKDLESNIPP ESEWGTVDAWDKNTPLPDDEV EVPFLKDIEFACGDGRVHDEDH NGFKLRFSKV\VQPRVGC*QG* G*LLYLDSV**GDPLEST
15124	45492	A	15211	62	301	SWMSSPRAFSSSTCLETAAPTR MATALTSAACRLPPAAGSGSP WAPAPYRWRARRRTGPMSDR Q*RTSQPCPEPAAASR
15125	45493	A	15212	1	1665	MQDSAHLRRLPPAASRRVWLA LGSCPLPLESSPAHRAYERPSVA HQPAVPGARRSLEVPSEVPLTV PALTPPRIPAMLTAVCGSLGSQ HTEAPHASPPRLDLQPLQTYQG HTSPEAGDYPSPLQPGELQSLPL GPEVDFSQGYELPGASSRVTCE DLESDSPLAPGPFSKLLQPDMS HHYESWFRPTHPGAEDGSWWD LHPGTSWMDLPHTQGALTSPG HPGALQAGLGGYVGDHQLCAP PPHPHAHHLLPAAGGQHLLGPP DGAKALEVAAPESQGLDSSLD GAARPKGSRRSVPRSSGQTVCR CPNCLEAERLGAPCGPDGGKK KHLHNCHIPGCGKAYAKTSHL KAHLRWHSGDRPFVCNWLFCG KRFTRSDELQRHLQTHTGTKKF PCAVCSRVFMRSDHLAKHMKT HEGAKEEAAGAASGEGKAGGA VEPPGGKGKREAEGSMASSSPD SPCSCDCFVSVPPASAIPAVIFA HELGPTPGRGAGGGVCPRRHS HSWEPAPGL*AVGGGGGASGQ AGDRGCHA*EAGRS/SCSRRGS GL*RAGTS*ISASS

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15126	45494	A	15213	3	471	GRPSSPGVHGSSTQTPAHVGSF PGCGPIPPD/ACRRSKIRGPGGW GGVGG/CRDGRNSR/DLRNLPC PFLFLPGP*AAAPSPPWPAAGA APCGQCLDGWPHSYSHGHSSA AGRGGICRSPPLLAGELRPPGIQ YNGRTEVRGILSGSPCPPFSGAG
15127	45495	A	15214	3	449	PHQDLEEAMVLL*PPSP/PAWPT MRTRKRPSSKVSSTSRPLRKSIM TTYAVPSRAPTPA*PSASKPTNA FS/HMVGSEPRSHAHLDGRHRD SR*RKPRPLSGPRTLGGKSLRGS AGAGRGGVPRPRPLPENLDAPL WNSPGNSAGAAVQLA
15128	45496	A	15215	26	1126	EGPSSEAAHPGGTPREQDGAM DPARKAGAQAMIWTAGWLLL LLLRGGAQALECYSCVQKADD GCSPNKMKTVKCAPGVDVCT\ EAVVAVETIHGQFSLAVR\GCG SGLPGKNDRGLDLHGLLAFIQL QQCAQDRCNAKLNLTSRALDP AGNESAYPPNGVECYSCVGLSR EACQGTSPPVVSCYNASDHVY KGCFDGNVTLTAANVTVSLPV RGCVQDEFCTRDGVTGPGFTLS GSCCQGSRCNSDLRNKTYFSPR IPPLVRLPPPEPTTVASTTSVTTS TSAPVRPTSTTKPMPAPTSQTPR QGVEHEASRDEEPRLTGGAAG HQDRSNSGQYPAKGGPQQPHN KGCVAPTAGLAALLLAVAAGV
15129	45497	A	15216	1401	1983	AQRAQALECYSCVQKAD/DGC SPNKMKTVKCAPG/VDVCTEA VGAVE/SHPFWIWPRPFNAAPPP LSAWPGPYDTALQARPLY*QL QARGAES*ELVH/GQFSLAVRG CGSGLPGK/NDRGLDLHGLLAF IQLQ/QCAQDRCNAKLNLTS/RG LDPAGTSPPVVSCYNASDHVY/ KGCFDGNVTLTAEPTTVASTTS VTTSTSPQ

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15130	45498	A	15217	1	964	MNVKGDTQGNTRVRVDNIGG VGAQTVNGIELIEVGGNSAGNF ALTTGTVEAGAYVYTLAKGKG NDEKN\SPSVYRP/EAGSYISNIA AANSLFSHRLHDRHSCLQPLKI LVTGGAGFIGSAVVRHIINNTQ DSVVNVDKLTYAGNRESLADV SDSERYVFEHADICDAPAMARI FAQHQPDAVMHLAAESHVDRS ITGPAAFIETNIVGTYVLLEAAR NYWSALDSDKKNSFRFHHISTD EVYGDLPHPDEVNNTEELPLFT ETTAYAPSSPYSASKASSDHLV RAWKRTYGLPTIVTNCSNNYG PYHFPEKLIPLVILNALE
15131	45499	B	15218	44	405	
15132	45500	A	15222	1	498	MTRSLLSVFEEDAGTLTDYTNQ LLQAMQRVYGAQLNLLHTELA KQL\ETQWFYLSYNSEKRISQTL SAMWRGRAAQA/TQGHWVWG MVEAVCSKVSTLKDLFGLASN EHDLSMAKYSRLPKKKENEKL AAFGQPTWCDPAERVGFLEPV GPDPGAKSAPSPRDRASTL
15133	45501	A	15223	1	1224	
15134	45502	A	15224	1	1353	
15135	45503	A	15225	1	2580	
15136	45504	A	15226	1	3117	
15137	45505	A	15227	1	1260	
15138	45506	A	15228	1	2142	
15139	45507	A	15229	1	1413	
15140	45508	A	15230	1	4049	
15141	45509	A	15231	1	381	MLMLNIGFKNFQFEHLKCSHGS YSEDIGFPNAGALSGAMFLLEE KHLLFGLKEEERLRASIRRESQ QRRMREKQHQRGLSASY\WNLI DTMRRRKARSP/YSLAAIKNRY KGGIRDQKPSYDSLNLCMT
15142	45510	A	15232	1	467	DHSSSPAREQNWMEN\EFDELT EVGFRRWVITNSSELKKHVLTQ CKEAKNLEKRLGELLTRITSLE KNINDLMELKNTARELHEAYTS INSWINQAEERLSEIEDQLNEIK REDKITEKMKNSTTVRVAASM QSKLLQGVAEEGPLRLTRSASF
15143	45511	A	15233	1	1140	
15144	45512	A	15234	1	2640	
15145	45513	A	15235	1	714	
15146	45514	B	15236	1	546	
15147	45515	B	15237	1	735	
15148	45516	B	15238	50	1603	

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15149	45517	A	15239	1374	2220	QAENSHININKKDVHSETPSEG HQRKRPKDHSSSPAREQNWME N\EFDELTEVGFRRWVITNSSEL KKHVLTQCKEAKNLEKRLGEL LTRITSLEKNINDLMELKNTAR ELHEAYTSINSWINQAEERLSEI EDQLNEIKREDKITEKMKNSTT VLVSTWGSQLEQNNLPHIISPLF HSTHDLNISFYGGCLLQACSSK LLQGLAEGGPLRLTRSASFFAA KLCLTKHFLPTEMILIKSRKTTP DTQPRRLYLLQGVVDQTSRKG PTALNIRQKTFAAAPPHR
15150	45518	B	15240	1	1311	
15151	45519	B	15241	46	212	
15152	45520	A	15242	3	371	EPLPPEPPAVPSEVELQHLRKEL ERVAGELQSQVKNNQHISLLNR RQEERIREQEERLRKQEERLQE QHEKLRQLAKPQSVELK\SQEV QSLQQQPDHF\LGHL\QQYV\AT LSAARWAAYQQLD
15153	45521	A	15243	392	558	
15154	45522	B	15244	52	689	
15155	45523	B	15245	400	603	
15156	45524	A	15246	5	1158	RKFWRWMVVMAAQHSQAAQ GQRR**VSKGP**PGPMGGPVL GHWWHSGGISLAVPSLPPPGKS SVFLFLFSASFSDMKLNPGTVSP RLIFGSYDDGFLVETVVKFDFQ LWQKTPLHRAAGERRRAEQRG KLSFVMP

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15157	45525	A	15247	1	1808	MAEETQHNKLAAAKKKSATGF HREGPTSSATLKDLESPCQERA VVLDSTSVKISRLKNTIKSLKQQ KKQVEHQLEEVTAPDNLVPWV GLSWGIGGILGACLLLCHLCLP LEKKANNERQKAERELEVQIQT LIIQKEELNTDLYHMERSLRYFE EESKDLAVRLQHSLQCKGELES ALSAVIATEKKKANQLSSRSKA RTEWKLEQSMREEALLKVQLT QLKESFQQVQLERDEYSEHLKG ERARWQQRMRKMSQEICTLKK EKQQDMRRVEELERSLSKLKN QMAEPLPPEPPAVPSEVELQHL RKELERVAGELQSQVKNNQHIS LLNRRQEERIREQEERLRKQEE RLQEQHEKLRQLAKPHCAFSRS *TMRTRAHLQLEQQVKELQE/Q ALARVFLQVELKSQEAQSLQQ QPDHYLGHPAAEHLEAASQQN QQLTAQLSLMALPGEGHGGEH LDSEGEEAPRPMPSVPEDLESR EAMVAFFKSAGASAQEKQAQL QEQVKEQRVCCQRLAHPVASA QKEPEAARGPGAPGPGGESSSF MDHLKEKADLSE/PGEKRTLLH P/PTG/GDRRHQKTHHLLSEPGG CAK/DAALGPGHHQAGAQGGD
15158	45526	A	15248	2085	2700	YPGKRGLEWT*ANSNRPAAEG PDE\SSSLPATEQSWMENDFDE LRKEGFRRSVITNFSKLKEDVQ THRKEAKNLEKGLDEWLTRINS IEKTLNDLMEMKTMA*ELHDT CTSFSSRVDQVEERLSVI*DQM NEMK*EEKFREK\RVKRNEQSL QEIWNYVKRPNLHLIGVSEIDR ENGTKLENTLQDIFQENFTYLA RQANIQIQEI

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15159	45527	A	15249	378	1744	QTERNSININKKDIHTKTPSVRH HHQRPKLHKTTKMGKKHSRKA ENSKNQSGSLPPKECSSSPAVE QSWTENEFDEFTEEGFR\RIESQ MNEIKGEEKFREKRVKRNEQSL QEIWDYVKRPDLRLIGVPDSDG ENGTRLENTLQDIIRENFPNLAR QASIQIQEIQRTPQRYSSRRATP RHIIVRFTKVEMKEKMLRAARE KELKIKKLTQNCLTTWKLNNLL LNDYWVHNEMKGEIKMFFETN ENIDTTYQNLWHTFKAVCRGK FIALNAHKRKQERSKIDTLASQ LKEIEKQEQTHSKASRRQEITKI RVELKEIETQKSLQKINESRSWF FEKINKIDRPLPRLIKKKREKNQ IDTIKNDKGDITTNPTEIQTISRE YYKHLYANKLENLEEMDKFLD TYTLSGLNKEEVESLNTSITGSE VEAIINSIPTKKKSRTRWIHSRIL PEVQGGAA
15160	45528	A	15250	935	1269	LIEGKLTERNSININKKDIHTKT PSVG/PPSSKTKDRSSLPAIEQS WMENDFDELTEVGFRRSVITNL SKLKEDVRIPHKEATNLEKRLD EWLTRINSIEKTLDDLMELKTM
15161	45529	A	15251	401	497	KTFSPFYFS*RRRTVRDINGFTE Y*EPEKLLG
15162	45530	B	15252	220	940	
15163	45531	A	15253	1	1476	

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15164	45532	A	15254	1	2423	MNGKNKTNIYQEPTVCQALHW TLARIGKEEPRRGQRGEGLLCS RERQPRGLSSPGTAAPAAPAAP TPPALPGHRTRSGSPEGPEPILR RGGSADAPGRVKTWVNRPAAF VGKCLGDGSADTACDQAMKG QRGSNRKRKTSHSLTFPTSSDM HAGGLSAAHPCAHSRAPPPASP SPYKGSLGTRTDGLTDSRADSA ASGARALGVDGQPQPSPPRRAP PRPVGADGSSRGPQPGRRRVER RGPATQPGDSRALPEPRGVPAV HPAGSGSEWERPPPAAPSPEHR DKMLPGLRRLLQASARRPQPFP EAARWVWSPCFSSGTLCPSFQS ERPLLPFQGASFPGTTLHQRLCP VAALHGSGKGQKWQQSHCYA AAVMEEPPAPGRSSESLQGPLS WAGGAPASACLLLMLLALPLA APSCPMLCTCYSSPPTVSCQAN NFSSVPLSLPPSTQRLFLQNNLI RTLGARHLWVQPAHPVALLQQ PLHHLPGHFPPL\QALEELDLGD NRHLRSLEPDTFQGLERLQSLH LYRCQLSSLPGNIFRGLVSLQYL YLQENSLLHLQDDLFADLANLE PTSFLHGNRLRLLTEHVFRGLG SLDRLLLHGNRLQGVHRAAFR GLSRLTILYLFNNSLASLPGEAL ADLPSLEFLRLNANPWACDCR ARPLWAWFQRARVSSSDVTCA TPPERQGRDLRALREADFQACP
15165	45533	B	15255	47	482	
15166	45534	A	15256	1	636	MRDPNTKRSRGFGFVTCATVE EVDAAMNARPCKVVGRTVEPK RAVSREDSQRPEDTEELHLRDY FEQYGKIEVIEIMTDQGSGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGSGNFGGGRGGGF GGNDNFGRGGNFSGHGGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVNYNNQSSHFGPM

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15167	45535	A	15257	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
15168	45536	A	15258	1	286	
15169	45537	A	15259	1	1674	
15170	45538	A	15260	235	1370	KREGEGRLADTFVSLLLSARGR RRRSIVKVSLHPAVMSKSESPK EP\EQLRKLFIGGLSFETTDESLR SHFEQWGTLTD\CVVMRDPNT KRSRG\FGFVTYATVEEVDAAM NARPHKVD\GRVV\EPKRAVSR EDSQRPGAH\LTVKK\IFVGWH* RKTTFWGGKKKRAKKHHLRD YFEQYGKI\EVIEIH*LDR\GQWP RKRGFAFVTF\DDP\DSVDKIVI QKYHTVNGHNCEV\RKALSKQ E\MASASSS\QRG\RSGSGNFGG GRGGGF\GGN\DNFG\RGGNFS\ G\RGGFGGT\RGGGGYGG/SVG DGYNGFGNDGSNFGGGG\SYN DFGNYNNQ\SSNFGPMKG\GNF G\GRSSGPYG\GGGQYF\AKPR\N QGGYGGSSSSSSYGSGRRF
15171	45539	B	15261	1	660	
15172	45540	A	15262	2	486	KMRQRERAQGKK/VAPAPAVV K/KQEAKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVKWPRYIR LQRQRAILYKRLKVPPAINQFT QALDRQTATQLLKLAHKYRP/G DKGALAKLVEAIRTNYNDRYD EIRRHWGGNVLGPKSVARIAKL EKAKAKELATKLG

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15173	45541	A	15263	3	845	PPKMPKGKKAKGKKVAPAPAV VKKQEAKKVVNPLFEKRPKNF GIGQDIQPKRDLTRFVK\WPRYI RLQR\QRAILYKRLKVPPAINQF TQALDRQTATQLLK/LVAHKYR P\ETKQEKKQRL\LARA\EKKAA WQKGTSPTKRPP\VLR\AGS*HP VTTLVE\NKKASAGWWIAHRR GFPSSLVVFLP\ALCREKWGSPY \CIIKGKARLG\RLVTRKTCTTV AF\TQVNLGRQRALLLKLVEAI RTNYNDRYDEIRRHWGGNVLG PKSVARIAKLEKAKAK\ELATK
15174	45542	A	15264	1	5796	
15175	45543	A	15265	1	2212	MPRVEKNIPGRRNSKGFEDPLE VTQDVTREWAKKVVWKREKA SKINGAYFCEGRVRGEAIRIRT MKMRQQATLTMTVDKGDNVN ISFKKVLIKEEDAVIYKNGSFIH SVPRHEVPDILEVHLPHAQPQD AGVYSARYIGGNLFTSAFTRLI VRILPPQPENIKISNITHSSAVIS WTILDGYSISSITIRYKVQGKNE DQHVDVKIKNATITQYQLKGLE PETAYQVDIFAENNIGSSNPAFS HELVTLPESQAPADLGGGKML LIAILGSAGMTCLTVLLAFLIILQ LKRANVQRRMAQAFQNVREEP AVQFNSGTLALNRKVKNNPDP TIYPVLDWNDIKFQDVIGEGNF GQVLKARIKKDGLRMDAAIKR MKEYASKDDHRDFAGELEVLC KLGHHPNIINLLGACEHRERGD RRHLENQVTPTLILRFSNTLSKR HTRRLYPEPGSEGPTPTEPRSLL AQQSEIKLHGGSEPPLLIFRQTG SGVDLQQTPTNLQLRVLTVRR KTDKRKGHPHQKPICSSPSSKT KEGFRRSNYSKLKEEVQTHGK EVKNLEKKLDKWLTRITNAEK SLKDLMELKTKARELCDECASL TSQFDQLDKRVSVMEDQMNE MKQEEKFREKRIKRNEQSLQEI WDYVKRPNLCLIGAPESDGEN GTKLENTLQDIIQENFPNITRQA NIQIQEIQRTPQRYSSRRATPRHI

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15176	45544	A	15266	1	743	PPLLIFRQTGSGVDLQQTPTNLQ LRVLTVRRKTDKRKGHPHQKPI CSSPSSKTKEGFRRSNYSKLKEE VQTHGKEVKNLEKKLDKWLTR ITNAEKSLKDLMELKTKARELC DECASLTSQFDQLDKRVSVME DQMNEMKQEEKFREKRIKRNE QSLQEIWDYVKRPNLCLIGAPE SDGENGTKLENTLQDIIQENFPN ITRQANIQIQEIQRTPQRYSSRR ATPRHIIVRFTKVEMKEK\MLR AAREK
15177	45545	A	15267	1	618	
15178	45546	A	15268	200	618	EVSRNNTRTKTSYKQDMNTSK GF*KDTST*PVT/KERSSSPATEQ CWTENDFDELREEGFRRSNYSE LKEEVRTNGKEVKNLEKKLDE WLTRITNAEKSLKDLMELKTM ARELCDERTSLSSRCDQLEERV SVMEDEMNEM
15179	45547	A	15269	158	594	SGSSICCSPISTVLQPPLLTPRQT GSGATSSK/SPTDLQLRECSSSP AKEQSWMENDFDELREGFRRS NYSELKEEVQTHGKEVENLEK KIDEWLTRITNAEKSLKDLMEL KTMAREQCDECTSLSSRRDQLE ERVSVIEDQINEMK
15180	45548	A	15270	3	1453	LSDLELAAQSIIFIFAGYETTSSV LSFTLYELATHPDVQQKLQKEI DAVLPNKERSSSPATEQSWTEN DFDELREEGFRRSNYPELKEEV RTHGKEVRNLEKKIRQM\VTRII NAEKSLKDLMELKTMARELRD ECTSLSSQFNQLEERVSVMEDQ MNEMKKEEKFRRKRIKRKEQS LQEIWDYVKRPNLRLIGVPESD GENRTKLENTLQDIIQENFPNLA RQANIQIQEIQRTPQRYSSRRAT PRHIIVRFTKVEMKEKMLRAAR EKEIQTTIREYYKHLYANKLEN LEEMDKFLDTYTLPRLNQEEVE TLNRPITGSEIEAIINSLPTKKSP GPDGFTAEFYQRYKEDLVPFFL KLFQSIEKEGILPNSFYEASIILIP KPGRDTTKKENFRPISLMNSDT KILNKILANRIQQHIKKLIHHDQ VGFIPGMQGWFNIRKSINIIQHI NRTNDKTHMIISIDAEKAFNKIQ QPFMLKTLNKL
15181	45549	C	15271	111	269	

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15182	45550	A	15272	94	4505	YLDMMSFVQKGSWLLLALLHP TIILAQQEAVEGGCSHLGQSYA DRDVWKPEPCQICVCDSGSVLC DDIICDDQELDCPNPEIPFGECC AVCPQPPTAPTRPPNGQGPQGP KGDPGPPGIPGRNGDPGIPGQP GSPGSPGPPGICESCPTGPQNYS PQYDSYDVKSGVAVGGLAGYP GPAGPPGPPGPPGTSGHPGSPGS PGYQGPPGEPGQAGPSGPPGPP GAIGPSGPAGKDGESGRPGRPG ERGLPGPPGIKG
15183	45551	A	15273	1628	1832	RRRRKARERRRLAAEQGRRMK EQCKDGFSE/QASGALKLMGSN EGEFKAEGNSKFTYTVLEDGCT KHTG
15184	45552	A	15274	1	362	
15185	45553	A	15275	1076	1240	LRQLL*LCPSWRLCLLGGWQL HLFF*RHHFVHLVSQRCSIAMS PSPRRCFSLHL
15186	45554	B	15276	480	1167	
15187	45555	A	15277	3	379	
15188	45556	B	15278	13	369	
15189	45557	A	15279	112	1112	WPPASPSASVIRTVKEFALTNPE KSSTKETERKETKAEEELDAEV LEVFHPTHEWQALQPGQACPC RNPTYGLNLQTGEREAKLQYE DKFRNNLKGKRLDINTNTYTSQ DLKSALAKFKEGAEMESSKED KARQAEVKRLFRPIEELKKDFD ELNVVIETDMQIMVRLINKFNS SSSSLEEKIAALFDLEYYVHQM DNAQDLLSFGGLQVVINGLNST EPLVKEYAAFVLGAAFSSNPKV Q/EWEAIEGGALQKLLVILATE QPLTAKKKVLFALCSLLRHFPY AQRQFLKLGGLQVLRTLGAGE GHGGARRARGHTALRPCHREK CSPRRRLS
15190	45558	B	15280	54	385	
15191	45559	B	15281	274	776	

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15192	45560	A	15282	362	1323	HQLGRSALLDTRTVSMQKAKN GDAVTEPQVA/ENEANGKDTA EVDLLTKELEDFEMKKATARA VTGILASHPCSTDVHIINLSLTF HGQELPSDTKLELNSVRHYGLI GLNGTENSMLLSAVGKHGVPIP EHIDIYHLTREMPPSDKTPLHSL VTVSSPRQRDDMSDGHLCTAR RHTDIRDDRSPDAPDTARSLAR STITTRRIFALATPSRTLQQVCS ALAYTSHPAARTQPLASTALTR RYMLPSPQLPSLRDHRRTNPLH SAVATIPHTTTGEADVSLLCIGL STLHYALVYHVSVLTALSAQS MSATDASIIFFEPKR
15193	45561	A	15283	3	537	
15194	45562	A	15284	1	455	MPRPEKLGKTQVPPLAECLTKD SFLGQKQASLGPLTFRDVTIEFS LEEWQCLDTVQQNLYRDVMLE NYRNLVFLVISS/HFTQDFWPD QSIKDSF/QRIILRTYARCGHKN LRLEKIVKVSMRKHQIIHTGKK PYKCEECAKLLASPQPLENMR
15195	45563	A	15285	1	397	FAVLMAHYDVQEEDPVLTVIT YMGLSVSLLCLL\LAALTFLLC KAIQNTSTSLHLQLSLCLFLAHL LFLVAIDQTGHKVLCSIIAGTLH YLYLATLTWMLLEALYLFLTA RNLTVVNYSSINRFMKKLMFPV
15196	45564	A	15286	191	1332	AIETQAITDNCSEERKTFNLNV QMNSMDIRCSDIIQGDTQGPSVI AFISYSSLGNIINATFFEEMDKK DQVYLNSQVVSAAIGPKRNVSL SKSVTLTFQHVKMTPSTKKVFC VYWKSTGAG/CSQWSRDGCFLI HVNKSHTMCNCSHLSSFAVLM ALTSQEEDPVLTVITYVGLSVSL LCLLLAALTFLLCKAIRNTSTSL HLQLSLCLFLAHLLFLVGIDRTE PKVLCSIIAGALHYLYLAAFTW MLLEGVHLFLTARNLTVVNYS SINRLMKWIMFPVGYGVPAVT VAISAASWPHLYGTADRMLAF KATAQLFILGCTWCLGLLQVGP AAQVMAYLFTIINSLQGFFIFLV YCLLSQQAKHKFTPMEVPRQN HRCLQQN
15197	45565	A	15287	263	397	GRPPAPAARVSGPASVSAG*KR VSASGSVGVRSMRRGSALLPPN F

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15198	45566	A	15288	1	278	MKFHDRGQMQPKPSPAEAVNS APQREPEGSILRAADPLVWAAK AMSASR/RGS/CGGSSADPRHTE RTPTEPDADTRFQPAETLAGPK TRAAGAG
15199	45567	A	15289	5	545	SFMTEAKSSPNPAQQRLSTQRP SESRKVPSSELQTLSCGLQRPCL HPGRPGPDPYYASASTRTRSPS ARHAVWGRRGCYPEA/AVRAR EGPHPTLAPASTYGLASPPRAD SAHRPRHRSLTRLLPNRKLGGS SADPRHTERTPTEPDADTRFQP AETLAGPKTRAAGAGGQPWDS ANASPP
15200	45568	B	15290	121	822	
15201	45569	A	15291	1	1308	MLRMVGIEISNGQWSTPPCQVL HLEGNDIYNPKEQGLGNTCRW GWMAAGTRRNLCWAPFPFLNP VASLVLHSTIQIALQESKDRVL GTLINSPLVTSTDKANWSLRLA LEVGDGGGLVGLSPQPVGSGA MSRCPNCTRKLIGSGISPTSSTL AEEQGSVVKTHSHQGGARCSK EKGWQILLILVAGLCQLVVVV QNVGVRKIPRKYLAALRVAIGH ALAIERRRIRVDVADQAQDTDR DDRSFGRDRNRDSDKTDTDWR ARSATDSFDDYPPRRGDDRFGD KYRDRYDSDQYGRGYWYEYR DGPCRDMDRYG\GGSGRRAFG SGY/RRDNDYRGGRDRYEDRY NRWDDGSCSSRDDFSRDDCRY NDRRPPQRPKLNLKPHNTPKGD DSSASTSQSSRASFVFGGAKPV DRAARETKVEEWLQKEQDKLQ HQLDEAKLE
15202	45570	A	15292	2	293	
15203	45571	C	15293	56	298	
15204	45572	A	15294	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS

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15205	45573	A	15295	3	1024	CGGIHSVLRGCSLEPAFFYLRSA FSPTISACRHPMEDSMDMDMSP LRPQNYLFGCE\LKADKDYHFK VDNDENEHQLSLRTVSLGAGA KDELHIVEAEAMNY\EGSPIKVT L\ATLKMS\VQPTVFPWGAFEIT PTQWSLRLKCG\SGPVHI\SGQH FSKLLEEDAE\SEDEEE\EDVKL\ LSISGK\RSAP\GGGSKVPQKKS KTLLLMKDDDDDEED\DDED DG*WMDFGWMEEAEEKAPSE RNPIRDTP\AKNAQKSNQNGKD SKPSSTPR\SKGQESFKKQEKTP KTPKGPSSVEDIKAKMQASIEK GGSLPKVEAKFINYVKNCFRMT DQEAIQDLWQWRKSL
15206	45574	B	15296	1	1107	
15207	45575	A	15297	1	1968	MLASMGVVAKEMKYLSSPYPQ HAFHTRIKSLMTVNFQAQLWL PNEAGPTGDGDWGGDTHGCPS FSPHLPRFIQKQPWGTGRRLLQ EHFSCKSLVPVIPSRDIEAFHLH ADLILNTLPSLVIIIGQIESHSEEL RARVSTYESGEDTIQCITVTWK PKYGATRWKDPGSPDGPLEER RLEDLSTRNNSIRLFRGCGYRV KQNSSQRPNKVCGLPDTGVLL QTKCGLVRNSQRSAQTNTKQH EELFSTAGIPENLSRRQEVLPGH GFTGWVGWTWKLTSGEGVTF HHLSATHKLSHASCRQGNFKP KGAMSVTRSTVHPHLAFLSAEI NGKCGRPCVFLGIWAINCGMAI LYERLSALVCVSVSERHLDYT MRFLFDIPPSTLEARIGSPLWAL SLHPLRSSTVTSSVELILPECTV AVLEIQYVFLGDTILFTTVGKA RSGTRDRDGGRAQIMQVLQGK GRELDAAAQPEGQLLREVRVL GVPFIPRARVDAWLVHTVAVG SADEAHGLLGAAAASSTGGAG ASVDGGSQAVQGGGGDPRAAR SGPLDAGEEEKAPAEPTAQVAD AGGCASEENEVLREKHEAVDH SSQREENEERVSALKENSLQQN NDDENKIAEKPDWEAEKTSESR NERHLNGADTSFF\SLEDLFQLL

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15208	45576	A	15298	1	2104	MKHLKRWWSAGGGLLHLTLL LSLAGLRVDLDLYLLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRALGVPFVPRTSV DAWLVHSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGG\CASEE NGVLREKHEA\VDHSSQHEENE ERVSAQKENSLQQNDDDENKI AEKPDWEAEKTTESGNE\RHL\ NGTDTSFSL\EDLFQLLSSQP\EN SL\EGISIWGDIPLP\GSISDGHEF FKHIYHVNFQPRLIS\QD\VNLH EAILLCPNNTFRRDPTARTSQSQ EPFLQLNSHTTNPEQTLPGTNLT GFLSPVDNHMRNLTSQDLLYD LDINIFDEINLMSLATEDNFDPI DVSQLFDEPDSDSGLSLDSSHN NTSVIKSNSSHSVCDEGAIGYCT DHESSSHHDLEGAVGGYYPEPS KLCHLDQSDSDFHGDLTFQHVF HNHTYHLQPTAPESTSEPFPWP GKSQKIRSRYLEDTDRNLSRDE QRAKALHIPFSVDEIVGMPVDS FNSMLSRYYLTDLQVSLIRDIRR RGKNKVAAQNCRKRKLDIILNL EDDVCNLQAKKETLKREQAQC NKAINIMKQKLHDLYHDIFSRL RDDQGRPVNPNHYALQCTHDG SILIVPKELVASGHKKETQKGK
15209	45577	A	15299	2	342	RRRFRVAAAAVGTA*AVVLSA RPSETWETRGRR*\RICPSSWP* GI*VNNG*K*RRHSVCQCSLWF PARCIKPYHSMARTQPGTRNKE NGPAGPTALDNVASSDDTGRH RPQT

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15210	45578	A	15300	710	1831	IRMKSKEIIARCIKPYHSMARTQ PGTRNKENGPAGPTALDNVASS DDTGRHRPQTTQLAPGFAHPLQ LASFRRMVLFLSGEGRSRGGPE LQFPASCRRGEGSPGVRESGSG GIAATSTPNYPPNQDSKEHDIR GAEHQKQEQPAKPPHTARSAY PPQKSSYPANAKATRHSPETAA AKEARAPAAAQPQRHQPNPSP APHTRPATAATRQPERRVPSPT HRHPAATRLSPRRQSPSPRPHH DRRGFPRLAETLQHPMCPLPLV ASAGHHRHHRLLLLLAPQAPER EASDEI\VFSGRSRSRGCPTEFQE SAMCFPNPGLPDSCGESQAVTI LILRKFQKVIWVIEVPLDYKKG SWEYFSRMETIIMPFENIQSE
15211	45579	A	15301	77	1041	IPSCVVSGIAAAF/HPGLASDAP ARASSWWTHVEMGPPDPILGV TEGFKRDTNSKKMNLGVSAYR DHNGKPYSIHKAEAQIAAKNLD EDYLSIGRLAEFCKASAEVALG ENSEVSKSGRFVTVQTISGTSAL RIRASFLQRFLKFSQDVFLPKPT WGSRTPIFRDTGMQLQGYRYY DRKTCGFDFTDTVEDISKTPEQ SLLLLHACSHNPTGVDPGPKQQ KEIATVVKKT/RNLFALFDMAY QGFASGNGNKDAWAVRHSAN\ IRHCRCQSYTKNMVLHSEGVA GFTMVCKDADEAKRVESHLKI LMCPMYSNPPLNGTRLLLPF
15212	45580	A	15302	1	1263	
15213	45581	A	15303	1	1146	MTGRQSLSPVLSLSSLDSMSFT TRSIFSTNYLFLGSVQVSNYGA RPASCMASVYAGAGGSGSRISV SRSTSFRGGMGSGDLAAGMAG GLAGMGGIQNKKETMQSLNDR LASYLDRVRSLETKNRKLESKI REHLEKKGLQVRDWSHYLKTI EDLRVQIFANTVDNAGIVLQID NACLAADDFRVKSLMTNVTWL PLETEMEALKEELLFMKKNHEE EVKGLQAQIASSELTVEIEKSTT VVTTQSTKVGDAEMTLTELRR TVQSLKMDLDSMRNLKASLEN SLREVEARYTLQMEQLNRILLH LESEMAQSRAEGQHQIGEYEAL LNIKVKLEAESATYHRLLDDDD FNLGDALDNSNSMQTI/QKTTT RRKVVSETNDTKVL

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15214	45582	A	15304	184	370	
15215	45583	A	15305	40	1411	RGDPRVRRRTQSLSPVLSLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL ESKNPEHLEKKGPQVRDWSHY FKIIEDLRAQIFANTVEQCPTTV L/LRIDSA\RLA\ADDFRVKYE\T EAGPCAQSVENNIHGLCKVIDD TNVTRLQLETEIEALKEELLFM KKNHEEEVKGL*AQIASSELTV EVDAPKSQDLAEIMADIRAQYD ELARKNREELDKYWSQQIEEST TVVTTQSAEVGAAETTLTELRR TVQSLEIDLDSMRNLKASLENS LREVEARYALQMEQLNGILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
15216	45584	A	15306	392	1449	GPWEMLMTIKSHPDAERQPQR VKKLTQVFWSSASLRER/GKTY LFWPKLKKAAEIPAAYREALDE ALGISGGGRDVGERVYKGPSM MANPQKPVLEALSSNKYLHILC AKHCDRHEGYKDEIKVKEASS RVNGCVEAMLSAPLPLDRRNE HVESKGKPFTMGLSPRVLSASR RDGLRERKGSFFRTVVLHDTKT DSNSDTETNSSTPPRTLLEMQIL SPTWTYEISSSRTLGCGPSVFQQ RASYSPSVSGPRLGCPLMDGGR MRCPPGNPESCVSEANLIPISVP VAPHAHQHLVLSVFWKITIVIG GKTCVAQNHSNEAKMKQRPEI NHASPPGAFAWSQSGEPIASAM TVPA

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15217	45585	A	15307	1	785	MWDVGQDSSLLRGAGGPGLQL WFGRLQLHLGGLREHRDAWV HSRGLGSCSGMQGAATPTQNG RGSCLSPAPASSMEHAAPAVPP CCSWCDSSSRSRWPATATTETG PRTVPSAQESAVGLLTASLLKG DSGSTGFCPLLMSLAAPGTQQC SLGFCCTFERKRSSVSPAAPGTA APELAAALMLMPRKNQIAVYE LLFKQGVMVAKEGVHLPRHPE LADKNVPNLHIMKAMQ\SLKSQ GHREEQFAWRHFYWHLTREGI QSIQ
15218	45586	A	15308	1	392	
15219	45587	A	15309	1	716	
15220	45588	A	15310	150	372	RRSNEWGVPVPVPARTGGG/HG QKTPPSPPLPPSSPPPSPSPPPPPA \APAKIPPPLPLPPLPPREAPPAP GPALP
15221	45589	A	15311	218	740	KSCPETVSRRKNVGSIKKHQGD KFNPVCLKMTTKTEFVLCGWV PCRCL/REGEEETVTTLDYSHCS \LEQVP\KEIFTFEKTLEELYLDA NQIEELPKQLFNCQSLHKLSLPD NDLTTLPASIANLINLRELDVSK NGIQEFPENIKNCKVLTIVEASV NPISKLPDGFSQLLNLTQ
15222	45590	A	15312	96	297	
15223	45591	A	15313	469	5174	KMTSLAQQLQRLALPQSDASLL SRDEVASLLFDPKEAATIDRDT AFAIGCTGLEELLGIDPSFEQFE APLFSQLAKTLERSVQTKAVNK QLDENISLFLIHLSPYFLLKPAQ KCLEWLIHRFHIHLYNQDSLIA CVLPYHETRIFVRVIQLLKINNS KHRWFWLLPVKQSGVPLAKGT LITHCYKDLGFMDFICSLVTKS VKVFAEYPGSSAQLRVLLAFYA STIVSALVAAEDVSDNIIAKLFP YIQKGLKSSL
15224	45592	A	15314	267	495	GCLL**CLCIRL/SKNRAERALR PYSDVEALRLSSDFPFRQRPKG GSGWSLLSVEINQYYGPRVMIG RSNSEVVLVL

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15225	45593	A	15315	3	3027	AMEQAGTRPAATEHPRLRRPM PWLLLLPLLLLLLLLLPGPAASQ LRYSVPEEQAPGALVGNVARA LGLELRRLGPGCLRINHLGAPSP RYLELDLTSGALFVNERIDREA LCEQRPRCLLSLEVLAHNPVAV SAVEVEILDINDNSPRFPRPNYQ LQVSESVAPGARFHIESAQDPD VGANSVQTYELSPSEHFELDLK PLQENSKVLELVLRKGLDREQA ALHHLVLTAVDGGIPARSGTAQ ISVRVLDTNDNS
15226	45594	A	15316	1	775	MPCVNGKYNSTIQAGLQMAQI LQDEGPYEVGIDEETGSQKGDG IIRSSRKLLFTMALFLETNLLKD PLSRERRWRLDELDSGGREKG VAVFLRSAGIRQVQVAMEQAG TRP/AATEHPRLRRPMPWLLL/L PLLLLLLLLPGPAA/SQLRYSV PEEQAPGAL/VGNVARALGLEL RRLGPG/CLRINHLGAPSPRYLE/ LDLTSGALFVNERIDREACLGS AGANPVAVSAVEVEILDIN/DNS PRFPRPNYQLQVTARCWWTSW
15227	45595	A	15317	2	165	
15228	45596	A	15318	1239	2251	TCSSRARRPRRGRTVSQVRGPA PWAPRRARLQQRGSLRGAARS PASPTSA/PSYSRASASAGPAAL QPQGAVTPGPSANLAAPGGTL VPAEGPRMPPVTAQSASSHPAP SASQPSSPAAASRGSLSVPQEVT ATLLASASSPTLDATRDAPATP RIAAPPGSATSSRGLGSQAQGSS LGTKESISDSFGLGSPAVTQRTT APPDSAALSQDTRPEAAGSWPG PQTGACSVGSGTDRRDTAAAT EAQHLSSESKEKTSAQKSGNCF GILKADFTISTLMDPEEMKDQF LRQVRLPSTDALKKQSISNYRP PGKGKPQQYLGDSAWNMVSA GTIEGFYKE
15229	45597	A	15319	46	2859	

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15230	45598	A	15320	240	924	NGEQKCILCHIVYSSKKRH\SHE CRRCGPTEVSLSAYAKHISGQL HKDNVDAQEREDDGKGEEEEE DYFDKELIQLIKQRKEQSRQEPS SSSQEVNSDDSSSATFSVSVFYV WLKTILLLTWPKEVKRLDTPGL ELWLVPNMAELSEPEGPVDWK ERCVALESQLMKFRVQASKIRE LLAEKLHHNERLEYRDQRKDS ASFQRKKQFTYKASGIEMASDL SKAPLEIRG
15231	45599	A	15321	3	755	LRLPRRSTRTRRGIWVRTGAAM GKVNVAKLRYMSRDDFRVLTA VEMGMKNHEIVPGSLIASIASL KHGGCNKVLRELVKHKLIAWE RTKTVQGYRLTNAGYDYLALK TLSSRQVVECVG\NQMGVGK\E SYIYIVANEEGQQFALKLHRLR RTSFRNLKNKRDYHIHRHNVS WLYLSRLSGMKEFCYMKQFCD EQGSQLRIHMMGGQMWAVPIC QPRDLFVWFVLRAEACAGCGA TSQQRGALGVTSTCYRD
15232	45600	A	15322	1	1028	MNKTITTQEEVLPLQADVVQRE EELNSLKQKLAAALLAEQEPQP ERLVSELQL\PRKAAVFQDEILR SSRQLVLPELGVHRHVLVVCC GGLRCPLAGGLAAASVGRLGL VDCDVVEMSNLAYQVLHGEAL AAQAKAASAAASLRGLNLAPP PAETVTNCADGGMLRVLTGVL GCLQPLKVLKIAASLGPSYSGS LLLFDALRGHFCCIRLRSCRLDC AACGKWPTVTHLLDYEAFCGS SATDKCRSLQLLGPEDRVSVTD YKRLLDSGAPHLLLDIRPKMEL PRKAAVFHDEILRSSRQLVLPEL GVLRHLLVVGCGGLRCPLAQY LAAAIVGRLGLVAYDVV
15233	45601	A	15323	92	778	QGTRRWSLGTCSLMTRTQFEV CTKVCVQESLQRPGEELKTRCP SVGAGYVNYGTPAHERI/GAAV KTGREADKPEVTKQTQFSTRK DE/TSLFGVPLQ*LLARHRAPP* RRT/RRLLEVARTPMLPAQASR SELAARQDSAWASPAAPASPN/ RSVLRRCLLSARPPLCGPL/LRV LPSWRRQQIRENSAED*LHSEY RANRIRRRRGHPEN/WTKS*LE NPENLTRRSSSAPAPC
15234	45602	A	15324	142	500	

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15235	45603	A	15325	3	343	
15236	45604	A	15326	1164	1648	PLMTSAPWPSCCCWRSLSSGRP AGRQRQLPTSITTANQPAPSRR KKSTSRKKQRNLPAVSPAMVAI V\RRSCDLYRWSVLHYASQERR VRDAAKPESD\RKRTTTKTRR/H WRYIKELESRQPGVADMRQQP TQLVEVPWNEQTPEQRQQTLQ RQHGRETRCSV
15237	45605	A	15327	28	417	
15238	45606	A	15328	2	440	
15239	45607	B	15329	1	441	
15240	45608	A	15330	22	584	IRGRVDPPSAVEPPPKMQIFVKT LTG\KT\ITLEVEPLGYG*KNVK AQASRDK\EGI\PPDQQRL\IFAG KQ\LEDGRTLS\DYNIQK\ESTL/ HIFVLRLRGGAKKRKKKSYTT\ PKK\IKHKRKKG*SLAV\LKYYK \VDE\NGKIS\RLRRECPS\DECGC WGVYGQVTFDRHYCG\KCCLT LLFQQTRMTSNCMS
15241	45609	A	15331	3	954	LDARRHWEGTPGFTHTSPDAW ADAWGKMAGEKVEKPDTKEK KPEAKK\VDAGGKVKKGNLKA KKPKKGKP\HCSRNPVLLRGIG RYSRSAMYSRKAMYK\RKYSA AKSKVEKKKKEKVLATVTKPV GGDKNGGTRVVKLRKMPRYY PTEDVPRKLLSHGKK\PFSQHV RKLRASITPGTILIILTGRHRGKR VVFLKQLASGLLLVTGPLVLNR \VPLRRTHQKFVI\ATFTKIDISN\ VKIPKHLTDAYFKKKKLRKPRH QEGEIFDTEKEKYEITEQRKIDQ KAVDSQILPKIKAIPQLQGNLRS VFALTNGIYPHQLVF
15242	45610	A	15332	670	1008	WCILGVTPSLMSRTALFLSRHT FFA/RSHSAASKL/EKKKKEKVL ATVTKPVGGDKNGGTRVVKLR KMPRYYPTEDVPRKLLSHGKK PFSQHVRKLRPSITPG\TILIILTG\ RHRG
15243	45611	A	15333	1	708	

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15244	45612	A	15334	1	1754	MRNEISDLTEELHQKEITIATVT KKAALLEKQLKMELEIKEKML AKQKPWACLVNAMPAIQVVFN LGRFRKCQDPHKAQEWVYPGY SGSDCEVFPEIMTSKNREEAMP EWKLWKKVVLSGATDAPSWD GPTFTDLNVFAGNMGLSDCTLS LGKIWKIPGHFLHTSGPVSFHT KGLLNTPTKERWVGGFGSEGR GVPEPGGCFGVLAVPRRTPPSA AAMTGGERLGRAWAGDRAAA SRSAPVPGTFGMMGWRPVAFG KNAKAYRGFGGIVTSLTPSCDK VTLLFVRILPGSGQSRDQSSPEK LTDTKSTSNKAYGFPECLRRPE STHIFFYDHQLGSEQPRGTKGT PLKWVSQKTLERETRQCQALVI WTDCDREGENIGFEIIHVCKAV KPNLQVLRARFSEITPHAVRTA CENLTEPDQRVSDAVDVRQEL DLRIGAAFTRFQTLRLQRIFPEV LAEQLISYGSCQFPTLGFVVERF KAIQAFVPEIFHRIKVTHDHKD GIVEFNWKR/LSTL*PHGLPSSL SVVCGVRSLSCRSVGFCWRSTP DPVCLCITSGGCRTASIAEQQKL LPDPSYRSFIPEGQPPI
15245	45613	A	15335	3	125	
15246	45614	A	15336	764	1005	
15247	45615	A	15337	1	3533	MELVNCVLMSTLGNTCCPMAI AMFRSSSSLPRPGHSLTGSPLRV NLIHIKFPLNDFHQNVVKIKNK DPPLGAAIGKESCPIADNELHSL ERRPLSPKLVQALGVAGLSRPG PPHTGCAIWLLLITDHKLLSEIL YDLLHQGLDILADPPDEGGIPR GKNLVELLQLPGLEEDKAFQKE IGLKILVFKAYSTLSSDGPPLFS ALRSLQGVQSSKVGESREEKSQ TEEEDPGNPWVPQSLGASVSSS GKWGCLRTKP

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15248	45616	A	15338	1	2800	SISGPGQEAVPLRPKAEPPEGSG MVWDRQTKMEYEWKPDEQGL QQILQLLKESQSPDTTIQRTVQQ KLEQLNQYPDFNNYLIFVLTKL KSEDEPTRSLSGLILKNNVKAH FQNFPNGVTDFIKSECLNNIGDS SPLIRATVGILITTIASKGELQN WPDLLPKLCSLLDSEDYNTCEG AFGALQKICEDSAEILDSDVLD RPLNIMIPKFLQFFKHSSPKIRSH AVACVNQFIISRTQALMLHIDSF TENLFALA
15249	45617	A	15339	8	450	TWSWSPQAPSWARPSSQARAV SLLVARGQLCQGSRRRSGVGSR VDAGAARTALRTLGTRPRLRRP CGLGSHETKAAASGQDGQRGS RGRGSLGGRELGANEPLYQ/WR AHTLTVLFILTCTLGYVTLLEET PQDTAYNTKSEIAVVHLS
15250	45618	A	15340	246	559	MPVAVMAES/AFSFKKLLDQCE NQELEAPGGIATPPVYGQLLAL YLLHN/GQRIWQRDFPGIYTTIN AHQWSETVQPIMEALRDATRR RAFALVSQAYTSIIADDFA
15251	45619	A	15341	129	915	RSGTQGRSAATAALNVIAGATP EGQSWGLAVRTVQRRGRPAK MPVAVMAESAV\SFKKLLDQC ENQELEAPGGIA\TPKVYGQLL ALYLFHNDMNNARYL*KRIPPA IKSANSELGG\IWSVGQRIWQR DFPWG/IYTTINGHQWSET\VQP IM\EALRDATRETAPLPWVSQA YTS\IIAR*FCQPLLGLPV\EEAV KGIL\EQGW\QA\DSTTRNGSCP GKPVCRGPWDVFPFNKFISLYS EP\APV\PPIPNEQQLARLTDYV AFLEN
15252	45620	A	15342	1	529	MATLTISRAQTEDEADYYCHRI KLVKEGLDERTHKAYLSSSGK GCEFHMVKPGSPLGPDILGSWA QSALIQPPSVSGSPGQSVTISCT GTSSDVGSYDYVSWYQQHPGT VPKPMIYNVNTQPSRVPDRFSG SKSG\NTASMTISGLQAEDEAD YYCCSYAGSYPVVFGGGTKLT
15253	45621	A	15343	399	737	WISGGNSCATT/LSDAGLSTTSN SIGSAT\GARQAESASSQSGGGA LGRHCGASGKCAESLRREPVGS ATNQWAPGWVVGRPASDSSHV VIGLGRSAWSPAEVTPSLIPGRG RTK

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15254	45622	A	15344	1	4320	
15255	45623	A	15345	1	966	MNVNLAEESKGKETVGDEIKG GGIQMVMLASQPLTSYCAARFI TGHGQKLKSELKKTLQVIMLNI QKVRIPTRDGYNEKDILSTGKN VEKLELSNIAGYPSNIEKKEYQE QSVLSCCSERKDANPKSVVCSF FMQEQCTKGEKRFLIPGTLSVD RHLRYFGILPTVSNAAVVKEVP TVSNAAVVTEAPTGSNAAVVT EAPTGSNAARVMEVPTGSNAA VVTEVPTGSNAAVVTEAPTGSN AAVVKEAPTGSNAARVMEVPT GSNAAVVKEAPTGSNAARVME VPTGSNAAVVKEVPTGSNAAV VKEVPT/GSNAAVVKEAPTGSN AARVMEVPTGSNAAVVKEAPT GSNAARVMEVPTGSNAAVVKE VPTGSNAAVVKEVPTGVTLRW SRKRPRE
15256	45624	A	15346	1	702	
15257	45625	B	15347	238	546	
15258	45626	A	15348	632	2361	FQSRTFLKNWNPGEQSQKII/CF QLGERAYQTDVLVKVPRQSSV FSENQRMNNPERWFESTGCGK TYNQNRAFNQHQRFHSGEKTY EHNECGKAFSWPSILSKHQRIH TGKKLYTCEDCGKSFSVHSYFI QHCKIHTREKPYECIKCGKAFS THSSYVQHLKIHTGEKHHECNQ CGKAFSHSSNLIHHQRIHSGEKP YKCKECGKAFNRQSNLIQHQRI HSGEKPYDCKECGKAFSTQLFL IQHQRIHTGEKPYECNECAKSFS LNRTLTVHQRIHTGEKPYRCNE CGKSFSQCSQVIQHKRIHTGEK PYICNECGKSFGARLSLIQHQRI HTGEKPYGCREKPYECSECGK AFSQSFNLIHHQRTHNGEKSYE CNECDKAFSLLSSLVQHQRIHN GDKPYECHKCGKAFSQGSHLIQ HQRSHIGEKPYECNECGKTFGQ ISTLIKHERTHNGEKPYECSDCG KAFSQSAHLIHHQRIHTGENPY ECSECGKAFNVCSSLIQHHRIHT GEKPYECSDCGKAFSQHSQFIQ HQRIHTGEKPYMCNECEKSFSA CLSLIQHKRIHTGEKPYVCAKC

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15259	45627	A	15349	3	354	EAFGGERVSSTMSGLSGPPARR GPFPLALLLLFLLGPRLVLAISF HLPINSRKCLREEIQQGPASDW RVRDLRPVWGRWRPAQ/RTSRS QILLAIFSTPKRMQPRGNLPLTT EDYDMF
15260	45628	A	15350	283	393	YVYRRYGRFE*NDPSSALMST* GKRCQDCLDQRENKK
15261	45629	A	15351	1	351	
15262	45630	A	15352	1	867	
15263	45631	B	15353	1	1323	
15264	45632	A	15354	1	3669	
15265	45633	A	15355	362	1039	LESYLQLPSAEGKTVSVFGETC ATPVGP/AAGPHTQ/LAQNIVTS WLTGGRFIELKTVQILDRLELE KPCIDAEDECFNTEWSTEFTLL KAWDEYLKAWFALHLLEAMF QPSDSGKSFIFNMSVGYNLEGQ PLNPKNYPSQGVPRVLKSHRQD YLVGNKLSWADIHLVELFYYV EELDSSLISSFPLLKPHTHVDNT KKGSHPHMCAYTDYVNNPND RMPQREITFVS
15266	45634	A	15356	74	208	QRLTKLRETSRRLLSWQRSPSS TTSMHGAEWSPPRWLLAAAGV EFEEKFIKSAEDLDKVRNDGYL MFQQVP\RLRLMG*SWSRV
15267	45635	A	15357	308	735	NQRCTWAYSMTMEIFLISCVKT LSVRYAVQQLKTGVFCSLETQP SKMAPAKKGSKKKKGHS/AIIE VVTQENTINIQKHIHEVGFKKC APRALKEIQKFAMKEMGTPVV LIDTRLNKAVWAKRIRNVTNRI HLCLSRKCNEDKE
15268	45636	A	15358	3	323	LSSLASMSFTTCSAFTNYWSPG SVQVPSYGTQPVSHAASVYAG LGGSGSRISVSH\SPMAGGLAG MGGIQNEKETMQSLRDRLASY LDRVRGLETENWKLESKIQEH
15269	45637	B	15359	1	991	

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15270	45638	A	15360	40	1030	RGDPRVRRRTQSLSPVLSLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL \ESKIREHLEKKGPQVRDWSHY FKIIEDLRAQIFANTVDNARIVL QIDNARLAADDFRVKYETELA MRQS\VEN\DIHGLRNVI\DDTN YHTDLQLETEIEALKEELLFMK KNHEEEVKGLQAQIASS\GLTV EV\DAPK\SQDLAKIMA\DIRAQ Y\DELAR\KNREE\LDKYWSQQI EESTTVVTTQSAEVGAAETTLT
15271	45639	A	15361	1	438	LHSDDLSLQMLRCSPVATAASY TSGPGAPISSSSFSRVGSSSFQGG LGGGFGGASGIGGITAVMVNQS LLRPLNLEVDPNIQARF/VHTQE KEQIKTF/NNKFASFIDKVRFLE QQNRMLEAKWSLLQQQKMAQ SNMDNMFQSYINNL
15272	45640	A	15362	176	1455	EIFPLVIQKSYKVSTSGPRAFSS R\SYTSGPGAPISSSSFSRVGSSS FQGGLGGGFGGASGIGGITAVM /VQVLHTQEKEQIKTF/NNKFAS FIDKVRFLEQQNRMLEAKWSL LQQQKMAQSNMDNMFQSYIN NLRWQLETLGQEKLKLEAELG NMQELVEDFKKKYHDEINKHT EMENEFVLIEKDVDEAYKNKV ELESHLEGLTDEINFLRQLHEEE IWELQSLISDTSVVLSIDSSHSLD MDNIITEVKAQYKEIANCSWAK ADSMYQIKYEDLQMLARKHGD NLRCTKTDISEMNQNVSWLQA EIKGLKGQRASLEATITDAEKR RELAIKDANTKLLELEAALQW AKQDMAQQLRVYQELMNVKL ALDIKTATYKKLLEGEESWQES RMQNMSIYSKTTSGYAGGLSS AYGGLTSPP\LSYGLSS
15273	45641	B	15363	70	915	
15274	45642	C	15364	62	217	
15275	45643	B	15365	1	612	

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15276	45644	A	15366	3	841	STPKMPKGKKAKGKKVAPAPA VVKKQEAKKVVNPLFEKRPKN FGIGQDIQPKRDLTRFVKWPRY IRLQRQRAILYKRLKVPPAINQF TQAL\DRQTATQLLKLAHKYRP ETKQEKKQRL\LARAE\KKAAW PKGTFPTKRPPV\LRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPAL\CRKMGVPYCIIKGKAS LGRIVHRKTCTTVAFTQVNSED KG\ALAK\LVEAIRTNYNDRYD EIRRHWGGNVLG\PKSV\ARIAK LEK\AKAKELATKLGLNVHC
15277	45645	A	15367	2	1006	WINLKGNLLRKRSLTSNFWPCK LRSRKRHTTRNLRMNLWLSSH PPQQSNTKPWCCQLSCSTSLLT LLGTSLPLLSYLIHLIPPGPRQYP VIHRTSTLLLQHISVGKEKFHKS QHWGFCNNVMMLQLQLSPLK GLSLVDKVNRPPALSGTRVLAS KTAWRIFQEP/SEPKTKAAAPG VEDEPLLRGNPCRFVIFPIEYHD IWQMYEKAEASFWTT\EEVDLS KDIRHWESLKPEERYFISHVLVF FAASDGIINENLVERFSQIVQITE ARCFYGFQIAMENIHSEMYSLLI DTYIKDPKEREFLFNAI/ETMPC VKKKADWALRWIGDKEATYG
15278	45646	A	15368	3	1368	QAQPMGRVGGMAQPMGRAGA PKPMGRAGSARRGRFKGCWSE GSPVHPVPAVLSWLLALLRCAS TMLSLRVPLAPITDPQQLQLSPL KGLSLVDKENTPPALSGT\RVL ASKTARRIFQEPTEPKTKAAAP GVEDEPLLRENPRRFVIFPIEYH DIWQMYKKAEASFWTAEEV\D LSKDIQHWESLKPEERYFISHVL AFFAASDGIVN\ENLVERFSQEV QITEA\RCFYGFQIAMENIHSEM YSLLIDTYIKDPKEREFLFNAI\E TMPCVKKKADWALRW\IGDKE ATYGERVVAFAAVEGIFFSGSF ASIFWLKKRGLMPGLTFSNELIS RDEG\LHCDFACLMFKHLVHKP SEERVREIIINAVRIEQEFLTEAL PVKLIGMNCTLMKQYIEFVADR LMLELGFSKVFRVENPFDFMEN ISLEGKTNFFEKRVGEYQRMGV MSSPTENSFTLDADF

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15279	45647	A	15369	2	621	RFIKMLSRHHQHVHHVLPLLRA PLPVAMEEEIPALFIDNGSGM/C KSSFA/GDNALRAIFPSIIGHPRH QGVMVGMGQKDSYVGDQAQS KCGILTLKYPIKHGIVTNWDDM EKIWHHVFYNELCVALEEQVV LLTEAPLNPRANREKMTQIMFK TFNTQAMYVAIQAVLTLHSSGC TTGIVMDSGDGVTHTVPIYERH TLPHTILHLDL
15280	45648	B	15370	1	966	
15281	45649	A	15371	2	228	
15282	45650	B	15372	1	816	
15283	45651	A	15373	256	384	RKLLNEAPC*PMR*HSLLNRLA TSCNSWTVPVVPKFSKLRRGL
15284	45652	A	15374	145	375	KIAGKNRLNRNQCKERKVQVL WISEKKKQREAVEDSPSLDCCH KFPPGS*ERLHG*KRGQWF*PP HTVEKQMRSCLL
15285	45653	A	15375	319	482	
15286	45654	A	15376	4776	5910	VCSTAGDVNGVCLLYDLLHIA VASGSAKGECFFARKPLLAEGV IYDCLQEFKEKKLVPATPHAQV LSYEALLSAHDTIAQKDFEPLLP PLPDNIPESEEAMRIVCLVKNQ QPLGATIKRHEMTGDILVARIIH GGLAERSGLLYAGDKLVEVNG VSVEGLDPEQVIHILAPRPCLSP MSLADLPPLPREVLVLAGKLPV PSSSFLLQPREDCQGPQPSSLIT WFAPLETEPGVDRAMSRGTIMF KVVPVSDPPVNSQQMVYVRA MTEYWPQEDPDIPCMDAGLPF QKGDILQIVDQNDALWWQARK ISDPATCAGLVPSNHLLK/RIWT EPGICIFTKRLRCSGKQREFWW SQPYQPHTCLKSTLCEYCNCPT
15287	45655	A	15377	2	405	WSLVTRRALARVGLPG/SPPPRL LLLPLLLGWGLRVAAAASASSS GAAAEDSSAMEELATEKEAEES HRQDSVSLLTFILLLTLTILTIWL FKHRRVRFLHETGLAMIYGLEK ITIGVLDITGWPYCTIQPYNGFL
15288	45656	A	15378	1	3804	
15289	45657	A	15379	349	622	RPDVANLAFLARKEGTKRGFLS KKTAEASRWHEKWFALYQNV LFYFEGEQSCRP\GMYLLEGCSS GGTSPRSFRSSSRDSPISIPLHPT AK
15290	45658	A	15380	314	483	

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15291	45659	A	15381	352	822	DPRRVQAFPAKMKFNPFVTSDR SKNRKRHFNAP\SHIRRKIMSSP LSKELRQKYNVRSMPIRKDDEV QVVRGHYKGQQIGKVVQVYR KKYVIYIERVQREKANGTTVHV G\IHPSRVVITRLKLDK\DRKRIS DRKAKSRQVGKEKGKYKEETI EKMQE
15292	45660	B	15382	80	432	
15293	45661	A	15383	11	888	VKCRKAEGRRESRLQTFEESQA VEAAMANVPWAEVCEKFQAA LALSRVELHKNPEKEPYKSKYS ARANM\EEVKALLGPAP\EDED ERPEAEDGPGAG\DHALGLPAE VVEPEGPVAQANRLRL\AVI\EF HLGVNHIDTEELSAGEEHLVKC LRLLRRYRLSHDCISLCIQAQT WRCIGVRDPPTSSCAFLSTSPTP VHSVKKIQTPGPLRPSNSTLVD DMESSFQTCFASPLSQDYVNGS NQEEIGTGVDRCIHKFLDIARQ NISFLQKRLQLSVQKPEQVINED VDVSELRNE
15294	45662	A	15384	1864	2705	WPGKVLAHRGLHPWHRDPHGS GGGAGQELRRQGGCLEQLLYD AAHAQRLPPLDSVLPRAALPQD CQRASACEGDPTLLRPSHSPGH PRGAEER/VPSTACLQRSWEGR/ WNRALQQVGGLKSPWRGEYK EPRHPPPNQANYHQTL/ACPAE R/CFRQGPQGPGQLRRQQAEPL SSSLLSHQSPQSQTSLLP*L*AR RSLGCGNPYLCPPWSQPLPETP AHQSGKQPSRSRNCSSWK*NYS STACPSHFLWRSRSKFSRASAST ASPCRMTVRRTHQRPLKARGTP
15295	45663	A	15385	1113	1378	RPHAESFVSGGIPDPPGPGPGST GPGPL/ERQPCSLTSWPREPPSSS SMKMLTQGPSLTAPYKGTILGE VNPAHAISSSARNTSSRTSV
15296	45664	A	15386	285	722	TPAHPGVPPGQSGRHRHW/QSA ARSQLQPSAW*PKTGSLFATTW RCQTRASTCSAHWPLMAASPG AGGSSMASWR/DRP*PCPPPPAP HLPEAAFLLR/CHDACP*NTGSA VPRGSCQPPAQQWDQGLAATR WGQAERLPRIYNWALAPP

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15297	45665	A	15387	207	605	FQASAERFGTEDD/GSLRTRPPV MQSHQWPWRRPRPLVSRGRPQ TTPERHDSGGSLPLTPRMESHS EDEDLA/EGCRWP/EAGTVGVP GPRAQGAAQR/QAVLARKKHR RRPSKRKRHWRPYLELSWAEK QQRDERQS
15298	45666	A	15388	193	407	ACPKTSKNLRQRRLWNLAKHE F/SVDMTCGGCAEAVSRVLISLE VRVKYDIDLPNK/KVCIESEHS MDTLLATL
15299	45667	B	15389	321	625	
15300	45668	A	15390	275	690	SLWPPVIRG/SPKGNRPAILTYH DVGLNMANKKSGDHPEREGTP RSFREVVSAFGPGSSKLQIPKGS APRCGVPGRGARRELQSFRAGP RTQGSPVGPRCQSRRLRSAQEE SAKARHGGLRAHRSFSWDIRM SSKERKFS
15301	45669	A	15391	2	137	PGRYRPN*LLLSDASPGAGNEF QSTFLTPTILPSLRFPVLYTPNS
15302	45670	A	15392	1	648	MSLRKLTIMVEGKGGPNIPHAC GCRQRSSIKVSLLPAVTSKSESP KEPEQLRKLFIGGLSFETTDESL RSHFEQRRTLTDCAVMRDPNT KCSKGFGFVTYATMEEKYHTV NGHSCEARKALSKQEVASASSS QR/GRSGSGNFGGGHGGGFGG NDNFGHGENFRGHSSFGGSHG GSGYGGSGDDYSGFGNDGSNF GGGGSYNDFGNYSNQSSNFGP
15303	45671	A	15393	1	3629	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCLRVDGQQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAAATSNVHMVKKISI TERSCDGAAEMKWEDQNIGD

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15304	45672	A	15394	1	1515	MGQVFRVVTGVGEQPGHPDQF PYIDSWLSIIQNHPKWLQACFET YCKTLMAQIKPGTIERDCKASV KEKDSQEKQKKPVLQAPPEELE SPALYAPIYPSLARLRQEAAPA APRGSDSEESTPQATPCREEPEP LPEKETSSSYRSNAVHFLIHNPT WADCKQLLQSLFNTEEHHRVI QAAFQWLENNAPAGTGYIRQY AQQALPIEADTGWDPNQAQGL QSLQWYREALLNGIKAGGKKA TNIGKVSEVCQKPDESPSEFYER LCEAYQLYTPFDPEAAGNQCM VNVAFVSQAQGDIKRKLQKLE AKAVLRGKFIALNTYIKKAERA QTDILRSHLKELKKQEQTKSKA SRRKDVTKIRAELNEIETTTTKI QKINETKSWFFEKINTINRPLAR LTKKSREKLQITSLRKEMGDTT TDTTEIQKIIQGYYEHLYAHKLE NLEEMNKFLEKYNAPSLNQEEL HTLNRPIRNSEIEVVIKKLPTKK/ SPGQDGFRAESYQIFKEALV
15305	45673	B	15395	1	1077	
15306	45674	A	15396	69	290	YYFDSPIHPLHLSGTLRPGGSRQ FPCDPQFLCRLLHTLASL*SLPG DLLRGLLHKLVCRVERLDLASL YAVGR
15307	45675	A	15397	62	201	
15308	45676	A	15398	3	429	LPSSVPRQPKMQARCLSRSIRA VEIYESDLEEGQGLLHEFSQFVL DRPPPTQSRYAQELVHTCYLHT LASL*SLPGDLQRGLLHKLVCR AERLDLASHHAAVGRSELFFW TPYTHSPPGAGVGHPFPWHTRL PWGVPAEGHQ
15309	45677	A	15399	303	612	PSSSIPVYHCSLRGICIPVLGLKR AANVGVSLEASPPLLSTPGGLGI CLSCGGTRTVGSRVGSIFPW*G EGTTGITGSISCKGSSDVGSNRT SGVDFPRRVE
15310	45678	A	15400	1	273	

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15311	45679	A	15401	1	406	MEEGWIRLPDGRVAAPQLLGA AVVLAVQETTHRGQESLEKLL GRYFYISPLSALAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWWVLGLTDFKN EATDPPGVKLQTFLVSVTTHKG SVDPNSEKQQDLLQRAKEQSFH SVEGDPSRDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSR*RAI SCCPSH*LPSAKCISVSGIGGFL VSLTSRMKPRTLLE
15312	45680	B	15402	1	930	
15313	45681	A	15403	391	617	LQLQPTG/CNFLYFYVGYMKIL GFCFHHIVEERGGCLWYPCFYC NLSLLGG*RSCSHTRIVPSLLMP KLGPGGQVC
15314	45682	A	15404	1	1860	
15315	45683	A	15405	1	531	
15316	45684	A	15406	2302	2691	
15317	45685	A	15407	520	2883	
15318	45686	A	15408	3690	4727	ENCHWGCEHPCDIGSSIILSPLA YWEQYHRVTYISRDTEGSIIVFP ALVTMLRNLFIILAGSSDPHFHT PMYFFLSNLSWADIGFTSATVP KMIVDMQSHSRVISYAGCLTQ MSFFVLFACIEDMLLTLMAYDR FVAICRPLHYPVIVNPHLCVFFV LVSFFLSLLDSQLHSWIVLQFTF FKNVEISNFVCDPSQLLNLACS DSVINSIFIYLDSIMFGFLPISGIL LSYANNVPSILRISSSDRKSKAF STCGSHLAVVCLFYGTGIGVYL TSA\VSPPPRNGVMASVMYAV VTPMLNLFIYSLRNRDIQSALRR LLSRTVESHDLLSQDLLHPFSC VGEKGQPH
15319	45687	B	15409	1	3195	
15320	45688	B	15410	1	1819	

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15321	45689	A	15411	399	1089	LLTPRTDLQEMPLDNAEIEWYT DGSYLRGEVFQWYDHLALIFVP QTGIEDVIWHIEALPNYIQKVCE RRNPYNQILSLQCAQHEIFLVS WKLVCKQLEGDDDMLVGTTA SNLLLESEQSTSNLNEKINHLEY EDQYKDNNFGEGNDGGILEDK LISN/NMGGPDSPDSVNPVE/P/M PTMTDQTTLVPNEEEAFALEPI DITVKETNAKRKRKLIVDSVKN LDSKTIRAQLNDY
15322	45690	A	15412	3	809	FKDDDMLVSTTTSNLLLESEQS TSNLNEKINHLEYEDQYKVDNF GEGNDGGILDDKLISNNDGGIF DDPPALSEAGVMLPEQPAHDD MDEDDNVSMGGPDSPDSVDPV EPMPTMTDQTTLVPNEEEAFAL EPIDITVKETKAKRKRKLIVDSV KELDSKTIRAHLSDYSDIGTTLD LAPPTKKLMMWKETGGVQKLF SLPAQPLWNNRLLKLFTRCLTP LVPQDLIKRRKGGEADNLDEFL KEFEHPEVPREDQQQ*HQQRD VIDEPII
15323	45691	A	15413	1	595	MVNRSHFRGVGEPCHQQNSHG HLNSITETSNSPTLRAAPLQPTR DPSDMAVFEIDELPEGAVKPPA NKYPIFFFGTHETAFLGPKDLFP YKEYKDKFGK\SNKRKGFNEGL WEIENN\PGVKFTGYQAIQQQS SSETEGEGGNTADASSEEEGDR VEEDGKGKRKNEKAGSKRKKS YTSKVTKKLLIVINVICISIKHF
15324	45692	A	15414	41	785	GKGWAGGASGPANHGPAAGG RSPGMLRGDQGLPGRGAAGM ARPRSRE\YKAGDLVF\AKMKG YPHWPARIDELPEASVKPPTNK\ YPIFFFWHPMKPAFLGPQ\DLFP Y*EYRGKFGK\SNNRKGFNEGL W\EIENNPGS/IRFTGYQA\IQQQ SSFRTEGEGGNTADASSEEEGD RVERDGKG\KRKNEKAGSKRK KSYTSKKSSKQS\RKSPGDED\D KDCKEEENKSSSEGGDAG\NDT RNTTSDLQKTSEGT

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15325	45693	A	15415	1	1272	MWSGAGPGLAVWPQLVTVLSL SLSRLNCKWGLSFLACLLLGD MADAAMQHYGVNGYSLHAM NSLSAMYNLHQQAAQQAQHA PDYRPSVHALTLAERLADIILEA RYGSQHRKQRRSRTAFTAQQL EALEKTFQKTHYPDVVMRERL AMCTNLPEARVQVWFKNRRA KFRKKQRSLQKEQLQKQKEAE GSHGEGKAEAPTPDTQLDTEQP PRLPGSDPPAELHLSLSEQSASE SAPEDQPDREEDPRAGAEDPKA EKSPGADSKGLGCKRGSPKADS PGSLTITPVAPGGGLLGPSHSYS SSPL/SPLPSAGAIPPAHGGHQQ PGALLVLRSRGSGPCCCSGGCC CALPGRQHGPAGLTA/SASPTTS PCQQPLLP/SQGVWGSPLLPAPP AGLAPASATLNSKTTSIENLRLR AKQHAASLGLDTLPN
15326	45694	A	15416	1	1152	
15327	45695	A	15417	8	82	
15328	45696	A	15418	1	1350	MGSEKDSESPRSTSLHAAAPDP KCRSGGRRRRLTLHSVFSASAR GRRARAKPQAEPPPPAAQPPPA PAPAAAQGPPPEALPAEPAAEA EAEAAAAAAEPGFDDEEAAEG GGPGAEEVECPLCLVRLPPERA PRLLSCPHRSCRDCLRHYLRLEI SESRVPISCPECSERLNPHDIRLL LADPPLMHKYEEFMLRRYLAS DPDCRWCPAPDCGYAVIAYGC ASCPKLTCEREGCQTEFCYHCK QIWHPNQTCDMARQQRAQTLR VRTKHTSGLSYGQESGPADDIK PCPRCSAYIIKMNDGSCNHMTC AVCGCEFCWLCMKEISDLHYL SPSGCTFWGKKPWSRKKKILW QLGTLIGAPVGISLIAGIAIPAM VIGI\PVYVGRNIHSRYDGKEN\S KHKRNLAITGGVTLSVIASPVIA AVSVG\IGVP\IMLAYVYGVVPI SLCRGGGCGS
15329	45697	A	15419	2	540	

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15330	45698	A	15420	1	530	SRTTPGKAPKETWGQDAGSGK GGQGPPTRKPPRRTSSHLPSSPA AGDCPILATPESPPPLAPETPDE AASVAADSDVQVP\GPAASPKP LGRLRPPRESKVTRRLPG\ARPD AGDGDHLSAVAERPKVSLHFD TETDG\YFSDGEMSDSDVEAED GGVQRGPREAGAKE\VVRMGV LAS
15331	45699	A	15421	1	2989	MLLVMYWAPAPPPVHMSQFLT TGPKCLELSLDHGRDSQEITAS GLLWLQHAACGLAQWNQKPH PPFLTLLQAEEPFERARSCDIYIR IKMLQTAQQHQVGLAPTERKE ALRGSQSPQKSASGQRPGSLDR ELLMLIKISKCLRVPSGPSSVLG TESTGPVPGELVLCQQDAGATQ EGVCYGRELMICRCDSFPRLME PWGVKGTPEVFRTDLITAMKIP DSYQLSPDDYYILADPWRQEW EKGVQVPAGAEAIPE
15332	45700	A	15422	218	404	
15333	45701	A	15423	1	422	
15334	45702	A	15424	160	470	LTMLFAACVFSGDEIMASEERQ PMEEEWSRSSTISGEDGERWTP DTAGKAAQGIAGDVVWVSPLP PSKVSAASKPPKS\HHPFFKWH NFSNLMKMFYKMYFSKN
15335	45703	A	15425	21	375	TFENTRFWDVQIPVPTGERRNE WALPPPGAGSVPAGGWSRPLTP GRCDSQGRGRSRRAAPLSRSPL PPLRRSPTLPGEPPPAHRPLRVH PRHGPRPSHL\ACLNSQAPDASR LRASANQ
15336	45704	A	15426	155	340	

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15337	45705	A	15427	1	2658	MIINTIITTTTTTITIIFIITIMSSSPIT ITNIITIIQHHHHHNDQRPSLGK CRGLYIRVRKVPGERATANSRC PINAQGIESCWNGVMALWLGP NSTCSRLPELTDSEDCQPADSP GDEDPKPWWDPPHEAPLTGYF HPYGAAFVPRHAGNFKDRREV PHQDTSFCSAGQFWILPSACKT GRVALTLTLLIGAYQTLTEADV KGLTAARAASPGAKWRTQFPC PAGTCSSQAGNGQLEDCLPYPP GPSAPVGSLSRSSANGEFIIGRVI KAMNNSWHPECFRCDLCQEVL ADIGFVKNAGRHLCRPCHNRE KARGLGKYICQKCHAIIDEQPLI FKNDPYHPDHFNCANCGIKLG VFLTDRKDLTADAQELKGELY CLPCHDKMGVPICGACRRPIEG RVVNAMGKQWHVEHFVCAKC EKPFLGHRHYERKGLAYCETH YNQLFGDVCFHCNRVIEGDDE GDGFAHRYSPYDSCEVDQSPLE GQQLKSIRKGPLAQSQPLPTPV MLHPGCKTQIREAPGSAALESV RRRPRPGLVPEEESESAAVEAV RHIHLQNFSRSLLETLNGQKLG GHFCDVTVCIHEASLRAHRCGL AIGSPSFQDKLLLGPSEIRVPSV VPVQTVRQLVELLYSGSLVVA QSEAPQVLMAASVLRIDSYRR MHADYRTRSSAPASTSAPAPLP TPVPPPLAPEQLRHRLRHLLAA
15338	45706	A	15428	708	892	
15339	45707	A	15429	2	713	
15340	45708	A	15430	212	1246	DLPLAVHGQVSDSGAQAVASR SGDESSIVCLKEESTVNMTFRCS LPLAVISVVSFTAKCQVKSEFII GRVIKAMNNSWHPECSAVTSA RKFWQILHLSRMLVDRKDLTA DAQELKGELYCLPCHDKMGVP ICGACRRPIEGRVVNAMGKQW HVEREQYMDPGILSALIDPKYL LILSHRGLHMKSMKGFYFAKL YYEAKEYDLAKKYICTYINVQE RDPKAHRFLGLLYELEENTEKA VECYRRSVELNPTQKDLVLKIA ELLCKNDVTDGRAKYWVERA AKLFPGSPAIYKLKN/DGWVRG QMVPKPDDEGVQVRGRSGRPD AGWRLNRRSSVGGSAWRLRPQ

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15341	45709	A	15431	129	444	WGGPGRQPDGGRVPGRCGPRR PATWESPAACRPRPQSRHHSFE *GGSRSGSSHKRPCPSSPAVLRA RDQVVLHTSFEATEGDSSHEDR STPLARRCLCSHRSGEA
15342	45710	A	15432	1	2446	METSLMVQVCGGRDCNALLPG NLCSQPTQVLPLEVDGDDGPG GLPLNAAPPSSVPPVPPSEALPP PACPSAPAPWRSIISRLFGTSPA AEAAHPPPGGALDFGALRTSSC LSQSHGHIPGGPGLGLGAVRVP VPSEEDPASLFTEPVPAAEAPAT VQSVEDFVANDRLDRSFLEDM TPARDEKKVGAKAAQQDSDTG RASRAPEQQIPHGGHWRGHSRS YERFRPPDMVSAGPGPSDGEAL GGNPIVAGFQDDVDLEDQPRGS PPPPAGPVPSQDITLSSEEEAEV ADPPKGPAPAPQQCSEPETKWS SIPASKPQRGTAPMTAAASPWP GGASVHTGLEKCSSTRPPAEIEP GKGEQASSSESDPEGPIAAQML SFVMDDPDFESEASDTQCRAVR RVLPAQRAENAYGSAFQPGAL KPECRPTLKGGPGPVPSKAGKK TEATSPRPTGGASPLAHGATVG AAWGLGMASWPIGSSLAPTRA RTREPRLQRRVGSELPGDPCSG SGASCRQVCARGRATSVRLPAL ESLWPLSSDGSAAAREGLEGPR LRQAAAPGGPGPPLPPLSRPPSP ARRMRGGAAVAGRGAAAPLE GRVRLGVGFLAETAVRAGAGA LAAADAPPGSRTPRARPLVAAG SGAAGGRCPVPSRRQREAPSPL GGAGVDLQLECLTSEKAGVGA ATGGVLEALARAIRQKKEIEEIQ

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15343	45711	A	15433	26	963	FMIWAGQNRKVQDFVIQLRML TPVVPPPQAAPNAQQPRAAASA PQTRVRAPRWPLGNVVVLGTE DAAGPSRPASEPPASPALPGPAL ELGLPNHPKQT/HRPRLAPRRSH PKDSCTIFKLNSFLKNIKFNNSV GDQVNLDYKLISGTEYDILNFW NFRILAKTGCSKDGHRNPRSRP TQEEGSGKPKKSLVKERSGAQE DLPVPPEEKLELSGTSMGPCCFS KTSYGIPHIIYILSYKGTTATAG HRWPAAYPAPLNCSVPPPETTM PVSDLGSPLHWASRIATPPSMW LCCLLAAALRVLAVSNSSAEVY SQS
15344	45712	A	15434	803	1305	RSKPCRSSHNVFSWWAHSRPC CPWSGYSSRLCCLSCCITLGPY QLKNRQQRNGSYKSFGNYLCV GNRLLFWVWIIFQGKGRS/WLP RSDWVTSYKVMVSNDSHTWV TVKNGSGDMIFEGNSEKEIPVL NELPVPMVARYIRINPQSWFDN GSICMRMEILGCPLPGWEH
15345	45713	A	15435	2	377	ARELLKAVWRPHKVAVMHCR GHQRASTLVGLGNSRADSEAR KAPSAPFRASVTAPLLPQAPDL VPTYSKEENDFLQAKGGQVME EG*IRLPDGRVAAVVLAVHETT HRGQELLEKLLGWYFYISH
15346	45714	A	15436	77	679	KMKTNQMGLKSKVVEMNATIS EIRLNINRKDVEYQQEILQLEAV WKLHKVAVMHCKGHQRASTL VGLGNSRTDSESPKAASAPLRA SVTAPLLPQAPDLVPTYSKEEK DFLQVEGGQVMEEGCIRLLDG RVAVPQLLGAAIVLAVHETTHL RS/ESSLGKLLGQLFSTISHFVSL CQNLTQRCVTCRQHNARQGPA VPPGMQ

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15347	45715	A	15437	2	881	HARCTGIAARAGLLDPRHTGEA LAARSRIDLARRPHWPRGCGTG GGGGGCAGLGGAWLRGNDVA VPARALVTAAPASSSMSPPIPA AARPVSSS\PAASPSPRCGLRAG PAELRCPRRLRQARAEEPPRAG PAPGRRRPTPGICPAPLSPRLRA GGTAPSLPGVTRGSRVGRRLRP SLGGAGCRVGKRPPRLLPPGRR CSTGLPPPAGTGAPAGVCWED GDPGHELAAALLRRLGGQIRAL AGHRTAGWAQHGLSPREAVRP APAARGTLLLRRSNSRRHLQNP ANFGGTLAT
15348	45716	A	15438	3	502	GRRDSCLPGVVAPRACLHPRG QVPRLGSVGKMATPGMSWQQ HYYGGSAAKFAPSPATAQLAG HSMDYSQEMHLKMSKKIAQLT KVIYALNTKNDEHESAIQALKD AHEEEIQHILAETREKI\LQYKS KVTEELDLRRKIQVLESSLEDHI KMKQQALTEFEAYKHR
15349	45717	A	15439	29	230	LQIDCKNKPAILRGPTDPLKEA DCYCRTWERPQILLPKWEGTR KPILVI*QNKAHQHAPQITLLHQ
15350	45718	A	15440	73	335	FFWGGIEEPCFVILSGSVFWFLL IWVGASASPVVGDVFGRGGSPF PTSTVGAFTVLWGVSWVLKRV CGSSWDC*FVLAINLELKFTM
15351	45719	A	15441	373	513	
15352	45720	A	15442	1585	1649	KNSNIQHSPKITLVHQQWFQTK KKFLIYLKKNSGGLVDP*MVHT TRLCADNPQYQPRARKSHS*VK GESTTLREHPMGQKNLNNSLQP
15353	45721	B	15443	1	696	
15354	45722	B	15444	49	525	
15355	45723	A	15445	113	474	SIPYKNKEEEEGKGGEYYIKGT CHGTKGSEQQPSALDLPSDRAY PNEKEPEN*LW*LI*QNKAL*HS PKNHTSSP/RNGSKPRKKSLINL KKNSGG*LLS*LGRHQRKVKPN ARKSKNQYKK
15356	45724	A	15446	47	614	TGCPRCKQNSTCIAAVKMEGPL SVFGDRSTGETIRSQN\DVTITN DGATILKLLEVEHPAAKVLCEL ADLQDKEVGDGTTSVVIIAAEL LKNADELVKQKIHPTSVISGYR LACKEAVFYLTENLIVNTDELG RDCLINAAKTSMSSDIIGINGDF FAN/MVVDAVLAIHARHRGQ/P RYPVTLLY*SHGES

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15357	45725	B	15447	707	1826	
15358	45726	A	15448	108	397	
15359	45727	A	15449	1726	2464	SKAVQLEAGGLLQLFCCKMAP DPNITDVFGRTALHYAVYNEDT SMIEKLLSYGANIEECSEDEYPP LFLAVSQRKVKMVEFLLKKKA NINAVDYLGRSALIHAVTLGEK DIVILLLQHNIDVFSRDVYGKL AEDYASEAKNRVIFELIYEYER KKHEELSINSNPVSSQKQPALK ATSGKEDSISNIATEIKDGQKSG TVSSQKQPALKDTSDKNDSVSN TATEIKDEQKSGT\VSSQKQPAL KDTSDKNDSVSNTATEIKDEQK SGTSVFSETTGLEGYK
15360	45728	A	15450	2	675	
15361	45729	A	15451	1	467	DHSSSPAREQNWMEN\EFDELT EVGFRRWVITNSSELKKHVLTQ CKEAKNLEKRLGELLTRITSLE KNINDLMELKNTARELHEAYTS INSWINQAEERLSEIEDQLNEIK REDKITEKMKNSTTVRVAASM QSKLLQGVAEEGPLRLTRSASF
15362	45730	A	15452	2	632	
15363	45731	B	15453	355	894	
15364	45732	B	15454	99	716	
15365	45733	A	15455	1	1140	
15366	45734	A	15456	1	1476	MEVNREKQLNELEVIGSEEQNL EEEGLMIGGVAVRLVPDDIVIP GGVNATNGTEARDALRVKVA MSVTLLSGIIQYLLSALGWSYY TVDGVSQKNPRALGVTADQLH AIFTTMSDEQASFRFGFVAIYLT EPLVRGFTTAAAVHVFTSMLK YLFGVKTKRYSGIFSVVYSTVA VLQNVKNLNVCSLGVGLMVFG LLLGGKEFNERFKEKLPAPIPLE FFADHNSSPAREQKWMENEFD EWTEVSFRRWVITNSSELKEHI LTQCKEAKNLEKRLEELLTRITS LEKNINDLMELKNTAQEFHEA YTSINS/RNQTEERVSEIEDQLN EI*CKDKIR\EKKRMKRNEQSLQ EIWDCVKRPNLRLTGVPESDGE NGTKLENTLQDIIQENFHNLAR QANSQIQEIQRTPQRYSSRRATP RHIIIRFTKVEMKEKMLRAARE KGRVTHKGNPIRLIADLSADTL QARRQWEPIFNILKENFQTRISH
15367	45735	A	15457	1	1185	
15368	45736	A	15458	1	2367	

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15369	45737	A	15459	1	744	
15370	45738	B	15460	337	1515	
15371	45739	A	15461	1	1197	
15372	45740	A	15462	1	714	
15373	45741	A	15463	142	601	HQRTKVYKFTKMRKNQPKKPE NSK/TQNPSSPSKDHNSLPAREE NWMENEFDKLTEVGFRRWVIT NSSELKEHVLTQCKEAKNPDK RLEKLLTRIISLEKNINDLVELK NTA*ELLEAYTNINSQIDQVEEK I/S/SIEDQLNEIKLEDEIREKKKK
15374	45742	A	15464	153	474	QTKSNNVNIKKQDVHTKTPSEG HQHQRPK\DHNSLPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLEKRLQEL LTRITSLEKNINDLMELKNTA
15375	45743	A	15465	1	2172	
15376	45744	A	15466	1	1640	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPDHLTPAGNC YVVRRNEDCIGFFSGFYNVISL GVYLVEQQKGWEDTHSKTPSK GHQHQRSKVDKSTKMRKNWS KNAENSKNQNALSPPNDRNSSP ARAQNWMENKFDKLTEVGFR RQVITNTSELKEHILTQSKEAKN LDKRLQELLTRITSLEKNINDL MELKNTARELREAFTSFCVNCE AVSLITSLREDSHWLEDSKGHR M/RRHQE*KCEYFHPPHPGLQF YQLPESDSHSDPLWPHGGSFLS
15377	45745	B	15467	50	1603	

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15378	45746	A	15468	528	1413	QTERNSTSTSKTPSEGHQHQRP KVDKSTKMGRNQCKKA*\NSK SQNACCPPKDHSSLPAREQTW MENEFDELTEVGFRRWVITNSS KLKEHVLTQCKEAKNLEKRLE ELLTRITNLEKNINDLMELKNT ARELREAYTSINSRIDQAKERM SEIVDQLNERNDRENGTKLENT LQDITQDNFPYLARQVNIQIQET QRMPQRYYSRRVTPRHIIVRFA KVEMKEKMLRAAREKDTSVK QKVNKDIQELNSALHQVDLIAI YRTLHPKSTEYTFFSAPHHTYS KTDHIVHSILCDSG
15379	45747	A	15469	368	679	SSQLNKAPSLFNPVSEEFCLWL LLLQKELLTRITSLEKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK
15380	45748	A	15470	865	2055	QTERNSININKKDNYAKTPSKG HQQQRPKVDKSTKMRKNQHK KA*KFPKPGMPSSPPK\DHNCSP ARE\QNWMEN\EFNEFDELTGA GFRRWVITNSSELKEHVVTQCK EAKNLEKRL\QELLTRITSLEKN INDLMELKQDITQENFMKHTQ VSIAQADQGRKERV\SEIEDPTL MDIKCEDKIREKK/IKKRNEQSL QEIWGYVKRPNLRLISVPESDG ENGNK*ENILQDIIQENF/PFPNL TRQANIQIQETQRTLQRYPLRR ATPRHIIIRFTKVEMKEKMLRA AREKGRVTHKGKPIRLTENLSA ETL*ARRE**PILNILKERNFQPR ISYRAKLSFISK/GKREIKSFIDK QTLRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKLKRPLT
15381	45749	A	15471	1	315	
15382	45750	A	15472	1	2775	
15383	45751	A	15473	1	1017	
15384	45752	B	15474	1	3105	

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15385	45753	A	15475	1	1115	MKWLLLLGLVALSECIMYKVP LIRKKSLRRTLSERGLLKDFLK KHNLNPARKYFPQWEAPTLVD EQPLENYLDMEYFGTIGIGTPA QDFTVVFDTGSSNLWVPSVYCS SLACTNHNRFNPEDSSTYQSTS ETVSITYGTGSMTGILGYDTVQ SGYHHGNHRLNLKGLCSSKRSS TTPPLYDLGQVASPPSGSVSSC DDQSGSVVIFGGIYSSYY\TGGL NWVPVTVEGYW\QITVDSITMN GEA\IACAEGCQA\IVEPGTFFVT GP\TSPIA\NIQSDIEA\SEELDG\D SVLICSAISS\LPDI\VFTI\NGVQY PVPPS\AYILQSEGSCISGFQG\M NLPTESEELWILGDVFHPASTLT VF\DRANNQVG\LAPVA
15386	45754	A	15476	1	765	
15387	45755	A	15477	470	479	PRNPSSFLQVQVQHRFLQLFVP FHFVFFLASLYVMVTLTTWFR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT
15388	45756	A	15478	1	896	CLPFGGPKPNPWDKDGGCQGR PQPRHLPGPGTAAQRRQQCPSE KSLL/CRWPSLTASTCSRLFYIL LHVGAS/CNLLPPAVKDSSGKG VGQDTQVLSGSGAVYRVCAGT ATFHLLQAVLLVHLHSPTSPRA QLHNSFWLLKLLFLLGLCAIAF CIPDEHLFPAWHYIGICGGFAFI LLQLVLITAFAHSWNKNCNEAS YLAEVFGPLWIVKVYSYEFQKP SLCFCCPETVEADKGQRGGAA RPADQETPPAPPVQVQHLFLQL FCLPLRLLPWLTLCHGYPYQLV QASAGCGCKPFAPYSL

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15389	45757	A	15479	1	1016	MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARIVP GFIRIARPRDGSFAYESVPWQQS ATQPAGSLSVVTTVWGVGNAT QSQVLGNPMGPAGSPSGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQQGVYSRGGYP GAPGFTTGYAGGPGGLGLPSH AARPSTDFTQAAAAAAVAAAA ATATATAT/GHRGCSPGEAEPG AEP\DGAMGAGQSFNSQFLQHG GPRGPSVPAGMNPTGIGGVMG PSGLSPLAMNPTRAAGMTPLY AGQRLPQHGYPGPPQAQPLPRQ GVKRTYSEVYPGQQYLQGAYP VHSGLSQFPTWQETPRHP
15390	45758	C	15480	1	585	
15391	45759	B	15481	1	885	
15392	45760	A	15482	3	440	GPWPRPVAYLSKQLYRVSKGW PPGLRALAEMALLAQEADKLT LRQNPNI/IGPHAVVTLMTTKG HH*FTNARLTYVKIPT*PLKF/G NTLNPTTLLPVSESPVEHNCVD VLDSVYSSRPNLRDHP*TSVDC ERYVDRSSFTNRCKVTR
15393	45761	A	15483	3	368	
15394	45762	C	15484	109	276	
15395	45763	A	15485	1	1710	
15396	45764	A	15486	221	784	QNSLRSMCQKEKKMAAGVLT HTC\GPWPRPVAYLSKQLDRIS KGWPPGLRALAATALLAQEAD KLTL\GKT*I*RPPHAVVTLMNT KGHHWLTNARLTKYQSLLCEN PHITTEVCNTLNPTTLLLVSESL VEHNCVEVLDSVYSSRLNLRD HP*TSVDW*LHVDGSSFTNPCK VTLKKMTSAAPVTPRS
15397	45765	B	15487	509	661	

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15398	45766	A	15488	1370	2243	LGKLRLESCGLVAAVRPHSGGL AMPLPNATRPASGRSED/AELK LALEHGHRSESLQGRKHRGVH DNSDIPQAALVGGTTMIIGHVL PDKETSLVDAYEKCRGLADPK VCCDYALHVGITWWAPKVKA EMETLVREKGVNSFQMFMTYK DLYMLRDSELYQVLHACKDIG AIARVHAENGELVAEGAKEAL DLGITGPEGIEISRPEELEAEATH RVITIANRTHCPIYLVNVSSISA GDVIAAAKMQGKVVLAETTTA HATLTGLHYYHQDWSHAAAY VTVPPLRLGIPPH
15399	45767	A	15489	307	600	VSRRASSGSPVPLGSLHLQHSA PA/PSAAPKPRSPPARLSRPHLR GESAAPSPLSPGPASLAAAAAA RVPAQPSPAPSTTPAPRTTLAPR VPHRLAPAP
15400	45768	A	15490	3	222	
15401	45769	B	15491	1	1131	
15402	45770	A	15492	136	201	
15403	45771	A	15493	3	556	ELPRRLVCSKLRADPGRLTPDA CARPGMSRYLLPLSALGTVAG AAVLLKDYVTGGACPSKATIPG KTVIVTGANTGIGKQTALELAR RGGNIILACRDMEKCEAAAK\D IRGETLNHHVNARHLDLASLKS IREFAAKIIEEEERVDILINNAGV MRCPHWTTEDGFEMQFGVNHL GHFLLTTWC
15404	45772	A	15494	11	559	
15405	45773	A	15495	1	312	MAPAADREGYWGPTTSTLDW CEENYSVTWYIAEF\SWLMSGF LPTPSSLRDLTASRWVRSLPPSR SPAGRQPGPAEELPKASPCPWG KSLSRPFASFSASSGPS

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15406	45774	A	15496	2	1605	WQLPHPPAAPSARQILRACQLS SVTAVAQSCLYGKQLC/GLTTG NIAGAGLLFFGGGIGGTILYAK WASHFRERVEKTIPYSDKLFEV VLGSAPYNVPLPKKSTQSGPLK ISSVSEVTKEFKQPASQLQKQK GDTPASATAGDTVLVPGVQHE ESLKTDHPAIDEGKPTPALSEEA SSSSIRERPCEEIAACLAQEEKQ EQVKTESLAKSFEDALRQTANV TLQAIAAQNTVVQAVNAHSNIL KAAMDNSEIEGKKKSAKWHTV QGALKEHRKAVDEAANALLKA KEEVQAAQFESKLVSQYHELV GQAQDDFKRQLDSITPEVLPGW KGMSVSDPADKLSTDDLNSLIA RAHRHIDQLNRELAEQKATEK QHITLALEKQTLEEKVQEQELK YEFEQNLSEKLSEQELQFHHLS QEQVHNFTLDINTAYARLRGIE HAVQSHAVAEEEARKAYQLW LSVEALKYSMKTSSAEMPAVPL GSAVEAIKANCSDNEFTKALAT AIPPESLTHGVYSEETLRVRFYA VQKLARRVAMID

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15407	45775	A	15497	89	2490	PKCCFFCLLSGETAAAQSCLCG KVVLRPLRPCRRYSTSGSSGLT TGKIAGAGLLFVGGGIGGTILY AKWDSHFRESVEKTIPYSDKLF EMVLGPAAYNVPLPKKSIQSGP L*ISSVSEVM\KESNRPASQ\LQK QK\GDTPASATAPTEAAQIISAA GDTLSVPAPAVQPEESLKTDHP EIGEGKPTPALSEEASSSSIRERP PEEVAARLAQQEKQEQVKIESL AKSLEDALRQTASVTLQAIAAQ NAAVQAVNAHSNILKAAMDNS EIAGEKKSAQWRTVEGALKER RKAVDEAADALLKAK*LLMDF NKEELEKMKSVIENAKKKEVA GAKPHITAAEGKLHNMIVDLD NVVKKVQAAQSEAKVVSQYH ELVVQARDDFKRELDSITPEVL PGWKGMSVSDLADKLSTDDLN SLIAHAHRRIDQLNRELAEQKA TEKQHITLAL\EKQKL\EEKRAF\ DSAVAKAFRNIHRKLKYRA*TG QKR*KEVRDAME\NEMRTQLR RQAAAHTDHLRDVLRVQEQEL KSEFEQNLSEKLSEQELQFRRLS QEQVDNFT\LDINTAYARLRGIE QAVQSHAVAEEEARKAHQLW LSVEALKYSMKTSSAETTS\IPL GSAV\EAI\KANCSDNEFTQALT AAIP\PESLTRGVVTVKRPLGAR F\YAVQKL\ARRVAMIDETRNSL YQYFLSYLQSLLLFPPQQLKPPP
15408	45776	A	15498	1	1212	MPKKRQALVEFEDVLGACNAV NYAADNQIYIAGHPAFVNYSTS QKISRPGDSDDSRSVNSVLLFTI LNPIYSITTPTRLNVFKNDQDT WDYTNPNLSGQGDPGSNPNKR QRQPPLLGDHPAEYGGPHGGY HSHYHDEGYGPPPPHYEGRRM GPPVGEYGPHADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVE KVKISLKKQSPGGRPMGEEWL\ DGYAVDRAITHLNNNFMFGQK LNV/CVGAQAREGSRGTGERK GGEWGPAEEHSEAEVLTHTEM GCGSVSKQPAIMPGQSYGLEDG SCSYKDFSESRNNRFSTPEQAA KNRIQHPSNVLHFFNAPLEVTE ENFFEICDELGVKRPSSVKVFSG KSERSSSGLLEWESKSDALETL GFLNHYQMKNPSINLVT

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15409	45777	A	15499	1	645	
15410	45778	A	15500	3	677	SPPNPRAPYLFPASLQNPANWS PHFQYLPILSQPRSVLTAFRQQA QPRISMPQAQTPFRPQMERLDQ NIRRSNQPQHSLKPKLIQSKALT LFNSVKAEKDEEAAEEKFEVTR VVHIRGLIDGVVEADIVEALQE FGLISYVMVMSKKRQALVEFE DVLEACNAVNYTADNQIHIAG HPAFVNYSTSQKISRPGNSDD\R SVNSVLLFTILNPIYSITTDVLYT
15411	45779	A	15501	2	1712	DEQRRRSGAMVKMAAAGGGG GGGRYYGGGSEGGRAPKRLKT DNAGDQHGGGGGGGGGAGAA GGGGGGENYDDPHKTPASPVV HIRGLIDGVVEADLVEALQEFG PISYVVVMPKKRQ\SLV*FEDVL GAGNAV\NYAADNQIYIAGHPA \FVNYSTSQKISRPGDSDDSR\SV N\SVLLFTILNPIYSITTDVLYTI\ CNPCGPVQRIVIFRKNGVQAMV EFDSVQSAQRAKASLNGADIYS GCCTLKIEYAKPTRLNVFKNDQ DTWDYTNP\NLSGQGDPGSNPN KRQRQPPLLGDHPAEYGGPHG GYHSHYHDEGYGPPPPHYEGR RMGPPVGGHRRGPSRYGPQYG HPPPPPPPPEYGPHADSPVLMV YGLDQSKMNGDRVFNVFCLYG NVEKVKFMKSKPGAAMVEMA DGYAVDRAITHLNNNFMFGQK LNVCVSKQPAIMPGQSYGLED GSCSYKDFSESRNNRFSTPEQA AKNRIQHPSNVLHFFNAPLEVT EENFFEICDELGVKRPSSVKVFS GKSERSSSGLLEWESKSDALET LGFLNHYQMKNPNGPYPYTLK
15412	45780	A	15502	1	528	NHQIRNDFTISPGVKADSRTSPI PQQPASSFDITEAAVSFAKDSLA GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP\ TQALNFTFKDKYKQIFLDGVDK RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVGK AGAERELRGFGDCLVKIYKSDG IK
15413	45781	A	15503	1	1452	

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15414	45782	A	15504	2	991	RSAGVKAGSRPSPVLQQSASSF NMTDAAVSFAKDFLAGGVAA AISKTAVAPIERVKLL\LQVQ\H ASKQIAADKQYKGIIGCVVRIP KEQGVLSFWRGNLANVIRYFPT QALNFAFKDKYKQIFLGGVDK RT\QFWRYFARNLASGGAAGA TSLCFVYPLDFARTRLAADVGK AGAEREFRGLGDCLVKIYKSDG IKGLYQGFNVSVQGIIIYRAAYF GIY\DTAKG\MLPDPK\NTHIVI\S W\MIAQTVHCCCPG*LPYPFDT RS/VRRNE*MQSGRK\GT\DIMY TGTL\DCWRKIARDEGGKAFFK GAWSNV\LRGMGGAF\VLVLYE *KSKKYT
15415	45783	A	15505	1	613	
15416	45784	A	15506	1	1695	
15417	45785	A	15507	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSAMEDEINEMKRE EKFREKRVKRNEQSLQEIWDYL KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSLRRATPRHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL
15418	45786	A	15508	1	3156	
15419	45787	A	15509	1	879	
15420	45788	A	15510	1	804	
15421	45789	B	15511	1	1230	
15422	45790	A	15512	2	827	
15423	45791	A	15513	1	1011	
15424	45792	A	15514	1	1722	
15425	45793	B	15515	1	780	
15426	45794	A	15516	1	2712	
15427	45795	B	15517	1	855	

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15428	45796	A	15518	3	1263	GRTIQTKGKEV\ENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERVSAM EDEMNEMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTPQRYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRAILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQEIQRTPQR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK
15429	45797	A	15519	1	1137	
15430	45798	A	15520	1	1578	
15431	45799	A	15521	1	1656	
15432	45800	A	15522	1	1120	
15433	45801	B	15523	1	1541	
15434	45802	B	15524	1	1632	
15435	45803	C	15525	53	352	
15436	45804	A	15526	1	973	MGKKQNRKTGNSKMQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELQRVSAMEDE MNEMKREGKFREKRIKRNEQS LQEIWDYVKRPNLRLIGVPESD GENGTKLENTLQDIIQENFPNL ARQANIQIQEILRIPQRYSSRRA TPRHIIVRFTKVEMKEKMLRAA REKGRVTLKGKPIRLTVDLSAE TLQARREWGPIFNILKEKNFQP RISYPAKLSFISEGEIKYFTDKQ MLRDF\VTTRPALQELLKEALN MERNNRYQPLQNHAKM
15437	45805	A	15527	1	2896	
15438	45806	B	15528	50	658	
15439	45807	A	15529	1065	1260	RSHALALDSAGSSSPESPH*RAS IPHTALGQNAGSWAGTAHSHH GPFLWSDPRHPQVVPHRTCCP
15440	45808	A	15530	96	219	EFSTKPRLSGP*SSWEMLILEPL APDTTIDLKLLYSDRDF

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15441	45809	A	15531	5459	6324	LLANVSQLLADISQLLANFTQL FSHFSQLLTYLSKLFTHLPQLLT HFPKLLTHQPELFSNQSQLHPNI T\RYSPTSPSYSPTSPNYTPTSPN YSPTSPSYSPTSPSYS/RDLTKLL PFQPTIHTTVSNLYPKLTQLQPQ FAQLQPNLTQV\PPTSPSYSPSSP EYTPTSPKYSPTSPKYSPTSPKY SPTSPTYSPTTPKYSPTSPTYS\Q PLQSTPQPLPSTHLLAPLTRPLP PSTRPPAPPTRPPPPKAQPTLPLP LVTRPPAPPTVSQARLSARMTV TRRTEGTWGAAAG
15442	45810	A	15532	13	941	SVVLRPLLVVAAATATTPVAA AAATNTAKKTATVMVGEMVA GERGVLQMGHDITRFFYSNIQT VINNWLLIEGHTIGIGDSIADSK TYQDIQNTIKKAKQDVIETFEN QVPRILNDARDKTGSSAQKSLS EYNNFKSMVVSGAKGSKINISQ GGGSQGGRGGPPISMWLLALC LVGLAGAQRGGGGPGGGAPG\ GPGLGLGSLGEERFPVVNTAYG RVRGVRRELNNEILGPVVQFLG VPYATPPLGARRFQPPEAPASW PGVRNATTLPPACPQNLHGALP AIMLPVWFTDNLEAAATYGGC FRVPKKA
15443	45811	A	15533	207	696	TNLQEKNKQPHQKVGKRYKQT LLKRRHLCSQQAHEKMLIITGH QRNANQNHNEIPSHTS*NGDH* KVRKQQMLERMWRNRNAFTL WVGV*TSSTIVEDSMAIPQGSR TRNTI*LSHPITGYIPKGL*IMLL *RHMHTYAYCGSIHNSKDLEPT QRSINDRLD
15444	45812	A	15534	1	307	
15445	45813	A	15535	1	381	LPPPHDRLWCVMFPTLCPSVLI VQFPPMSENMRCLVFCPCNSLL RMMVSSFIHVPTKDMNSGIL*S RPADIELFSINLVNKKIFLKGKF GDPLSLQRQLRNIVFSMPCCFPS FLLPWVFSQLSVKPH
15446	45814	A	15536	134	278	DPAFLAPSPV/LMKQAPQATSG LMEPPGPSTPIVQRPRILLVIDD AHTD
15447	45815	B	15537	1	840	
15448	45816	C	15538	1	891	

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15449	45817	A	15539	1	3102	MYSHVITVCRHVKNGDILLLNR QPTLHRPSIQAHRARILPEEKVL RLHYANCKAYNADFDGDEMN AHFPQSELGRAEAYVLACTDQ QYLVPKDGQPLAGLIQDHMVS GASMTTRGCFFTREHYMELVY RGLTDKVGRVKLLSPSILKPFPL WTGKQHINRTKDKNHMIISIDA EKAFDKIQQPFMLKTLNKLGID GTYLKIIRAIYDKPTASIILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEK
15450	45818	A	15540	1	779	IPMKDHDAIKLFIGQIPRNLDEK DLKPLFEEFGKIYELTVLKDRFT GMHKGCAFLTYCERESALKAQ SALHEQKTLPGMNRPIQVKPAD SESRGEDKKLFVGMLNKQQSE DDVRR\LFEAFGNIEECTILRGP ERQTAKGCAFVKYSS\HAEAAG RPSTRLHGSQTMPGAFVPVWV GQVSADTDKERTMR\RMQQMA GQMGMFNPMAIPFGAYGAYA QALMQQQAALMASVAQGGYL NPMAAFAAAQMQQMAALNM NGLAA
15451	45819	A	15541	1	1413	MEYYAAIKKDEFISFVGTWMK LETIILSKLSQMQKTKHRIFSLIV LCDITDILKEFTVAEAGGFALNE IMKEICKSRFSAKVSLHWKMW HSTASLGYHRVNVTNPDPLNLC LGHCWLGLRDTGQKQACGGP GVCPGMFRRACGGNAPCKEAP SVTEASSPDGSVLCLGSHVPITP APLSSAQMVCHMVEDRRTVEL ILGATHNLFFSTSPLTWSLRAIP GNCVLFLKDYVTEPVRSQSILHI AGPTFKQTPNLPFLKFPEATKA HGPNVYQNDSTCPEPTAQVSH WSSVSSTLIASPVPGPEDRKLFV GMLNKQQSEDDVRRLFEAFGN IEECTILRGPDGNSKARPLASSQ GAPSVKYSSHAEAQAAINALH GSQTMPLMQQQAALMASVAQ GGYLNPMAAFAAAQMQQMAA LN\PNGLAAAPMTPT\QANGQP AAEEI\FANGIHPYPAQSPTAAD PLQQAYAGVQQYAGR

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15452	45820	A	15542	254	883	DLRKDSPWEHRQCDKREPGNS APPAPHSWGFAVFNPRAGDVR QLCKRADTRTPSPRAPFGSAGA CRGCGRAGARSLASPKARTCIS SARRRAGGPLQLGAGSGQAKR PDR*TRREGANA*KTLHL/HSSL APSPGGVLAGFQEPPGRPQVAC CAATAAGGIRAGERR/PAAAAA AAPWAQKLRRLRLQRRGPPGC R**MVSFPRLFSGSTSR
15453	45821	A	15543	1	768	MCDFGKSTSLPASPTSSSANGR DNSTYRLKEQGGFMHSVASRD SCAESARYTDAHYAKSGYGAY TPSSYGANLAASLLEKEKLGFK PVPTSSFLTRPRTYGPSSLLDYD RGRPLLRPDITGGGKRAESQTR GTERPLGSGLSGGSGFPYGVTN NCLSYLPINAYDQGVTLTQKLD SQSDLARDFSSLRTSDSYRIDPR NLGRSPMLARTRKELCTLQGL YQTASCPEYLVDYLENYGRKG SASQVPSQAP\PSRVP

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15454	45822	A	15544	85	2249	SAEAMSGDGATEQAAEYVPEK VKKAEKKLEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEIKAKNYDK GEKLFQRCLMKVLHIDLWKCY LSYVRETKG\KLPSYKGKMAQ AYDFALDKIGMEIMSYQIWVD YINFLKGVEAVGSYAENQRITA VRRVYQRGCVNPMINIEQLWR DYNKYEEGINIHLAKKMIEDRS RDYMNARRVAKEYETVMKGL DRNAPSVPPQNTPQEAQQVDM WKKYIQWEKSNPLRTEDQTLIT KRVMFAYEQCLLVLGHHPDIW YEAAQYLEQSSKLLAEKGDMN NAKLFSDEAANIYERAISTLLK KNMLLYFAYADYEESRMKYEK VHSIYNRLLAIEDIDPTLVYIQY MKFARRAEGIKSGRMIFKKARE DTRTRHHVYVTAALMEYYCSK DKSVAFKIFELGLKKYGDIPEY VLAYIDYLSHLNEDNNTRVLFE RVLTSGSLPPEKSGEIWARFLAF ESNIGDLASILKVEKRRFTAFKE EYEGKETALLVDRYKFMDLYP CSASELKALGYKDVSRAKLAAI IPDPVVAPSIVPVLKDEVDRKPE YPKPDTQQMIPFQPRHLAPPGL HPVPGGVFPVPPAAVVLMKLLP PPICFQGPFVQVDELMEIFRRCK IPNTVEEAVRIITGGAPELAVEG NGPVESNAVLTKAVKRPNEDS
15455	45823	A	15545	12	427	SAEAMSGDGATEQAAEYVPEK VKKAEKKLEENPYDLDAWSI\L IREAQV**YRITFPSLWVQSHYL VLPVNNIFIILTL*MLFIGFQF*N QP\IDKARKTYERLVAQFPSSGR FWKLYIEAEVTILFYFFLYQYCS IHL
15456	45824	A	15546	150	469	SAEAMSGDGATEQAAEYVPEK VKKAEKE\LEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEVTILFYFIFS YISIAAFTVVIENKLGT
15457	45825	A	15547	1	834	
15458	45826	A	15548	443	732	SFMRWQKGQLPQLCLHRESHC SPYPQPSFLGMEP/ADIHETTFN SIMKCDVDIHKGLYANAVLSSG TTMYPGIA\NRMQKEITALAPS MMKIKIIAPA

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15459	45827	A	15549	1	1214	MEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPSIVGRPRHQGV MVGMGQKDSYVGDEAQSKRG ILTLKYPIEHGIVTNWDDMEKI WHHTFYNELRVAPEEHPVLLTE APLNPKANREKMTQIMFETFNT PAMYVAIQAVLSLYASGRTTGI VMDSGDGVTHTVPIYEG\YALP HAILRLDLAGRDLTDYLMKILT ERGYSFTTTAEREIVRDIKEKLC YVALDFEQE\MATAA\SSSSLEK SYELPDSPRSSTNWQLSGFRLPL RHSFQPSFLG\MESCG\IHETTF\ NSIMK\CDVDIRKDLY\ANTVLS GRTPPCTLGIADRMQKEITALA PSTMKIKIIAPPERKYSVWIGGF HPWAWLSHLSSKMWVQQARS MTESGPLHSSTANGFLGGLLTL VAFTPFLWTKP
15460	45828	A	15550	1	2355	MKQITFAPRNHLLTNTNTWTPD SQWLVFDMRTSGASFTGETIER VNIPTGYVEKPNKQCRHSVTRY GHGGHSDHTPSLTVATVATQIT PRHSGHGSHCDRNLSLATATA ATLITPHHLLWPRWPLGSHSVT WCGHGGHSDHTPSPTTATAVT RITSRHPLRPQQSLGSHPVTHYS HGSHSDCIPVTRYAHGGHSDHT PSLAMATAATQMALCHSLWPR QPLGYLVNKIRRKRCTDGVSPS GKAPVFDTGIPWFESRYPSHLL RVSGSPPGYWGIAKRHQILNVS NMFGKFKTNLLGYRQAVRHRI LIPAFRGSNPRTPANLFKTLTLIS NMRALENDFFNSPPRKTVQFG GTVTEVLLKYKTAIEKRLEKLA VDPHRDRAQMLKVENVQQAW QQWINKLPPARREDEDVKEIR WMIEELRVSYFAQQLGKNSRA ESMLWSFHKAAIEAARTNIIQA QTRVEAAQATERRIAADIDDSE LKAPRDGRVQYRVAKPGEVLA AGGRVLNMVDLSDVYMTFFLP TEQAGTLKLGGEARLILDAAPD LRIPATISFVASVAQFTPKTVET SDERLKLMFRVKARIPPELLQQ HLEYVKTGLPGVAWSFLYSINQ TICLRLDSIEAKLQALEATCKSL EEKLDLVTNKQHSPIQVPMVA GSPLRTTQMCNKVR/CVNP*AT VVPPPVPQPTTQQYQGLDAGA

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15461	45829	A	15551	1	956	MSSGRRDALARGLGNSGDGAP HLGEHRQLEDVGGVTVTVTWT GRLQAAGCWTRSVSSTAAAGR REPSTRDGAALSTEPPDPPERLG HRGSRAGLTALGHVRTRGSSQ RGGRPEPWEHWLENGTRRTEL VDGVSYESWRRRPCRGQLESR LVLENHVATDEDEPALKCQRL EINCQDPSIKSFLYSINQTICLRL DSIEAKLQALEATCKSLEEKLD LVTNKQHSPIQVPMVAGSPLRT TQMCNKVR/CAMHWLCVSCIF TCLPGWRPAAPDQGPAAISLCS LPSSSQGHREPLALGLPSALPPA HRQRLRGSATVPIPP
15462	45830	B	15552	161	925	
15463	45831	A	15553	31	856	GGFLHHASFFVGRGRTLLMYFS LLGATPKPEPEPEQVIKNYTEEL KVPPDEDCIICMEKLSAASGYS DVTDSKAVGPLAVGCLTKCSH AFHLLCLLAMYCNGNKGPEHP NPGKPFTARGFP\ASATFQTTP\ GPQELVPYTPQITAWDLEGKVT ATTFSLEQPRCVFDGLASTNDT VWLVVAFSNASRGFQNPETLA DIPASPQLLTDGHYMTLPVSPD QLPCDDPMAGSGGAPVLRVGH DHGCHQQPFCNAPLPGPGPYR WVVPTGALGLGLCLG
15464	45832	A	15554	827	1371	GSSAGEASSSLRRLSPSQPISRPL LPAGEKVLVVWIEDQTSHNIPL SQQSKT/TLFNSMKAERGKEVT EEKLEARRGWFMRFKERSCFPN VKVQGEAANADIEAVACYPEY LAKITDEGGYTEQQIFSVDETA LYWKKMPSRTFLARRKNCHSH PSFSSQHLVQSAAINIKAKSSTS KKIMTP
15465	45833	A	15555	799	906	FLNKLAFALRCGLALNSFLRKI QEPSLG\SKSGSLS
15466	45834	A	15556	143	560	

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15467	45835	A	15557	1059	1940	QQMQQEMRRKSKWMAMLGK WETYQNS/TKGHLMKRVYKGI PMNVRAEVWSVLLNIQEIKAK NPRQYRVMKEKGKRSSEHIHQI DLAVSQTLRNHMFFRDRYGTK QQELFYILLAYSKYNPVVGYCR DLSHIAALFLLYLPEEDTFWAL VQLLASERHSCRVGEQLPLGLH AARPGDGHPGQPRHLPCVASLL GAFRTSLLTVPKEPGTDPPEPKS DAFHPHQQKASHPPRGCPLCPG ATPSGSDSVQLALRNLRVLLPF SCSGSSCPWYPRKEALHPGGLE EQRGLQPLMGLVTG
15468	45836	A	15558	123	448	ALAAAVYPSHSERTGEEAKKIC SVR*LLRSAQEEI/FLRGKNSRT GVL*KLLQRK*RYQRALGLAM LSEWTISPKGPVSTGITKPMLTA SRVTVPRMTMSALLDFIHGA
15469	45837	A	15559	1	6387	
15470	45838	A	15560	52	3218	
15471	45839	A	15561	3602	4015	GSVESPLGQKTPRTSSASPCWPS TNLYRMELELYGPHVTSQVVK STRCAPIRWSAAPSILCEVRVPV TMWTCLPLPATGRLSMW*IWP RQWPCVLTSATQS*LTRCGGGT RAVSLAPQSHL*VCPAQSSWTS IILWT
15472	45840	A	15562	932	1316	RVQDIPAKRGIPQFRPKIKGIGQ SYKQHYPARPWNVLAQKVV/V FEDQDALLPCLLTDPVLEAGVS LVRVRGRPLMRHTNYSFSPWH GFTIHRAKFIQSQDYQCSALMG GRKVMSISIRLKVQKAVNRA
15473	45841	A	15563	1	263	
15474	45842	A	15564	66	185	
15475	45843	A	15565	1	4217	MRLAEERAALAAENADGEPGA DRRLRLLGTYVAMSLRPAAGA WERCAGSAEAEQLLQAFLGRD AAEGPRPLLVVRPGPRGLAIRP GLEVGPESGLAGAKALFFLRTG PEPPGPDSFRGAVVCGDLPAAP LEHLAALFSEVVLPVLANEKNR LNWPHMICEDVRRHAHSLQCD LSVILEQVKGKTLLPLPAGSEK MEFADSKSETVLDSIDKSVIYAI ESAVIKWSYQVQVVLKRESSQP LLQGENPTPK\VELEF

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15476	45844	A	15566	26	494	RPGCGEWLGNAELWGQECQL HYSPPVSPWENSSGPRFSISKTG SLIPPLLNDICQNQKPQIILSHPA RCLGLLDHFPQQWERRQAQNR AETG*GQRSAQGQTFRQRPLSV SGNCRVPPRATVSRK/PRPAPAY ALSLKSPRRRPPRTGPAPPGLVP
15477	45845	A	15567	1	1242	
15478	45846	A	15568	114	1219	VDLPPGAPVRQSGSHGSVLRDH KTEGEARVLPLHQRVGKAGGR GATPGPHVHEDPVTICCGHSFC RP/C/ICLSWEEAQSPANCRACR EPSQKKDFKTNILLKNLVTIAR KASLWQFLSSEKQICGTHRQTK KMFCDMDKSLLCLLCSNSQEH GAHKHYPIEEAAEEHREKLLKQ MRILWKKIQENQRDLYEERRT AFLWRKRTLRLKGMTSGAQGT SQKVALGLLQQPLCHTVRAQS NSARVHKQRGGDAVSSGAGIP DPKAQRFPATLRSQAFTCTAGR RWGSGETVLHPLQRAGVRGAV AELHRQLLLSSSAAGFEECEGL CTSGPHITQGPDHQELYLSHEG VWTLFTCTGDRWKVLSGVPCP

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15479	45847	A	15569	1	2694	MRMAATAWAGLQGPPLPTLCP AVRTGLYCRDQAHAERATDVV LLAPFCQPKTRSHGTCPPTERDP RGEGSTEYPGRVDGIQGWGTR ALTGWTDRRLLCQACQTLPPR HWFLPGARGWLGGSPCAHGQE SLPSQPSPILLRVESVKSRMLRR RAQEEDSTVLIDVSPPEAEKRG SYGSTAHASEPGGQQAAACRA GSPAKPRIADFVLVWEEDLKLD RQQDSAARDRTDMHRTWRETF LDNLRAAGLCVDQQDVQDGN TTVHYALLSASWAVLCYYAED LRLKLPLQ\DYPTRPPTGRPAC/ CAWLGIPNVLLEVVPDVPPEYY SCRFRVNKLPRFLGSDNQDTFF TSTKRHQILFEILAKTPYGHEKK NLLGIHQLLAEGVLSAAFPLHD GPFKTPPEGPQAPRLNQRQVLF QHWARWGKWNKYQPLDHVR RYFGEKVALYFAWLGFYTGWL LPAAVVGTLVFLVGCFLVFSDI PTQELCGSKDSFEMCPLCLDCP FWLLSSACALAQVREEAGRLF DHGGTVFFSLFMALWAVLLLE YWKRKSATLAYRWDCSDYED TEERPRPQFAASAPMTAPNPITG EDEPYFPERSRARRMLAGSVVI VVMVAVVVMCLVSIILYRAIM AIVVSRSGNTLLAAWASRIASL TGSVVNLVFILILSKIYVSLAHV LTRWEMHRTQTKFEDAFTLKV
15480	45848	A	15570	1	924	MISQFIPENYFSGKSSATSGWA RAQRDFRVGAGSARPALLSGRL APPALGSERLSTRASSCGGLPR ATPRGRAPPPATRHPVPSTAQR LRSAAARQRLAGSSARGRDAL GKASWAPESVLEVLARAVRQE KEIKGILLGKEEVKLSLFAGDMI VYLENPIISAQNLLKLMSNFSK VSGYKISVQKSHAFVYTNNRQS ESQIMSELPFTVATKRIKYLGIQ LTRDVKDLFKENYKPLLNEIQE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTFFTE LEKTK\FIWNQK\RAHIAKTIL
15481	45849	A	15571	1	825	
15482	45850	A	15572	1	1488	

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15483	45851	A	15573	1	1476	MPIKVDWIKKSRTHTPRDTMSP KRGINISIQEYRNTPDASILSELR LERDTNTQVYTYEQEHTNKNN GHQAIDKQNKGHIRRESDRGEY YPLDCRPTGSLTDKGWGMLLC GMMTAGKPTPILTFLLDVGLPG GTAINKSSVIRVRNREEGNVEK WGERQVDQRDAVMRVRCGIR NNVEAGLKYGPGTMKVSLSVF YTTQQCRRYLSVLCFAGLARAS VPFNEDFQMSLDEKLFSNLHPL GSSSSPPKSLLHCPLLEHQFTML GFSDLGAQLASPSGSHTRAAGV AACQPAPTLTWLSPWVARGLG TLEQGVVLVGEARAAQEPMEW VGGSCMVGCRSRALPRGKAAK AWREIQRSAGAGGAPVSPWSG GAPSRACPPSASSVRFLCAARR LACNTYSPVLYCVRNWWILGL TDFNNEATDPRDPFLANVPGQL AAVAIGTCDGNVYSAGDRDYR FALESILKACTLALALEEVGPPA VQDKIGADP\TGLPF
15484	45852	A	15574	140	448	GFLGACAGREFKMAPP*SSLSG *KLSVSPCPGLLISAEGPEAVFSI V*NARVRGFILEVSETKNPPIPD TISTKHASLMSDSYREKKLVPV VYPHSSTPSFQ
15485	45853	A	15575	1	1001	MEAPQGALEQDGPAVLSQQRH RKKPFTATPIDPSYHRSHAISLS VIIGYCVPPSHAAEMAAYGWT MGKSKLMAGQWITQSQVFCDS STDGPRQHKAQTAILTKLQSQQ RSTNNSTVSHRQQWVNCRLLR VKCQRLRAHKELLPVQRWLWR QGRCVPTTSLVAVSETAGAGA AALALSRLCRCLQVSASARPFS SRTLSPQPKCWAMAASHQPIKG ILKNKTSRTSSMVALSEQPCRT VHEELSKKCQKWDEMNILSTY HPADKDYGLMKIDEPSPPYHG\ LTGDDENACSDTETTETMVSDI LAKKLAAAEGLEPKYWVQEQE SSGEEDLLAEE
15486	45854	A	15576	1	1851	
15487	45855	A	15577	73	418	GKPDGDKVSQHLLLWKG/YSF/ PPSLMKLSLAGYEILS*KFFSLR TLNIGPPLSSGFRVSAERSTVSL MDFPLCITQCFSPAALNIFSFIST LVNLTIMCLGVALLEQYLCCVL
15488	45856	A	15578	2	460	

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15489	45857	A	15579	1	2031	MATEVFLIPYALLQCSLASYPS KPGIYVPSPQMWVGSVTCSDQ KNTIEVLVPKAYTLARQQYKSL SEQVYSCHQGTLNTRAQESAAS LLKPARPRTRQKKETPNTSEHQ KEQTLDTPPLRTVTLTTRVRGFI LEVSETKNPPISDTMGLDISKQE EVLGRESDEQGEQSQGLSEMQ TALAMLLTREPISAKQAPHEPP RRQEDNTQAREGETRSRKTRA EGQKGHAHAENERNAKERESE RKRQEAEDENGKEKQERNEGT HARHMKRRKRDEKKRQGQNK PGNKRPEGNEEAQRRRKKNRE RQRFSFYQSGPSAAGLLVFAGG PLQSLFAWVSPLEAAEQQRFLS VPSSGPLRKFCLYFGFVGNATP LRGLNTHGRLLTPAHGTRRRHT RPLNSPVPEKAGSTTESNGSPY GQNPGPLPPKGNRAQGEKWM GRRIQGTTRPRAREANHKKMT QIMFETFNTPAVYMAIQAMLSL YTYGCTTGIVMDSSDGVTHTVP IYEGYALPRAILCLDVAGRDLT NYLMKILTEHSYSFTTMAEREI VCDIKEKLYYVTLDFEQEMAT AASSSSLEKSYELSDGQVITIGN ELSCCPEALFQPSFLSMESCDIH KTTFNSIMKCDMDIRKDLYTNT VLFGGNNMYPGIANRVQKIVTL VWMGSSILALLSTFQQMWVSK\
15490	45858	A	15580	485	886	VPYFHFTCSHSSASQLPFLQMM KIAKTCSLGLNRLPEAKLKAFP TPRVTSL/WPRQRGRPRR\GCGR NRSGSLVSAARGVGGRSQAAA ARRDAPSPPATSRMPPRQGSVS WGCARNAPGRRADPEVRRQPG PSCT
15491	45859	A	15581	1	435	
15492	45860	A	15582	2	339	HRCSTGAFSTAASNSNADRPPP ARRRGLPR/RGPP/SRRRSPRPPR REPWPRTRRPRTRTAKARRRAT LEGRCRRACGHWQPRAAAAA AAAAAAVAAAAAAAAAAAAA GASATW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15493	45861	A	15583	1067	2093	RRNTSSKCRSRNCRCPRSPHRH RPSLRPRSQQPKCKCRPRSRRSS RAPSSRRSRPQGLVPC*RAPPW PTSRWPGSPGFPLLNCSRKGRC RPRHPSQPRCPCRSLRWCPSRQ LWSPHRESPPCP*TSRGSAWRS VSHRRQQDRPWWTQPVHMQQ LLKLKQQAVQQQKAIQPQAAQ GPAAVQQKITAQQITTPGAQQK VAYAAQRALKNPVSYHTHLPG PETGRGPASADPDPGCKTSSSCS TANTRGQHPASCLCFPAGFSTD CGAHAGDGGRAAGADDPCSDR DCPGGSAETHSAAGGDHGVGP APDSRRSQPSPGARQLRQPKPA AQVTDEGPCCQAKDTY
15494	45862	A	15584	10	607	RALCGESRLPLARKLS*AKKSV QRSTLQSRRIWVCWFHFAN*SL F*KQGRT*ESPL*L*LIPAS*RPS TSESPPL*KANFQQPHRGL*EKV AEGRRGP**EY\YTSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSS SNNSSNSRHRRRRRRLLSFLSR RRRHSRCCLSRSRPRRRPRRHP ARLWLRSRCTDQRKNFQLPRK TV
15495	45863	A	15585	217	1012	AKNDSKRQNFGHRGQPTFGAD KAKGERVRTSSTIRRTSYLDTIT GPYLTGQWPRDPHGHYPSCMK DKATQTP\SCWAEEGAEKRSHQ RSA\SWGSADQLKEETPTDLQQ NAQQKLYKPEEVGCLISDFLKE KENCQPRILYAGKLSSECTPDE EAVNIVEMITKDLEYYINLVDK EWQGLRGLTPILKEVLRVKCY QTASHATKKSGMKGKVSQFGK LHCYFKKLPQLPLPSATAILISQ LTSTRQELHHKKDCNLLKTQMI
15496	45864	A	15586	2	387	
15497	45865	A	15587	1	165	LFMFFCLLYIR*QLLHPGYNAPF QNTAATRGRGIAQTAPEAAFQL FLHQRVRFHC
15498	45866	A	15588	172	359	PDGDGIESINYLGQYGHFHDIDS SYP*AWNVLPFVCILFYFIEQWF IVLLEEVFHIPCKLDS
15499	45867	B	15589	1	2850	
15500	45868	C	15590	1	2835	
15501	45869	C	15591	78	491	

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15502	45870	A	15592	1	5721	MAVLSLPLAPPTLMPPAHFNLV EMQVKATLKEYWQRKSPGIPA GANRKKKINGSSPDTATSGGYH SPGDSATGIYGEGHASSATLED LELRQPTPSTSPNDCSLYPSPQS SSNSSSLHAPHSQYRELAVALH SSSAIISQLSENINSLNNENKSAL QLERQVKELKLGELKETVTSDP SNNGWEAVTSLWEGERLPARG AEEPRGSESTAAARPVPVSPAA VRGRLVAGEPGSYQPAETAAK AQLSLMALPGEGY
15503	45871	C	15593	178	1287	
15504	45872	B	15594	52	855	
15505	45873	C	15595	1	1698	
15506	45874	A	15596	302	617	NLAVNPSGPGLFLIGKLLIIASIS EHVIGLFRDSTSSWFSLGRVYV SRNLSVSSRFSLVFDDGDVQMG FWCGCPLCLLVFLLT\AGPSAA GLLEFAGGPLQTLFA
15507	45875	A	15597	1	2762	MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIQGCDFSGTCRQ TLSILTQPLRQWGLEGIKKPNS WIISEESVSNGGPPLLIPRQTAS GVDLQQTPTDLQLRVLTVRRK TNKQKGIASTSTKRTSTPKPHL YVTIIKDQSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWDYVKRPDLRLIGVPD SDGENGTRLENTLQDI
15508	45876	B	15598	1	1989	
15509	45877	B	15599	1	762	
15510	45878	A	15600	686	850	GQPERKVGLPTKGSPSD*QRISR QKLYKPKESGGQYSTFLKKRIF NPEFHIQPN
15511	45879	A	15601	2	382	
15512	45880	A	15602	1	993	
15513	45881	A	15603	3	460	SPCWGQLLQATQP/ATAFAQKD LLVGAVLFGHNGSLSSRNTLAF SMDVGPSQWMWGLLNGCGAS AHRQCTRCTLQVTIALEGPLAP LKLAWHKKIYIFLGEAAEIRRD QLEAERELFHSRAEQGRLFVGR PGQAAHLMLPPGDCVSIWTQH MIT
15514	45882	A	15604	1	130	
15515	45883	B	15605	1	561	

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15516	45884	A	15606	94	420	EKAVGRWIFQSKRYRSPCEKPY SKGLQVQRTVPEGPSKAARAA QAPGPNLLPCLPT/PQTPEFIISEP LANMYSCGNQNTLMEELAEQA QQHDEMLHMHHALKEALSIIS
15517	45885	B	15607	46	747	
15518	45886	A	15608	186	364	AFAPAPCTLVPGVLRGPPILLRE TGLAH*CPAVISPPKSLPWLPTA YSVESQQVILFGL
15519	45887	A	15609	155	511	GAAVAGTQNLCLGGGGAVGG S*RGALNGEGLLHPGYNAPFQN TAATRDRGIAQTAPEAAFQLFL HQRVRFHC*FLLWREGRGR*AR REPLSRPQPPAGPLGGALPAPPL PDASTLVGVG
15520	45888	A	15610	1352	1684	MSIRSAWCRAEFNSWISLLTFC LVDLSLVFDDGDIQMGFWCGC PFCLLVFLLT\AGPSAAGLLEFA GGPLQTLFAWASAVVAAEQQI LVSSKCCCLIVPLEVLSQRSTWP
15521	45889	A	15611	98	367	
15522	45890	A	15612	426	738	VCVWGDPPGPAGGHGEAAATL WKEKVDLKERVEKLELQFIHLS GQTDTIGRKYISQGAVSETQHW ERRTSSGWP\GPGGDEGEPAGA AGQVLQLVGDHKEGHGKF
15523	45891	B	15613	86	1411	
15524	45892	A	15614	950	1493	GTVFLWRRRGTLIFRVSGFSAL FFPPSLWFYLPFVFDDGDLQME FWYELSFLLMLLLFLCACWFSF *QSGPSAAGLLEFAGGPLQTLF AWVSAAVAEEQWILVNRKCCC LIVPLEVLSQRSTRPCEVSVHPY VHCCLGIEELNIYCSLHSLGLFE AILLGKAFEELGCCDPSLFATV
15525	45893	A	15615	1	5731	MDSHRPTAWPAAVLAGRSPVA AESERYCSRQPPLPRRQALLSV LVLASDTRLPFPWSSQTFCGILS KPLVLSGPLQTQGETNNENGLV GGGEVGMQPLVLFERSLFPGRC CVLERRIVPWMRQESYSSSSPI WFVDSDELNLTSVLECLEDDK NNNLLHQQLKWLICGLCRLYN LPKHLDVAMPDQPLPMGQSGP SAAGLLEFTGGPLQTLFAWVSA ALAAEKQILVNCKCCCLIVPLE VLSQRSTWQYELKEYW
15526	45894	A	15616	2	521	

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15527	45895	A	15617	1	1261	MSEHNITEECQQENQSIEQWRSI AHSDSIEVSWLHEVIKTYLKAK STKLDLMKKLKELSSQPSRKPK PFIPSQEGTGDNDVIYSTERLSK LLNQKKGSTRLYDKPLSNLLNQ KKVSTRTEGLTVDSRADMRNV TTILLSTESSSTDSSSSMDSSSSM DSSSSIGRVETATCAMIPVQKSK RSGPPQGPSAATGDGAEGRFLP RCSRPWADRLAWSQPRRHLAP GPSAATGDGAEGRFPPLCSCCG TDRLAWPQPQGHLALLPRCGE CGRARELPGDCCLHAEGGCSSV LEVLARAIRQKKEIEEIQIGKQE VKLSLVADDIIFCLENATDSSRN LLELIKEFSKVSRYKINGHKSVA LPYINSYQAENHIKNSTPFTIAA TNNNNKK\KNLGIYLAKESKDS YNENYKTATERNHRWSQAR
15528	45896	B	15618	60	499	
15529	45897	A	15619	134	1416	RTSICWTMDSSVQNTVLGPTRS SVKGVMEWLQYLQMERR/CTL SISMESMPRVAEDAGDVGAAE PLHLEPPAGPLEVEQQLQAEIK HLRKTLESLAGQLQAQVEANE GSSHLNRQQDERLREWKAELW EEQGETGRSSVQKDRTTISHAL SQNHQLEEQLAKERLEATSQQ NQQLQSQMSLMALPGEGDELG SKEEEEAPQPMPSILEDLKSREA MVAFLNSALVSAEEEQQAQLH GQLKEQRVCCQHLAHPVALAQ KEPEAAAPTPRTGGDSAVWTV DLQVEKTKFIMFTIKPGEVVNK DMAQSIYRSGKNLDKDMYGH DLEARRKTNRPLETTFYFLSYE LDYSRCFIGCLKCLCLPSPSATI GSFLKPSQKQKPVCLLYSLQNH EPIKPLFFINYPDSDSYRHTQVIR ILLSGSIHVQVPATKTPL

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15530	45898	A	15620	1	1665	MGGHVGGRHRMLTPKLIPETL AAGSMKINPEEPNRPPINGAPG GPALPLAAGDSGSEQAGEPALA ASELQGWDSTLGSPGSLRGTGI VATRSGSRGFRLSPASLGRRSR DRKTKELAFAGSGLATRGQRA SSDAAAGPPLSRCSPARTPQLPV RGSLTGPRAPAPPRARVCLLSC SCRQPFPPLTGGLNVGRPSGPS WKICPRSLPSASAETGIRRRRAA AHPPLQQPPLCGESLPSVQCSA NADSSIPVPSRWSQDACRNTGA AGPPGYPACVNNRNRTDKNSQ LDETHHMKTKVTDRGGFGAFT MLLRVVDTGHTSCSGSVEWDP RLYGDQADLSRSGHLDRPGAH HDYYTAIKKCEEGKSLDTTVK VKAGVNGFGRIEHLVTKPAFNS GKVDIVTINDPFVDLNNMVYM FQYDSTHGKFCGTVKAENRKL VASGNPITVFQ/ERDPSKIKW\YI AESTCIFTTMEKAGADLQGGA KRVIISAPSADAPMFVMDVNHE KYDNSLKIVSNASCITNCLAPL ANVIHNFGIVEGPMTTVHAITA TQKIVDGPSGKLA
15531	45899	A	15621	2	1105	GRVGCSTVSRIFSCVASRATSLR TPMGKVKVGVNGFGRIGRLVT RAAFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFHGTVK AENGKLVINGNPITI\FQER\YPS KIKWGDAGAEYFVESTGVFTT MEKAGAHL\QGGAKRVIISAPS ADAPMFVMGVNHEKYDNSLKI ISN\ASCTTNCLT\PLAKVIHDNF GIVEGLMTTVHAITATQKT\LD GPSGKLWRDGRGAF\QNI\IPAS TGAAKAVGKVIP*AERGKLTG\ MAFRVPTANVS\VVDLTCRLEK PAKYDDIKK\VVKQGVGGPPQG AILGYTEH\QV\VSSDCNSGPPV FPPFDAG\AGIALNDHFVKLISW YDNEFGYSNRVVDLMAHMAS
15532	45900	A	15622	121	221	
15533	45901	A	15623	189	538	

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15534	45902	A	15624	3	1015	DRAGPPGAPRLGQQLLCAIILL GLAAKKKEINITIIKQLLKKFLN KKPSYGLERQMETTQNLVDSY MAIVNKTVWDLMVGVMPKTI MHVMINNTKEFIFSELLSNLYS RGDQKTLMEESAEQAQWRDE MLRMYHVLKEALGIIGDINTTTI ST\PWGPVDNSWLQVQSVLARR R/SPGLAPTAPSLPTPHRLSLGA LGTGSVPTLLHHPGSSSVSSLSG LVA/DCFGLPKARGGPGQRLPF PSLPGRLFCDLAVAPPAPKAAP FICDFVYCCDQASEPVGCQGQT APHRLHGSPLGIPQAPPGSIQA WLRAAVFWKGALCPRCGRHIQ EFLLHRCTLVSL
15535	45903	A	15625	547	1242	PKALIKTSNKSSLSYQLTTHSGT MACPWIRHEVLLSRLGFLVLEN TNMDKRPSKLLRWLERQMETT QNLVDSYMAIVNKTVWDLMV GVMPKTIMHVMINNTKEFIFSE LLSNLYSRGDQKTLMEESAEQ AQWRDEMLRMYHVLKEALGII GNINTTTIST\PWGPVDNSCLQV QSVLAGCSFIILVQAVFLLYQA WWLLFWAPQGERWPWTSGLE DTVTREEGSPKGLSISL
15536	45904	A	15626	108	308	AQKHHLT*LSFLPRH*ILT*NLT KIPTSKIKKTPRSRSPRRSTSCFL DNLAPSCGCSGKGSSWRIC
15537	45905	A	15627	687	1910	KDHQLRKKLRRRGKQGAFTAA LPPGSPRPPLRGGRSGGVGLGV RGQRTPQAPQAVTPSEGPEPLW GPVLGGGGEHRRGTGASAAAG ASMRRLGAAGGGAGAGPQRG VGARVVVSEEANSPGAAITSNR ETQDANEGLSAPRPECLLHPTC RLLYVPLIVRDWVCHTRSVVLL QVVNVTGIAVGTGLASAYDTL MSQSFGVKNLKRVGIILQRGVL ILMLCCFPCWADLVNTERILLL LKQDPKSPGWTRECFQEWGSYI HLVIPSMFMVCTEQWTFEIGNF LAGLIDVMELGTQGIICELASV AYMNYFRLNPQPPISDFTINLAF LTLTERKILGYIQLRKGPDIVGP YGLLQPFTDAVK\FTKEPLWPS TSTITLYIIAPTLALSIIVLLALPT RMLAATPRPRGT
15538	45906	A	15628	1	1173	
15539	45907	A	15629	3	1447	

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15540	45908	A	15630	1	215	MDPKQEEIPDSPEKEFRRYRIAE WIRIHQPIICCLQETHLTHKDSH KLKV/KGWNKAFHANGHQKSA ARETK
15541	45909	A	15631	1	1524	
15542	45910	A	15632	1	575	MALSERSQPQDHVSHDRIYVK HPEYANLYRQKVDYTLPRVSIS IHVGQAGVQIGNARWELYCLE LAIQPDGQMPSDKTIGGGDDSF NMFFSEIGAGKHVPRAVFVDLE PTVVDRCLGHWMAAFLGE\EV HTGTYRQLFHPEQLISGKEDAA NNYSRGHYTIGK/EDLVLDRIH KLLTSQCRKPKATMWLSQAT
15543	45911	A	15633	208	465	
15544	45912	A	15634	107	827	EARRPCTLHLRSALHPATMCEL YSKRDTLGLRKKHIGPSCKVFF ASDPIKIVRAQRQYMFDENGEQ YLDCINNVAHVGHCHP\EVVKA ALKQMELLNTNSRFLHDNIVEY AKRLSATLPGETLCLLFYKFRG YWPSSTNPSSRPAAPASPPAAE RAGDFRAGRKPSVPGSRSVSGS PRGPCSRLSLSTFCTRYCPLSAL TSGPGCPYPMCFFLSPRVSRLLY SSHMVAGCRALRRCKNSH
15545	45913	A	15635	3	1218	GGLWEKMAAAA\QSRVVRYLS MSRSAITA\IATSVCHGPPCRQL HHALMPHGKGGRSSVSGIVAT VFGATGFLG\RYVVNHLGTAW GSQ\VIIP\YRV*IKY*QSMHLSFP WG*PGGQLSVFLGNWGTARD* RFLFRRVSYNTGNVGSSILFGTR LGETKNF\DFWRDVFVKIPQAIA \QLSKGSWEFEKFISCFHIWNGG II*KALS*DI*GNKAVGEKVVRD AFP\EAIIVKPSDIFGREDRF\LNS F\ASMHRFG\PIPLG\SLGWKTV KQPVYVVDVSKGIVNAVKDPD ANGKSFAFVGPSRYL\LFHLVK YIFAVAHRLFLPFPLPLFAYRW VARVFEISPFEPWITRDKVERM HITDMKLPHLPGLEDLGIQATP LELKAIEVLRRHRTYRWLSAEI EDVKPAKTVNI

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15546	45914	A	15636	2	799	GLWEKMAAAAQSRVVRV\LS\ MSRSAITAIATSVCHGPPCRQL HHALMPHG\KGGRSS\VSGIVAT GFGA\TGFLRRYVVNH\LGRMG SQVIIPYRCDKYDIMHL\RPMGD LGQLLFLEWDARDKDSIRRVV QHSNVVINL\IGTRP/WKSKNSD YEDVFVKIPQAIAQLSK\EAG\V EKFIHV\SHLNANIKSSSRYLRN KNRKREKEEMKKDLLSKKEPE PEDLENSQLIHIAKNEKACFEEN TKSVAEQPFDEEIVDATHQLTS YLGRSQE
15547	45915	A	15637	560	1394	RKSSSVHNAASGLLGSRAPGAH RHLGRCRCRHRLVSPSPAMAE DLSAATSYTEDDFYCPVCQEVL KTPVRTTACQHVFCRKCFLTA MRESGAHCPLCRGNVTRRERA CPERALDLENIMR\KFSGSCRCC AK\QIKFYRMRHHYK\SCKKYQ DEYGVSSIIPNFQISQDSVGNRIE NNTGIKQIPGAPAFGDGRVGCR QRNAKTELLAAAGESPCTMSL GSGPNLGPSPRSKSSSVTSPQPC FTEHPRERFVSFPVHYVLEGSR MSFLLWSLKTDRIFGH
15548	45916	A	15638	1	1026	MKVVCKEVKFEKQCPEAVLLH WEQTDDDENKRCDLREPRKPE THTKGPGLLVPTTQPGRNEGQS GADGKHARCSKTSCCLSGKEPS FIITEHCPLVPVQNTTIKPDSGIR ILQTLDSRETFTMSTALDVLQM KEEDVLKFLAAGTHLGGTDLD FRMEQHICKRKSGGIYIINLKRS WEKLLLVAPAIVAIENPADVSV ISSSSTGQRAMLKCAAATGATP IAGHFTPGTFTNQIQATFPNPRV LVVTDCRTGHQPLAEASYV/NN LPTIALCHTDSPLHHVDIAIPCN R/KAHSVDLMWMLAREILPM\R GTIARKHWWE\DPEEIEKEEQA AADKALTKEEFQGE
15549	45917	A	15639	20	441	TAEIAIPCNNKGAHSVG*MWR MLAREDLRMRGTISGEHPWEV MPDLYFYRDTEEIEKEEQAAAD KAVTKEEFQGEWTAPAPEFTAT QPEAADWSEGVQVPSVPIQQFP TEDWSAQPATEDWSAAPTAQA TEWVGATTDWS
15550	45918	B	15640	88	531	
15551	45919	A	15641	1	1302	

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15552	45920	A	15642	150	957	KAGASCCGSANPYVSVGKSCV LLAMAQLQTRFYTDNKKYAVD DVPLSIPAASEIADLSNIINKLLK DKNEFHKHVEFDFLIKGQFLRM PLDRHMEMENISSEEVVEIEYV EKYTAPQARSNAWFHDDWISSI KRGRG\RILTGSYDKTSRIWSLE GKSIMTIVGHTDVVKDVAWVK KDSLSCLLLSASMDQTILLWEW NVERNKVKALHCCKGHAGSV NSIAVDGSGTKYFGLRIEPKPA VSLVEEINSLSYRWTADNYKV GSGGKEEED
15553	45921	A	15643	3	393	VFCCPHCSLTFSKSFSSFSRLVR HQQTHWKQKSYLCPICDLSFGE KEGLMD/HLEGL*RQGPGQSSH HKCRVILGQWLGFSHDVPTMA GEEWKHGGDQSPPRIHTPRRRG LREKACKGDKTKEAVSILKHK
15554	45922	A	15644	335	537	VYFKQVTLDSSCRL*ERQVKST SSWNILSSTWRLPFCPTSVVLRF LTWICLRTISTSSISWFPADSS
15555	45923	A	15645	153	828	

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15556	45924	A	15646	1	2002	MLESAGNQDIEDVDIVLRQIQV KNRSTTEVGQNGNLQVEVSYT QAHIAPRPLASQGTWPHFVSSA PQPCFQVQNHSKYQNLYYSGFI RETEPISKGDVGEWLSAGKGES SAMFASEQEISKDEQGTPVLGS FYWEVDSPRKESSQAWAPGQE WIKLERDTTEEKMFEQLKPIEP VQKTLPWVGEVAATLQEAMK RDCWREARVKKKPVTFEDVAV NFTQEEWDCLDASQRVLYQDV MSETFKNLTSVEGKKKELREQ HPSLRDEGTSDDKVFLACRGA GQCPLSAPAGTMDRTRVLQAS QAGPP/FFFATTVGKCFSRRSYL YSHQFVHNPKLTNSCSQCGKLF RSPKSLSYHRRMHLGERPFCCT LCDKTYCDASGLSRHRRVHLG YRPHSCSVCGKSFRDQSELKRH QKIHQNQEPVDGNQECTLRIPG TQAEFQTPIARSQRSIQGLLDVN HAPVARSQEPIFRTEGPMAQNQ ASVLKNQAPVTRTQAPITGTLC QDARSNSHPVKPSRLNVFCCPH CSLTFSKKSYLSRHQKAHLTEP PNYCFHCSKSFSSFSRLVRHQQ THWKQKSYLCPICDLSFGEKEG LMDHWRGYKGKDLCQSSHHK CRVILGQWLGFSHDVPTMAGE EWKHGGDQSPPRIHTPRRRGLR EKACKGDKTKEAVSILKHK
15557	45925	A	15647	1	1048	MPSLAELFEGSSKAFGAAASQL NFPVASGEMLKFKYG\LRNPLH AVAAEPIASRTSRLNLFFQGKPP FMTQQQMSPLSREGILDALFVL FEECSQPALMKIKHVSNFVRKY SDTIAELQELQPSAKDFEVRSLV GCGHFAEVQVVREKATGDIYA MKVMKKKALLAQEQVSFFEEE RNILSRSTSPWIPQLQYAFQDK NHLYLVMEYQPGGDLLSLLNR YEDQLDENLIQFYLAELILAVH SVHLMGYVHRDIKPENILVDRT GHIKLVDFGSAAKMNSNKMVN AKLPIGTPDYMAPEVLTVMNG DGKGTYGLDCDWWSVGVIAY EMIYGRSPFAEGTSARTFNNIM

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15558	45926	A	15648	101	220	KRQQAFGLLDLHQWFARGSQG FRLQTEGCIIGFPTFEV*RHSGFL SCQSSCTGSFSSVWADVPLMFE GAAQPV*PVPSRGSADFRPLSIC *RSSRILLVKRCENSGVR
15559	45927	A	15649	597	808	ITMKSQRQIIKKAVTTKEMKSV CRRD/TPAFMFIAALFKIAKIRIQ RLCLSTDEWIKKMWYIHTMEY YSTLK
15560	45928	B	15650	161	3156	
15561	45929	A	15651	14	270	
15562	45930	B	15652	787	1821	
15563	45931	A	15653	1	2412	MAKSKGCSAATLASTHQILVTP WSCDNQKCLQTLPNVPGGTKL LLCEDHWFRNDSCNQAIPTIAT LLSFPSLQASLWTTHFLSPLNH HPVNPDSHLEQPPGQSPRLNFE AGDPERAPHALGCKRSRTRATS DRQPMASRDPGWGKASVGKA CALGSAVLPAGNDCTTDNLGL GSAGFEDLRLRLGQGPPRRQGA LQAAPRKASSCAAGQRLAPDSS FSRKRRPSRQRLGCETAAVADT AEAKSSEAPAFGWSTMDEAGS SASGGGFRRALDEPPNSRIFLVI SKYTPESVLRERFSPFGDIQDIW VVRDKHTKESKGIAFVKFARSS QACRAMEEMHGQCLGPNDTKP IKVRVPGSGCPRGKEWASWTSL HLLLCRGEGGVEHPFPAADQT APGLGTGAALRRGSPPTKLRRV AGKGTGCGVFAPRERTRQPRPP GDRTAVAGLP\SPSPSLIHQLLSS LPNSS*PTLSTFLTFLSQMPRFP YIKNGKTL/PFPQVFIAQSRSSGS HRDVEDEELTRIFVMIPKSYTEE DLREKFKVYGDIEYCSIIKNKVT GESKGLGYVRYLKPSQAAQAIE NCDRSFRAILAEPKNKASESSE QDYYSNMRQEALGHEPRVNMF PFGHGVVQYFNVASAIYAKYK LHGFQYPPGNRIGVSFIDDGSN ATEKMATQMVAAQLASMVWN NPSQQQFMQFGGSSGSQLPQIQ

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15564	45932	A	15654	375	2059	DSSVWQTPQKQRAVRPLHSGG APWTKLAALRATRGFRPGVDS LDEPPNSRIFLVISKYTPESVLRE RFSPFGDIQDIWVVRDKHTKES KGIAFVKFARSSQACRAMEEM HGQCLGPNDTKPIKVRVPGSGC PRGKEWASWTSLHLLLCRGEG GVEHPFPAADQTAPGLGTGAA LRRGSPPTKLRRVAGKGTGCG VFAPRERTRQPRPPGDRTAVAG LPLSLALTNPPALEFTAKLVLA YFEYFSDLPLSDAQISIYKKRKN STFPQVFIAQSRSSGSHRDVEDE ELTRIFVMIPKSYTEEDLREKFK VYGDIEYCSIIKNKVTGESKGL GYVRYLKPSQAAQAIENCDRSF RAILAEPKNKASESSEQDYYSN MRQEALGHEPRVNMFPFGHGV VQYFNVASAIYAKYKLHGFQY PPGNRIGVSFIDDGSNATDLLIK MATQMVAAQ/RLHQWCGITQV SNNL/WQFGGSSGSQLPQIQTD VVLPSCKKKAPAETPVKERLFI VFNPHPLPLDVLEDIFCRFGNLI EVYLVSGKNVGYAKYADRISA NDAIATLHWKDSEWGET
15565	45933	A	15655	257	412	
15566	45934	A	15656	3	866	HAASPCCCYEEKQSPLQKHLRV CSLRTWSLAARVAEGTAETVD PSAAPKTSVWSSRVCWGRLLA TISPSVNETDTCGMEDRRLVVC RPWRAQCHMKAWGWRHPEEG GTHSGAPSAVLQALAVAIQLGG HLADPLLQVDPLSSCGAVSLDI LIYLVFYYRTASVPETYIVKTLF KKLESQSLIQSNVLTRSNSMKA ERGEEAAKEKSEASRGWFMRF KERSCLHNIKMQGEAASADVE AAASYPKDLAKITDEHGYTKQ Q\FDVYKTAFCWRVMLKKYVK LLFVLCPLP

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15567	45935	A	15657	333	1034	RLSTTVMRGAFVF\MHKMPRL WLDYCQF\LMDQGRVTHTRRT FDRALRALPITQHSRIWPLYLRF LRSHPLPETAVRGYRRFLKLSP ESAEEYIEYLKSSDRLDEAAQR LATVVNDERFVSKAGKSNYQL WHELCDLISQNPDKVQSLNVD AIIRGGLTRFTDQLGKLWCSLA DYYIRSGHFEKIRKAPVNGGPT WMVGQNSVPRFQTRRLTPLKR KGPLVTDFREKQPTPLAQE
15568	45936	A	15658	172	346	ARPCRWCPGS*TSASAPGPGLR PCPP\GGDRTPASPPLHNQAAA APPGPGTWRGAAAS
15569	45937	A	15659	293	482	
15570	45938	A	15660	468	791	LAKCGCLEARGRARQTSGRPRP TDGGP*SPCWETGKGHPVLGR RGS/PGKQGL*SLPQSCQGQWR CAASRLLSSKNSWACMGSREA VSQETGTSSSSLGLMRPSDKKP
15571	45939	A	15661	366	609	
15572	45940	B	15662	321	739	
15573	45941	A	15663	1	1815	
15574	45942	A	15664	1	1911	
15575	45943	A	15665	437	1125	PVSCSGHSRWAAAAISIALSMIE TVNMVFTFYSRHHGTISTRVL/I GKRPERQDGQDTVNLGTLEET ASPSPVVTTSPPQPMLPSAFPPL SEEINPALPEATVMASPEAVAR QDNVDSAQEPPPTPLCASRPTT RQKSWWGARGEVESVTHEEM HYTGKELLEFSNLYKEKSGEQA WEWILRVWDNGGRNIQLDHPE FVDLGPLSRNSAFNVAVRGVK KGSKSLFAWLGEI
15576	45944	C	15666	49	186	
15577	45945	A	15667	80	877	GAERLPEGPGKRMVFRRFVE\V GRVAYVSFGPHAGKI/VSAMVD VF\DQNKGFWSNGPCTQVR\RQ A\MPFK\CMQLT\DFILKFPHSAH Q\KYVRQSLGRREDINTKLGQP TRWGQGRFESQEEKEKPRLTDF *SVF*S**RAKEN*RDRINPRNE V*EAFKRAAFPGKASSQKKAPG Y*GVLLAAAAAAAAAAAAAA AAAAAAAK\VPAKKIT\AASKK APAQKVPAQK\ATGQK\AAPAP KAQNGSKSSKPQKAPAPKASG KESISGNHKK
15578	45946	A	15668	253	1218	
15579	45947	A	15669	1	1819	

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15580	45948	A	15670	1	2422	MCPILREHRGSTEGKRRQKRLP LELTLKDEEVLAHRQEIEVAKA SPSKGNIIIHFGYKGVEYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKLELTKAEK HVHNFMMDTQLTKRHCPWAA TIQPKLSFLISLPGCDYRGESAR ARPLSHPPLQLGLGKDARYLRI CDRSLLCVCAAAGNAGLRPRD SPHTLLHWRSRSPYFFSPKPVPP QLLGGQPAAHSRRDDLGEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPAPGQGDVMPIVLVRPT NRTRRLDSTGAGMGPSSHQQQ ESPLPTITHCAGCTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPPP RSSHLHCQQQQQSQDKPCPPFA PLPHPHHHPHLAHQQPASGGSS PCLRCNSCASSGAPAAGAGDNL SLLLRTSSPGGAFRTRTSSPLSG SSCCCCCCSSRRGSQLNVSELTP SSHASALRQQYAQQSAQQSAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHHPHPAHHQH HQPQARRESNPFTEIAMSSCRY NGGVMRPLSNLSASRRNLHEM DSEAQPLQPPASVGGGGGASSP SAAAAAAAAVSSSAPEIVVSKP EHNNSNNLALYGTGGGGSTGG GGGGGGSGHGSSSGTKSSKKK NQNIGYKLGHRRALFEKRKRLS
15581	45949	A	15671	1	246	SEPPHRGPTGALPSGAVRRGPL SSRPQIGRSTDSLHCVPGKATD AQRQPVKAAGSGAVPCKATG WSCPKL*EPISCINVTIC
15582	45950	B	15672	43	741	
15583	45951	A	15673	687	1012	FHTSRPFWNISELSRFCIQKYKK PWHSVSDFYRYQFFICQGTACC PASLRM*HCPN*ILQGTSSQNCC SCSGKSCSPMQQRHRSTVCSGS GTFCVGSCESFEGTYFSR

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15584	45952	A	15674	1	1640	MSCDTNGEVEGGRVDSKTRGR QEVERNTETHLGSGLNCDIPLIF LTYEWRGILEYKIFSVKTGEVL GKPGQLGHPTGQTTFFETGTQV TSMQEMGSYSFGQPHPVALQG TAPLPAAFTGWRLASVAFPGTQ CKLSVDLPIWGLEDSGPLLTAP LGSAPVGPLCGGSDPTFPFCTA LTGPSAASLLEFARGPLQTLFA WVSAEVSAEQGFFVNHECCCLI VPLEVLSQRSTRPCEVSVCPYW GVPPRDRSNQCPSGFTLDSVGP FCADEDECAAGNPCSHSCHNA MGTYYCSCPKGLTIAADGRTC QDIDECALGRHTCHAGQDCDN TIGSYRCVVRCGSGFRRTSDGL SCQDINECQESSPCHQRCFNAIG SFHCGCEPGYQLKGRKCMDVN ECRQNVCRPDQHCKNTRGGYK CIDLCPNGMTKAENGTCIGECL AVSVTEIS/CAVNKSNIDECKDG THQCRYNQICENTRGSYRCVCP RGYRSQGVGRPCMDIDECENT DACQHECKNTFGSYQCICPPGY QLTHNGKTCQGKLPFKQIESGG
15585	45953	A	15675	1	669	MGFCHDGRSIAFRGERGNDESA IEMIKVSHLKQYLAVVFRDKPL ELWDVRTCTLLREMSKNFPTIT ALILTGRCASLKWRSKPKKEEF MGYRQWNPTQESSKGDFEIQL EGGPSMATVYRTEMQPVQIGIE LLPSPLSFHPSPNSGIPNDPSWL LSTATLHPPTGVERSSSPATEQR WTENDFDELREEGFRRSNYSEL REDTQTKGKEVENFEK\NLEECI
15586	45954	A	15676	1	323	MAHESAEDLFHFNVGGWHFSV PRSKLSQFPDSLLWKEASALTS\ SESQRLFIDRDGSTFRHVHYYL YTSKLSFSSCAELNLLYEQALG LQLMPLLQVRCSCFLGVVDQ
15587	45955	B	15677	1	1443	

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15588	45956	A	15678	1	708	EVTASPQGVSAVSKGDQKWT LGKGLTFIKAVGSIQRNRWRG WQLKALYQCTTIAGATGVFLR VYRALDVLQMEEEDVLKFLAA GIHLGGTNLDFQMKQYIYKKK CDGVYIINLKRTWEKLLLAACA IVAIENPADVRVISSRNTGQRAI LKFAAATGATPIAGRFTPGIFTN QIQATFQEPQHLFFTDSRADH/S PLTEASYVNLHTIAPRNTDSPLC YVDIAIPCKKGAHSVGL
15589	45957	A	15679	78	757	REIFINVRSLLMACFVKEEDVL KFLAAGTHLGGTNLDFQMEQY IYKRKSDGIYIINLKRTWEKLLL AARAIVAIENPADVSVISSRNTG QRAVLKFAAATGATPIAGRFTP GTFTNQIQAAFRE\PRLLVVTDP RADHQPLTEASYVNLPTIALCN TDSPLRYVDIAIPCNNKGAHSV GLMWWMLAREVLRMRGTISR EHPWEVMPDLYFYRDPEEIEKE EQAAAEE
15590	45958	B	15680	1	1767	
15591	45959	A	15681	98	412	
15592	45960	A	15682	521	600	PSPGES/PPLQPDPPVPPWPPPEE EPRA
15593	45961	A	15683	117	285	
15594	45962	C	15684	12	468	
15595	45963	B	15685	1	840	
15596	45964	A	15686	1	1173	
15597	45965	A	15687	1	2931	MDLFMNVAMLRAARYLWSEA VSGFGAQDPKSLALRTHCQTSG WSLTEQDPYNNVIRTTIEALAA TLGGTQSLHTNVFDEALGLPTD FSARIARNTQIIIQEESELCRTVD PLAGSYYIESLTDQIVKQARAII QQIDEAGGMAKAIEAGLPKRMI EEASAREQSLIDQGKRVIVGVN KYKLDHEDETDVLEIDNVMVR NEQIASLERIRATRDDAASDTR EIVDLTNGNIKTFNGSIIIYARFD TGRHLFSGGNT
15598	45966	C	15688	1	1779	
15599	45967	B	15689	22	1531	
15600	45968	A	15690	98	412	
15601	45969	A	15691	521	600	PSPGES/PPLQPDPPVPPWPPPEE EPRA
15602	45970	C	15692	175	454	
15603	45971	A	15693	332	494	RKEMASGFSKGPTLGCC\RRAL PDGDTQLQLLLRGNHDSVLGA KRRDKGEAGPD

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15604	45972	A	15694	2	1276	HTLHSLVTILGTWALHSGPALL LPRPGSGLDFLLSPVLPSPQPPG LPTPTPFTNAVQLLLTLKLVSLA SEVQDLHLAQRKEMASGFSKG PTLGLL/RRRALPDGDTQLQLLL RGNHDRPVLPLPHLPGLAGAAL PRGSA\SLRPLLRRAWPAPLFGL LFLLSSHLFPLEAVREDAFYARP LPARLFYMIPVFFAFRMRFYVA WIAAECGCIAAGFGAYPVAAK ARA\GGGPTLQCPPPSSPEKAAS LEYDYETIRNIDCYSTDFCVRV RDGMRYWNMTVQWWLAQYI YKSAPARSYVLRTAWTMLLSA YWHGLHPGYYLSFLTIPLCLAA EGRLESALRGRLSPGGQKAWD WVHWFLKMRAYDYMCMGFV LLSLADTLRYWASIYFCIHFLAL AALGLGLALGGGSPSRRKAAS QPTSLAPEKLREE
15605	45973	A	15695	134	601	RDGEQPLWAWGSPCSPVAPTL CILWAPSSGPGPSFRPSPAPATP WLWPGLSPISCDSEPSASWACP LPCPSPKPDRWLLTLKLVSLAS EVQDLHLAQRKEMASGFSKGP TLGLL/RRRALPDGDTQLQLLL RGNHDSVLGAKRRDKGGQTTII FVQV
15606	45974	B	15696	76	504	
15607	45975	A	15697	11	706	HITRGRSCTRWTSSAMAKGAPR VILLCLFGAALCLTGSRALQCY SFEHTYFGPFDLRAMKLPSISCP HERFEAILSLDTGYRAPVTLAR KGCWTGPPAGQDAIEPGRAAA RLLG\VRGCTTDKCNAHLMTH DALPNLSQAPDPPTLSGAECYA CIGVHQDDCAIGRSRRVQCHQD QTACFQGNGRMTVGKGLEGW KGLGKGYGGRAAMRVVIPDRP NRETWPCSEVGGMTLV

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15608	45976	A	15698	2	1642	DEGRAKGHHTWQQTRENESQA KGETPYKTIRFRETYYHKNSMG ETTPMIQLSPTGSLPQHVGIMG ATIQDKIWVRTGLPGFPGTPGL PVSSGFPGSPGFPGLQGPPVSYG PTGIPGPIGPPGPPGLMVSSGPP GLPGPKVILGLNFQGPKGEKVS KGLQGPPGPPGQISEQKRPIDVE FQKGDQVSNGDRGPPGPPGIRG PPVSTGGEKGEKGEQGEPGKR VSEGKDGENGQPGIPVSSGDPG YPGEPGRDG/EKGKNVMGPPGP PGFPGERGQKGDEGPPGISIPGP PGLDGQPGAPGLPGPPGPAGPH IPPSKLGDTCFNCIGTGISGPPGQ PGLPGLPGPPGKL\GAPGAPGFP GSKGEPGDILTFPGMKGDKGEL GSPGAPGLPGLPGTPGQDGLPG LPGPKGEPVSCTFKGERGPPGN PGLPGLPGNIGPMGPPGFGPPGP VGEKGIQGVAGNPGQPGIPGKF GDPGQTITQPGKPGLPGNPGRD GDVGLPGM*GLPGQPGLPGIPG SKGEPGIPGIGLPGPPGPKGMLL
15609	45977	A	15699	246	433	GLFPLEPGANGI*GC/SGRIRAQ RWLPGRPKFTGESFIR*PPRVAK ESGQLIWFGCVPTQISS
15610	45978	A	15700	179	5262	RSCGSRRRMKLRGVSLAAGLFL LALSLWGQPAEAAACYGCSPG SKCDCSGIKGEKGERGFPGLEG HPGLPGFPGPEGPPGPRGQKGD DGIPGPPGPKGIRGPPGLPGFPG TPGLPGMPGHDGAPGPQGIPGC NGTKGERGFPGSPGFPGLQGPP GPPGIPGMKGEPGSIIMSSLPGP KGNPGYPGPPGIQGLPGPTGIPG PIGPPGPPGLMGPPGPPGLPGPK GNMGLNFQGPKGEKGEQGLQG PPGPPGQISEQ
15611	45979	A	15701	155	623	FNYLPPGPSHN/DVGIMGATIQD KIWGPPGLPGFPGTPGLPGERG FPGSPGFPGLQGPPGLPGPTGIP GPIGPPGPPGLMGPPGPPGLPGP KGNMGLNFQGPKGEKGEQGLQ GPPGPPGQISEQKRPIDVEFQKG DQVSNGDRGPPGPPGIRGPPVS
15612	45980	A	15702	581	687	KKGAGQVV/DDVQLAQRLAQA NEIVLSWNCWMLCKQY
15613	45981	A	15703	7	123	

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15614	45982	A	15704	1	374	RFRKAQCTIVERLTNSMMMHG RNNGKKLMTVRIVKHAFEIIHL LTGENPLQVLVNAIIN/DVSPLR RVNHAIWLLCTGAREAAFRNIK TIAECLADELINAAKGSSNSYAI KNKDELERVAKSNR
15615	45983	A	15705	2	892	QAFLPITPDQLSNYKVFAKKTA LWQNDDVHSQHKGEYRNAAG EPKYRNSVTTHSEGKWQSEKG KDLGVGYWSMACYKLGHIAG NEQQKHICGGIAKKWKQPKCP PTGKWPAVVKPATESEGGGAK KEEKAHLPRVVEKELHESSRHI RHSIESVLLQAFTQKDYTAVKE KYAKYLPHSAERYAAKRFRKA QCPIVECLTYSMMTHGRNNRK KLMIMRIVKHAFEIIQLLTGDNP LQVLVNAIINSGPREDSTLTGRA RIVRRQAVAVSPLSRVNQAIWP QCTGALE\AAFRNIKTIA
15616	45984	A	15706	1	536	
15617	45985	A	15707	8	437	
15618	45986	B	15708	255	1058	
15619	45987	A	15709	609	1489	LPLSLPRAARPAVAPHLPPREPG PALPLPPPQPPRPPSLPGSAQGC NS*RTGTAAAGAGPFAPASMSL RVQTPCWPQRGAREPPGSCAS WLFCAVWQMVRAHSGCPLAPP PAAAAWVAAQLQP*DGHEGPG G*ET/S*VLRLRPTPTPPLPTWCC TVRPRRPVLPFCLIMRRRTAGPP CAPIAAAPTTPSSLRRGKVPTGR PPVL*G*AAVMLTMAVTITRTV TTSCNAAAVMPPKTGTAHRAP LTPGTV*RDLCLVKPTAQMPPS APPWTAPPRVAVAPVIVLPAIS NLGAFA
15620	45988	A	15710	173	530	GRERGDKGGAVQTLQDLVNV HLGLTYPPRPCGHSPPSWASPQ APLQPPLRGEPGHGWGS/PSGL GQGKSEGLGPAHLPRAARPAV APHLPPREPGPALPLPPPQPPRPP SLPGSAQGCNS
15621	45989	A	15711	1	227	
15622	45990	A	15712	238	498	
15623	45991	B	15713	1	1017	
15624	45992	B	15714	590	649	

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15625	45993	A	15715	3	843	AVFLSTSNEAVYKIFDDSPCPFT AKTCNPETFPSSNESRQCPNAR CQFAFYGGESGYHRALLGLQIF NAFMFFWLANFVLALGQVTLA GAFASYYWALRKPDDLPAFPLF SAFGRALRYHTGSLAFGALILAI VQIIRVILEYLDQRLKAAENKFS Y\CLMTCLKCCFWCLEKFIKFL NRNAYIMIAIYGTNFCTSAR\NA CFLLMRNIIRVDVLDKITDFLFL *GKLLIVGIVGILAFFFFTHRIRI VQDTSPPLNYYWVPILTVIVGS YLIAHGFFQRY
15626	45994	A	15716	1	449	FRGMGDERPHYYGKHGTPQKY DPTFKGPIYNRGCTDIICCVFLL LAIVGYVAVGIIAWTHGDPRKV IYPTDSRGEFCGQKGTKNENKP YLFYFNIVKCASPLVLAGI\QCP TPQICVEKCPDRYLTYLNARSS RDFEYYKQFCVPGV/PRTIKKA NGVLEAGNSPCAYLKITPSLGT DY/PWFLLEFQCPTPQICVEKCP DRYLTYLNARSSRDFEYYKQFC VPGVQEQ
15627	45995	A	15717	627	1665	EQAGQALSTAPVGDGHELLCE VGSSSFRDVLGTSMGLCGGY/G GAS/GMGGITAVTVNQNVLSPL NLEVDPNMQGMHTQEKEQVK TLNKSASFVDKVLFLEQQNKM LETNWSLLQQQKPAQSNMDN MFESYINNLLGQLEILGQEKLK LEAELGNMQGLCMFFVKEDFK KKYEDEINKPTEMENEFVLIKK DVDDAYMNKVELEFRLEGLTD EINFLRQLYEEEIPELQSQILDTS VVLSMDNSRSLDMDSIIAEIKY EELQTLAGKHWDDRRLTKTKIS EMNRNISRLQAEIEGLPQRPEQ RASLESVIADAEQRGELAIKDA KTKLSELEAAQQRAKQDMAHG

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15628	45996	A	15718	3	3908	STQQKTARSNMDNMFESYINN LRRHVETLGQEKLKLEAEL\GN MQGLVEDFKNKYEDEINKRTE MENEFVLIKKD\VDEAYINKVE LESRLEGLTDEINFLRQLYEEEI RELQSWISDTSVVLSMDNSRSL DMNSVIAEVKAQYEEIANRSQA EAESMYQIKDEELQSLAGKHG DNLRCTKT*DLLR*TRNISRLQA EIEGLKGQRAFLEAAIADAEQC GELAIKDANAKL/SELEAALQR AKQDMAWQLR\LMN
15629	45997	A	15719	1	804	MKPRTLVVSVTVLKDGVSRVC SFRCSDVSRISSFQWVRGLADF RNEATDPHGLLDDILTLRQDKG SFMICWLKGKAPPGDPAPPRITP TVRFSTMDLSAASHRIP\LSDGN SIPIIGLGTYSEPKSLWATNHVP EMVRPTLERTLRVLQLDYVDL YIIEVPMAFKPGDEIYPRDENGK WLYHKSNLCATW\EAM\EACK\ DAGLVKSLGVSNFNRRQLELIL NKPGLKHKPVSNQVECHPYFT QPKLLKFCQQHDIVITAYSPLW TSTNP
15630	45998	A	15720	476	906	WKQHSHHQTWYLLTSEACKD AGLVKSLGVSSFNSR\QLELIQN NPGLKPKPVSNEVECHPYYTQP KLLKFRQQHDIVMIAYSPLGTT RNPTWTNMSSLPSLKDALLKR CNKITAQVILRFNIQQGVVVIPK SFNPEKIKENLQA
15631	45999	A	15721	138	217	RHAPQVLGGLSEGT*GGHRCPA RGHW
15632	46000	B	15722	8	578	
15633	46001	A	15723	1	3087	
15634	46002	A	15724	1	2232	
15635	46003	A	15725	1	2085	
15636	46004	A	15726	1	1512	
15637	46005	A	15727	1	1260	
15638	46006	B	15728	1	2145	
15639	46007	A	15729	1	1353	
15640	46008	A	15730	1	1741	
15641	46009	A	15731	1	1995	
15642	46010	B	15732	1	3464	
15643	46011	A	15733	2	109	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL
15644	46012	B	15734	90	1247	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15645	46013	A	15735	1	1698	MELKAKAQELREECRSLRSRC NQLEESVSVMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLTGVHESDGENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKGWVTHK GKPIRLTVDLSAETLQARREWG PIFNILKEKNFQPRISYPAKLSFI SEGEIKSFTDKQMLTDFVTTRP ALQELLKEALNMERKNRDTHR LKIKGWRKIYQANGKQKKAGV AILVSDKTDFKPTKILKDKEGH YIIVKGLIQQEELTILNTYAPSTG APRFIKQVRSDLQRDLDSHTLII GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDIYRTLHPK STEYTFFSAPHHTYSKIDHIVGS KALLSKCKRTEIITNYLSDHSAI KLELRIKKLTQNHSTTWKLNNL LLNDYWVHNEMKAEIKMFFET NENKDTTYQNLWDTFKVVCTG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKTL/QKINESRS WFFERINKIDRPL
15646	46014	A	15736	1043	1536	TSTELSTPNQQNIHFFQHHTTSI PKLTTYLEVKLSS*KKH*TWKG TTGTSCC/INHAKIVTHRLKIKG WRKIYQANGKQKKAGVANLV SDKTDFKPTKIKRDKEGHYIMV KGSIQQEELTTLNIYAPNTGAPR FIKQVLSDLQRDLDSHTLIMGD FNTPLLTLDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHPKSTE YTFFSAPHHIYSKTDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTKNRSTTWKLNNLLLN DYWVHNEMKAEMKMFFETNE NKDTTYQNLWDTFKAMCRGK FIAVNAHKRKQERSKIDTLTSQ LKELEKQEQTHSKASRRQEITKI
15647	46015	A	15737	1208	1387	KPWQKNYVTHAQASVADLIK WKKGYQ*LKIK*MK*SKKRSLE KKE*KETNKASKKYGTI
15648	46016	A	15738	308	487	KPWHKNYIMHAQASVANLINW KKGYQ*LKIK*VK*SEKRSLEK KE*KEMNKASKKYGTM
15649	46017	A	15739	220	1101	
15650	46018	A	15740	1	1534	
15651	46019	B	15741	365	3904	

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15652	46020	A	15742	79	506	EPSQRHSQDLQGWSQEHQVCL HRVGWGHCATCILPAATASHE GPEAW/TARLLVPQTAVGICSA FSGLPTSTHEPTGMHFLPSEAHE KPRTQPDQKRGRDDLPCTPSTC LHTSLFLDTGQEFGTCRMAGLK EHVAGDNRERRQ
15653	46021	A	15743	2	71	ELKF**FPILSPSRKTSPLRQGS
15654	46022	A	15744	1	627	MKAEIKMFFETNENKDTTYQN LWNTFKAVRRGKFIALNAHKR KQERSKIDTLTSQLKELEKQEQ THSQASRRLNQEEVESLNRPIT GSEIEAIINSLPTKKRPGPDGFTA EFYQRYKEELPK/YLLKQLQQS LRIPNQCAKITSIPKHQ*QTNRE PNHE*TPIHNCFKDNKIPRNPTY KGREGPLQGELRTIAQRNKRGH KQMEEHSMLM
15655	46023	A	15746	1	3828	MQLPVQTIAADGYVIKLQKRTT EDGHQSPERHQFPHLSSYSEQE TTRVPFAKAVASGFPGDTTLVF CASPQPSPQVHLPTQAVADIFSE FHEHYARISTAPSVTLSKANMM GSEFPTARLSNSKYPETLEVGES AQPVPMYTWKTVAQDRKDGV SPPLLEKQSITKSISNKPVELSSK VVEVDASKADHMKKMASMGL VHSMAGSGLVLSRSEILKEISSL RNGCAIYRSEFISTDPSSWVVPR PRTNEENNGES

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15656	46024	A	15747	1	1639	NCLSDHSAIKLELRIKKLTQNCS TTWKLNNLLLNDYWVHNEMK AEIKIFFETNENKDTTYQNLWD TFKAVCRGKFTALNAHKRKQE RSKIDTLTSQLKELEKQEQTHS KASRRQEITKIRAELKEIETQKT LQNINESRSLFFEKINKIDRPLA RLIKKKREKDQIEAIKNDKGDIT TDPTEIQTTIREY\YKH\LYANKL EY\LEEM\DKF\LDTYTLPRLT\Q EEVESLNRPTTGSEIEAIINSLPT KK\SPGPDGFTAEFYQRYKEEL VPFLLKLFQSIEKEGILPNSFYE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIISIDAG KAFDKIQQSFMLKALNKLDIDG TAIRQEKEIKGIQLGKEEVKLSL FADDMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDINKWKNIPCSWVGRINI
15657	46025	B	15748	1	1563	
15658	46026	A	15749	1	4332	

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15659	46027	A	15750	1	2319	MRIDGAQELTLALPFASGVACR DVKPGPRRRPLRYRCFQKPSNR LGSASLGAGFWAGRRDAKSGH DDDPSGALFSVTMDRDLEQAL DRAENIIEIAQQRPPRRRYSPRA GKTLQEKLYDIYVEECGKEPED PQELRSNVNLLEKLVRRESLPC LLVNLYPGNQGYSVMLQREDG SFAETIRLPYEERALLDYLDAEE LPPALGDVLDKASVNIFHSGCV IVEVRDYRQSSNMQPPGYQSRH ILLRPTMQTLAPEVKTMTRDGE KWSQEDKFPLESQLILATAEPL CLDPSVAVACTANRLLYNKQK MNTDPMEQCLQRYSWPSVKPQ QEQSDCPPPPELRVSTSGQKEE RKVGQPCELNITKAGSCVDTW KGRPCDLAVPSEVDVEKLAKG YQSVTAADPQLPVWPAQEVED PFRHAWEAGCQAWDTKPNIMQ SFNDPLLCGKIRPRKKARQKSQ KSPWQPFPDDHSAWLRPGSETD AGRAVSQAQESVQSKVKGPGK MSHSSSGPASVSQLSSWKTPEQ PDPVWVQSSVSGKGEKHPPPRT QLPSSSGKISSGNSFPPQQAGSP LKRPFPAAAPAVAAAAPAPAPA PAAAPALAAAAVAAAAGGAAP SHSQKPSVPLIKASRRRPAAGRP TRFVKIAPAIQVRTGSTGL/IGH QRGGPSPGSPGISGSGLQSSGGP LPDARPGSSAGCPAPLCLG\QQP

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15660	46028	A	15751	409	1874	YDSYIVVIDDADITRGDDAVPR DHHSSTSMVVFRHIRLDVIVVD GDDQHRRMVGRRCRSAWFRR GSLDVDQVIGDTAAGRLNVMG DITRDARRDKVKNERYGVAPS VAFGLGTANRLYLNYLHVTQH NTPDGGIPTIGLPGYSAPSAGTA ALNHSGKVDTHNFYGTDSDYD DSTTDTATMRFEHDINDNTTIR NTTRWSR/S/WTWSRTANTKDV SNKILTNQTNLTSTFYTGSIGHD VSTGVEFTRETQTNYGVNPVTL PAVNIYHPDSSIHPGGLTRNGA NANGQTDTFAIYAFDTLQITRD FELNGGIRLDNYHTEYDSATAC GGSGRGAITCPTGVAKGSPVTT VDTAKSGNLMNWKAGALYHL TENGNVYINYAVSQQPPGGNN FALAQSGSGNSANRTDFNPQK ANTSEIGTKWQVRGSSRVNVM HEVNTPHQCVRFRPARSAPGCC QSPCHRSGKHMQYGLSKCQPG QYNSVKSGERVNGVTFQ
15661	46029	A	15752	421	441	P*ARMPSPLGPPCLPVMDPETT LEEPETARLRFRGFCYQEVAGP REALARLRELCCQWLQPEAHS KEQMLEMLVLEQFLGTLPTEIH AWVRGQRPGSPEEAAALIEGLQ HDPGQLLG
15662	46030	A	15753	1	346	PAFGGSAPSERLELHVDGPPPRP QAPGD/CGVGRSWRAEM/HDR ALRGTNPRRHLRSCCARARRRP *RRSAPPGPRAN\PS*SSWGPSTP GNYRCRYRSWVPHTFKSELND PVELLVA

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15663	46031	A	15754	1	2091	MKPGLRRRRGRGLGCGLGPQL RATWSGAVLAGRDAVLRCEGP IPDVTFELLREGETKAVKTVRT PGAGAKLELIFVGPQHAGNYRC RYRSLVAHTFESELSDPVELLV AVAATLNIHLRLVHMLHIPAAG EGSFREGTHFLKPSPVKMPLVF RVGRRRVLNQGPQGVPIPIPRSC EHLNWQKGLCGVTKCAAPLLR GPPCPAVLRKEIPFVSLKPGLMS SKASEAEPLGPRLGSHQSTAAA LGPRYNGSADAIRPHTAWAVIQ TTISRFTWSLTQVNVPSRTVSLA VRRDRYMTSRTTTNPEEGCRG TFWARRNGCSPSACAVAEAAL EACLADVRYPVVALSCGRLQK RRDFRETNAAMSNKEKSLASA RFFVEVQVTLGALCTVQATGQ SMLVFSTTQMSSYSEKFLTSKH ASLSPRLQLADRWRDQGMKW QSPQWGELRPAASHTAEQEPGL AASKAFRDLQNLSNSAFLSLTS LSAGHQCISAIVVMMSKKEITP QGQLAAASFGELQPVALKCPW LKSQHVESWL\RPEAHSKEQML EMLVLEQFLGTLPPEIQAWVRG QRPGSPEEAAALVEGLQHDPG QLLGWITAHVLKQEVLPAAQK TEEPLGSPHPSGTVESPGEGPQD TRIEGSVQLSCSVKEEPNVDGQ EVAPSSPPLAAQSPEGNHGHQE PASTSFHPPRIQVSSPKWEV
15664	46032	A	15755	1	208	
15665	46033	A	15756	3	373	EVAQMPRVSTPATLPSLPQPAL MAPWTVPYDQLMEEEKARAR YAGTIQKWTAAALQPLSRTSLK DSGEGTSKWGRSVDTTQPLSPA IPVIFQ*AHEQSGHSGMDGGYA WALQHGLALTNTDLA
15666	46034	A	15757	3	266	
15667	46035	A	15758	3	587	YPASAGLMLQNFGVIGLRYHF AIHSPAAGGLLDGLHAVAAIQG ITKIETTPNHQRAPAHWTLLTQ QAHLQPSPLHFNLPLTLCLMHC PTAIPHCFADARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVG\AYGAQLL
15668	46036	A	15759	1	1566	

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15669	46037	A	15760	1	981	MVAIAKVLIAYKEDSDSHNQPN TRMTVSKGPVSAVEGGRRGQD SDDCVEENDAVRTWPPSRILRT ESHPSPHTCSWRRHLLSSCPYT GMSFPIPSSGNISSTHAVISFPPL SEEMNPMLPKATVMTSLEAAA RQNLKSRQAPRCEVESVTHEEV YYTRKELFEFSNLYRKKSGEQI REWILRKTDGSWRITVDYRKL NQMVTPIAAAVPDV/VVSLLEQ INTSPGTW\LCHNLIWRDLDCFL LPQNITLVHYTDDIMQIGSSEQE VANTLDLLPALMASW/ENSP*SI DRGRED*SLVHKWFCTICRHHP KVDSCSTTAPF*DIPEGQQL
15670	46038	A	15761	349	718	AGPEGTTTAECP/I/CQQQRPILS LRYGTISWG/DQSATWWQVDY IRTLLSWKWQSASAKTTIHGLT KCLIHHDIPHSIASD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHHPCSFPN
15671	46039	A	15762	143	469	ARIQ/GSRNQGVEVEVAPLTVT PSDPLANVLLPVPATLPSAGLEI LVPEEGRLPPGDTTMMPLNWN LRLPHGHFGLLLPLNQQAKKG VAVLGGVIALDCQDEISLLLYK
15672	46040	A	15763	1	2712	
15673	46041	A	15764	3	578	LKSRQAPRCEVESVTHEEVYYT RKELFEFSNLYRKKSGEQIREWI LRKTDGSWRITVDYRKLNQMV TPIAAAVPDV/VVSLLEQINTSP GTW\LCHNLIWRDLDCFLLPQN ITLVHYTDDIMQIGSSEQEVAN TLDLLPALMASW/ENSP*SIDRG RED*SLVHKWFCTICRHHPKVD SCSTTAPF*DIPEGQQL
15674	46042	A	15765	1	461	MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAF\LPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVP
15675	46043	A	15766	1	1371	
15676	46044	B	15767	54	864	

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15677	46045	A	15768	2	1148	PRGRNRRRKTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI P\EWFHCLSKLIHLLIPGMQPLT WQ/HALFSIPVHKGYINSLALC/ Q*CYLERT*LLFTSTRYHTGPLH **HYADWIQCARSRKQTGLTG KGQRFVLTERDTY\YGFTYPAH NASAKTTIHGCTECLTHPHVIPH SIASEQDTHFTAKEVWQWAHG NGIHWSYHVPHHPEIARLIEWW NGLLKSQVQCHLGDNTLQGW GKVLQKAVYALNQYPIYGTVS PIARIHGSRNQGVEVEVAPLTIT PSDPLAKCLFPVPKTLCAACLE VLLPGGGMLPPGDTTTIPLNRK LRFPLEHFGLL
15678	46046	A	15769	917	2352	DTISHQLEWRSLKSQETTGIAEI SATIKDLKGAGVVIPTTSLFNSS VWPVQKTDKSWRMTVDYCKL NQVLTPNAAAVPDVVPLLEQIN TSPGTWYAAIDLANAIFSIPVHK AQQKQFAFSWQGQQYTFTVLP QGYISSLALCHNLIRRDLDGFLL LQNITLLVHYVDDIMLIGSSEQE VANALDLLVRHLCVRGWEISPT KIQGPSTLVKFLGVQWCGACR DILSKVKDKLLHLAPPTTKKEA QRLVGLFGFWRQHIPHLGGLLQ PLYLVIQKAAIFEWNPEPEKVL QKVQAAVQAALPLGPYDPTDPI MLEVLVADRDAVWSLWQALI GESQQRPVGFWSMALPSSADN YSPFERQLFACSWALVETECLT MGHQVTMQPELPIMNWMLSDP SSHKVVQAQQH\QEVAQMPRV STPATLPSLPQPALMAPWTVPY DQLMEEEKARARYAGTIQKWT AAALQPLSRTSLKDSGEGTSKW
15679	46047	A	15770	1	861	
15680	46048	A	15771	5	90	
15681	46049	A	15772	1	324	MVQEASEVIGQLQSSAAK*AM HWAGFSYLTKKSLNAN
15682	46050	C	15773	1	726	
15683	46051	A	15774	364	543	ARGAARSMKHTSGDETKRQKL D*VRLTGIRASREEVTKEAGPR KRIMCSGMDELNGGLQL
15684	46052	B	15775	1	1056	
15685	46053	A	15776	1	282	

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15686	46054	A	15777	167	954	KRVTSKLKSPRRGSPHCSRNPV LLRGIGRYSRSAMYSRKAMYK\ RKYSAAKSKVEKKKKEKVLAT VTKPVGGDKNGGTRVVKLRK MPRYYPTEDVPRKLLSHGKK\P FSQHVRKLRASITPGTILIILTGR HRGKRVVFLKQLASGLLLVTG PLVLNR\VPLRRTHQKFVI\ATFT KIDISN\VKIPKHLTDAYFKKKK LRKPRHQEGEIFDTEKEKYEITE QRKIDQKAVDSQILPKIKAIPQL QGYLRSVFALTNGIYPHKLVF
15687	46055	A	15778	1054	1403	MVEGGILRVNTSVECKTGPFFF SPHILWREPFCSVQVGKKKKEK VLATVTKPVGGDKNGGTRVVK LRKMPRYYPTEDVPRKLLSHG KKPFSQHVRKLRPSITPG\TILIIL TG\RHRG
15688	46056	A	15779	1	388	
15689	46057	A	15780	1	456	MKLPEEGSLSDICCSAIFAVLQP LLVIPRETGSGVDLQQTPTDLQ LRQTESQIMSELPFTVASKRIKY LGIQLTKDVKDLFKEIYKPLLSE IKEDTNKWKSIPCSWLGRINIVK MAILPKVTYIFNAIHIKLPMTEL EKTK\FIWNRKRACI
15690	46058	A	15781	1	504	
15691	46059	A	15782	1	1836	

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15692	46060	A	15783	285	1949	RGEMNSRGRNNLSIINKTDFPFI ALNAHKRKHERSKIDTLTSQLK ELEKQEQTNSKASRSHEITKIRA ELKEIETHNKPFKKISESR\SWFF IFYF\ERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITTDPTEIQT TIREYYKHLYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGSEIEAIINSLPTKRSPGPDGFT AEFYQRLKQCRKAHLDPVSLT HRSGPGAREDRLSDSGDASRGC WNLSQHAAVTSPESEERRIRTL SCRSVGVCRRSTPDPVCLGISSG GCRTVNIGEQQMLLPDRSSGSF VSEGYRPCEVSAPTGGCPPVRC LMINTVSLIGVKFTEVFDSINISE HLELACLQDHNSLLAREQNWT EDEFDELTEVGFRRWVITNSSE LKEEVQTHCKEVKNLETRLDE WLTRITNAEKSLKDLMELKTM AGELRDACTRFSSRFNQLEERV TEIEDQMNEMKQEEKFREKRIK RNEQSLQEIWDYVKRPNLHWL GVPESDRENGTKLENTLQDIIQE NFPNLARQTNIQIQEMQRMP
15693	46061	B	15784	596	1414	

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15694	46062	A	15785	610	2986	QTERNSININRNGHQHQNPICRS PSSKTKGSIKPQRSGRNQSRKA ENSKDQRTSSPTKDCSSSPATE QRWMENDFDELTEV/VLQKPG RDTT\KQKEKFRPISLMNIDVKI LNKILANRIQQHIKKLIHHDQV GFISGMQGWFNICKSINVIHHIN RTNDKNHMIISIDAEKAFDKIQ QPFMLKTLKKLGIDGTYLKIIRA IYDKSTASIILNGQKLEAFPLKD RTRQGCPLSPLLFNIALEVLARA IRQEKDIKCIQLGKEKVRLSLFA EDMIVYLENPIVSAPNLFKLISN FSKVSGYKINVQKSQVFLYINN RQRESQIMNEFPFTIARRRIKYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNMPCSWIGRINIM KMAILAKVIYRFNAIPIKLPMTF FTELEK\TTLKCI*NQKRAHIAK PILSQKNKAGGITLPDFKLHYK AAVTKTAWYWYQNRDIDQRN RTEPTEIMLHIYNHLIFDKPDKN KKWGNDSLFNKWCWENWLAI CRKLKRDPFLTPYTKINSRWIE DLNIRPETIKTLEENLGNTIQDIA MGKDFMSKTPKAMATKAKIDK WDLIKLKNFCTAKETTIRVNRQ PTEWEKIFAIYSSDKGIISRIYNE LKQIYKKK\NNPIKKWAKDINR HFSKEDIQAASKHVKKHSTSRIF MQIKTTLGYHLTPVRMATIKKS KNNRCWCGCGEKGTLIHCW/M
15695	46063	A	15786	1	906	MVNQKRYHIPGGTAEISGTIKK LKNAGVVIPTTSPLNSPIWPVQ KTDGSWRMTMDYHKLNQVVT PIAVAVPYVVALLEQINTFSCT WYAAIDLANTFFSFSVHKA/HK K*FAFSRQGQQYTFTVHP\YDN YSPFERQLLACYWASVETEHLT MGYQVTIQLELPIMNWVLSDPS SHKLGHAKQHSIIKWKWYIRD RARAGPEGTARIHRSRNQGVEV EVAPLTITPSDPLARFLLPVPTIL HSAGLEVLVPEGGTLPLGDTTT IPFNWKLRLPPGHFRLLLPLNQ QAKKGVTVFAGVIEAIKMK

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15696	46064	A	15787	1	909	MVLEVSVSDRDAVWRLWRAPI GESQQRSLGFWSKVLPYSADN YFPFERQLLACYWALLETDRLT VGHQVTLQPELPIMNWVLSDPS SHKVGHVHQHSIIKWKWYIRD QTRAGPEGTTTPVITQ/WDAHE QSGLSGRDG\KGQRFVLTGVDT YSGYWFAYPAHNASAKTSIYG FTECLIHCHGIPHSIASDQGTLFT AKEVWQWAHAHGIHWSYHIP HHPIAAGLIEWWNGLLKSQLQ CQLGDNTLQGWGKDLQKAMY SLNQRLIYSTVSPISRIHGSRNQ RVEVEVAPLTITLSDPLAKFFFL
15697	46065	A	15788	1	754	MQNNVDSFQEPPPTPLFSSRPIA RLKSKQAPRGEAESVTHEELESI RLRAKTSDKISSLTFRRGWGKV LQKAMYALNQHPIYGTVFPIPRI DGSRNQGVEVKVAPLTITLSDP LAKFLLPVLSALHSAGLEVLVP EGGILPPGAGDMRMIQLNWKL SLPPGYFGLLLPLSQQTKKGVT DLGGVIDLDYQDEISLLFHI\KV NGKLQQPNPDRTTSGPDPSGM KVWVTPPGK/EPQPAEGLAEGK GNTEWVVEE
15698	46066	A	15789	686	1506	VETVHLMLQIGEFKKTDVS/WK TVDYHKLNQVVTPTAAAVPDV VSLLEQINTYPGTWYAVIDLEN AFFSVPVHNAHQKGFAFSWQG QQYTFTVLPQGYINSPTLCHNLI RRDPGHFSYPQDITLVHYIDDI MLIGSSEKEVANTLDLLPIYQV TLKAANYEWGPEQEKAVQQV QAAVQAALPLGQHNPADPTVL EVSVADRDAIWNLWQAPIARIH GSRNQGVEVEVAPLTITPSDPL AKFLPPVPATFCSAGLEVLVPE GGMLPPGEIETIPLK
15699	46067	A	15790	422	537	VNQFGVIFCAAIIN*YECLKQSF KTQTDYFPSPLNTSQ
15700	46068	B	15791	1	519	

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15701	46069	A	15792	53	753	SLGTGTLRVLLGTAEAQMLQFS HLYADYGGKPALEDINLTLESG ELLVVLG/PSGCGKTTLLNLIAG FVPYQHGSIQLAGKRIEGPGAE RGVVFQNEGLLPWRNVQDTVA FGLQLAGIKKMQRLKFAHQML KKVGLEGADKRYIWQLSGGQR QRVGIARALAANPQLLLLDEPF GALDAFTRDQMQTLLLNLWQE TGKQVLLITHDIEEAVFMATEL VLLSSAP\GRVLERLPHI
15702	46070	A	15793	2348	2760	LWLVCINCFIPAFLLMLRWLPR LKPLSQLSVPTYRLPSVPFLKPT GMESPEAISRVSGKGIL*RDSDA YSVSLSYHYPHRHPSSIIVDHRS SIDP*PIVDHSSSIAKRSGTFPLG YWEVFVQLTFGQQRQASGILQ
15703	46071	A	15794	2	415	HPGLETTDLLSPLPAALEPQGQ GRPSIQGAPRGSFTRIEAGTPHV PAPCPAAQRNQGWGLVGAWL GFMAP*EQSVASSWK*PLMKS QYSREVISHLPLVPMQQGRPVM TQSMWGWLVWFPALFLVQIGH LVMSSGHS
15704	46072	A	15795	428	885	GISMKLSRISAI/NWNKISDDKD LEVWNR/LTSNFWLPEKVPLSN DIGAWQTLTVVEQQLTMRVFT GLTLVDTLQNVIGAPSLMPDAL TPHEEAGLSNISFMEAGHARSY SSIFSTLCQTKDVDAAYAWSEE NAPLQRKAQIIQQHYRGDDPLK K
15705	46073	A	15796	1	1125	
15706	46074	A	15797	57	303	SHKHYADALLYPAPDVCTAC* LLRGNRRDQSKS\TAKRHLTAA HFRFVRMVRHGNH/SRLRPDSF R*PVSPDR*PPLRAAHFR
15707	46075	A	15798	3	430	
15708	46076	B	15799	1	1338	
15709	46077	A	15800	380	1043	WTRWRASAADNLAHGRWGEQ KLVVTTGASGAPDRQAARCGC IWRKISWYRSKGSKHPLTPKEV EKTGWGLKIRGMGKQQIA\ERV KEAARILELDGLLKRRPRELSG GQRQRVAMARAIVRDPAVFLF DEPLSNLDAKLRVQMRLELQQ LHRRDQVEAMTLAQRVMVMN GGVAEQIGTPVEVDGDDTLEIL GADNLAHDAGRAEAGGDWRI RSARRSSTCAH

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15710	46078	A	15801	1	900	MAAIAFLITWFLSHDKKRIRILK RLSGGGNMADEFPGGAVVFTV LNLTHWLEDWGLPVHWRSSC MPSGLEYLIVLIFKGVIVAVHLL IVDALNLIRRIHAV/QGSPCVET CQHALDQLIMHSQPTHAVAVF DDENRSSGWRHQGLPDYKAGR PPMPEELHDEMPALRAAFE\QR GVPCWSTSGNEADDLAATLAV KVTQAGHQATIVSTDKGYCQL LSPTLRIRDYFQKRWLDAPFID KEFGVQPQQLPDYWGLAGISSS KVPGVAGIGPKSATQLLVEFQS LDGIYENL\D\AVAEKWRHKL
15711	46079	A	15802	1	1350	
15712	46080	A	15803	1618	2082	
15713	46081	A	15804	1	803	MINLIGSDVNYDWLKLPLVHL HWYDKEVRPGRKVGHLNLTDS DTSRLTATLEALIPLLPPEYASG VIWAQSLIRCVKHRIRHCAPIAG CGTGCRPDKTRQASHQAQMSN AYDYSEIQGIGKQKAANRVAEP RTYHSFASITDRRADLLKPGNH AQDGRLTAARRADKHDELFIG NFQKADNRGQVSDSVEGNSNC APVKPAPIPTERIPLALMASMPA CASSMPIHACGGTPSPAQAARK ISGSGFEFLSWEASAQKVKNSR SSSAAKIVGAFRETEASPTEICC ARRSASKERMPG*ARADPHRA HTAGVNGVNARLRIFNADTCL RRHAQPCTGGEKDFRVRFRVF KLGSIRAEGEKLAQLQRR

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15714	46082	A	15805	1	1655	MRGHNWIDMDQARQQSTPHT DRKICHKNDRPRTTPLRKIDAH PHTLIILPAESTLSTTKYKLRAL LVENTNKDKSAVSVVFRGSVL HQQAANFPNLMLCFQLKNGVN ACNDFIMLFVDDNAAGSIERAA SPCINEKQHAFSESVPAIAAVRG LGSMIAVEFNDPQTGEPSAAIA QKIQQRALAQGLLLLTCGAYG NACKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKLT PVIQPRASGEYNEEFSLLPVVN YLKDKLSNPVRLVKDYLDGVD VAEGELVVLENVRFNKGEKKD DETLSKKYAALCDVFVMDAFG TAHLRAGFLLTGI\GKLRCSLRC AGPLLAAELDALGKALKEPARP MVAIVGGSKVSTKLTVLDSLSK IADQLIVGGGIANTFIAAQGHD VGKSLYEADLVDEAKRLLTTC NIPVPSDVRVATEFSETAPANL KSVNDVKADEQILDIVRDLDAA NVVINAVFSYVTNVWGWAFE WYMVVMLFGWFWLVFGPYAK KRLGNEPPEFSTASWIFMMFAL
15715	46083	A	15806	1	1359	
15716	46084	A	15807	670	1008	
15717	46085	A	15808	455	1137	GTKPRDIDHILGTFITPGMPKGG KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHD VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG
15718	46086	A	15809	465	888	RGLVALSSERRCRLRRRNHPES GTRSPDPAGAASLSRRFFYAPP GTPETGCGYSSRSRSQRKR/LST WRCNS*ETPKSPPKACCRPARIP APRSSSVKKASACGPAAVMKK RCRKASITPISKITCAIHRMRRW TCTKRAAF
15719	46087	A	15810	417	707	IQIHERSWRYLHWWSSVRRRA A*YGAPL*RDGIQRGTRRISQV YQ*SSVRQLRRDASASGSAPRV CREYAAACYLRHEHWSCDAVS PTPRMLKSFV
15720	46088	B	15811	1	4350	

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15721	46089	B	15812	1	2862	
15722	46090	A	15813	1	1471	MLHSRGFLAEVFGILARHNISV DLITTSEVSVALTLDTTGSTSTG DTLLTQSLLMELSALCRVEVEE GLALVALIGNDLSKACGVGKE VFGVLEPFNIRMICYGASSHNL CFLVPGEDAEQDGTGTSGIGAQ KKKMYANNGAIDRKLLFEATF VTIEKCCDTNQKGDDTHALGQ PIRGHDKSLAGSFCYACRSEEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNIAGDLTAVIAPDGS RNGTQYDAWGKAVRTTQGG\L TRSMEYD\AAGRVIRLTSENGS HTTFRYDVLDRLIQETGFDGRT QRYHHDLTGKLIRSEDEGLVTH WHYDEADRLTHRTVKGETAER WQYDERGWLTDISHISEGHRV AVHYRYDEKGRLTGERQTVHH PQTEALLWQHETRHAYNAQGL ANRCIPDSLPAVEWLTYGSGYL AGMKLGDTPLVEYTRDRLHRE TLRSFGRYELTTAYTPAGQLQS QHLNSLLTYRHANFAL
15723	46091	A	15814	1	1367	MSKLLERFRYFKQKGETFADG HGQVMHSNRDWEDSYRQRWQ FDKIVRSTHGVNCTGSCSWKIY VKNGLVTWEIQQTDYPRTRPD LPNHEPRGCPRGASYSWYLYSA NRLKYPLIRKRLIELWREALKQ HSDPAADNDLIARFQSFTNQPFI ANRLTGNDRARFNLTFIVNNQH ATAITTTGTFLPEWSTTFIITLIL QSKVQAIDLTKEAIVTVGCNTIS TTVHEVVSASIGIATKFWQHIGP CFYVIYDTVVTTIVESRTTEYSP DVVTGLITRITTPDGRASAFYN NHHSQLTSATGPDGLEIRREYD EWGRLIQETAPDGDITRYRYDN PHSDLPCATEDATGSRKTMTW SRYGQLLSFTDCSGYVTRYDH DRFGQVTAVHREEGLSQYRAY DSRGQLIAVKDTQGHETRYEY NAA/GDIRQCESDLQSPSCSQYR AIDGESLSETARYSVHQ

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15724	46092	A	15815	357	1733	TADSPETLRCQTSGENARGAGT VERAGKSLWRSLR*SHRP*STR TGDIHCQIQTNFSLFN*QHPGQH R\YGSGTAIINQSLITHDPEYPEN LPAAPLVRYGWTPRGELAVVY DRSGKQVRSFTYDDKYRGRMV AHRHTGRPEIRYRYDSDGRVTE QLNPAGLSYTYQYEKDRITITD SLDRREVLHTQGEAGLKRVVK KEHADGSVTQSQFDAVGRLRA QTDAAGRTTEYSPDVVTGLITR ITTPDGRASAFYYNHHNQLTSA TGPDGLELRREYDELGRLIQET APDGDITRYRYDNPHSDLPCAT EDATGSRKTMTWSRYGQLLSF TDCSGYVTRYDHDRFGQMTAV HREERLSQYRAFDRRGTVIAVK ETQGLETGFEYHFPVPDGVIAP KG/SRNGNSQSVGKRRSTEDIR G*TRWRGYTADRRAAKTHARV E*HLRARPRVCALFFPKQCERH
15725	46093	A	15816	1595	3228	DNNAKLFRAGQMKVLKPYVDS GKIKVVGDQWVDGWLPENAL KIMENALTANNNKIDAVVASN DATAGGAIQALSAQGLSGKVAI SGQDADLAGIKRIAAGTQTMT VYKPITLLANTAAEIAVELGNG QEPKADTTLNNGLKDVPSRLLT PIDVNKNNIKDTNLPAAPLVRY GWTPRGELAVVYDRSGKQVRT FTYDDKYRGRMVAHRHTGRPE IRYRYDSDGRVTEQLNPAGLSY TYQYEKDRITITDSLDRREVLH TQGEAGLKRVVKKEHADGSVT QSQFDAVGRLRAQTDAAGRTT EYSPDVVTGLITRITTPDGRASA FYYNHHNQLTSATGPDGLELR REYDELGRLIQETAPDGDITRY RYDNPHSDLPCATEDATGSRKT MTWSRYGQLLSFTDCSGYVTR YDHDRFGQMTAVHR\EEGL\SQ YRAYDSRGQLIAVKDTQGHET RYEYNIAGDLTAVIAPDGSRNG TQYDAWGKAVRTTQGGLTRS MEYDAAGRVIRLTSENGSHTTF RYDVLEQYCGQVIKAHAVSRF
15726	46094	A	15817	1	627	
15727	46095	A	15818	701	895	

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15728	46096	A	15819	1412	1705	LASISTSCAPPKVNCGVMAIFLA SDSRLWSGLRAQATSRSTLSLM TRSGLWLAIQ*NALRSWLASHE TKRPPSTLGGNTVPS*ALRLGIL ASSRILL
15729	46097	A	15820	344	547	
15730	46098	A	15821	1	1518	
15731	46099	A	15822	1693	2455	VLAAFTRSKQRYGAPRLTDELR AQGYPFNVKTVAASMRRQGLR AKASRKFSPVSYRAHGLPVSEN LLEQDFYASSPNQKWAGDITYL RTDEGWLYLAVVIDLWSRAMA LLRRKSPGNVIVHTDRGGQYCS ADYQAQLKRHNLRGSMSAKG CCYDNACVESFFHSLKVECIHG EHFISREIMRATVF\IISNVITIGG GGTVAARGGVP*AVKSNVNDV RRNCLARSSNNGWIFPPVVVNG WRQQALTIVAGICC
15732	46100	B	15823	1	1407	
15733	46101	A	15824	1	3252	
15734	46102	A	15825	1	2409	
15735	46103	B	15826	1	2802	
15736	46104	A	15827	1715	1824	
15737	46105	A	15828	410	720	PGSRAVIGWSMSPRMTAHWPA MPCRWRCGGVRTYAPEPTG*R RWLQNCSACSS**LRKTSRKNR TT*RTPARSSSAPPLMLKQPFTR QWPLNTPWKPPRLSPS
15738	46106	A	15829	905	1008	SCDSYRLSSRAAAVTPMRSASF RASGFLLVILFVCRVSVVGCRV LAWSGGSVFRRGVPLAWTVLR WVRRRCGCGVGRCRGLSAVV YPSGIITVDSARSWRIMGRSGSP LA\TVGLAGCWSQPRL*TDAFS KLQGFRVFTGDTICM
15739	46107	B	15830	1	3148	
15740	46108	A	15831	1896	2062	SVCYPGRN*IPSG*N*PRIWSDP VQRRERAGKKWLHENPGWRK **PDYHYRSEAD

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15741	46109	A	15832	1	1456	MSTEIARLKRQLADGMKSWLS SKRPRHTSRAPEMKYVFIEKHQ AEFASKQCAACSGWPATAGNV VSAADKDKHASAVPPHCDSVV LAAFTRSKQRLPLNVKTVAASL RRQGLRARPPGSSARSATAHTA CLVRKSVGAGFLRQWPEPKWA GDITYLRTDEGWLYLAVVIDL WSRAVIGWSMSPRMTAQLACD ALQMALWRRKKPRNVIVHTDR GGQFGDRWK/ALANALNIPLDQ LSARISANPKGGF\IYLAREVNP DMADYIKKLKLPGIHVREESRR YYPSGEVTAHLIGFTNVDSQGI EGVEKSFDKWLTGQPGERIVRK DRYGRVIEDISSTDSQAAHNLA LSIDERLQALVYRELNNAVAFN KAESGSAVLVDVNTGEVLAMA NSPSYNPNNLSGTPKEAMRNRT ITDVFEPGSTVKPMVVMTALQR GVVRENSVLNTIPYRINGHEIKD VARITTEEDFNHASAARFVCAA AERALQNHH
15742	46110	A	15833	2	929	
15743	46111	A	15834	1	472	
15744	46112	A	15835	1	513	
15745	46113	A	15836	1	254	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTGAA YSLSRDQKRV/LRYEPVSQFRLS ETQKHQSVCHAFIRIPVSVS

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15746	46114	A	15837	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIG\LQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCLALHRIETEL MGKFDEGKLPTDPHLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK
15747	46115	B	15838	1	1734	
15748	46116	A	15839	1	971	
15749	46117	A	15840	1	1143	
15750	46118	A	15841	1	556	
15751	46119	B	15842	8	1000	
15752	46120	A	15843	1	1169	MLTLILLDLQFMAQLAGYQMS FNSTKSKQTKNNFAVGYRTGD FQLHTNVNDGAEFGGSVYQKV CEELDALINLAWTSSTSCTRFG LAAKFQLKPIAFISTKVNHWLT GVSYTPPLEAGVKLNLSALCDN LKTCHTSHGSVMAETAVINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAMRLY ESLCQYRKP\DGSGIVSLKIDWII ERYQLPQ/TYQRMPDFRRRFLQ EEFESLNRQITGSEIVAMINSLST KKSPGPDGFTAEFYQ
15753	46121	A	15844	1	1509	

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15754	46122	A	15845	1	558	
15755	46123	A	15846	1	1773	
15756	46124	A	15847	1	2256	
15757	46125	A	15848	1	812	MEVLASWATFTLGQTEQHVD WISAGAAPQGPIVKQLPSPVPPT EQLEQEKPVTIGSAPSTPNKLLL SHSNCQLPRPLRSITNISACFSLE LAIDHRGFPHSPGARSLYSNSVF GTYQLCDLCDNLKTCHTSHGS VMAETAVINHKKRKNSPLIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPW/FIKRSPE*RRGKFPFT QMGQD
15758	46126	A	15849	1	1773	
15759	46127	B	15850	1	1755	
15760	46128	A	15851	1	726	MPASGNENDLNMPSGTIEIFVR CYVEVERIMSAWTEQPNEHRT MMWSVLLQPCDNLKTCHTSHG SVMAETAVINHKKRKNSPRIVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRG/LYSV HINPYLIPFFIGLQNRFTQFRLSE TKEITNPYAMRLYESLCQYRKS
15761	46129	B	15852	356	671	
15762	46130	A	15853	1	2121	
15763	46131	B	15854	721	2739	
15764	46132	A	15855	1	5828	MQEQQQASSLIRSGNGRLPGSG AQRTPCHIRRDGSQRRVCDDCK QQWWKAKYNIPSGLHACTATL EETHILDSGAHVQVFYKGQLH VMRVPCTDYFDTQKNPNLSHL HGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQN
15765	46133	B	15856	537	1318	
15766	46134	B	15857	1	411	
15767	46135	A	15858	1	1356	

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15768	46136	A	15859	1	1215	MPYDRPFTVMAAFPLCPACDK EYRDPLDRRFHAQPVACPECGP HLEWLKMGKIVAIKGIGGFHLA CDARNSNAVATLRARKHRPAK PLAVMLPVADGLPDAARQLLT TPAAPIVLVDKKYVPELCDDIA PDLNEVGVMLPANPLQHLLLQ ELQCPLVMTSGNLSGKPPAISN EQALADLQGIADGFLIHNRDIV QRMDDSVVRE\RRNAAPF/AGA VLSQHLGDLSDDGIQMQWRER YSLMQNIYDFTPQYVVHDAHP GYVSSQWAREMNLPTQTVLHH HAHAAACLAEHQWPLDGGDVI ALTLDGIAQPDERSRSEDVDRA HQRGHERDRRRRRSGTSHLTR VDLKEDGKGLKIVRQSLPYGTA SGTHGLYFCAYCARLHNIEQQL LSMFGDTDGKRDAMLRSPNR
15769	46137	B	15860	74	2050	
15770	46138	A	15861	2	703	LQARFPLSWRNFPITFACYAGL FCLSASIIYP/DHLCPVSVPRAFA GPRHRRHLLVLHRGCGLRH/TK RPGPGPGPARALAIWPPDPGC* RCRRPSLPASSLRSSATPTCTST QPALEWCVAVYAICFILAAIAIL LNLGECTNVLPIPFPSFLSALAL LSVLLYATALVLWPLYQFDEK YGGQPRRSRDVSCSRRHAYYV GAWDRRLAEAILTAINLLTYVA DLMHSAHLDFSKV
15771	46139	A	15862	1	849	MAQPLAKQWTPVSPRALLVSIS SMPPRPAADVTVCRHRNCTLRE LLYGFAYAAAQQLNLHGDVCN DGDG/VEVRLREDPETFLVQLY/ QHCPPLA\RTGGTMNTQIVPDA ATCPASLSEMNTPGERRYRYPF INCTHYGPSFPIIRAMPYDRPFT VMAAFPLCPAC/DKEYRDPLDR RFHAQP/VACPECGPHLE/WGIG GFHLAC/DARNSNAVATLRARK H/RPAKPLAVMLPVADGLPD/A ARQLLTTPAGAGLWLGGNGYP RAPDNANSTAMSCASHAHSFG GGHPRGR
15772	46140	B	15863	1	2688	
15773	46141	A	15864	1	1578	

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15774	46142	A	15865	1	877	MQAAHRLRPAYRIKTGKPPAL ADYHPAYQEMLSRKQDRVIDQ IDFGIKDTVEILHMGQIQSMGRE FALSLRFSIHGHNVHGNESPEM GPERRSGFYDEWSPERIIQYYRP AREQLMNELVQILKNTRQHLM TGVSHMIPFVVSGGILLAVSVM LYGKGAVPDAVADPNLKKLFD I\GVAGLTLMVPFLAAYIGYSIA ERSALAPCAIGAWVGNSFGAGF FGALIDAFPRLSEEINPALPEAK VMACLEAVARQDNVDSPQELP PTPLFASRPITRLKSWWAPGGE VESGTHKK
15775	46143	A	15866	3	423	
15776	46144	A	15867	633	771	NNRSHPALCTNRPPRTRLVFYP LLAPNA*LAALQKGWAYGAGH NA
15777	46145	A	15868	1	4014	
15778	46146	A	15869	1	180	SGHPFIPLKDLTQIAIGDVFNNN LILWANREIIHSVP*RY*HDANI QCFVVISSFVRSQQ
15779	46147	A	15870	815	1905	IFQEHIMDHLPMPKFGPLAGLR VVFSEM/WRAEVIWIENVAWA DTIRVQPNYPQLSRRNLHALSL NIFKDEGREAFLKLMETTDIFIE ASKGPAFARRGITDEVLWEDKP KLVIGHLSGFAHQVSQISTHQG SSNWVSPDQLQCNTQTNSPKQ LFSTHCMQCRPNSTTNSRQFQS NPVNHALNHQSKPHHPLVYAQ HKAKRAHRAKSITASRKQATTF QQVGAPAGGHTHTSSSHPQTT KALEQVKHLTTRQAILSKAKPQ ATSPIPRDTGPLRGRQFHALNPS TTVIGQPANQRIGQHGHPQFKP KTPFWPQPKEKVPNRQCTSKTY SNGEQNIPQTYAIRTKNRSTYPR NLKQQPLNPGKAKT
15780	46148	A	15871	1	361	QTTGISFQGRGGAGPGVPTRTQ/ CLRCHGGRHG/HPSHLCKPNKG DPRKIRLKMSWR*PWFAIGPRD WSSSRPKPTSPRGSCRSFIEASK MSAPVVWSTKTHSSRSMLSFSL MEDFVTALSIL
15781	46149	A	15872	1	447	

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15782	46150	A	15873	1	1424	MLLEQLSQHKLDMIISDCPIDST QQEGLFSVRIGECGVSFWCTNP PPEKPFPACLEERRLLIPGRRSM LGRKLLNWFNSQGLNVEILGEF DDAALMKAFGAMHNAIFVAPT LYAYDFYADKTVVEIGRVENV MEEYHAIFAERMIQHPAVQRIC NTDYSALFSPAKLRRALYHPAS TELHPACGKDFRQLYRRIQNQI QRHALWHKIFDVEIPHPILIIAR VSANMPHTGCRIAIEWPGKVVE AILRLTNDAPEYLPIGFNHKSK MRSEGMNPYQRQFMELALSNQ VLKCGEFTLNRGRKSPYFFNAG LFNTGRDLALLARFYAEALVDS GIEFDLLLAPAYKGIPIATTTAV ALAEHHDLDLPYCFNRKEAKD HGEGGNLVGSALQGRVMLVD DVITAGTAIRESMEIIQANGATL AGVLISLDRQERGR*CDHRRNG DSRVDGDYSGQWRDACWRVD FARSSGTRARRDFGDSGS*A*L QLQSDLYHHPERPDCLPGREAG NGGTSGGG
15783	46151	B	15874	1	1086	
15784	46152	A	15875	484	729	CTQFRKTCFTCKASNGFCFATS CNLIYTSEIICRGPTG*HNLIASL LQRIDNLRKFIVIPTLKYLTRCR LDDNIMIFYAQGI
15785	46153	A	15876	1717	1971	PANAWAEMWEYSAWQRRMYS MG*TSKVVVHPGATDRW*NTN GCYRIFWIAAPFVPAAVIHGNIL PTHGACVHKGFGRAPAGAAVE
15786	46154	B	15877	1	765	
15787	46155	A	15878	103	823	VPACAGLKKEARSLLASPPRLL NTKLQASCRALFSPPIQSRQTTG ISFQGRGGAGPGVPTRTQ/CLRC HGGRHG/HPSHLCKPNKGDPRK IRLKMSWR*PWFAIGPRDWSSS RPRPTSPRGSCRSFIEASKMSAP VVWSTKTHSSRSMLSFSLMEM PARMPITSSMPSTPLRQGSVKFE DFVTALSILLRGTVHEKLRWTF NLYDINKDGYINQEEMMDIVK AIYDMMGKYTYPVLKEDTPRQ

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15788	46156	A	15879	1	2926	MVKDASQSQASLGLDAFLPAS GVQYTHERSPDSPLKSQECPSG VVNEDTFKQIYAQFFPHGGLMS ENGTGKKASVFGSTGSGALLLE EGERRREQPLIEMRKPPHVLIN YQAKVGGNSIPSPSLCKPAFPPL PSWAVDLASARQKEDASRSLQ NKEEDFYTSQPGFPALALGCCL RVNLLLGHRGISAGSSYRPITST PCHLCKLGQEVFAKPLNLQDQ CQQNLVMQVLKLVLNCLNFDF IGSSADESADDLCTV
15789	46157	A	15880	1	1521	
15790	46158	A	15881	1	1182	MDKFLDTYTLPRLNQEEVESLN RPITGSEIVAIINSLPTKKSPGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTKKENFRPISLMNIDAKILY KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLAQNLLKLISNFNKV SGYKINVQKSQAFLYTSNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRAHIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYCYQNRHIDQWNR\PSEI TPHIYNYLIF
15791	46159	A	15882	1	690	
15792	46160	B	15883	1	458	
15793	46161	A	15884	1	719	
15794	46162	B	15885	1	3552	
15795	46163	A	15886	1	321	
15796	46164	A	15887	1	362	
15797	46165	B	15888	1	489	
15798	46166	B	15889	1	1660	

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15799	46167	A	15890	1	1593	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKRIKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIIQENFPNLARINKI DRPLARLIKKKREKNQIDTIKN DKGDITTNPTEIQTTIREYYKHL YANKLENLEEMDTFLDTYTLPR LNQEEVESLNRPITGAEIVAIINS LPTKKSPGPDGSIAEFYQRYKE E/PADKQLQQSLSIQNQCTKITSI LIHQQQTNREPNHE*TPIHNCFK ENKIPRNPTYKGCEGLLPGELQ TTAQGNKRGYKQTEEHSMLM GRKNQYRENGHTAQGNF*IQC HPHQATNAFLHRIGKNYFKVH MEPKKSPHRQVNPKPKEQSWR HHTT*LQTILQGYSNQNSMVLV PKQGYRSMEQNRALRNNAAYL QLSDL*QT*EKHAMGK/EFPI**
15800	46168	A	15891	1	1177	
15801	46169	A	15892	1	3663	
15802	46170	A	15893	1	1995	
15803	46171	A	15894	1	4191	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ

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15804	46172	A	15895	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRSLH AKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWIHDEMKAEIKMFF ETNENKDTTYQNLWDAFKATA SKTNKEKEKNQIDTIKNDKGDI TTDPTEIQTTIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESLNRPITGAEIVAIINSLPTK KSPGPDGFTAEFYQRYKEELHI NRAKDKNHMIISIDAEKAFDKI QQPFMLKTLNKLGIDGTYFKIIR AIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMTVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIPCSWVGRIN IMKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQK\RARI AKAILSQKNEAGGITLP
15805	46173	A	15896	1	1740	
15806	46174	A	15897	1	880	
15807	46175	A	15898	1	2777	MGKKQNRKTGNSKKQSTSPPP KERSSSPAMEQSWMENDFVEL REEGFRRSNYSELQEDIQTKGK EVENFEKNLEECMTRITNTEKC LKELMELKTKARELHEECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKRIKRNEQSLQEIWD YVKRPNLHLMGVPESDGENGS KLENTLQDIIQENFPNLASTLSD HSGIKLEINSKRNPQNHANTWK LSNLLLNAHWVNNEIKMKVKN FFELNDNSDTIYQNFSD
15808	46176	A	15899	326	3096	QTERTSTPKTHLYVTIIKDQK*I KPQRRGKNRGEKLETLKSRAP VLLQRNAVPQQQRNKAGRRM TLTS*EKKSSDNQTTPSYRRKF KPMAKKLKTL/RKKLDECITRIT NAEKCLMELMELKAKARELRE ECKSLRSQCNQLEER\INKIDRP LARLIKRKREKNQIDAIKIDKGD ITTDPTEIQTTIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESLNRPITGAEIVAIINSLPTK KSPGPDGFTA

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15809	46177	A	15900	1	2047	MENDFEELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTQKCLKELMELKTKARELR EECRSLRSRCDQLEERVSAMED EMNEMKREGKFREKRIQRNEQ SLQEIWDYVKRPNLRLIGVPET LHPRDEAHLKNLIDAIKNDKGD ITTDPTEIQTTIREYYKHLYANK LENLEETDKFLDTYTLPRLNQE EVESLNRPITGSEIVAIINSLPTK KSPGPDGFTAEFYQRYKEEL/PD KQLQQSLRIQNQCTKITSILIHQ QQTNREPNHE*TPIHNCFKENKI PRNPTYKGCEGPLQGELQTTAQ GNKRGYKQMEEHSMLMGRKN QYHENGHTAQGNLQIQCHPH* ATNAFLHRIGKNYFKVHMEPK KSPHRQVNPKPKEQSWRHHTT *LQTILQGYSNQNSMVLVPKQR YRSMEQNRALRNNAAYLQLSD L*QT*EKQEMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKR*T*NHKNPRRKP RHYHSGHRHGQGLHV*NTKSN GNKSQN*QMGSN*TKELLHSK KKKNY*QTEQATCKMGENFHN LLI*QRANIQNLQ*TQTNLQEKN KQPHQKVGKGHEQTLLKRRHL CSQK\NHEKMVTITGHQRNAN QNHNEIPSHAS*NGNH*KVRKQ VLERMCRNRNTFTLLVGL*TSS
15810	46178	A	15901	1	3285	
15811	46179	A	15902	1	3681	

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15812	46180	A	15903	1	1854	MKAEIKTFFETNENKDTTYQNL WDAFKAVCRGKFTALNAHKR KQERSKIDTLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QKALQKINESRSWCFEKIHKID RPLARLIKKKREKNQIDAIKND KGDITTDPTEIQTTIREYYKHLY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGSEIVAIINSL PTKNSPGPDGFTAEFYQRYKEE/ RENKIPRNPTYKGCEGPLQGEL QTTAQGNKRGYKQMEEHSML MGRKNQYRENGHTAQGNLQIQ CHPHQATNDFLHRIGKNYFKV HMEPKKSPHRQVNPKPKEQSW RHHTT*LQTILQGYSNQNSMVL VPKQRYRSTEQNRALRNNATY LQLSDL*QT*EKQAMEKGFPI** MVLGKLASHM*KAETGSLPYT LYKNQFKMD*RLKR*T*NHKN PRRKPRHYHSGHRHGQGLHV* NTKSNGNKSQN*QMGSN*TKE LLHSKRNYHQSEQATYKMGEN FRNLLI*QRANIQNLQ*TQTNLQ EKNKPPHQKVDEGHEQTLLKR RHLCSQKTHEKMLIITGHQRNA NQNHNEIPSHTS*NGNH*KVRK QQVLERMWRNRNTFTLLVGL* TSSTIVEVSVV
15813	46181	B	15904	1	2718	
15814	46182	A	15905	1896	5031	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFFSAPHHTYSK TDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNPTQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDT FKAVCRGKFIALYAHKRKQERS KIDTLTSQLKELEKQAQTHSKA SRRQEITKIRAELKEIETQKTL\Q KINE\SRSWFF\ERINKIDRPLAR LIKKKREKNQ
15815	46183	A	15906	4	133	

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15816	46184	A	15907	95	1875	PFFGRKNYRLPSKNMPRRCRSS PLPCSMKMTI*CVLTSTATITRL PAASAQW*LDGRTLVTKNSFR YLHTLHTMGPAPEPNLTILWSE ELPIAFKKYAAQVSIVTSSLQYE NDDLMRTDFNSDDYAIACCVS PMVIGKQMQFFGARANLAKTL LYAINGGVDEKLKIQVGPKTAP LMDDVLDYDKVMDSLDHFMD WLAVQYISALNIIHYMHDKYSY EASLMALHDRDVYRTMACGIA GLSVATDSLSAIKYARVKPIRD ENGLAKDIQGTTEPQFRNSHSR TSGTVTLYLPVSTFVGTGFFIRV DPPKKPLKIRKIEFVEIYEPFSEG QAKAQADRCLSCGNPYCEWKC PVHNYIPNWLKLANEGRIFEAA ELSHQTNTLPEVCGRVCPQDRL CEGSCTLNDEFGAVTIGNIERYI NDKAFEMGWRPDMSGVKQTG KKVAIIGAGPAGLACADVLTRN GVKAVVFDRHPEIGGLLTFGIP AFKLEKEVMTRRREIFTGMGIE FKLNTEVGRDPRASSFYEEKQL IARKALPFIDNKTTMAADSSST VMELLKLLQDRSGLTLLTNSAE AIHVLAQSEIKVVSTGGELNKN TLSLQGRITKEIIRRYHVDIMWL PDELRVEKGFSPDTLKLLEAKG QKVALKEAMGSTQSIMVGPDE RRTGFSYLRYQNLMIRVKF
15817	46185	B	15908	271	2118	
15818	46186	A	15909	597	743	
15819	46187	A	15910	573	1066	IRAQNGSPWLSFLVDSVCVLKA CVDAVMRAGICSVS\YWQYQS GVGANSSALSGFSQGAIMMLES IKAEPGLASRVIAFNGRYSSLPE TASTATTIHLIHGGEDPVIDLAH AVAAQEALISAGGDVTLDIVED LGHAIDNRSMQFALDHLRYTIP KHYFDEALSG
15820	46188	A	15911	1	2652	
15821	46189	B	15912	1	1494	

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15822	46190	A	15913	1	1733	MGVGSKGTIFGSTTTQHGSFIPY LTGYLTYTHGHSPANPKPAVG GQILTAVLPAHDGYVSRIMTM NTQLTTPLTTATHTARQTASLIS VIGRQLRCFRHSSQPSVLTHVR DDSTQYAQLDMANGQPTSHGY EHWAQLMYATDRRYGRHMSD AARQGCSDTGIVKFSHPEPEMS VRKFTSARSGCVRSGAWNVTV SAQTRVSQALTTLLRRVHKSPM NALTVPAVMAEAPSQAHGRRQ TRRLSLHQTLRLLLTTPDWVGV IRRCVPVVWGCLEHLDTAGFPL PNSHTMPLPIGWNDTRKRLHHS AHNGQHDVAQGRRVLGRKVG LTHPKVQQQLGVDGLSLFCVY LVWYIGLHLRRPFRLAYTICPSL VYGADLRVIVRLFSDSHHFMAF GNPQPKHLDCQEYALFLLNSM PDNTAEHYRNKIAIYLHCLPED DRIKAINEIRMAIHQVSPFREEP VDCVLWVKYSQLMPNDYNPN NVAPPEKKLLQKSIEIDGFTQPI VVTHTDKNAMEIVDGFHRHEI GKG/SHASLKLRLRGYLPVTCL EGTRNQRIAATISHNRARGRHH ITAMSEVTPELRLLGW
15823	46191	B	15914	1	273	
15824	46192	B	15915	169	292	
15825	46193	A	15916	2	844	KGGVYKTSVSVHLAQDLALKG LRCLLWKGT\PPQGTPSMVSRE GDPALHN*CKTQLLCLSYLGEK DDVTYAIKPTCWPGLDIIPFCLA LDRIETEL\MGKFDEGKLPTDPH LMLRLAIETVAHDYDVIVI\DSA HNRG\IGTINVVCAADVLIVPTP VE\MFDYTSALQFFDMLRDLLK NA\DLKGFEPDVRIFVTKYSNSN GSQFP\WMEEPIPECLPKHGSKK NNVRNANEVGKGQIRMRT\VFE QAIDQRSSTGAWRNALSIWEPV CN\EIFDRLIKPRWEIR

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15826	46194	A	15917	1	681	MSIGGSGNSLCTRPKQQQGGTG LKQYEVSVPGTLRCLACPQACT LRKEHWIHFAPKSNYDSCRYIE EYFAYEASFMSVQLTELVIKSL EDLASLFMIHKKNPVSIPHTVW YADDIRRGEREAADVLGLTLYE LMLRAGEAAFQVCRSAYPDTR HWLVLCGHGNNGGDGYVVAR LAKAVGIDDTLLAQESDKPLPE EAPLAHEAWVNAGGEIHALNI GW\PESEHLIV
15827	46195	A	15918	3	774	VKCSEKCLFLPLGQFSQFIQKLR \VIFLDPLFIRKGQGVTPTAFAM HLHEYISQGLESILGALDIEGSY DKQRTITIATTPSVGALVLPVIY RAIKTHYPQLLLRNPPISDAENQ LSQFQTDLIIDNMFCTNRTVQH HGLFAANMVLICREGNPLLSLE DDREAIANAAHVLLLPEEQNFS GLRQRVQEMFPGRQINFTSYNI LTIAALVANSDMLAIIPSRLYNL FSRCWPLEKLPHPSLNEEQIDFS IHYNKFSLR
15828	46196	A	15919	1	741	MITVLLIATQFAPYFTEMALKG GFSFAGESAQISALSVGNMFGW SISELMSLGIIGVVVAVGIVASV VLFLRVLSMSWLKEVIGTEKAV IAMCHLRALPGDPSFDAQLGM NWVIDKAWDDLMALQNGGVD AVMFSNEFSLPYLTKGLVPALV AREILVRGMYVRGRKMVAFLV CCVALAISAMYELIEWWAALA MGQGADDFLGTQGDQWDTQS/ GYVLRAAWRINDGDIPRSLSLP PATALWLDNRI
15829	46197	A	15920	1	678	MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVDA VMFSNEFSLPYLTKVRPETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHQ HRIGAGEVKTLFNIVPEAAVYL GNRDICSIAKSTVFNNHPDALC VSGLTAGTRTDSALLKRVKETV PDT\VVLANTGVCLENVEEQLSI ADGCVTATTF
15830	46198	A	15921	624	734	TRTLRQIVDSRAIPFT*ERLHSPI NQPKNPYPPESV

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15831	46199	A	15922	1	1923	MPFALGGGDLEETPRSDPGVTF ACSLAQPMRKPTGVLGNRFHD TQEPPVPGGPGLRGFHLWHAPP LDRPAQFAAIRTDSELMSSANP KSFTASPLMTFTPARSRINYRY YPAGTRAKGENEAAFAARIHSF LPYRRPVFWATTMGQAKSAIK PMSTAVTRDASVFQTEYERSRF GARPWPLRKAPEAMGRGFHEI GVQCEAPTANTLEPSRRGAVM AAGLSFQRTPWREVLGRGEGSF LGAGSDPVLRALSLASTPFPGE KHVGSWGMGRIVLRSFALASSS LRHSGERIPGTVLPCDDIFACHQ RNYAEVFGIWRTTSSVLQPIEPV EPKCISQFLYIVLERRSSSSLISLS FNSASLCRSRHDARYVLQHALF CFTTNDFGQIFTTFFVSGGSGTR MSLPAEFGVIAQSDQKVLFIDA DLAVVIRITCLPSTSMSWLKEVI GTEKAVI/AMCHLRALPGDPSF DAQ/LGMNWVIDKAWDDLMA LKMVRPETTAAMARI/IGQLMS DIRIPFGVNV/LWDPVASFDLA MATGAK/FIREIFTGAYASDFGV /WDTNVARSRRIRASTVFRLAQ RCQPDASEYGFRMIARVFVDVR GDQNSEASLRVGSGIGPRTCAP VAWQSRRFPRLLDRSDDVKRF QADTDSLVLH
15832	46200	A	15923	480	900	KTRYSCRGETWSNPQSSQLSAL IAAVRHPATSNAVCRSARSCCIL RALRAIQFHTGCSAGNVAPEW CQFAPCWRKPLK\EESDSVFMR VIKESLWQELADITDKTQLEWR EVFQDLNHHGVYHSGEVVGLG NLVCEKCHFH
15833	46201	A	15924	1	431	SKVFAVAGCVVLMTTMPDSCN SWQKCRNKTMNKKIHSLALLV NLGIYGVAQAQEPTDTQAPGVS TITADEIRKNPVARDVSKIIRTM PGVNLTGNSTSGQRGNNRQIDI RGMGPENTLIL/IDGKPVSSRNS VRQGYRLECGDG
15834	46202	B	15925	1	1352	

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15835	46203	A	15926	31	546	CYCILFVSFPSNRPLCCRSAGVC QRYTPDPFCLGITSRGCRRAKIT ACSFLWKLHPRGALARCQPELS CWRCLST\LLEGVSPSGGTGVR DPYEEAVCPLAELKCCAGRSA VLFRAGRQGRLSLLKLFPQLPF SPCVLCLSKLVPVSPNSTRTSKL LSIPYSRGPALLEVLS
15836	46204	A	15927	2	479	
15837	46205	A	15928	1082	1386	ADPFQEREAEKYANPIPSREFIL EHLTKREKPASRDELAVELHIE GEEQLEGLRR/RQCYALPERLD LVKGTVIGHRDGYGFLRVEGR KDDLYLS\SEQMKTC
15838	46206	A	15929	3	401	
15839	46207	B	15930	1	3675	
15840	46208	A	15931	1749	1941	SQIPTSEAQVMSNLMGTNGVLR PARAYRNEAVLS*ALVSAMYS QTFRNASFGVPQMFSTTSGV
15841	46209	A	15932	5	1465	KRSTTAQIRWISPLTSLKPRSKR QSKSCATKPKKWYVAAPCCWC SPTGISLKTRLPVPAPMAVGAIQ TRLVDQSLRCDANIIVETASAR DPHHFAVLLGFGATAIYPYLAY ETLGRLVDTHAIAKDYRTVML NYRNGINKGLYKIMSKMGISTI ASYRCSKLFEAVGLHDDVVGL CFQGAVSRIGGASFEDFQQDLL NLSKRAWWRCRLSATIGCCDC TRGYLGGARITGQISSITVWGVI IPVVGLCIIGWFWFSPTLYVDS WNPHHAPFFSAVGSSIAMTLW AFLGLESACANTDVVENPERN VPIAVLGGTLGAAVIYIVSTNVI AGIVPNMELANSTAPFGLAFAQ MFTPEVGKVIMA\LMEMSCAGS ILGGKFTIAQVFKSSSDEGYFLT IFSRVTKVDAPVQGMLTIVIIQS ELALMTISPSLNSQLKEMVNLA VVTNIIPYILSMAALVIIQKVAN VPPSKAKVANFVAFVGARNSF
15842	46210	A	15933	1	3666	

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15843	46211	A	15934	979	1626	FSATITPPFIALQRVRFHPLDAL LLFVISLWLQLGLPDELSRFTPF CLALPIIALAWHYGWQGALIAT LMNAIALIASQTGLLLGAGIQR LRELNQSLQKELARNQHLAERL LETEESVRRDVARELHDDIGQT ITAIRTQAGIVQRPGAGHPLTDA GNGAGRARYCQPSRMANR*IS VKRKVVEHRCFVDFTFTNDDG AVNVDRRAVRGVFIAAS
15844	46212	C	15935	1	666	
15845	46213	A	15936	1	1137	MGKFGHTEIGEVDVRDWSDAL QAKELQKLPGHSRKLEDPPTSL FMLLNPHSDQFSSNAHHHLHA TAIDDDYTDPTKSTYALGLNWS NSILGGFNISGYKTYSYDGDND SSNLNINWNKAFKHATVSVNW QHQLSASENNEDDGDLFYVNIS IPFGRSNTATLYTRHDDHKTHY GTGVMGVVSDEMSYYVNAER DHDEPTLPAQNKAQEVLLDVV LDEAKIGVASMLGSRVRVKTW SWFADDKQEIRQGGFAGWLTD GTPLWVTGSGTSKTVLTRYAT VLNRVLPVPTQVASGQCVEVE LFARYPLKKITAEKSTTAVNPG VLNGRYRVTFTNGNHITFVSHG ETTLLSEKGKLKLQSHLDREEY VARVLDREAK\STPP
15846	46214	A	15937	323	695	FTGPRRSLEIEVAELKQRLDSLL AIGAGGSVCWTLQGAWSPTRA KAGELKTQLATAASLR/MDKH RSNSVGPHDLYFTLLDDYLHV VDTALWLSGGKASLDGGTLLT NDAGEMLFAEHHFSAGPL
15847	46215	A	15938	1	235	
15848	46216	A	15939	98	593	MSKVRLMRNLSPAPPNAVAKG ESKPGIMSGWVF*AEWAYLITG *AKKKVYGSS/ARIHLRALRYY SNWRQYFAGYTFGRQYWQSPE DDHLPLLREFLARHEYMQKYL LGTESGIQGEELGASDGIKPEEV EWQTAAIEGKLDLLVTLDFRM SSTCLFSDIVLPTAT
15849	46217	A	15940	367	677	LSSCLRATQSAPAVRNWKARFL RCTVVVWQKRSSTGRNMYLPV RPTILKLRPTWHVTW*LSGASL RNWVHCCTRKKKVKCSSAVA* RKRNICPMKLHVSSTRK

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15850	46218	A	15941	1	921	MEMSSLEFLHSICSHLKCHLLY YIASAYNYDWYTQPAKLSFISE GEIKYFTDKQMLRDFVTTRPAL KELLKEAVNMERRNRWVDIGP GTELDCISQAYAQFVASTAECC GEGGIKAWDYVRMGFLSRMG VLNNWLTRRRKLLWSARSRIH LRALRYYSNWRQYFAGYTFGR QYWQSPEDDHLPLLREFLARYE RPMKKLAGRSSIAILAFRGHDQ RDYEFPSKSALNIN*LRWALAS VK*TTACATGVFPVSVTGARRF
15851	46219	A	15942	531	637	SIFARLNASRRC*TSALYALLVR LPIIQITAKGIL
15852	46220	B	15943	120	881	
15853	46221	A	15944	1	1583	MADRVDSKCSRSRPGAVAHNY NPSTLGGRGGRITFWLLSANPSI NRGTLEKESRTVAQRLSVLHGI NAPEFFDKAVFSSLVLTLRDEG YISDSGDAEPAETMKVYQLLAE LITSDLMIFNISATVLYITAFIAC SAAVDLTSLRGTRPYNQRAAA SKEIEDLKKKLTEGEEISGCDVS GSDGDDNEEGKIGEDEEKRNT GGNKVFPERTVETPATADAER KALETKLDVEEETRLQLNSRNR KKDLKTRQEHQSLPEKFSGLQK NVLLEAVIDPALIAQLRQAYEE AL\RIAQAPAKSVWQPEEYEEA EHEILLAFRALLASDSERFLPSA WQRFIQQLNYCSMEEIDELRWS LCTIAMNTAHLSFECVVLLAER LRWLQEENTGEIDEEELESFLY AIAKGNVFNFQTILHLPVAVQN DTIDFYQMFARIWLPGAPGAYC DGLHTSKRTTCTTSTHQRQRKD TPPALNPHTATCTPPHTWLGAP PPASMRSGPHNAPTPPFTGSTPR HTHDHTNITNANIPHNVNSN

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15854	46222	A	15945	1	1228	MGVLNNWLSEEESLWIQSRIHL RALRYYSNWRQYFAGYTFGRQ YWQSPEDDHLPLLREFLARYER PMKNCWKILDIEETTDVDIIRRA YLALLPSFHPETDPQDFKQLRQ AYEEALRI\AQSPAKSVWQPEE YEVAEHEIL\LAYRALLASDSER FLPSAWQRFIQQLNYCSMEEID ELRWSLCTIAMNTAHLSFECVV LLAERLRWLQEENTGEIDEEEL GSFLYAIAKGNVFNFQTILHLPV ARRPDICTQHNDQSRCEGYQIL SDKRGHQHGGGITALYQCGNA DPRAKGERLFFDAPAKDSTQTR AEDAHYAGSNNMSPPDQQGDG RKQIWESVRVHTPVRCQQRSLP VTSYLNGGEIFNLIGLICRTRRIA ARWVKSHRNRARSFECLKRHR FVVAFNRRKPGLV
15855	46223	A	15946	71	323	AAGAVVSAMPKAKGKTRRQK FGYSVNRKRLNRNARRKAA\R GSNDLEAEASLPEKKGNTLSRD LIDYVRYMVENHGEDYKVSGS
15856	46224	A	15947	48	627	AAGAVVSAMPKAKGKTRRQK\ FGYSVNRKR\MSRNAKRKAAR\ GLECSHIRHAWDHAKSVRQNL AEMGLA\VDPNRA\VPSRKRKV KAME\VDIEEEA*KNLYRKPYV LNDLEAEASLSEKKGNTL\SRD LHLTMYRYMV\ENHGE\DYKAI A\RD\EKNYY\QDTPKQI\RS\KIN VYKRFYPAEWQDFLDSLQKRK MEVE
15857	46225	A	15948	796	1301	LTKKDYISPNARKAFVQRLPER NLLTRGLKRQRQPCLSCWCGG QARMPKAKG\KTRRQKFGYSV NRKRLNRNARRKAAPRIE/CVR GLGFRVAVGLGRDGPRDDGSA MSLFAGSSHIRHAWDHAKSVR QNLAEMGLAVDPNMAVPLRK RKVLTWQGLGPCLLYSSPAILT
15858	46226	A	15949	512	675	SQDFGPPSAAPSPSGMP\PGPSG CSSHRQQEDPPDGAAAPPGHGL RPGRLQELLV
15859	46227	B	15950	1	717	

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15860	46228	A	15951	587	1387	RARSRILGNPLRPLAPAPSNDV GVQRA\FRPIRCRKAQPVPGSV ANRRRLRQHTRPDPLGTNRSEP GWWDRSWSPDQAKSGQSCVA KIKNKNHMIISTDSEKAFDKIQH RFMIKTLSKISIQGTHF\KIIKAIC DKLTANIILNGEKLKAFPLRTE MRQGCPRLSLLFNIVLEVLAKA IRQEKEIKDIQIAKEEVRLSLFA DDMIVYLENPKDSFRKLLELIK EFSKVSGYKIKNQYCENDHTA VSGVGSFQWICGLADVKNEAA
15861	46229	A	15952	3	3201	SERGFRAGDLRYPTHFLSTNSV LASVTASLKEHPRGTLLSDGSP ALSRNVGMTVSQKGGPQPTPSP AGPGTQLGPITGEMDEADSAFL KFKQTADDSLSLTSPNTESIFVE DPYTASLRSEIESDGHEFEAES WSLAVDAAYAKKQKREVVKR QDVLYELMQTEVHHVRTLKIM LKVYSRALQEVL\QFISTAIGRL FPCADDLLETHSHFLARLKERR QESLEEGSDRNYVIQKIGDLLV QQFSGENGDRLIEK
15862	46230	B	15953	83	1969	
15863	46231	A	15954	1	444	SSESAVEFSEPASGSSPSWELGS EGAIRDKKTSLGAHVGLSALGR ALENTIAFQGKETDVQKSYDSP QGDCL\QDVKGKRPTLE*PSLE NPETRRFLDASYAWRESCLSW HHHTAHDIFAGKPVDPLPGSTR GQDSAVCSQGQFLIVR
15864	46232	A	15955	2	236	SEGAKRDKKTSLGAHVVLSAL GRALEKTIAFQGSS/APSKGRKL RSRKVMTRPKGIAWQDVKGKR PTLE*PSLENPEVR
15865	46233	A	15956	1	459	KKVGNYYTTPIYRFRMKCHLC VNYIEMQTDPANCDYVIVSGA QRKEERWDMADNEQVLTTGE RHPLTCLGAL/DPESALGPPKPS RALIVAEHEKKQKLETDAMFR LEHGEADRSTLKKALAHT\DHI QEAQSAWKDDFALNSMLRRRF REKKKA

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15866	46234	A	15957	564	1189	AAPKMGERKGVNKYYPPDFNP EEAWLSSTDYHNSHPFRERASG SCSQGI\LIIRFEMPYNIWCEG\C RTNFGMGVRYNAEKKKVGNY YTTPIYRFRMKCHLCVNYIEMQ TDPAN\FDYVIVSGAQRKEERL GHWRTMNRLLTHRGIEEEAEA WKTDAMFRAGTMGRPTAAHF KKALPKLEPHSGRPRAPWKDD FALNSMLRRRFRVPSKP
15867	46235	A	15958	2	1047	FVDGKLHGRGSTDDIGPVAGWI NALEAYQKTGQETPVNVRFCL EGMEESGSEGLDELIFARKDTF FKDVDCVCISDNYWLGKKKPCI TYGLRGICYFFIEVECSNKDLHS GVYGGSVHEAMTDLILLMGSL VDKRGNILIPGINEAVAAVTEEE HKLYDDIDFDIKEFAKDVGAQI LLHSHKKDILMHRWRYPSLSLH GIEGAFSGSGAKTVIPRKVVGK FSIRLVPNMTPEVVGEQVTSYL TKKFAELRSPNEFKVYMGHGG KPWVSDFSHP\HYLAGRRAMK TVFGVEPDLTREGGSIPVTLTFQ EATGKNVMLLPVGSADDGAHS QNEKLNRYNYIEGTKMLAAYL
15868	46236	A	15959	163	1388	RLVERWRPSGTLFKYIDENQDR YIKKLAKWVAIQSVSAWPEKR GEIRRMMEVAAADVKQLGGSV ELVDIGKQKLPDGSEIPLPPILL\ GRLGSDPQMKTVCIYGHLDVQ PAALEDGWDSEPFTLVERDGLT WCSSCRGPYCRGSS/DRLSWKL PSVMWGDSREPHLARLD\HPSG LEPQRPGSTWGGGDDRRGGRA LSRQLPYAGYAAAQCKGEVRP QVSSSRLVVECSNKDLHSGVY GGSVHEAMTDLILLMEEHKLY DDIDFDIEEFAKDVGAQILLHSH KSHLHLDLLPVVVRLLGQALFH TAHFPDNIPSSSKDILMHRWRY PSLSLHGIEGAFSGSGAKTVIPR KVVGKFSIRLVPNMTPEVVGEQ ACGAGTRESMSSLGYPSRAED DSGLSALPSQPQPFILYAT

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15869	46237	A	15960	3	433	FETLFSQVQLFISTCNGEHIRYA TDTFAGLCIQLTNALVERKQPL RGIGILKQAIDKMQMNTNQLTS IHADLCQAITTPAMAV\SHIMLE SYKKYILVSLILLGKVQQLPKY TSP/QLVGRFI\KPLSNA\YHELR HKLY\STNNPC
15870	46238	A	15961	46	1481	TSGSDVAAREDLRWIAAAPPPR AAAFSRACCLRRSGRPGENMA SALEQFVNSVRLLLSQ\GCSCFP GQMTQLCELINMSGELLAKNLS HL\DTVLGAL\DVQEHSLGVLA VLFVKFSMPSVPDFETLFSQVQ LFISTCNGEHIRYATDTWQETV LLKSMVLVLVVIYYQPLRGIGIL KQAIDKMQMNTNQLTSIHADL CQLCLLAKCFKAALPYLDGDM MDICKENGAYDAKHFLCYYYY GGMIYT\GLKNF\ERALYFYG\Q AITTP\A\MAVRHIIVW/ESYKKY ILVSLILLG\KVQQLPKIFHLKLV G*IPLSLLSNAYHELAQVYSTN NPSELRNLVNKHSETFTRDNN MGLVKQCLSSLYKKNIQRLTKT FLTLSLQDMASRVQLSGPQEAE KYVLHMIEDGEIFASINQKDGM VSFHDNPEKYNNPAMLHNIDQ EMLKCIELDERLKAMDQEITVN PQFVQKSMGSQEDDSGNKPSS
15871	46239	B	15962	1	3411	
15872	46240	A	15963	689	925	
15873	46241	A	15964	1	244	GSAPQSCASPAPVSRSAAPGTA EAAEPWAIVPGVEQKNYYVCV PLGLIGNCTVTSSGI\SLDCADW CLKWKSILMESLEVP
15874	46242	A	15965	469	604	
15875	46243	A	15966	286	433	
15876	46244	A	15967	4356	4643	DCPLARNKSKPQTVCLKARQTF QAINFSRALRITGYLTSFPSLSRS TLPSSAGDFRASAWA*SGPTV* TLTSVPSVGINSSYIYEPVFRTLL SGE
15877	46245	B	15968	1	1472	

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15878	46246	A	15969	918	1619	KTHVLSWGSPKSTWKAGWLQ KQKTTQEKKAESKAPIEEEPAG AGLNKDKETEERSDGERVAEV APEERENVAVAKLQESQPGNA VSCSGGRRKEDEREDWGKRTQ RTHPPAAAQAPGQCPPGSTEVG AGGGLRWTPSPGRQPAGVAAD MGITVLTVPLQRCLQNSWAKE PVLVVSFVIGSLTVILPPLSPYTK YSIMINEATPYNYPVPVHDDGN M/PDMCSHPQGPQGPSLEWL
15879	46247	B	15970	183	459	
15880	46248	A	15971	864	1197	GSFRLGHGRIPPFHLRGMKESL GPDFGDPCPVCPLNSGPGPP\GV SAGGAGAGCGGMGRRDAWVP TGPVAESPGGHLAPISPGRQGA PWGGPCGQLGAGTLGQAVCG MTQDP
15881	46249	A	15972	1	441	
15882	46250	A	15973	3	182	
15883	46251	A	15974	23	475	PLEKGRQFYPQYEDQITIFTDYL EEYPDTDELVWILWKQHLLKT EKSKLLSDISARLWFTYRRKFSP /ILGGTGPSSDAG\WGCMLRCG QMMLA\QAL\ICRHLGRDWSW EKQIEQPQEYQRILQCFLNRKD CCYSIHQMAQMGVGEGKSIGE
15884	46252	A	15975	224	418	
15885	46253	A	15976	743	1220	WCWGHRVRLVLAAGPSSRGVL LLLVVLPSWASFLVRVCAWVG VLGDDGVLGGFLLWLGVVGRP LAVLRADLAVCVGVVCACVPF VVLPICAALVRVGCSLVEAALG \LGARPLKTFFAVVVPLTKGGV VAGSMLVFVPAVGEFVIPELLG GPDSIVIGRV
15886	46254	A	15977	3	3492	RKHKVGILYCKPGQSSEEEMSN NEEAGPAFEKFLSLIGEKVCLK GFTKYAAQLDVKTDSTGTHSL YTMYQDYEIMFHVSTLLPYTPN NRQQLLRKRHIGNDIVTIIFQEP GALPFTPKNIRSHFQHVFIIVRV HNPCTDNVCYSMAVTRSKDAP PFGPPIPSGTTFRKSDVFR\DFLL AKVI*RLRNAAEQVPTSFTPWA TRTRQEYLKDLAENCVSNTPID STGKFNLISLTSKKKEKTKARA GAEQHSAGAIA
15887	46255	B	15978	402	2884	

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15888	46256	A	15979	294	1721	AVRPGRHDPSAGLRSAAAASQ* VRGHPGGLCA*GSIQGPGASAA EGPPAHSRAA*SKGGAELRTR* AGGRRPAGPHAQRP*LP*GPRV PLRPPSGTFLLP/PPACTPITSRPS *KSCSRASTPPTWSS*IPASGTSP GMVRTPGEA\PGEPGEPVPVPG PGAARVLPPGVE/PRPCLWARK SPGVFFRPSSGGRRPPS*KTKWS KPTSTAPPR\P*T*LRCTGLAFPL PPREGEPALGRGALEWTCAPLP LPAAAGPRGRRLGCGAAPPPPR GRVDQEEK\PGPRVEGPPQANR NHPALPLSPPLPSPT/*PPPAWVP TPALAAAPAPVPTASSSHSPSPG NAPVPTGSPRCLFFLRPYFPVGS ILLPFRCPLISPCRFLRRRQFYG WSSAAYALLPHTPLSAACPSGP TTALHGQPQSSCSCCQEATFTV KSGVVQSGRPSLRQFYVHDFCK IQPQQLLVSHATTKATTDRYST ASCVAR
15889	46257	B	15980	35	314	
15890	46258	A	15981	1	197	
15891	46259	A	15982	3	3889	
15892	46260	B	15983	172	287	
15893	46261	A	15984	8	166	
15894	46262	A	15985	250	1095	
15895	46263	A	15986	366	870	NHSLAKKGTAHGLGMEKCCGR SPFFSFFPSWIAKPTLRSSSSWPH SSSSPSMSSPLQRAVGDT\KRAL SASSSSSASLPFDDRDSNHPSEA CTTPGGGWEVADGNTDSLLAD EGSDFEDSFNRNVKKKAAKRPP KTTPV/AKQPKKGSRVVHRHSR KQSEPPANDLFNAV
15896	46264	A	15987	30	229	ALETNIGSSYNYGSEDQAEFLC VVSKELHSTPNGLSSESSRKTK\ CYKPEAPGCEAPDHLQGLGVPI
15897	46265	C	15988	1	930	
15898	46266	A	15989	1	609	

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15899	46267	A	15990	1	875	MRMEAGEAAPPAGAGGRAAG GWGKWVRLNVGGTVFLTTRQ TLCREQKSFLSRLCQGEELQSD RDETGAYLIDRDPTYFGPILNFL RHGKLVLDKDMAEEGVLEEAE FYNIGPLIRIIKDRMEEKDYTVT Q\VPPKHVYRVL\QCQEEELTQ MVSTMSDGWRFEQLVNIGSSY NYGSEDQAEFLCVVSKELHSTP NGLSSESSRKTKSTEEQLEEQQ QQEEEVEEVEVEQVQVEADAQ EKGSRPHPLRPEAELAVRASPR PLARPQSCHPCCYKPEEPGCEA PDHLQGLGVPI
15900	46268	A	15991	1	2448	MRRGETRSRRPPQCWAFAHVV SRSSRRGEFFSFDRWKKHRSEV RESAQVPTTKREPVLFQHKINIK IVIALVDILFALGLGNLVCVSPV QLFSVQTDSRATGDQRLPSWT AQRYGTRTLGPDGFTERCPYGP SPESLLCSALPWLRDLGMPVAE APQVAGGQGDGGDGEEAEPEG MFKACEDSKRKARGYLRLVPL FVLLALLVLASAGLEMLSDPGS RSYGSGLLPAWAKCPKAPHQR SLIPPDYAPGVNHPPPQERCSM GLRTQGTLGRHRVLSAQQVAF SVSLLMAKIAFAKQKSDDIIPDF KLFMVTLVHRPNRLSARVLTM VPVLPAPCPMLLPLLEGYKAEV MVSQVYSGSLRVLNRHFSQDL TRRESSAFRSETAKAQKMLKEL ITSTRLGTYYNSSSVYSFGEGPL TCFFWFILQIPEHRRLMLSPEVV QALLVEELLSTVNSSAAVPYRA EYEVDPEGLVILGQYCEWKPPG RRMQTPRPAMRMEAGEAAPPA GAGGRAAGGWGKWVRLNVG GTVFLTTRQTLCREQKSFLSRL CQGEELQSDRDETGAYLIDRDP TYFGPILNFLRHGKLVLDKDMA EEGSQVWTVTSGGWGDRNAV LTGMGRALSLFLWLIQYLKFCL VRAWVLEEAEFYNIGPLIRIIKD RMEEKDYTVTQVPPKHVYRVL QCQEEELTQMVSTMSDGWRFE

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15901	46269	A	15992	1	573	MPGLLSRPRRGSLRARPCGGGE ALPEHVAIDVCPGPIRPIQQISG YFPHFPRDLPHDAPARPATASA GRRRPSDGARDHDKDGDHLFG SLTIQHRPW/PAPSPDFPFTPFAV LYPG\LKPMDHNGLADPCVKL HLRPGARKVPEACQLAPDLQD SSCLTAITKAHDVLTVFLPAAL KIQGNKYLTFIECQKLF
15902	46270	A	15993	500	2022	WTREKEPPGVETHGKASRTTL GLSLWCCLHLSEIQSSFISDCAR PRCSGRLPGSGPMLLATPHVLA TVVASSCSKQLWWLPPKVATD QQQMKLKGLFIAGAPPGSPR/G VQPHLQPIRNMSVSRTMEDSCE LDLVYVTERIIAVSFPSTANEEN FRSNLREVAQMLKSKHGGNYL LFNLSERRPDITKLHAKVLEFG WPDLHTPALEKICSICKAMDTW LNADPHNVVVLHNKGNRGRIG VVIAAYMHYSNISASADQALD RFAMKRFYEDKIVPIGQPSQRR YVHYFSGLLSGSIKMNNKPLFL HHVIMHGIPNFESKGGCRPFLRI YQAMQPVYTSGIYNIPGDSQTS VCITIEPGLLLKGDILNSEILFGV DELSLTGFGLKCYHKKFRSPAR DVIFRVQFHTCAIHDLGVVFGK EDLDDAFKDDRFPEYGKVEFVF SYGPEKIQGMEHLENGPSVSVD YNTSDPLIRWDSYDNFSGHRDD GMEGAQHPQIGQDTPPGPSDPP
15903	46271	A	15994	171	720	LSGSSAGKVAAPCVPPSNHELV PITTENAPKNVLDKGERPSRGG NTRKSLE\TTASTGSPR/GVQPH LQPIINMNVSRTMEDSCELGPV YRTERNIAVSFPSTANEENFRSN LREVAQMLKSKHGGNYLQRN VSL/RRLSPSLRHPGPWPPSQEP GMCQGEPGPPATLWPMPCGPT VLESPGGPGP
15904	46272	B	15995	145	972	

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15905	46273	A	15996	2	1096	WPVLTAAGCWLQDPAGHRGG RAGGAGRAVLFQLQAGRAELR GLRARGWARSWAPAPGCQRTG RDAAAAGRRAGRAGALLGFTC LLLAALCGHLGPSWRGGLAPG GEWIWLRASETRGPSGPRPALM GSQKIRNITRTRHGPLHWLHSG CTTATPFCLTRSCSDAACSLKG LPCLCPCGLSVLIRVRLELRRHQ RAGHTIPRIFQAVVQRQPERLA LVDAGTGECWTFAQLDAYSNA VANLFRQLGFAPGDVVAIFL/E GRPEFVGLWLGLAKAG/MEAA LLNVNLRREPLAF/CLGTSGAK ALIFGGEMVRAPPPNAQAPPLT PVSPADRLFYIYTSGTTGLPKA AIVVHSSARPSCPSSRTLRAAHR
15906	46274	A	15997	397	597	SIKSPEIHSPSTRIRMGCSSLPTE EAHAEGVIELSRIKCVEIVKSD/ DRIPCHYKYPFQVSPSGGSSP
15907	46275	A	15998	1922	3886	EGDNKLRPRIRRKLFPLVVLRG DAQGAPPFKNWIMNNFILLEEQ LIKKSQQKRRTSPSNFKVRFFVL TKASLAYFEDRHGKKRT\RKGS IELSRIKCVEIVKSDISIPCHYKY PFQVVHDNYLLYVFAPDRESR QRWVLALKEETRNNNSLVPKY HPNFWMDGKWRCCSQLEKLA TGCAQYDPTKNASKKPLPPTPE DNRRPLWEPEETVVIALYDYQT NDPQELALRRNEEYCLLDSSEI HWWRVQDRNGHEGYVPSSYL VEKSPNNLETYEWYNKSISRDK AEKLLLDTGKEGAFMVRDSRT AGTYTVSVFTKAVVSENNPCIK HYHIKETNDNPKRYYVAEKYV FDSIPLLINYHQHNGGGLVTRL RYPVCFGRQKAPVTAGLRYGK WVIDPSELTFVQEIGSGQFGLV HLGYWLNKDKVAIKTIREGAM SEEDFIEEAEVMMKLSHPKLVQ LYGVCLEQAPICLVFEFMEHGC LSDYLRTQRGLFAAETLLGMCL DVCEGMAYLEEACVIHRDLAA RNCLVGENQVIKVSDFGMTRF VLDDQYTSSTGTKFPVKWASPE VFSFSRYSSKSDVWSFGVLMW EVFSEGKIPYENRSNSEVVEDIS TGFRLYKPRLASTHVYQIMNHC WKERPEDRPAFSRLLRQLAEIA
15908	46276	B	15999	58	1526	

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15909	46277	A	16000	3	378	GASPDLGGRVLGAGASAESPR GRPFGPSPLGGPPVPGCQCAAP SLRDPWGLWAPVLQMTGSYEF KLNQPPEDGISSVKLSPHTLPSP GLSPSWET\SVRLYDV\PGNFM AVKYQ\HTGARPGNGPF
15910	46278	B	16001	83	2851	
15911	46279	A	16002	296	1186	AENHPGP\LVVEGKMTAPERM KHESNYLRGTIAE\NLNDGLTG GFKGANFLLIRFHGMYQQDDR DIRAERAEQKLEPRHAMLLRCR LPGGVITTKQWQAIDKFAGENT IYGSIRLTNRQTFQFHGILKKNV KPVHQMLHSVGLDALATAND MNRNVLCTSNPYESQLHAEAY EWAKKISKQLLPRTRAYAEIWL DQEKVATTDEEPILGQTYLPRK FKTTVVIPPQNDIDLHANDMNF VAIAENGKLVGFNLLVGGGLSI EHGNKKTYARTASEFGYLPLEH TLAVAEAVVTTQRDWG
15912	46280	A	16003	225	386	GLCIPVVRSPCQLWGQKGPCM LRDEGRVFT*LSTKKNCPGNMR RKYETVDCRR
15913	46281	A	16004	386	739	PLLIHWRFATIEEADDHRLAAG ARTFQ/PLCGPPQAQAVWR*AQ *FQFADRFPASRWRRASSGRRF SRSGRARRCQSVAKRRRQIHEC GRSTPDCRCRMRQQYRCCRDA RRYQNRAPRR
15914	46282	B	16005	10	1468	
15915	46283	A	16006	3	1267	GRSRR**PPSAVPHD\PAVQRER DTQSLSVII*MQIYNFSNTTHLT NHNTFLTFHKTFTAETFQHIGP QPTTDTPYHTAEAYCCQLVKLI RRQALRRCWQGAAILKCNSKP TNHCTS

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15916	46284	A	16007	1	1673	MTPICTVFRALSRLPDLWHRSI GTLTEALPQTDKRQEQIAVALT SYSGLYGLGYGSKEIQLTYSGT ESGIWPFPYSPNATHKGCGRHR FACPIAPHFLVIEPQSALGSCPSP VEVDPGGCVFGAIRLLVLRDAP SFSRLLNTLASGESLQGGPGFV GVSKVYAFLVVRNPTGTPMFT GTFEIPKWPTFPIPPVFGRLGSF VLQLQGPRSPGQCEYDRELVSG SRSVSSCLLVLGTLHLLSYKDA GVDIDAGNALVGRIKGVVKKT RRPEVMGGLGGFGALCALPQK YREPVLVSGTDGVGTRRRLAL VLKRFVFIGIDLVAMCGNDLVV QGAEPLFFLDYYATGKLDVDT ASAMISGIAEEKSEILDGSKVSD GDVLIALGSSGLHSNGYSLVRQ ILEVHRAAADDVLSDADAVSW RAPYQTSSGLRKKINQGAVSFV DLHLSEVAQMVNYGFFGDIDV AVIEASALAPDGRVWLTSGIRN APTWLLRAKKVIIELNHYHDPR VAELADIVIPGAASRRNNGSIFH AMDRLGNPHVQIDPEK\IVAVV\
15917	46285	A	16008	425	595	
15918	46286	A	16009	315	721	QCFRALGGHRRIADRGENIQV WIEPGC/INDLLKWLNALDEKY RSRLVWARSSKNSLCASEANW LEMNNRLSKGDLPCIRPILIIMLI R*TCSYGFTALR*TQNAAGGGD SLAGGIGIFTLVFFTLPAYAIRW LPR
15919	46287	B	16010	652	858	
15920	46288	A	16011	238	2526	
15921	46289	A	16012	21	522	IPCCRSTRKTSGAGLSITSEQRR AAVSRISVTSSLLASAG/VRYRQ HHARDRVRERPVDKL/PR**TPC SARLSLYGPSR*WW/MARVLIF VTLPVRSRIVTVSPMRIGFSNRII RPEIKLAKISCKPKPRPTPSAAT SHCNFDHSIPIIEKPTSPPISISRY LVMVVMA
15922	46290	A	16013	2	527	

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15923	46291	A	16014	1	1734	MVNGCDSTNASSYANVNGCDS TNASSYANGERCDSTNASSYA NGQRVRSTNASSYANGERVRL DNASSYAIGERVRLDERTSYAN GERVRLDERILLANGDRVRHHE RILERKATFNNSGTTCCRAVYS RVSAMTAPDKAFTPHRQRCRLP DATLARLIRPQIPAPSVGRIRRL RRIGNSANCLMRRLRVLSGHKF PHHPSMPNVSANGYRSFPFMAS YMTPFFGYLTAWSYCLCGCRW GSLKSPPLALCPVLVPGDGAVD TRIDAVALVALANLAAVRLYA KSSSAAGIINFVVLTAALLAVT AACTVATYALRTGKNRQYRA MQSFRRSSIDNRVDTFFKGTGA LGISVTVIAVTCKSRLVYPIPVY TGLSLPQRPAVVKVNEGSMET KDLIVI/GAGINGAGIAADAAGR G/LSVLMLEAQDLACATSS/ASS KLIHGGLRYLEHYESACEALAE REVLLK/MAPHIAFPMRFRLPH RP/HLRPAWMIRIAENIS/DFVEP KLCLPRMGTRESVLPGVCRNY ESTITSVISVSPCERDMANYVPR HSAGYRRRFYPMTQPIKDAVEP VDQDWKAGKEMAASRS
15924	46292	A	16015	1	5895	
15925	46293	A	16016	170	371	
15926	46294	A	16017	216	477	
15927	46295	A	16018	2	263	
15928	46296	A	16019	1	2862	

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15929	46297	A	16020	1	1567	MKLNKAGFNVPESYSLLKMPP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLSGPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDVAHDSRSIQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLERKDLALNQAMIPLGSCT MKLNAAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLDAEIARIEKMGVP\IKCTTEV G\NTLTLEQVKAENRAVLVTVG LSSGSGLPLFEHSDVEIAVDFLQ RARQAQGDISIPQSALIIGGGDV AMDVASTLKVLGCQAVTCVAR EELDEFPASEKEFTSARELGVSII DGFTPVAVEGNKVTFKHGDLR TAPFLGVADKRNKSAGNHP
15930	46298	A	16021	62	329	
15931	46299	B	16022	289	334	
15932	46300	A	16023	1	2991	
15933	46301	A	16024	418	3156	
15934	46302	A	16025	1	2169	

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15935	46303	A	16026	800	2406	SSRRMFPPAIRLLLICLPARRWK SAL/GEEQLQNLQHISQEMGISP SLFSTQPLWQIAMVLQATQAQ KLGLRAEYGIDYQLLQAAKQQ HKPVIELEGAENQIAMLLQLPD KGLALLDDTLTHWHTNARLLQ QMMSWWLECEGGERERIFPVS KRMGKKLDAVFGDNHTASLTE TEEYRKSQVHFCICDKRERSSG NYQSIQGCRSAAFFIPSNSTRTK RGESMYRMDKLTTGAAYGAS AGSILNGMLNAYSPEQWNAIG VLTTAAAGAEMNPTLRNKLVG AIVGGSGAITIAAVMLGNADGL EGRRYYAYQDVVGVWTVCDG HTGTDIRRGHRYTDKECDNLL KADLRKAIIYISGYSGTNGIRDS LLFSSLWLIPVFLFPKRIKIIAAVI GVAFSRFIASHLAVAFESDPEAE IRQLNSRRVELERALSNHENDN QQQRIQFEQAKEGVTALNRILP RLNLLADDSLADRVDEIRERLD EAQEAARFVQQFGNQLAKLEPI VSVLQSDPEQFEQLKEDYAYSQ QMQRDARQPGVCP
15936	46304	A	16027	2336	3105	HGNAIALIASQTWRDHPVDLLL SLLVQSLT/GRLRELNQSLQKEL ARNQHLAERLLETEESVRRDV ARELHDDIGQTITAIRTQAGIVQ RLAADNASVKQSGQLIEQLSLG VYDAVRRLLGRLRPRQLDDLT LEQAIRSLMREMELEGRGIVSH LEWRIDESALSENQRVTLFRVC QEGLNNIVKHADASAVTLQGW QQDERLMLVIEDDGSGLPPGSG QQGFGLTGMRERVTALGGAFH ISCLHGTRVSVSLAQRHV
15937	46305	C	16028	1	1374	

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15938	46306	A	16029	1298	2896	GAFTCCATAGGCMNIRRKNRL WIACAVLAGLALTIGLVLYALR SNIDLFYTPGEILYGKRETQQM PEVGQRLRVGGMVMPGSVQR DPNSLKVTFTIYDAEGSVDVSY EGILPDLFREGQGVVVQGELEK GNHILAKEVLAKHDENYTPPEV EKAMEANHRRPARPSIMMPEIG NGLLCLALGIALLLSVYPLWGV ARGDARMMASSRLFAWLLFMS VAGAFLVLVNAFVVNDFTVTY VASNSNTQLPVWYRVAATWG AHEGSLLLWVLLMSGWTFAVA IFSQRIPLDIVARVLAIMGMVSV GFLLFILFTSNPFSRTLHLAYPN RCQPINWRGRHLVWYLLLFVIS LWLQLGLPDELSRFTPFCLALPI IALAWHYGWQGALIATLMNAI ALIASQTWRDHPVDLLLSLLVQ SLTGLLLGAGIQRLRELNQSLQ KELARNQHLAERVLETEQSVR RDVARELHYDIGQTITAIRTHA GIVQRLAADNASVKQSGQLIEQ LSLGVYDAVRPLLGRLRPAQLD DLT\LEQAIPLT
15939	46307	A	16030	15	277	KIGQKAPLGEARGGERT\SRTA KNFGYEEMLSELEA/HRRG/WL KRV*PRMKLPPEALVETFIAQLF DAPSQIMPLTSPIILLIAIEMGS
15940	46308	A	16031	1	2916	
15941	46309	A	16032	1	2862	
15942	46310	A	16033	1	3099	

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15943	46311	A	16034	1	1567	MKLNKAGFNVPESYSLLKMPP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLSGPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDVAHDSRSIQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLERKDLALNQAMIPLGSCT MKLNAAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLDAEIARIEKMGVP\IKCTTEV G\NTLTLEQVKAENRAVLVTVG LSSGSGLPLFEHSDVEIAVDFLQ RARQAQGDISIPQSALIIGGGDV AMDVASTLKVLGCQAVTCVAR EELDEFPASEKEFTSARELGVSII DGFTPVAVEGNKVTFKHGDLR TAPFLGVADKRNKSAGNHP
15944	46312	A	16035	367	849	NNFCSTTSHHGQHHHTDHRCG EQNVCHRDAICQTLFRTTKDDS NFICLIEAQSACHKDVNYNHDS QKNAADHHDKQQ*SPANFMPD TINDGFAERCINHQQNGRLVSF RNPFFIARHPVTNPRPGKMPQH KRQQQLQHNFTDLLKAAPCTV NIHHQTNQQW
15945	46313	A	16036	1	1066	MHQRPRTRNAVEQHRFSRQLY YALHAFEITIPPLRMRRGSIPAL VNNKLRSLEKRFSTRLKIDDDA LARLVSCAWPGNDFELYSVIEN LALSSDNGRIRVSDLPEHLFTEQ ATDDVSATRLSTSLSFAEVEKE AIINAAQVTGAFPWWLGDVKL TIPLTLGMVAAALTDLDDRLAG RLRNLIITLFCFFIASASVELLFP WPWLFAIGLTLSTSGFILLGGLG QRYATI\AFGA\LLNAIYTMLGT SLYEHWYQQPMYLLAGAVWY NVLTLIGHLLFPVRPLQDNLAR CYEQLARYLELKSRMFDPDIED QSQAPLYDLALANGLLMATLN QTKLSLLTRLRGDRGQRGTRRT GIL
15946	46314	A	16037	1	951	
15947	46315	A	16038	576	669	

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15948	46316	A	16039	1	1047	
15949	46317	A	16040	2	425	
15950	46318	A	16041	148	1052	RARRGVSVKAKKQETAATMK DVALKAKVSTATVSRALMNPD KVSQATRNRVEKAAREVGYFP QPMGRNVKRNESRTILVIVPDIC DPFFSEIIRGIEVTAANHGYLVLI GDCALQIQQEKPFIDLIITKQIDG MLLLGSRLPFDASIEEQRNLPP MVMANEFAPELELPTVHIDNLT AAFDAVNYLYEQGHKRIGCIA GPEEMTLCHYRLQGYVQALRR CGIMFCRFTAEGVQEIDYKDIA TLKNYITESGGVTELIHFFIAEY SDNQRANAGGGVEDEDIEVLES LRLNENHAIKERCRS
15951	46319	A	16042	3	741	
15952	46320	A	16043	237	1542	FHRLWTGRFLPSPPSRRGTDNA AGRTKMPPSPVIF/WFALAQFV GVKHSRSIPFAAVRSHKARIRSI SRSDVATSILPQLS*RMPF*SQK ALVARFPARQNCAFRLPGV*/L DPGMDHAAVVARLVTGRGGIV WFGRDFYRSVDDIHFGAWGDL AKECFDIVIPQTNTARTYPHAN AEIGVRTMKQINAAIGRQTNRM MAHWVIRSSRHYRRQLNSLCFI TGADVCRWFPQHIVPGRDSVA HVVVQHVITYRLLRGLLHFAG DGGVNAITVFIGTFAITVIHLLA HHFAQVRRRESNLRRVIVSVNR LSACLIELLLGDIPFIQHPRQHD VTPRDGTIHRVERVEGGRRFRQ PGYHRHFVQRQLVDRFSEIDLC RSTDTIGAVTKVNLVQIKLEDL VFRQQLFNANREEDFLNLTHQR AFWTEEEVSRQLLGNGTCPL
15953	46321	A	16044	1	1059	
15954	46322	A	16045	104	349	RSAASPWKTRKALVCCSAVVIS PALKISMIVTISVQAHG*LRKGS GVKAALSWWKFQPTMKPTITS SLTGRRISCRSRVKR

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15955	46323	A	16046	1056	2373	GPRLVQRSDHRPHDANYRQYL AGLSVHDDPLHGLAE\TIPDDL YEASAMDGAGPFQNFFKITLPL LIKPLTPLMIASFAFNFNNFVLI QLLTNGGPDRLGTTTPAGYTDL LVNYTYRIAFEGGGGQDFGLA AAIATLIFLLRIPRRTTALQGMR SNLNMESSRWARANRRLKAIN TLSLTLITQSCETYLIQNTRPELI TDTFREFFDTPVETAQDVHKQL KRLRRVIAWTGERETPVTIYSW VAAATRYQLLKRGVISNTKINA TEEEILQGEPEVKVESAERHHA MVNFWRTTLSCILGTLFWLWT GWTSGSGAMVMIAVVTSLAM RLPNPRMVAIDFIYGTLAALPY GGGRPVAVGVFYGGCYCTRDG LTRAPPPNAAPTAARYGPRTTP RTLRKGITDVRCEKRHHQRQA RNAGYQTVFSDLDRLRHPALR

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15956	46324	A	16047	1	2581	MVLMGLAQNIWQFLILRALLG LLGGFVPNANALIATQVPRNKS GWALGTLSTGGVSGALLGPMA GGLLADSYGLRPVFFITASVLIL CFFVTLFCIREKFQPVSKKEML HMREVVTSLKNPKLVLSLFVTT LIIQVATGSIAPILTLYVRELAG NVSNVAFISGMIASVPGVAALL SAPRLGKLGDRIGPRKILITALIF SVLAVIPIRHFEMRSKESRPSAW VTPKGEWGKGSVELVEIPTNDE TNDNIVAYWTPDQLPEPGKEM NFKYTITFSRDEDKLHAPDNAW VQQTRRSTGDVKQSNLIRQPDG TIAFVVDFTGAEMKKLPEDTPV TAQTSIGDNGEIVESTVRYNPV TKGWRLVMRVKVKDAKKTTE MRAALRVWNKPGQNHQHLGN GFYGQVYGGYLETMFGGAGAE VLYRPLDSNWAFGLDANYVKQ RDWRSAKDMMKFTDYSVKTG HLTAYWTPSFAQDVLVKASVG QYLAGDKGGTLEIAKRFDSGV VVGGYATITNVSKEEYGEGDFT KGVYVSVPLDLFSSGPTRSRAA IGWTPLTRDGGQQLGPGYTDLL VNYTYRIAFEGGGGQDFGLAA AIATLIFLLVAIMFPLLMVVAIS LRQGNFATGSLIPEQISWDHWK LALGFSVEQADGRITPPPFPVLL WLWNSVKVAGISAIGIVALSTT CAYAFARMRFPGKATLLKGML
15957	46325	A	16048	1	765	
15958	46326	A	16049	869	1012	MAISFMMSCFVT*VAANSAILL SMSWRA*SNSNGP*LANSILLS AAC

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15959	46327	A	16050	1	1854	MTLSCNSTDFEKTVTSVPALPD VVSDSDMSLNALSVTLADNVQ LSFRRDSYSGQPSVIYTTPQRPT AGSEDAPVWPEAFTEDVRHNR PPYPVIPRATRPACLARERMAM YMRPQIKTIGKAPAEEALSNPR MQGPQLSSASTIPVTPFHWLFG SHAAGHFSQHAHRTALTGHFS HLATTLKGLALEGNAIFTITRFT RPYGHKNTTPHSPLCSAPHSPIF NSRRKVYGQHGPQWWAFIHSH RPGGSSHSSILHCFALVCPGLVV QRDTPHPIIRPALCPPIAIAFSLSL WLGNPSFPSGTQHLQGPKTFQQ QASPSSKVCPKRLICTVIPQQRV ASHHHFHGHNRYYQLGLPVQH CTLQGVIRATHFIPRTARNQISH VSWGAGPAHSDSQGKQDLE/H EPIKPLDNSEKASKV/SQALETV TTTAEKVQRQ/PVIAHLIRATER FNDR/LGNQFGGFVLAS/HPMLL QDIFDKILQNIS/DPTLAATLKNT INTAVHSHLVPAGADGIFLLLRP FDAVCAAWIATAEYKDYPGMP GKTHLKIRLMRRERLIGIRFYSG LLPGTKAPYSRTLAFKRVLHTA LSLHLGLGKTCTTGFELCSLTLL EYASNAFTYWPDWHINRIKNK N
15960	46328	A	16051	249	724	EKVKKTQRKEIENVTNITGVRQ IELWRRDDLQHPRLDEVAEEVP VALVYNGISHVVMMASPKDLE YFALGFSLSEGD/IIESPRDIFGM DVGVPCACNGLEERRRALDG/R TVAGCGVCGVEQ/LLNDIGKPV QPL\PFTQT/FDLNKLDDALRHL NDFQPVGN
15961	46329	A	16052	71	408	RYLSTASQTNSIQIGAGLSRSRA FTTFGSKGILLSHTSVFIPRDRCT SFSMMPTCSASLTSHCPFQMTS LLSSHHP/FKKKKFGT\KTGHCL CPSLNCLPCCFSQIMVIKQVIL
15962	46330	A	16053	668	905	CLHVLHHLTSHCPFQMTKPYST IHFLPRMTSLLSSHHP/FKKKKF GT\KTGHCLCPSLNCLPCCFSQI MVIKQVILEKKKK
15963	46331	A	16054	834	1057	ARLLFMDLLDERTLVAVERPL\ VTSLLSSHHP/FKKKKFGT\KTG HCLCPSLNCLPCCFSQIMVIKQV ILEKKKKTK
15964	46332	A	16055	1	1011	

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15965	46333	A	16056	191	631	NLLRGNKMATQSSPVITDMKVI PVAGHDSMLLNIGGAHNAYFT RNIVVLTDNAGHTGIGETPGGD VIYQTLVDA\IPMVLGQEVARL NKMVPQVHKGNQAADFDTFG KGAWTFELRVEAGAGLEARLL DLLGKALNVSGCELLGHGS
15966	46334	A	16057	2	335	GARQQQKFVLIAGGFP*QLL*T NAVIGREFRNVQECIGLHTAGF ANAVTKHFGKCAIALHNMAFR IEDNHRSVEMVNGNNQLSGLFF LRHFYAGIPYQRQVINFPLGAH
15967	46335	A	16058	736	910	RVSTPRATGTVPQRDYPLSVVA TG*PDSFHTYLFVRTY*K*V*VL AYLNTRQNDGDFP
15968	46336	B	16059	17	1699	
15969	46337	A	16060	3	440	
15970	46338	A	16061	1	564	
15971	46339	A	16062	1	1062	
15972	46340	A	16063	203	425	LNNWIISWLLHMMCLMKVAN CFRS*DRRELAVSAFFVLL*AM RLRRSSSGFLANLAHLQKMKL NSSTYVPPTKH
15973	46341	A	16064	402	713	RGVAISLGQSKSHGYIHFQVAQ REPEILG\DSIKAVRWCSLHGRL M***M*RDLKQWFSAPEA*VSL GTLCVIGQKAVGSLALMSWEP TPRPMGLLSTSRTLYS
15974	46342	A	16065	944	1305	LPLWFISALRLAGIAVWCVLST GFEQIRMIKAFGLEDRQSAL/FA ADAEDTGKKNMRVAR/IDARF DPTIGWPSSLGLLFSNRTPWVPF PFFFQVPQ\LHTFIRGILIWKTFP FWIFPFPASSW
15975	46343	A	16066	1	756	

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15976	46344	A	16067	50	1191	CLTIAVFFPAPQCPEMFSIPCHT ARDGERAASMIQDYIFCFFSASF MKLKPERMHSHERAQTSDMLK DCRRHLPIGILMAGGMFAVLRK KHQGQTFIERPRISLTCMLPSW ATFLWLFTRIGQVLVTCLLMSR ECFVNE/VQVIATVVSVNPQVN PDIVAMIGASAALSLSGIPFNGPI GAARVGYINDQYVLNPTQDEL KESKLDLVVAGTEAAVLMVES EAQLLSEDQMLGAVVFGHEQQ QVDSRGSPIKGNRTCDNYIVIEG LIDYVNDMIENVSEEAFCVENR IMRHSDHHSCIVVRCLSLFALD LVLVVIAVSVVNPCLLEVTRLR AASIVSQPNLNISDTWGIGAILY GAYTCSCIADPHKMMSSGPMY SHSCVEK
15977	46345	A	16068	401	1518	LILFMST/ALLDAVVKKNRVRLI PYMLALYVLAFLDRSNIGLAKQ TYQIDTGLSNEAYALGAGIFFV VYAFLGVPANLLMRKLGARTW IGTTTLLWGFLSAAMAWADTE AKFLIVRTLLRAAEAGFFPGMI YLTSQWFPQRNRASIMGLFYM GAPLALTLGSPLSGALLEMHGF MGHPGWFWMFVIEGLLAVGA GVFTFFWLDDTPEQARFLSKQE KTLLINQLASEEQQKVTSRLSD ALRNGRVWQLAIIYLTIQVAVY GLIFFLPTQVAALLGTKVGFTA SVVTAIPWVAALFGTWLIPRYS DKSAAKRYTRPHRECGYFSAPY HPPKKVRNNAPHSGPGPICLIRL RVRVRPNLGIEVYKHDSPPNNA
15978	46346	A	16069	283	822	

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15979	46347	A	16070	1	1400	MTDLIQRPRRLRKSPALRAMFE ETTLSLNDLVLPIFVEEEIDDYK AVEAMPGVMRIPEKHLAREIER IANAGIRSVMTFGISHHTDETGS DAWREDGLVARMSRICKQTVP EMIVMSDTCFCEYTSHGHCGV LCEHGVDNDATLENLGKQAVV AAAAGADFIAPSGAMDGQYDV FVRNENYWGEKPAIKKITFNVI PDPTTRAVAFETGDIDLLYGNE GLLPLDTFARFSQNPAYHTQLS QPIETVMLALNTAKAPTNELAV REALNYAVNKKSLIDNALYGT QQVADTLFAPSVPYANLGLKPS QYDPQKAKALLEKAGWTLPAG KDIREKNGQPLRIELSFIGTDAL SKSMAEIIQADMRQIGADVSLI GEEESSIYARQRDGRFGMIFHR TWGAPYDQRPSQSKRVRQR*F QAQQD*MKKPTQSKWNRATR VRGGREILTKFVLTAPLKWLKR SNSRRVSFAG
15980	46348	A	16071	592	1427	IPIGVTPCFSTLRRTLFALLACAS FIVHAAAPDEITT\AWPVNVGPL NPHLYTLNQMFAQSMVYEP\LV KYQADGSVIPWLAKSWTHSED GKTWTFTLRDDVKFSNGEPV\D AEAAAENFRAVLDNRQRHAW LELANQIVDVKALSKTELQITL KSAYYPFLQELALPRPFRFIAPS QFKNHETMNGIKAPIGT\QPWN LQESKLNQYHGFGRNENYWGE KPAIKKITFNVIPDPTTRAVAFE TGDIDLLYGNQRLLPLDTFARF SQNPVYHTQLSQIWNQ
15981	46349	A	16072	1	1071	
15982	46350	A	16073	585	1072	RPARDVPLPIRGLQPSLRGPQQL PEKPAVEVRLDKWLWAARFYK TRALA\REMIEGGKVHYNGQRS KPSKIVELNATLTLRQGNDERT VIVKAITEQRRPASEAALLYEET AESVEKREK\MSPRGPPFVGAP KNPRGFLKLNALTMPHPDRRP DKKERRDLLR
15983	46351	A	16074	36	356	ASHTLARKSC*S/PSLLYQENQA HNQMPASELKASEIPFHPSIKTQ DPKAEEKSPRSKR*L*QRQVLP DPAADLSVKPPGPLMLPLCYLS GPADITVLKASQDGLIIA

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15984	46352	A	16075	1	2111	MNTPLQSAHTHLTLVEFIAYLV SDSPFPAASTLSLPTCNFDPCPT KLGAGTMPPAAAGGQRRPHAA PPAAYPHRNKVRAAEARTSRA VRREYEAGDEASGRRGRGGRM KSVQNARADRGMWVRERRAV VRGQENTVVVFAAAASPESDFL QIVLRDIAREMVPEYKSDLQPR TQMDAKKPRKCDLTPFLVLKA RKKQKFTSAKHLWVQRKGKG VEDHADWQGQIWVGVEGKSA EGQGLNLTGAFNRSPENKVSPQ GPALNALEIDSSYLDPQALALP QGWQGLLFPPLLGTELVGSKLS VQIQKPPSNIKNSRMTQVFHKN TSVTSLPFVDTKGKKNTVSFPHI SKKVLLKSSLLYQVSADGLDPE KAGERPGFSPKPVLERPRIVGKS TVAAEEENQAHNQMPASELKA SEIPFHPSIKTQDPKAEEKSPKK QKVTLTAAEALKLFKNQLSPYE QSEILGY\PELWFLGLEAKKLDT APEKFSKTSFDDEHGFYLKVLH DHIAYRYEVLETIGKGSFGQVA KCLDHKNNELVALKIIRNKKRF HQQALMELKILEALRKKDKDN TYNVVHMKDFFYFRNHFCITFE LLGINLYELMKNNNFQGFSLSI VRRFTLSVLKCLQMLSVEKIIH CDLKPENIVLYQKGQASVKVID FGSSCYEHQKGHLPSRLRSAVT TTSMILNKVLRFSEPKLPHLQFE

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15985	46353	A	16076	28	1327	GYKMPVITLPDGSQRHYDHAV SPMDVALDIGPGLAKKPLVIRQ GAAGLMAKLVDACDLIENDAQ LSIITAKDEEGLEIIRHSCAHLLG HAIKQLWPHTKMAIGPVIDNGF YYDVDLDRTLTQEDVEALEKR MHELAEKNYDVIKKKVSWHEA RETFANRGESYTV\SIVEENSAD DDKPGLYFHEEYVDMCRGPHV PNMRFCHHFKLMKTAGAYWR GDSNNKMLQRIYGTAWPDKKA LNAYLQRLEEAAKRDHRKIGK QLDLYHMQEEAPGMVFWHND GWTIFRELEVFVRSKLKEYQYQ EVKGPFMMDRVLWEKTGHWD NYKDAMFTTSSENREYCIKPM NCPGHVQIFNQGLKSYRDLPLR MAEFGSCHRNEPSGSLHGLMR VRGFTQDDAHIFCTEEQIRDEV NGCIRLVYDMYSTF\GFEKIVV
15986	46354	A	16077	1692	1776	
15987	46355	C	16078	1	1341	
15988	46356	B	16079	83	373	
15989	46357	A	16080	2	64	
15990	46358	A	16081	1695	2293	EMISNPFIPSSILPLAKIRNIGIMA HIDAGKTTTTERILYYSGYTRSL GDVDDGDTVTDFMAQERERGI TIQSAAATFEWKGYRVNLIDTP GHVDFTLEVERCLRVLDGAVA VFDASAGVEAQTLTVWRQADK HNIPRI\VFLNKMDKTGASFKYE VITISSLQKSGITKLCFFCVLKLV SQERCQASKCNKIEGQRFNQ
15991	46359	A	16082	1	2901	
15992	46360	A	16083	1196	1740	FWLKAMPTIVTASPRWFSC/LR EIRSAASAIASTAIQQAIARPSTV IATTLLSNSHGNSSDSTSVEMK AIINKLRILRGRSRPQRTRGPTPS SSANGTISQVNMVLKNGSPIEIL PSPSCLCTNGSSVPSNTTSIAAT SKTLFANSKDSRDHSALFTRER TLCPRAANSSSEPANHQHHKGE D
15993	46361	B	16084	49	398	
15994	46362	A	16085	378	566	
15995	46363	A	16086	1	2184	
15996	46364	B	16087	311	4963	
15997	46365	A	16088	12	335	
15998	46366	A	16089	1034	1400	

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15999	46367	A	16090	1767	2973	SGARRLAG*KPGNAVSAAPFYP YARPV/SMISPMLIPC*CWKC/D PAAKRQFRERTAVRCVAQFVD VGKLIPFWGLCVGIYATNSAET FLHRVVQLLNDSVEHTLQDAIT IRDEDFTATPSPADEVAYIQLSG GTTGTPKLIPRTHNDYYYSVRR SVEICQFTQQTRYLCAIPAAHN YAMSSPGSLGVFLAGGTVVLA ADPSATLCFPLIEKHQVNVTAL VPPAVSLWLQALIEGESRAQLA SLKLLQVGGARLSATLAARIPA EIGCQLQQVFGMAEGLVNYTR LDDSAEKIIHTQGYPMCPDDEV WVADAEGNPLPQGEVGRLMTR GPYTFRGYYKRSSVLGKGSDCS FGVFLPGLLPSASSVRRDSNVSI RNVVSLINSSRWKSGFTWHDN VLQLDGSFPLT
16000	46368	A	16091	845	1920	YPMMRK/RLMKLWREAKALHS DPFEPWASIIEDADKAKSSKQA RGRGGFVRSSWQEVNELIAASN VYTIKNYGPDRVAGFSPIPAMS MVSYASGARYLSLIGGTCLSFY DWYCDLPPASPQTWGEQTDVP ESADWYNSSYIIAWGSNVPQTR TPDAHFFTEVRYKGTKTVAVTP DYAEIAKLCDLWLAPKQGTDA AMALAMGHPPERESGRYRLIPV PASGYPPDPAPEWDQFPHVHEL CDTANGCPLPELASPAGYTSSIN RVSTCVSTLAKSSYRSRVRVKR LRRRFNGGVHFRRVVAVVIDQ HCRTAFTIHWLQREFTEEIKTAT SPLEAFKRPQNSLVVNALFRSN RNAAAAFSAL
16001	46369	A	16092	1	209	VSFMIIAALMMMGIDTGWLLV AAGFVGAIVIAS/ARPGRNSKRL IALISAIGMSIFLQNYVSLTEGSR DVA
16002	46370	A	16093	194	657	CLDHLRAVQSLRLPLSVPAAM RPGAAIGYTMVYGIIGMIN/FAH GEVYMIGSYVSFMIIAALMMM GIDTGWLLVAAGFVGAIVIA/S/ AYGWSIER/VAYRPVRNSKRLI ALISAIGMSIFLQNYVSLTEGSR GLATEMFLEKGDNGTEDGRAR
16003	46371	A	16094	1	3303	
16004	46372	A	16095	3	5071	
16005	46373	B	16096	144	326	

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16006	46374	A	16097	282	599	IPVSISGCHLAGAGTQTASGVP VHPHGHLAHQRQSFIGNTKTEC WPISSVPPHHW*A**TDIGAGSG DDQRVLDVWWNWRTKE*P*W W*PTNGLCRKVANRQAAR
16007	46375	B	16098	1	276	
16008	46376	A	16099	812	1084	
16009	46377	C	16100	1	1608	
16010	46378	A	16101	173	504	SADSKPVLPRTSASLVSASCSTR CGLRQASMESNNLTMVFGFSIG KVWMRS*NSATSLAKSRISFGT RRRWHSCSTN/SNTRRAMTMM TRPEFWRRQPCGLSIAAIESVIK V
16011	46379	A	16102	1	816	
16012	46380	A	16103	742	1182	PAFIECSKAQENNHKGNCYQSG SLVSR*AFLIRHTRPVITNARR*F *RKVFHQRHGIAGTGSWRGFPL NLH*RQTVVAFQSRRAIHPM*S GKGREWHHFAVGAADIKFIDIF WQHTEFGIRLNTRRAMTMMTR PEFWRRQPFTEIVA
16013	46381	A	16104	550	884	KRYGMAASFHSGEITTHRTPAP WRMVVMSPARSMAHDLAQTA WRG/APRPLPDTLATMTPQAY/ NSIQYDAEKSLWHNVE/NRQLD AQFFHMGMGFRRRTLWAGITN AQVCGWTA

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16014	46382	A	16105	2363	2856	MLTLWSSPTTTRRWRWAASSV ANTLA*MTLSMAAMLSPQVDV RFATLCHDLGKGLTPPELWPRH HGHGPAGVKLVEQLCQRLRVP NEIRDLARLVAEFHDLIHTFPM LNPKTIVKLFDSIDAWRKPQRV EQLALTSEADVRGRTGFESADY PQGRWLREAWEVAQSVPTKAV VEAGFKGVEIREELTRRRIAAA SDTIPQLNEHDIHRRRHNKAIN GERDQRNALNQLQEGFNRYQR HHKSGDQPNGKHRDIAACQEA PALVEIERRCAHHHRHRQQERK SEQHAARFGIANGDLVRVWNK RGQILTGAVVTDGIKKGVVCV HEGAWPDLENGLCKNGSANVL TADIPSSQLANACAGNSALVYI EKYTGNAPKLTAFDQPAVQAN TRPLRLARNQHRAFRCRITFHR FTRIMWVEEIGQRFGNHPFGRV RIQDSLCVCGALRYISATFNVW RKRAVTCVRSFGSDFTGSPPLR APKGESIRRLLALREAGIIHILAL GEDYKMEINESRTVLKTEDNSY SFDVFIDARGQRPLKVKDIPFPG LREQLQKTGDEIPDVGEDYTLQ QPEDIRGRVAFGALPWLMHDQ PFVQGLTACAEIAAACGPFDKD RIEGGIVVRMAKEGETLVLLDG TEAKLNADTLVIADHNKALAM GGIFGGEHSGVNDETQNVLLEC AFFSPLSITGRARRHGLHTDAS
16015	46383	A	16106	390	636	KFLSFRPDRVCVACAEEARAGL CLRQCITGHPEACLAIPVLVCVE CWGGTDADQPVAVFPSRFSQV SPDRGT*QWLCWKFL
16016	46384	B	16107	1	520	
16017	46385	A	16108	142	243	
16018	46386	B	16109	275	919	
16019	46387	A	16110	1	693	
16020	46388	A	16111	522	714	

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16021	46389	A	16112	1	900	STCSSRSHLHLIQASPILPNYVA TAVAARIIADVQGISDTCVIAQP SPPHPGALRTLVFTTDEPETPQP PGAAGFQLVQKKQVQLHNVLY VMTPHAFAQGTVTIYLPGEQQT LSVAPLKNVVQLVTQQHLRDR LWWPGAFLTDFAAKVKALKD/ YPNHVMAQRASGEAEADDDV AATIKSVRQQLLNLNITGRLPV KLDPDFVRVDENSNPPLVGDYT LYTVQRPGTEQGSFKVKRARA RVRQTRAPLFGPKSPAPEHMES ELEFELIGPSKSTSGNPRGLRSE RPVLFCLYPEMPTAAAR
16022	46390	A	16113	150	649	NALLGTCPGTARFPGTGSAPTL HPDASRSGRGRAACPRSAQWS PRPWQSVAGLAWLGAHWGSR STSRTAETTASKRGHPRSPAAQ LPPGPRPPRAPQLQRALQSVHP LSPRPAPLA/EPKLTAACWAEA VKITTVRYSDSCSRLLTDLGKP VQSMLLKDIRKVYNWQ
16023	46391	A	16114	153	740	THQLFLPPHHQEISQTTWLSAA WPRHTCAHSLSPLQPPVPFSRP HVPLPGPSKTWSDGPRLQSLPG/ RPSERTPRR/CRSASGQPPHLGG EERLCLAAPSGRICHCEGDDES PLITPCHCTGSLHFVHQACLQQ WIKSSDTRCCELCKYEFIMETK LKPLRKWEKLQMTSSERRKIM CFSDIPRHCRPMCGLVLVCAH
16024	46392	A	16115	1	1194	
16025	46393	A	16116	323	642	TGYARQKPVPALGWWTNVSAS TAPPIILPSITGSRLAVIKWLTVS AGKLSALLCASCQKGG/VGEM ANGNGERNHKQIGDTVLTPPQ HYRKIYQPIAARSCIRCVCGS

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16026	46394	A	16117	1	1782	MAGIRSTLIKEKNMITNYEATV VTTDDIVHEVNLEGKRIGYVIK TENKETPFTVVDIDGPSGNVKT LDEGLSLLLSLVSIVVIMKLFYQ YEQRFGMRSTSLLNVIGSNTIAI YTTHRILVEIFSLTLLAQMNAA RWSPQVELTLLLVYPFVSLFICT VAGLLNLTTVMPEQYRYTLPV KAGEQRLLGELTGAPCATLVA EIAERHAGPVVLIAPDMQNALR LHDEISKFTDQMVMNLADWET LPYDSF\SLHQDNYLLVAFQPFY QLTDDAAVGVLIVPVNTLMQR VCPHSFLHGHALVMKKGQRLS RDALRTQLDSAGYRHVDQVME HGEYATRGALLDLFPMGSELPY RLAIGVNVAQAEVLNLESGAK QVLQETFGYQQFRPGQEEIIDT VLSGRDCLVVMPTGGGKSLCY QIPALLLNGLTVVVSPLISLMKD QVDQLQANGVAAACLNSTQTR EQQLEVMTRPRIGDGTGALRK RVAQLAFKNQPMMVGNWAQS ILHGGVIASALDVAAGLVCVGS TLTRHETISEDELRQRYRGWGP LIFALIICAQAGASVLLLLVACC VQAIKSPSPALNYTMKNSFILPV
16027	46395	A	16118	380	1431	TALLIRDMPPYVEAYPNENLTT VMPEQYRYTLPVKAGEQRLLG ELTGAACATLVAEIAERHAGPV VLIAPDMQNALRLHDEISQFTD QMVMNLADWET\LPYDSFSPH QDIISSRLSTLYQLPT\IQGGVLI VPVNTLMQRVCPHSFLHGHAL VMKKGQRLSRDALRTQLDRAR YRHVDQPAHAGGKVLEMIVVG IATWLGFLLFGLNYSLLLAVLV GFSVLIPYIGAFVVTIPVVGVAL FQFGAGTEFWSCFAVYLIIQAL DGNLLVPVLFSEAVNLHPLHHR EQIGGNKMADRQCRKIVCATV RQLPEGGRGEMANGNGERNHK QIGDTVLKATGSKQGDGQNHG
16028	46396	A	16119	1	940	

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16029	46397	A	16120	114	1380	NRVHCRRCSGGDTGVSHLKGI NVKYRYELTDSVGVMASLGFA ASKKSSTVMTGEDTFHYESLRG RYVSVMAGPVLQISKQVSAYA MAGVAHSRWSGSTMDYRKTEI TPGYMKETTTARDESAMRHTS VAWSAGIQINPAASVVVDIAYE GSGSGDWRTDGFIVGISGVLKD GTGKPVQNCTIQLKARRNSTTV VVNTVGSENPDEAGRYSMDVE YGQYSVILQVDGFPPSHAGTIT VYEDSQPGTLNDFLCAMTEDD ARPEVLRRLELM\VEEVARNAS VVAQSTADAKKSAGDASASAA QVAALVTDATDSARAASTSAG QAASSAQEASSGAEAASAKAT EAEKSAAAAESSKNAAATSAG AAKTSETNAAASQQSAATSAST AATKASEAATSARDAVASKEA AKSSETNASSSADYAAS
16030	46398	A	16121	165	299	GILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW
16031	46399	A	16122	1	388	MGSKSWVTQKGPAKAQSSQV GRVKQATATDTGRTRDSHMER PKCSKGYLCLPYMALQQHHLL SDVTVRGFVAGATNILFRQQKH LSDAIVEVRLCGSDLVLYGTST PKNLIWVMVHVVGHRPDRR*C CCNA/SVRQTQISLRAFGSFHM AVSGSSSVSGCSLFHSAHLTAL CFSWPLLCYPTLGPH
16032	46400	A	16123	130	414	
16033	46401	A	16124	1	387	
16034	46402	C	16125	1	1611	
16035	46403	A	16126	318	401	
16036	46404	A	16127	519	658	YPGSQLLASKGTKLDGE*V*RS RLQKVGNNKLLQAKGACSNPT QES

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16037	46405	A	16128	1	1837	FRPRQLVAAKPSVFADVQSMES VGTGGGAEAEGGVRSRGLCPT RMLPGLAAAAAHRCSWSSLCR LRLRCRAAACNPSDRQEWQNL VTFGSF\SNVVPCTHPYIGTLSQ EKLYSTNVHKEGQGSHTLREE KVPSFVTAEGVGAKLISPLKQE PLQVRVKAVLKKREYGSKYTQ NNFITGVRAINEFCLKSSDLEQL RKIRRRSPHQDTESFTVYLRSD VDAKSLEVWGSPEALAREKKL RKDAEIEYRERLFRNQKILREY RDFLGNTKPRSRTASVFFKGPG KVVMVAICINGLNCFFKFLAWI YTGSASMFSEAIHSLSDTCNQG LLALGISKSVQTPDPSHPYGFSN MRYISSLISGVGIFMMGAGLSW YHGVMGLLHPQPIESLLWAYCI LAGSLVSEGATLLVAVNELRRN ARAKGMSFYKYVMESRDPSTN VILLEDTAAVLGVIIAATCMGL TSITGNPLYDSLGSLGVGTLLG MVSAFLIYTNTEALLGRSIQPEQ VQRLTELLENDPSVRAIHDVKA TDLGLGKVRFKAEVDFDGRVV TRSYLEKQDFDQMLQEIQEVKT PEELETFMLKHGENIIDTLGAEV DRLEKELKKRNPEVRHVDLEIL
16038	46406	B	16129	1	1065	
16039	46407	A	16130	1248	1658	PLALPEFISKSWKERLTDTTVLF LKARRQSLCLQIGGDPLES/ILQ AFCVLSVAKESQLYTYLHAIMR TLKSSIARGARTFQSTSDGTVKS RPSKIIFLPRLHDRFRFSALRHL DPKKLDLGDGSRSAHRPDRRFF
16040	46408	B	16131	969	1026	
16041	46409	A	16132	339	432	RYMVLSEFRSMQTGITKWKERI L*NCRKRE
16042	46410	A	16133	3	443	HTWNSDRTMYLQRRHIFFKNC FWLQAGYSLGAPSWRSLVTVW QIIFSDFYRKTLCNSNSPLF*SLC QRQSTLLGTLLIFCSYASSPEAI NSAAPRVRSPRTDPRKARSPRG VGGAEGNGSRDTEPKGGRPLA TPSQGERLMAGTVTK
16043	46411	B	16134	34	1426	
16044	46412	C	16135	62	217	

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16045	46413	A	16136	1	609	MIPVSEKSKIGQLNLMLKGKKT KGKKVALVPAAVKKQEAKKV VNLLFEKRPKNVGIG/QDIQPKR DLH\RFVKWPRYIRLQQQTAIL D/QFIQALDQQTATQLLKLAHK YRPETKQKNKQRLLA\RAEKKA ASKGDIPNKRPPVLQAGVKTVT NLVENKKAQLVVIAHDVDPVE LVVFLPVLHCKMGVPYCIIKGK ARLGHLVHRKT
16046	46414	A	16137	1	824	GTRPKMPKGKKAKGKKVAPAP AVVKKQEAKKVVNPLFEKR\PK NFGIGQDIQPKRDLTRFVKWPR YIRLQRQRAILYKRLKVPPAINQ FTQAL\DRQTATQLLKLAHKYR PETKQEKKQRL\LARAE\KKAA WPKGTFPTKRPPV\LRAGVNTV TTLVENKKAQLVVIAHDVDPIE LVVFLPAL\CRKMGVPYCIIKGK ASLGRIVHRKTCTTVAFTQVNS EDKG\ALAKLVEAIRSNYNARY DEIRRHWGGNVLGPKSVARIA KLEKAKAKDLATKLG
16047	46415	A	16138	1	799	
16048	46416	A	16139	1	344	MHQTTAKTPHTSYPNNYEEHN RRANRSKNYDRIRHTTIILKRTN PAQTITNLLKSRFNRYNYVQPR SCRSIFIHIPGERDLNLCIAPNPP AIFPTSIGYLGPDLNNLPTYAPFI TTNLTGPAPTTTHPVGNLGTTG NPEPGGCGILIVWCCVNWACL WDSVVAAPREPYMPAGLLRHR RHYRHRREDLIAVPAARQTDE NRRPALCHEYAVGHRKIKTNV EHTEPYILPLITHSQPLNRGAFF CPGVRFLVVSVLDFEKRLAFAS *SCGVQLRIRGKVQGVGFRPFV WQLAQQLNLHGDVCNDGDGV EVRLAYRVLVGQPQHYPRGRP
16049	46417	B	16140	1	1323	
16050	46418	A	16141	1	1356	
16051	46419	A	16142	1	1524	

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16052	46420	A	16143	173	2310	QQWASRTRRWRSLITTLCVDA RSQHDYIALSRLFHTVMLFDVP VMTRLMESEARRFIALVDEFYE RHVKLVVSAEVPLYEIYQGDRL KFEFQRCLSRLQEMQSEEYLKR EHLAAKPETVKRDWYVVDAT GKTLGRLATELARRLRGKHKA EYTPHVDTGDYIIVLNADKVAV TGNKRTDKVYYHHTGHIGGIK QATFEEMIARRPERVIDNRRGS LRQAGYAIHDGGNNSMAKNTS CGVQLRIRGKVQGVGFRPFVW QLAQQLNLHGDVCNDGDGVE VRLREDPETFLVQLYQHCPPLA RIDSVEREPFIWSQLPTEFTIRQS TGGTMNTQIVPDAATCPACLAE MNTPGERRYRYPFINCTHCGPR FTIIRAMPYDRPFTVMAAFPLCP ACDKEYRDPLDRRFHAQPVAC PECGPHLEWVSHGEHAEQEAA LQAAIAQLKMGKIVAIKGIGGF HLACDARNSNAVATLRARKHR PAKPLAVMLPVADGLPDAARQ LLTTPA\AP\IVLVDKKYVPELC DDIAPDLNEVGVMLPANPLQH LLLQELQCPLVMTSGNLSGKPP AISNEQALADLQGIADGFLIHN RDIVQRMDDSVVRESGEMLRR SRGYVPDALALPPGFKNVPPVL CLGADLKNTFCLVRGEQAVLS QHLGELSDDGVQMQWGQRLC RMGTQVLPPTFNIEKKVQSARY
16053	46421	C	16144	1	184	
16054	46422	A	16145	85	416	
16055	46423	A	16146	96	570	

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16056	46424	A	16147	2	1690	CCCCPCCCPCWGRVSGSVAGG PRQGLGLPLSLCISPGSLNKDPS YSLQVQRQVPVP/EGLCVIVSC NLSYPRDGWDESTAAYGYWFK GWTSPKTGAPVATNNQSREVE MSTRDRFQLTGDPGKGSCSLVI RDAQREDEAWYFFRVERGSPL TQKPDVYIPETLEPGQPVTVICV FNWAFKKCPAPSFSWTGAALSP RRTRPSTSHFSVLSFTPSPQDHD TDLTCHVDFSRKGVSAQRTVR LRVASLELQGNVIYLEVQKGQF LRLLCAADSQPPATLSWVLQD RVLSSSHPWGPRTLGLELRGVR AGDSGRYTCRAENRLGSQQQA LDLSVQYPPENLRVMVSQANR TVLENLGNGTSLPVLEGQSLRL VCVTHSSPPARLSWTRWGQTV GPSQPSDPGVLELPPIQMEHEGE FTCHAQHPLGSQHVSLSLSVH/S PSTAAGPLLLLGG*GSALQLLL/ SRPARPPLCAGGLGRSCWRGTA VRAPSRSPPAQPGPGPTAP*AS MEGSAPASGSAVRPGTSTGPRV ALSSSCYQGSWSMGEDLAWGL PWELASLPCSLSVPALSSSG
16057	46425	A	16148	3	1578	VTQLLCTSNGRRALEFALFPGR RFRPVATNHQSREVEMSTRGRF QLTGDPAKGNCSLVIRDAQMQ DESQYFFRVERGSYVRYNFMN DGFFLKVTGMEWGGNPCLSH WGGTLGTAYGLSREGSQGPLQ HKN/HPTTVSVPALTQKPDVYIP ETLEPGQPVTVICVFNWAFEEC PPPSFSWTGAALSSQGTKPTTS HFSVLSFTPRPQDHNTDLTCHV DFSRKGVSVQRTVRLRVAYAP RDLVISISRDNTPALEPQPQGNV PYLASPK\GQFLRLLCAADSQPP ATLSWVLQNRVLSSSHPWGPRP LGLELPGVKAGDSGRYTCRAE NRLGSQQRALDLSVQNPPENLR VMVSQANRTVLENLGNGTSLP VLEGQSLCLVCVTHRQPPSQAE LDPEGTGSEPLPALRPRGSWSW LVGSSGARRRVHLPRSAPTGAP RRTLLPSPCTTPRSCWAPPAPGR LRVCTAAAPPRPARPPLCAGGL GRSCWRGTAAQGLLRGSPPAQ PGPWAQTASPEPSMEGLNSGPQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16058	46426	A	16149	90	1029	MLLPLLLSSLLGGSQAMDGRF WIRVQESVMVPEGLCISVPCSFS YPRQDWTGSTPAYGYWFKAVT ETTKGAS\VAPNPP\SREVEMST RGRFQLTGDPAKGNCSLVIRDV QMQDESQYFFRVERGSYVRYN FMNDRVL\LKVTALTQKPDVYI PETLEPGQPVTVICVFNWAFEE CPPPSFSWTGAALSSQGTKPTTS HFSVLSFTPRPQDHNTDLTCHV DFSRKGVSAQRTVRLRVAY\PP ETFGISIFTVTNTPDPPENLRVM VSQANRTVLENLGNGTSLPVLE GQSLCLVCVTHSSPPARLSWTQ RGQVLSP
16059	46427	A	16150	270	1001	CCCTVYRAFIRKRLKRSSDSVY RRKNPSASYDRDAEASLAAVK SGEVDLHQLASTWAKAYAETT LEHARPEEPSWDEDFADVYHD LIHSPASETLLNLEHNYFVSISEL IGERDVELKKLRERQGIEMEKV MQELGKSLTDQDVNSLAAQHF ESQQDLENKWSNELKQSTAIQK QEYQEWVIKLHQDLKNPNNSS LSEEIKVQPSQFRESVEAIGRIYE EQRKLEESFTIHL*AQLKTMHN
16060	46428	A	16151	60	648	LAMSLSHLYRDGEGRIDDDDD ERENFEITDWDLQNEFNPNRQR HWQTKEEKGSLQRKEFFTDLV GLCFCAYRARDYSAPVNFISAG LKKGAAEEAELEDSDGFLRFFFI LFFH*LSFDFSFLQGGNFKPSQK GFAGGTKSFMDFGSWERHTKG I*FTYMNCCDRKTLFFFC*NSSG IINPIEAKQRKGKGAVGAYG
16061	46429	A	16152	237	450	LAMSLSHLYRDGEGRIDDDDD E/REENFEITDWDLQNEFNPNR QRH\WQ\TKEESTYGVWAERDS DDERPSFGG
16062	46430	A	16153	12	85	VSFLSMGSGHCIRSTRGSKMVS WSVIAKIQEIWCEEDERKMARE FLAEFMSTYVMMNIHMIVEKN T*SPFCPWARATVSGPPVAPKW SPGP
16063	46431	A	16154	49	481	
16064	46432	A	16155	20	248	
16065	46433	A	16156	493	728	VSFLSMSSGHCIRSTRGSKMVS WSVIAKIQEI*CEEDERKMAREF LAEFMSTYVMMVSGRAARSG WALPGPSMTPSPF

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16066	46434	A	16157	136	306	ASSSREGLTKFAKFTKFTKIHQI *ITLTSYSIKSLEKVCADLIRGTK EKNLKVKGPV
16067	46435	A	16158	563	1216	MMFWPELQPRVCWMGLSWVN HQNGRRRRKNQKHH*QKVPLL IMASK*KLLEFLNRETKASANL SETVTKPPLPQKNTAQVGASSQ TRKPNKLAPHPAVPAFVKNTCP SRPRERQTHFLRPRPEDRMVAL KPIKIVLPPVFMPFSSPQGIRSR MPTQHLYCRWVAPKALVPTCL PTHSLSRKEEKPKRMDTPFLPY SRPPSGEWLLIVLWFFNRSQRS
16068	46436	A	16159	1	143	
16069	46437	A	16160	40	230	KQAAQPAVATLSGPLPHCGSFV LSLFAINLVAAHSLGPHCLYEL* HSPRRSTASLREGPRLHS
16070	46438	C	16161	233	319	
16071	46439	A	16162	290	472	EFLDTFCYIPKVVDQ*D*THKQ QHNVAIIPHVSSAQMSTFC*RT MPTISDDPWHMASMRAV
16072	46440	A	16163	3	553	
16073	46441	C	16164	270	608	
16074	46442	A	16165	2598	2943	HSPRGSAASFLKSVRPRTHQFR TQEDRLSPGIQDQPGQPSNTPSL QKL*N*LGVMGRICSPSYLS*P WREDHLSPGG*GCSEP*LHHCT PAGVTKSDRVSKNK*INKNKIN NDNQ
16075	46443	A	16166	2	58	
16076	46444	A	16167	218	342	
16077	46445	A	16168	734	872	
16078	46446	A	16169	1233	1706	CLVFWLLYYPGLQLPFHLLPHS LGSGQQSSEESAATPSLAEGRR EAAFRCGPAGLARQAWRPHAR LPGPAAPLAAPSLAPLPTGRSG RWLPMLCAASC*SPSPAMSVYP QRRLGQGGAEDSEGGPVSRGC RAPGPQRPLAAPGEQTAARTQ AICLIW
16079	46447	A	16170	598	1159	CRQTGVKIYDVWFFWLLYYPG LQLPFHLLPHSLGSGQQSSEESA ATPSLAEGRREAAFRCGPAGLA RQAWRPHARLPGPAAPLAAPSL APLPTGRSGRWLPMLCAASC*S PSPAMSVYPQRRLGQGGAEDS EGGSVSRGCRAPGPQRPLAAPG EQTAARTQASVYLLLPHSPPLL SALHIHHLLPPS

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16080	46448	A	16171	834	1185	RSLFRHHRPSAAFPRTPCSDCPR CSAGTMEDCWLVLGSPELR*KS LHERPFHWLPSPSRARCCLPRSE TPAGPVPPRPGPRRARRPRGTS RPPPASSRGRGALGSLPASEPLP ARAT
16081	46449	A	16172	78	478	VVKNSLIFLVNQVLNSRDFHVF FKTT*NCPAQAHTAALYQGLGP ACSQRASHWMSSSSKRSSKSLK KSA*TAFSLAAKSIKSPGAASRL GNGKARLCQVRFPKEQVISALQ GHYPHKKRRWVRGNRLKLEST F
16082	46450	C	16173	1323	1656	
16083	46451	A	16174	77	231	RSCMTLMWPRSTP*FGLMERR RHMFDWLLITMLWMLPTKLGS SKLSPAA*F*SSCLIL
16084	46452	A	16175	1	255	STSKGEKPAIRAMAHFLEPHPIN FLGARARKADLSPT*YHFFKHL DNFLQGKCFHNQQDAENAFQQ FFKSQSTNFYAGSSFVTEV
16085	46453	A	16176	690	1020	SPVLQRAFKNGPGTANERTVQ WWFKKLCKGDESLEDEEHSG* PSEIYNNQLRAIFKADPLTITRE EVFPHPLYSPDLSPTSYHFFQHL DNFLQGKCFHYQQDAEHAFQE
16086	46454	A	16177	1	383	MHRSCGSDAYALLGERSVSLR RCAVRHAGGIRSANADISNDKA GEKPARRKTKGSCPTLIGAGLV QSLSPIQSAADAGELGSNGILPD VESLRIPVQYLANLLTAGDTKP VLRALKRMLAMRHYKRAETV DGKVDTRALEEVGLTEAQAQE MYRYLAIANYEDRFVVPSSHRE LAREAFPEKNGCGFTFGDGCH GSDTKFNLFNSRRIDAID*PCPD *RWTGTLGLPASGLFTRFIVTY VSIRTSDTSSMPHSTPSQA\TERS PNNA*ASLQTC

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16087	46455	A	16178	740	1977	SASASRSLEHITVTPSTGILTCFP STTPFGLAL/GGTLGLPASGLFT RFIVTKSSIFSVTPLVQPKPSCN GYSPPPPPVPHRREFQRRVIAEK IFCQHHRAKLNRLEERQYLTVN FRAIAQRVNIGITGLQITIDANA AINRQPGASCQGRFPGAVRCGG NYRIHFDIALAVQRWPECQNPF FPAPVTEISTADERPSPLTGCLQ RLVTFGSVIFGIINMIMRLAPIGR FGAMAFTIGKYGVGTLVQLGQ LIICFYITCILFVVLVLGSIAKAT GFSIFKFIRYIREELLIVLGTSSSE SALRRMLDKMEKLGCRKSVVG LVIPTGYSFNLDGTSIYLTMAA VFIAQATNSQMDIVHPITLLIVL LLSSKGAAGVTGSGFSVLAATL SAGGPIAGSGSGADPRYSTALC
16088	46456	A	16179	757	1037	FLDPSPEPNVTVTPSTGILTCFPS TTPFGLALGVDSPCPD*RWTGT LGLPASGLFTRFIVTYGVTPALD TGLM*LRSCGPPRSML*HRTQQ KC
16089	46457	C	16180	1	313	
16090	46458	A	16181	178	290	LLLGLASEN*HCPIASEAP*TTT DTELWVTLTVEGKS
16091	46459	A	16182	1	251	
16092	46460	C	16183	129	1136	
16093	46461	C	16184	117	364	
16094	46462	A	16185	636	748	LLLGLAAED*RCPIASEAPQTIT DTELWVTLTVEGKS
16095	46463	A	16186	37	444	DPQVGKLLQHCPARIKMTVTF NNHRKPQLSKFHQLYSEDTQQ QIIRETFHLVFKRDENVCKFLGT IWSLTTGKLNRGQAPLFGIFHT VELHLEIRSSCQGIVHF*LTCFSS CPCSGPFVNSPFYLPLESGHSK
16096	46464	A	16187	179	422	LQLGPKEKQSRVLGSFFQVPSC GKMGCGSSGSRHIGFPP\PQLSG GPLDPRQGSGISEMK*TE*GGY PKGSPQHYSRKHQGS
16097	46465	A	16188	1064	1374	KEQCLQALSSVKNREKRPSSFH PICWSAVSFSVGREGDMWPLAP FPDSENVAGAGALLLRLAALPG LSWALRPPPPAPVRSWATSGW* GGQGREPGRGIPPRW

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16098	46466	A	16189	44	515	VGGGGVQPSMTMGDKKSPTRP KRQAKPAADEGFWDCSVCTFR NSAEAFKCSICD\VRKGTSTRKP RINSQLVAQQVAQQYATPPPPK KEKKEKVEKAGQKRKPEKRPR KFSP/SVVTKKNTNKKTKPKSDI LKDPPS\EANSIQSANATTKTSE TNHTSR
16099	46467	A	16190	382	795	DSGRSWKRLLSPPRPMCDTWA LGSYPRLCFAVSPPFSCSLPLPSL FPHSPLLGRPKRQAKPAADEGF WDCSVCTFRNSAEAFKCSICDV RKGTSTRYLKICVTWVVVVI*Q VFIEHTAICALGVQWYKDRPGP CSYGA
16100	46468	A	16191	2	343	
16101	46469	A	16192	472	625	KTSLFQHWLWKVTIVIVMF**L RVNVGKLLNNIHRYNSENLASL GSQWKFP
16102	46470	A	16193	343	693	KTSLFQHWLWKVTIVIVMF**L RVNVGKLLNNIHRYNSENLASL GSTQIPLKAFTNPCHTSFTLCKH MVIQAHQEKQLIQQILYLGDLL ET*HFQAFWQALDENMTLLESI TGFEGF
16103	46471	A	16194	340	534	TAIMNDMVTI*TRKFMTNQRLQ RKQMVIDVLHPGKATVPYLILI EQLRFARHCAWYGGDSDETSH
16104	46472	A	16195	80	552	PIPHLEKFHAPTRRTFRGNQM\V IDVLSPPGKADQCP*AQEIPGKT *PKMYQDPHPDVI\FVFWIPELH FGSRGKTKLAFGNDFMTSLGFI AKEKWNPKHRTLQGHGPGME/ ERKKTSKGKPTERERQGTGLEG KFQGGLAKGPFFGAWAKRRNE VSSS
16105	46473	A	16196	248	474	YPETPESPTQLSSGQPHREQPPE MPESPTQPSSGQSCQEQPPETPE LPM*PCLAQPSQKHMIKG*QNN KHHENKM
16106	46474	A	16197	223	669	PRPSLPACSPWRIVDDCGSLKS WKRVCQWLQPCPNALPSCLGS PLRCEFSGFPRN*LGLGSTTGSF AVWGGLFSTIDCGLVRRPGPSP FHPVLPALTSVSLPPTPPGGPLA MVGSAMMGGWSGEWEILHLA SSTHPYPSLPSPAPPFLE

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16107	46475	A	16202	188	484	HFGRVEVGRSQGQEFQTRLAN KAKHHLYSFMNESQISPIGC*P M/PPKLIRKVHREKNCAGRNLT R\QRSGFKTGPPGPPARPSSPTLP PPPPLPRLPRRP
16108	46476	A	16203	36	409	
16109	46477	A	16204	651	893	NTSVKNNFSFMNESQISPIGC*P MAPKLIRKVHRERNCAGRNLT RAEKRLQTPGLPVPPARPSSPSS PPTPPLPAATPGGR
16110	46478	B	16205	13	441	
16111	46479	A	16206	3	205	NSSNSFSIQFCSFAGEELCSFGG EEAFWFLEFSAFLRCFFLIFRDL STFGL*CAPLEEKRHSGFWNFQ PFCAAFSSSSGIYLPLVFDAGDL QMGFLCGCPFC
16112	46480	A	16207	23	841	EKAKEFRRAEEKKKEVPAVPET LKKKRRNFAELKIKRLRKKFAQ KMLRKARRKLIYEKAKH\YHK EYRQMYRT\EIRMA\RMARKA\ GNF\YVPA\EPKLAFVIRIQRVS MGVSPKGSERCCKLLRPFVKIF NGNLL*KLNKGFRLTML\RIV\E PYIGMGGTPILKSVNELIYKR\G YGKIH\RKRIA\LTDYALIARSLG KYGIVCMEELNHEIYTVGKRFK EANNFLWPFKLSSP\QGG\MKK KTTHFVEGGDAGNREDQINRL HRRNELTRLTWIFF
16113	46481	A	16208	1137	1200	PPSAPAPG*LRPPALSSGSP*PPS APAPG*HAPPPSAGTPPP

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16114	46482	A	16209	1	1480	MNECRGVEITTVCSEDWIQRHL PGAVVPLKGEGNVGVATEDHY QEDSFGFGLRGTGKPLKLEKSR PGAVTHTSPSDGLTQYVPDSLT AMPAAAVVIWVIRPGCGVQQQ IGFLRHSNIDDIRPRTIIRAVAPV KLHGIRIKMASFTSATRLTDEQ VITAPADSGIVIPRFSDNWVAG GKTHLTHKDSHKLKVKGWKK AFHANGHQKQAGVAILTSDKT NFKATAVKKDKEGHYIMVKGL DQQENITILNIYAPNTGAPKFM KQLLIDVRNEIDSNTIIAGDFNT PLTALDRSSIQKVNKETMDLNY TLEQMDLKDIYRTLHPTTAEYT IYSTVHGTFSKIDYMTGHKTSL NKFKKSEIISSSLSDHSGIKLEID SKRNHQNHANTWKLNNLFLNN RWVNNEIKMEIIQLFELNNNND TTYQNLWDTAKVVLRGKFIAL NAYIKKTERAKKTIYSHTSGI*K QEQTKPKPSRRKEIIKIRAELNEI TTKKTIQKK
16115	46483	A	16210	32	398	ASERLGGPGSPG*/PVNPRTDGS GAAWLSQRAQCTQSDPRV*EV PEHLSPSTPSQEYRGLPAL\PHTS RPSHCLPACPLPSRTQPWVPVK PGPTACRGFLQHSPTPGSPSP*S FQGSSWWDTDL
16116	46484	A	16211	2	681	AEPWDEGGDGVPCRVPSSGSV* V*TLYLDSSVQLCGTEAPQHPV DGPPGGKLCHEGSLHLRQGQIP GPRLVLQFVQQAGVCGPGGNA VYSTPRDSASLVSGRTSMLFLR KFGKTWRKGKLHQRGPPASPV LGRECNWG*VIGRHPAQSS/SGP ACAKDAAELGAAMPGLVSGPL GAALQPRGAGVQLGAATGPGS CSK/RGSPKADAR/PRHSQEPGQ VPPHAPQGPGLS

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16117	46485	A	16212	102	1005	VQWSARPDATPLSTEPSLADYP EAQSHIPRRGPRRPEKQGRGGK PPRALGRERAGGGSRGPPASPD PLSRPCSQAPPPGASAGA*DAP ACRREAGSDGVPCRVPSSGSV* V*TLYLDSSVQLCGTEAPQHPV DGPPGGKLCHEGSLHLRQGQIP GPRLVLQFVQQAGVCGPGGTD GSGAAWLSQRAQCTQSDPRV* EVPEHLPQVDTHKGELYQ*PGG RDGPGWEEPPQCGMGVSEAHG GAGGPGEAGKGRLQRKFGKT WRKGKLHQRGPPASPVLGRPR PE*VLLRCD*EG*PPSAGQLL
16118	46486	A	16213	378	494	GTACLQIPQTQGV*QRGFLAEY IQWQLRMRSGSIPVRTG
16119	46487	A	16214	18	894	SVGSLCCLQETPGLRAFGVPWR SAQRRWPRRSAASLLSLVLPGR AHSPRPTLAPGPLEAQQPPPGG SALAQHSRTAPAGTSAACLWP VSEQGAAPMCQVTRPPGSQAP CSQPSAHAHKHLTTGSSSPAEA SALPRA*TGSRWETKSSERVSSF SA*GTACLQIPQTLRRRTG*RQ VGRRLPGSGGFDGCSIFS*S*PV TYSLRSVSATSSNEATQLGTT*S NSIIFEFCSAQSTAVRCRLFST*T DAPWSRSSSTTKTCFSITASCSA VLPLLLEALMEAPCPCLACSSA S
16120	46488	A	16215	340	582	
16121	46489	B	16216	93	711	
16122	46490	A	16217	1378	2081	LSRKKPNWPSSMPWYQFSLIWL MSVKTSPSWKPSSPWFSGWKS YSTLQLGWSRGGMLLLGVQM DLLEDWKGDEAAILGTVVQGK PPLDCSGSPRSK\APRTWAYTPA WGVRKLPASCA*ASLPARPGSA WPASGRSAAPPP/AARS*LICSM SVSRRLCMLVSATSLESSNFSSA WRSSSSGILPCRFSMSRESFTSA RCFMDSPASSSASLKLDSLPSSF WWRIRHSLRSPSDCG
16123	46491	A	16218	191	288	
16124	46492	A	16219	67	209	
16125	46493	A	16220	96	341	
16126	46494	B	16221	1	1185	

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16127	46495	A	16222	192	703	AMPSCTRAGLAFVCHVRRRGC LSCRGVIPASSQCLFPAPMGTTE ATLRMENVDVKEEWQD*DLPR PLPEETGVELLGSPVEDTSSTSN TLNFNGAHRKRKTLVAPEINISL DHSEGSLLFDDFLDTLDDLDIN VDDIETPDETDSLEFLGNGNEL EWEDDTPVATAKNMP
16128	46496	A	16223	8084	8251	TAGDERHGPSRVRMFRIKGRRL GWMGPLGRGKR*VTRGMWPG KGPAYPGSSASSF
16129	46497	A	16224	645	1317	WGASRLREPPSPRTLHSPRPGP ASAPPLRPLPQNRTPSPSAASTT APPQPSEASRLPA*KAKPKPHPP SAPRRGGSPPRHSAQPACGRRR PRSVGGAAPYAAERRNSAPQGP PQRLRRTAEGGKRPSNPRQRSH PRQRGDSLP*LGPWSRDRRAGR DGRDGSAGGTRRSPSPRYASPE PLGPAAPASPAGASWTGGPGRR ADDSWRASVFGAQSSACFPRA RVL
16130	46498	B	16225	72	378	
16131	46499	A	16226	151	372	GGQHWAKAWRQTLGPEMPER TGACGCGSL*PFTTPPPPAICVD GTFHKYVFTPDGNCNREAFDV YLDICDDDDF
16132	46500	A	16227	182	1083	HPGPCPDHEQVGSMGLVEDPV SPGLPLTLNLGPDNPPTCPAVLI WDDAREGKD*EG*SSLGIPPPP HGHPVLCDTHRIVIVLKNRQLC PF*DAASSSAAHPTPHLHTLGL CELPCGLLAPSLHTTPTSDSSLL PQDLASTKPGTSSAPFTINAHQS DIACVSLNQPGTVVASASQKGT LIRRVCMVGW*PHTT*HVGITA DLSSSINFSHDSSFLFPTLPCPCP PAHLPYLGLASAACRLARVGK VGPMIGQYVDSQWSLASFTEM PERTGACGCGSL*PFTTPPPPAI CVDGTFHKYVF
16133	46501	A	16228	202	517	GVHCHGFSAGQAAGQEPTSVH ETLLPHQLQDQSALRGGVQNR QRHQAAEGPGERAGAAVSVGL GEPQCH*VGAGRAARGPPILEV PAGGADAAAECPAGPHGCGG

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16134	46502	A	16229	141	633	WENARPEPSQGDLRAASVVSPR LPPRKGQGGLGYFGRGAGHAH GTAGQGASESETLLPHQLQDQC ALRGGVQNRQRHQAAEGPGER AGAAVSVGLGEPQCH*VGAGR AARGPPILEVPAGGGDAAAECP AGPHGQNARGQQSGISQLRHE REFLLRPFPQAPQL
16135	46503	A	16230	65	466	VVFAEAAEASLMTSGVGGGAA QSPRSRRGGWWPLGEMPYANQ PTVRITELTDENVKFIIENTDLA* GYRGKRLAALGRGRPKPGPRG RGRGCSGWGGGDVLPELPPCT RALALGACGAGPACRGCSAFTP LGF
16136	46504	A	16231	42	491	SGGKEAQGQSGTDQTVVVLSN PTYYMSNDIPYTFHQDNNFLYL CGFQEPDSILVLQSLPGKQLPSH KAILFVPRRDPSRELWDGPRSG TDGAIALTGVDEAYTLEEFQHL LPKMKGNKWEQKSHYKPDWD *NLSCLFRQVLNFVIVAPP
16137	46505	A	16232	531	976	NQSIVRVNVDNSLSIPVIAAELG VRKPSEKGMQQKKKTKDLGFR AGKESKTEWRK*GLQDMASQ MFASPLK*PVTAAFHDSSMPSS LLQIEMEQLFLEARLQLDSKSE ARRNQCDSMLLRNQQLCSTCQ EMKMVQPRTMKIPDDPKAS
16138	46506	A	16233	2	419	SFLLSSSYTRTKSILRWPSLKKR ESGFPLNSSNSGVRKSC*LSSDP KSGTIVCPRFSNTISPSSSSSSSSI CSKTFL\PSFSCLPQKAAPNLAR SWGLPGSRTARLSQGPDRGPRG VCRLGSGAAEPSQRRGKPSRDE IV
16139	46507	A	16234	27	792	INSIRILSTCKMGHPRFAPQAPG PLRTSEKGPAVLPAWGNSSSDH SSEPSVGFYFNEDSDGSHPVLQ MRACSPDPAQGARPSAEAPGQP *HSASRGSDPKVASEWRLPHAE ASPQLPGFSGAASPAPKHSCSSF SCLPQKAAPNLARSWGLPGSRT ARLSQGPDRGPRGVCRLGSGA AEPSQRRGKPSRGTHRPEPRAG GRLSPAERSPETEHAQCGRRGS LRND*TSPVLRGAQKEVGRRD CRGSSAILRAGEL

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16140	46508	A	16235	343	969	YDKTRLFNTVPLPPPHKKIIKKII QDIKGEILRAFPLRTGTKHRCPL SPLLFNILLEVLARAIRQEKEIKS IQIGKEEVKLSLFADDIIIYLESP KYSSRKLQELIKEFSKVSRYEIN VHKSVALLYTNSNQAENQIKKS TPFTIAAKNKIKYLGIYLTKDAK DGYKENYKTLMKEIIDDKNKQ KYIP*SWKGRINIVKTTILSTAIY
16141	46509	A	16236	15	403	ICESRRGRVCSALVRRYVGEGF GKAGSICMPQAPDKSSRWTILI RPPRFPPS\PSCSPGKEAPGGSEL /SPLPHAWPSDPVSPLGDRVTA NPAEIR*EPGPQSAAPGFREQRR RGQMG*IWYLTPTPPGGQ
16142	46510	A	16237	19	454	KGKSLLCTSPKVCRGRLRKSRK PETKVTHICMPQAPDKTSRWTI LIRPPRFPPS\PSCSPGKEAPGGS EL/SPLPHAWPSDPVSPLGDRVT ANPAEIR*EPGPQSAAPGFREQR RRGQMG*IWYLTPTPPGGQRPS SAASPRGFPLV
16143	46511	A	16238	276	898	MKGTAPWRCGSRRGRVCSALV PKVCRGRLRKSRKPETKVTHIC MPQAPDKTSRWTILIRPPRFPPS SILQSWEGGTGWLRTLPLPHA WPSDPVSPLGDRVTANPAEIRIL GEDPESPEETLNLILRTPIPPKPR GNAKSHP/GGHRSHR*EPGPQS AAPGFREQRRRGQMG*IWYLT PTPPGGQRPSSAASPRGFPPTNN SSRLPAEPE
16144	46512	B	16239	177	284	
16145	46513	A	16240	253	416	CCPVLPGPWAAGHPGD*PDGP G**AQPHKECRGGFAPLQVTLG PKQPSGKRVNK
16146	46514	A	16241	1401	2246	NIYLLLQVFDCWGLQGILGVSN PSYSIRRCYTAGQSPRGLPDPGR F*G*EESTGEQADCP*GSHRRSR SAAGAADGGLDPGAHTITCGC LSHRGRLVPAQKSSAAL*APSG AKPAPTVAPVHDPARQG*GGQ ARGQGARQPHSHREGLCEC*A VTTL*EPHLRNSSAPA*ERGPQG IRVPEGQSGDQESSAEEHHGGD PGGGKPRCGQHQEPLGAGWPS PAGVEPLLGGLQKGSDGAP**E PQRGCVDEAQQSSPGAVPEAK AIAVQPPAPDVFAAVARCD

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16147	46515	A	16242	30	461	IPAETTC/EPAKHFHCFTDGSSN GKASYSGSKGKVFQTPYISAQK VELVAVIEVLTAFDMPINVISDS SYMVHSTQLIENAQLRFHTDEQ LIIKTKKGGNRDYGTAQTQLNL ALLTFHFSSLPKGQMLPAAEQH LQKPAAKTQAE
16148	46516	A	16243	1	573	
16149	46517	A	16244	1	1689	
16150	46518	A	16245	1	1416	
16151	46519	A	16246	27	779	KNHFNWKDKFPPRLRISFLMVA TVKPPEPTPLKRLTEKPIWIEKW PLSK*KLEALEKLVTEQLENGHI APTFSPWNSPVFIIKKKSGKWR MLTDLIAINSVIQPMGALQPPGL PSPAIIPKNWPLIVTDLKDCFFTI TLAKQDCEWFTFIIPAVNNLQP AKHFHCFTDGSSNGKASYSGSK VKVFQTPYTSALTAELVAVIEV LTAFNMSINMISDSSYVVHSTQ LVENAQLQFQTDDTNDFIYPVA NSS
16152	46520	A	16247	2	394	
16153	46521	A	16248	63	1123	ELDVMGLPEERVRSGSGSRGQE EAGAGGRARSWSPPPEVRLVSL LRLNMSQKINDIWASISVAEFW GDIAKEFYWKTPCPGPFLRYNF DVTKGKIFIEWMKGATL*LCLF LVWGRSYTPNHWFFLVCLREG NEPGGQLDGREQVAARRVHGS YSVLLPAGIQKGDRVAILSNPFL HSLNPWGFLLSLRLSSLP*GPM DIVPTRQHGAY*GLECLLLPKD MDMGGSCQVPFEPTRLPL*AFL FSRGFPVRCCIVVKHLALTLSSH SLYTWTLQGQGTGVSCPHLELF TVLPCPSLQISWNQGIDLWWHE LMQEAGDECEPLPSLHLVVSRG GHKTLTCSPFFPQGVVHTVGGY
16154	46522	A	16249	35	219	ALGVHFVLGPVGDGSRAVDCG QQL\PTSSACTTSGLSISRRCSGI WRMNQKKQVRGPSPKE

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16155	46523	A	16250	1934	3213	WPAPPSQVPSLDYGLALWFDA YVSVHGTQETSQCSPESSLTPPR LCGLRILQPYAERIPVVATAGIT INFTLRGYAWPNGALPASTVPC GFAACPGEFLCSVNGRQAPAGS SGFLPPVPSLCPHTVCRATFQCK EDSTCISLGRFPWGSETHLLCPA PIPSVPGVPCGTFTFQCEDRSCV KSLSASPLPLLLCPPHHLPPSPD CGLQGPSSRIVGGAVSSEGEWP WQASLQVRGRHILGRGSFLPPH LTPPHPTPPHPSMASTVLWTVF LGKVWQNSRWPGEVSFKVSRL LLHPYHEEDSHDYDVALLQLD HPVVRSAAVRPVCLPARGRIEN RGSRLLRSHFCP*PRTGPISNAL QKVDVQLIPQDLCSEVYRSSPG KGGALTLLQSFLLSPFQGDSGG PLVCKALSGRWFLAGLVSWGL
16156	46524	A	16251	511	853	CCWNMALIQTFQMSMEIPLCTT LS*TALHLASANGNSGVVKLLL DRRCQLNVLDNKKRTALTKAV QCQEDECALMLLEHGTDPNIPD EYGNTTLHYAIYNEDKLMAKA LLLYGADIESKNKVEEEMKKH ESNNVGLLENLSNGVTAGNGD DGLIPQRKSRTPENQQFPDNESE EYHSHTEFLPSRIYP
16157	46525	A	16252	1050	1350	CDPQMCCCFRPEAATPG*REAA SAGPWDSAPPSPARTSLPSAHSS DYPLPRSRSSSASAASRSPPRPL STIARRLNPRRSGRSLPSGQPAG PSDPRGFCL

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16158	46526	A	16253	2	3486	SSQSGAAAGAFCGLCVDLELTA SCDLEADSEDRTEHLATLQLRP DFSGSRCPAPQKHLQTHRPHSK PWPIY*PT*RSYLAISPHSW*AP\ PPSRRRAPPAFHPHTQACPSTCY CHTLASRRGPSNGRYHRPGYPH PTAVQRDPPAGPRGCQSPC*HQ PPACRRPCGRHYR*HGQHDPPP WQ*HC*SRSPCHPPSQRDAVTW PFIHIPAED/SHTQPQKSP\PAFRP HTKTCPFTCYCHTFAGRRGPSD GRHHHLGYHHPSAVQWDPPAC *RGCWRPCQREPQTCPCFCGR/P PPGTSLA*PPHPRVPLKEKLCQY DEFSEGLRHSAHLNRHQRVPTG EKSVKSLERGRGVRQNTHIRNH PRAPVGDMPYRCDVCGKGFRY KSVLLIHQGVHTGRRPYKCEEC GKAFGRSSNLLVHQRVHTGEK PYKCSECGKGFSYSSVLQVHQR LHTGEKPYTCSECGKGFCAKSA LHKHQHIHPGEKPYSCGECGKG FSCSSHLSSHQKTHTGERPYQC DKCGKGFSHNSYLQAHQRVH MGQHLYKCNVCGKSFSYSSGL LMHQRLHTGEKPYKCECGKSF GRSSDLHIHQRVHTGEKPYKCS ECGKGFRRNSDLHSHQRVHTG ERPYVCDVCGKGFIYSSDLLIH QRVHTGEKPYKCAECGKGFSY SSGLLIHQRVHTGEKPYRCQEC GKGFRCTSSLHKHQRVHTGKK
16159	46527	A	16254	333	695	ISVFRSPGQSTSQHDAATWPFL HISGEGPTPSRRKAPPAFHPHTQ ACPSTCYCHTLASRRGPCNGRY HRPVYPHPTAMQRDPPAGPRG CQSPCWHYTPACRHPCGRHYR *HGQHDPPPWQ*HC*FGSPGQS TSQHDAVTWPFLHIPGERPTAS RRKAPPAFHPHTQACPSACYCH TLASRRGPSNGRYHRPGYPHPT AVQRDPPAGPRGCQSPC*HEPP ACRHPCGRHYR*HGQHDPPPW Q
16160	46528	A	16255	9	437	SCNMSLCRCNVCIRAAFKEGTP ALLVYSAILSFTPVSLAKSCSISI AIVSNILSWLDPFKRGVVSELSR LPSRVLL*L*LVHSLLKETSFRS SSFSSCRACFLRSSQ/STAGPCR HLCRPTSAGIGEQRRCRPESHH EIVDRGI

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16161	46529	A	16256	619	1138	SCNMSLCRCNVCIRAAFKEGTP ALLVYSAILSFTPVS*DPEAFSP HLPSNCWSLPPSLSSNVSRDRG AEAMQAGKSPWCVFPP*EPGPT GCEPPRTLPPAPFKLCSL
16162	46530	A	16257	408	801	SQRRGSVCRLVHGRHGQPGKG TSPHSSLWDWQPGPQPSGPPWP EGGASPGTPSLIPRS*SASCCFP WHPGCSC*GAPASQC*VALSPQ PWFPLPCLSVPSPVGAQATGPK HVRTPPGSDSAPPQLQPQSRI
16163	46531	A	16258	1	199	
16164	46532	A	16259	665	1006	IGSPDGRNVIRERTVTNETQTEG EREKEEERESFHTGDVLKVGDL GPQGSSREFQLLSNLTVPNFIDI QFPK*VSAAC*DGPSHTHSSYIS SSLFIIRASQSSPGDFSISVRY
16165	46533	A	16260	247	404	
16166	46534	B	16261	258	934	
16167	46535	A	16262	519	924	NRTIQADLLYPDDAGNPLPARN TRQASASADPPGARAGERRRG AAGPSPGR*QQAPGPPPPGEGA GARPG*EGDAAGGATRFVGED ARLLRAGCHRGGRGEAEEPLQ ALRHPGLQGLL*EGAPHGELAL VAFAHL
16168	46536	A	16263	121	214	
16169	46537	A	16264	139	272	
16170	46538	B	16265	1	1962	
16171	46539	A	16266	2373	2554	SATPWLPTGLAAPTPGLAAPGT RSPPGQT*PERSPAASPKRPERP ALDFQPPRQPPPPPP
16172	46540	A	16267	919	1653	WNCFVCSADTMAQIMAEQEVE NLSGLSTNPEKDIFVVRENGTT RRPLQPPPRGRAS*GGAGRLCS QLITEQADIALTRGAEVKGRCG WRPLGLRTQTLRGRLKRTSPAQ QESHNMSKGPEATCQLSGTLG* EQ*GF*LLLWALAVAGKHTAN SHHLSALVTPAGKSYECQAQQ TISLASSDPQKTVFCRTYDSGCF DQSSLLFFFPIAEHKCPVDEREQ LEETLPLILGLILGLVIMVTLAIY
16173	46541	A	16268	2	321	PAWPPWPGITGFCPQQDSPSNT FVVPAAHTV*CSHPCSYYKGIR QMVGLPQPLFHPDCPVTPQAHT DSLNTLGVLGGPPVCSDATLPQ IINALEEDPAAQKMQLAF
16174	46542	A	16269	120	327	
16175	46543	A	16270	540	791	

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16176	46544	A	16271	1688	1945	DRVSLLPRLRQENRLNPGGRGC SELRSHHCTPAWATE*GSVSKK KKKKKNQKKNQFDFISLALPPS PHCPPLSQSLLLQPSSSAN
16177	46545	A	16272	3	343	DIHHVRKSMEVNFLSYVVLTV AALPMLKQSNGSIVVVSSLAET AMKAVSGIVHMQAAPKEECAL EIIKGGALRQEEVYYDSSLWTT L\LIRNPCRKILEFLYSTSYNMD RFINK
16178	46546	B	16273	48	407	
16179	46547	A	16274	35	646	DLTGFIKFSLLLGLFMAYYYYS ANEEFRPGKYPCVSFWRNRFK KHRGA*VAYHLAKMGAHVVV TARSKETLQKVRVLCSQICVPS HAQMCSYI*DMTFAEQFVAQA GKLMGEAVSLTSSSELCPWGH QELLDIHHVRKSMEVNFLSYVV LTVAALPMLKQSNGSIVVVSSL AGKWDRDICGR*KKKKNARDD AVQTPGSKSAI
16180	46548	A	16275	221	393	LLYPANCVYMRCPQMLHFQGI QRPILL/HVSSGGAIHLQTGVET EEMRSAIAPDPIPLT

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16181	46549	A	16276	2025	4146	SDEWIISAGSVSGDYNSSAAVS KNDILLGIEHISVFSETNHSSEEA FIKTAKSQLVEIEPATQNPKTSF SYERLQALQETCKENKGVPKQ GDTFLSFSAACETDVSSVTPEK EFEETSATGSSMQSGSELLLKE REILTAGKQPSSDSEFSASLAGS GKSVAKTGPESNQCLPHHEEQ AYAQTQSSLFYSPSSPMSSDDE SEIEDEDLKVELQRLRFRHIQEV VNLQTQQNKELQELYERLRSIK DSKTQSTEIPLPPASPRRPRSFKS KLRSRPQSLTHVDNGIVVIDPLC VESNAASCQQSPASKKGMFTD DLHKLVDDWTKEAVGNSLIKP SLNQLKQSQHKLETENWNKVL QLESVYHREDEATWLPQLRAQI VAYPACAAAIASAHRRSMGVQ GFQEFLEKRCPGAVVPVDLLKL ARTVSRQQQQQHLHRQLPPTA ALAPGAPRAARGSVPLQPPLPP AALGAYSGGAGPIRHHHPAHH FHHHGQAQPGLHPPLPPPPPPQ LPGARVLVDAGSALPRLYGGY QTDWVCGGQWNAMLGYLSAL CQACAYPGGDGLELVVMFPGG LGKDRLAEWGRRCQAERQTAQ LIVGHVGNKGTPPPRAWFLPPA CLSHCVRLALIRFRF*VFQSLED HHLEVVAFFRENGFHGLLAHD SEYALYNIPSYYSSHALKLSWN GKNLTTNQFLMQEVAKQLGLK
16182	46550	A	16277	1	542	MRAPPKSGQLQHCRPSRGALRS GDLPWEINPLSSCSLLHEKDPP MTSGPQTNQPKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAPIPYFRTPTSY LCAPIPYVRTPTSYLCALTPFPL FWRHIRTSKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPGQGMPAAQ
16183	46551	A	16278	3	351	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLIS LRPNPLCPHPDL/GISVP*PLSRF SGGT*ELPNA*TAAA/AAF/LPEP PPPG/CLLQVPEI*PPGQGMPAA QDSS
16184	46552	A	16279	1	513	
16185	46553	A	16280	774	1007	ARSVTSSSELCGSWCLQASRHT HVPWCQL*KLPVVHLVQPQPC RGPAPGAALPAGSLEMPGTTEP ERGCHSPGLGIS

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16186	46554	A	16281	507	520	LLLGLAAED*CCLIASEAP*TQS LFGGLFTRTHMKFGAVTQIRGP PLGDKSPVLLLFALERQRRHVL SMDPKLRCWSRTGKAAFPWCL IIAEMPDYSPTFQRCQTTQGRLP WSFTLSSKSRFSGEGARACYKC QKSDHQAKECPQPGIPPKPCPIC AGPHWKSDCSTHLAATPRAPG TLAQGSLTDSFLA
16187	46555	A	16282	269	607	RARSEGAGLWSVVAPSAVSVFF VSDPRCAPFHRSPSCCSPVDRV CRCLRRVALAPAALVLVCSGSH SQSPWNSGLKLSDRLLLGLAAE D*RCPIASEAP*TTTDAELTIPGL
16188	46556	C	16283	1	1752	
16189	46557	B	16284	146	372	
16190	46558	A	16285	336	753	ARTPLAAASRGSGGTRGGAAW VAGDDLRGPAPGPAEPGPARRR RGKGTPSSRPRTQRRPRSAAMH GHRCPQPARRSREHPNTYPAGR RPPELRRGRSGVPPPRP*RRPGE APRAPRPRAAEL*ARLPRPSVRP APARRV
16191	46559	A	16286	1	768	FDELREEGFRQSVITNFSELKKD V*THRKEAKNLEKK\LDEWLTR INSVEETLNDPMELKTMAQELR DACTT*FREKRVKRNEQSLQEI WDYVKRPNLRLIGVPESDGEN GTKLENTLLDMIQENFPKLARQ ANIQIQEIQQIPQRYSSRRATPR HIIVRFTKVEMKEKMLRAAREK GWVTHKGKPIRLTADLSAETLQ ARREWGPIFNILKEKNFQPRISY PAKLSFISEGEIKYLTDKQMLR DFVTTRPALKEL
16192	46560	A	16287	345	894	EQRHNIPESLGHI*STSAGDTPA DRVWSGPPANSSRPAAEGPDC* KEN*QRARTS\NQNPICTSPSSK TKEAKNLEKRLDEWLTRINSIE NTLKDLMELKTRARELRDACR SFSSQFDQVEERVSVIEDQMNE MKKEEKFREKRVKRNEQSLQEI WDSVKRPNLHLIGVPESDGENG IKLENTL
16193	46561	A	16288	1	1206	

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16194	46562	A	16289	1	882	MAPVSASEDFWQCPETSLISQL ESAPGIQLMEARDADKSLIMHE IAPTSNRELPVHKISIAKPCSML MISWFFVNTGQSFQRKDQAAIF AVLQPLLVIHRQTGSGVDLQQT PTDLQLRDLTVRRKNNKQKGI ASTSRKRTSTPKPHLQDHSSSPA MEQSWMQKDFDKLAEVGFRR SVITNFSELKEDVQTHHKEAKN LEKRLDEWLTRINSVENTLNDL MELKTMAQELHDACTSFSRQF DQVEERVSVIEDKISEIKQEEKF REKRVK\RNEQSLQTIWDYVKR PNLHLIGVS
16195	46563	A	16290	1	1008	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGPGGLQPGQR VLYKQSIAQRARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMILATIIANC IVLALEQHLPDGDKTPMSERLD DTEPYFIGIFCFEAGIKIIALGFV FHKGSYLRNGWNVMDFVVVL TGRKAGLGCCGSGVESGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSELKEDVRTHRK EAKNLEKRLDEWLTRMNSVEK TLNDLMELKTMARELRDACTS FSSQFDQVQEMVSVIQDQISEM KREEKFREKRVKRNE/QSLQ*I WDYVERPNLRL
16196	46564	B	16291	1	1257	
16197	46565	A	16292	3	467	KTPFVGYQHQRPKVDKTTKMG RNQSRKAENSKNQSTSSPPKDP GSLPATEQSWTENDFDELTEVG FRRSAITNFSELKEHVLTRRKEA KNLEKRLDEWLTRINSVEKTLN DLMELKTMAQELRDARTSFNS *FNQVEKRISVIEDQIDEIK*EDK
16198	46566	C	16293	115	498	

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16199	46567	A	16294	2	1455	TERDSININKKDIYTKTQSVGRQ HQRPKVDKTTKMGRNQNRKA ENSKNQSASSPPKDCSSSPAME QSWMENNFDELTEIGFRRSVIT NFSELKEDVQTHCKEAKNLEK K\LDEWLTRINSIEKNLNDLMEL KTMAQELRDACTSFSSQFDQVE ERVSVIEDQMNEMKQEEKFRE K\RVKRNEQSLQEIWDCVKRPN LHLIGIPESDGENGTKLDNTLQ DII*ENFPHLAR*ANIQIQEIQEIQ RTPQRYSPRRATPRHIIVRFTKV DMKEKMLRAVREKGFKPTKIR RDKEGHYIMVKGSIQQEELTIL NIYAPNTGGPRFIKQVLSDLQR DLDSHTIIMGDFNTPLSTLDRS MRQKINKDIQELNSALHQVDLI DIYRTLQPKSTEYTFFSAPHRTY SKIDHVVGSKTLLSKCKRPETT TNCLSNRSAIKLELRIKKLTQNR SAAWKLNNLLLNDYWVHNEM KAEIKMFFETRTKIQHARISGIL
16200	46568	A	16295	395	656	FQLQRPASCSSPIQHRKHIPRKP A\SQSSLPHTGKSARQPQEPQNR ENCLLRILIRVASEATRRWTRPS EFSSRSENPRAHHPRRALR
16201	46569	A	16296	671	1126	RRKVSELEHRRPVWKCPRRPPE VRKPESARVSFSPRGGARRSRP GATRSPQPRVPAAASASFGFGG LGRGGRGERARRGRGPKLEGP ESSAVLA*RNFPSRPRRRRPGRA GVEIARLGGTGSSPRPCPKPDPT ASLSELFMIPSDIPRRRN
16202	46570	A	16297	2571	2716	THGMLEKRCCLQENMPIIPGKD FMTKTLKAIATKVKIGK*DLIKS FCT
16203	46571	B	16298	54	576	
16204	46572	A	16299	475	719	VTWIRNNNACFTLNWFYHERS HIWILKSTLQCGQIIIGNDVESR HK\CPKPS*LVGSVELEIADNVL PQKFPAAKTIFALYF
16205	46573	A	16300	395	830	LSPCHNSFFFFQAFDDIAKYFS KKEWEKMK*ATVPGPSLPLKK *TFCSFLGFKVTLPPFMRSVSLE FGNLYQQRKILM*L*STVEMSLI LFICDLHIVKIMPKKPAEEENGL KEVPEASGPQNDGKQLCPPGNP STLEKINKTS
16206	46574	B	16301	54	576	

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16207	46575	A	16302	475	719	VTWIRNNNACFTLNWFYHERS HIWILKSTLQCGQIIIGNDVESR HK\CPKPS*LVGSVELEIADNVL PQKFPAAKTIFALYF
16208	46576	A	16303	393	822	LSPCHNSFFFFQAFDDIAKYFS KKEWEKMKSATVPGPSLPLKK *TFCSFLGFKVTLPPFMRSNSLE FGNLYQQRKILMYF*STVEMSL ILFICDLHIVKIMPKKPAEEENG LKEVPEASGPQNDGKQLCPPGN PSTLEKINK
16209	46577	A	16304	1	447	
16210	46578	A	16305	75	565	LLFSGFSLLHGYLPHWYLCHLP RSRSLGLRDKRWKVKGDTDFL SPSHPEYLLKEENDGHLCSLSFR MGNQFSSPLPAYTPLECILNHW DGFYP*NLEEKHLIALRTKGWP NYDLQEGLSWPQEGTIHFNTT WQLELFCRHEDRWSEATYMQ AFYILQGNRDLG
16211	46579	A	16306	1	1620	
16212	46580	A	16307	128	223	
16213	46581	A	16308	1	1578	
16214	46582	B	16309	592	883	
16215	46583	A	16310	1	344	MHQTTAKTPHTSYPNNYEEHN RRANRSKNYDRIRHTTIILKRTN PAQTITNLLKSRFNRYNYVQPR SCRSIFIHIPGERDLNLCIAPNPP AIFPTSIGYLGPDLNNLPTYAPFI TTNLTGPAPTTTHPVGNLGTTG NPEPGGCGILIVWCCVNWACL WDSVVAAPREPYMPAGLLRHR RHYRHRREDLIAVPAARQTDE NRRPALCHEYAVGHRKIKTNV EHTEPYILPLITHSQPLNRGAFF CPGVRFLVVSVLDFEKRLAFAS *SCGVQLRIRGKVQGVGFRPFV WQLAQQLNLHGDVCNDGDGV EVRLAYRVLVGQPQHYPRGRP
16216	46584	A	16311	84	237	DGIVLSTYYHFYWHHF*ILEGP LPANTGDLCLPLQVQPDREQVR WALFKK

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16217	46585	A	16312	2887	3537	HLDRSGLFNIQVIPVCRKLGKE GNDEKQCVTTSRSNAAFFLLHF FLLATFTWMGLEAIHMYIALVK VFNTYIRRYILKFCIIGWGKPLK IFLVLFFPHENCQVYGKESYGK EKGDEL*VIKTFCDE*ISFVS*SG VMFFLNIAMFIVVMVQICGRNG KRSNRTLREEVLRNLRSVVSLT FLLGMTWGFAFFAWGPLNIPF MYLFSIFNSLQGKINCT
16218	46586	A	16313	302	547	QIGLWTPNFRARTFCVWTGGL VLCF*GFCFQEAAGARDTSSFA MGVSPWEFRHG*LWPEMRSME QILELLVLEEFLTITGQ
16219	46587	A	16314	1	1174	WEEKENKEYLKSLFEILILMGK QNIPLDGHEADEIPEGLFTPDNF QALLECRINSGEEVLRKRFETT AVNTLFCSKTQQRQMLEICESC IREETLREVRDSHFFSIITDDVV DIAGEEHLPVLVRFVDESHNLR EEFIGFLPYEADAEILAVKFHTM ITEKWGLNMEYCRGQAYIVSS GFSSKMKVVASRLLEKYPQAIY TLCSSCALNMWLAKSVPVMGV SVALGTIEEVCSFFHRSPQLLLE LDNVISVLFQNSKERGKELKEIC HSQWTGRHDAFEILVELLQALV LCLDGINSDTNIRWNNYIAGRA FVL\CSAVSDFDFIVTIVVLKNV LSFTRAFGKNLQGQTSDVFFAA GSLTAVLHSLNEVMENIEVYHE FWFEEATNLAHQT
16220	46588	A	16315	717	902	GALQSWPCYLPRQCGATVQNF CGVPTCMRKSTWSNLVVFRFP QDPSRCAN**LDCCTACTQ
16221	46589	A	16316	1	374	EHSEPPIGVQIVDYLLRQEKVT DRMDHSKVETETVLSFVDDIIS GAKSPCAMPSQVPDK/QAQEIA DKIYNLFNGYTSGKEQQTAYN TLLDLGSPTLHRVLYHYNQHY ESFGEFTWRCEDELGPR
16222	46590	A	16317	2	1293	

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16223	46591	A	16318	219	1912	PHPTRTRSAQSVQYIEKDWGPG EGLEEGGVLGQLVAFDSFTVSF HFVSAGNSPSDESEERERDPKV LTFPEYITSLSDSGTKHMAAGV RMECHSKGRCPSSCPLCHVTSS PDTPAEPVLLEVTKAALLNTQS FPCSLMQLLQEATMSSLWCSGT GDVIEDWCRCDSTAFGGCVPVS CSFLSAHRLRLSTVHEPSSTLVV LEWEHSEPPIGVQIVDYLLRQE KVTDRMDHSKVETGEHLLLHG LVLIQGDKTKTKKNALPHGFAP GPQYPRAMQEEQGEEEAVLLL QEAAVLLPLRVRDIRSCCFRHR ELLFLMLFPFLLLWAETVLSFV DDIISGAKSPCAMPSQVPDKQL TTIYFQPLIARFSFSSRKGLLRIM SSHCHGDCDVSTLDSYTVSAN HALPLPARFTLWGVDNTGRRS RPSDVIVYM*ITYFPFPPSSEIAD KIYNLFNGYTSGKEQQTAYNTL LDLGSPTLHRVLYHYNQHYESF ASF*LKYPLCLIHRKAGLILSQL GDLSSWCNGLLQEPKISLRRSS LKYLGCRYSEIKPYGLDWAELS
16224	46592	A	16319	1	2031	
16225	46593	A	16320	1	739	MKRAGSSGGRGECDISGAGRL GLEEAARLSCAVHTSPGGGRRP GQAAGMSAKERPKGKVIKDSV TLLPCFYFVELPILASSVVSLYF LELTDVFKPVHSGFSCYDRSLS MPYIEPTQEAIPFLMLLSLAFAG PAITIMVGEGILYCCLSKRRNG VGLEPNINAGGCNFNSFLRRAV RFVGVHVFGLCSTALITDIIQLY TGHQAPYFLTVRTPNYTSLNVS CT*NSYLAEDIRSRSDLTLTHSG

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16226	46594	A	16321	48	1359	GDKNQNPRNWPLGEGKGNSLG RKETGRSNSRSHSSRSKSR*QSS SRSRSRSHSRKKRHSSRSRSRTY SRSWSRDRMYSRDDRH*YEVIV DCSRHGREYKGREPRHGSGSLE RPTEQETSQPKIRKEIVETKGTA RGNCGTTGLLRPKTMMVERSY GPQDRVAVGTWPHPGTERWAS SWDVSSSVRHQSEGVVQGWEH RCTHKSQQEVGACVNFRTPKVI LIYNLYLPVSHQFSKTFMSIVIV QKNLYLHNDFRALNVTHIYRLT IPNTTTCFTATQDEDKQIFHTAA QHRSHTSSYQYLSLTRSHRYEI VFYTRGLGAPFPAGDGHGKFQ RLGKPYSHSVHFVIPQDKTQHIS INTPHKNSETTKQHTCSFAYGL YYYQQKEDNPYAWPQVPAAA EMVSRLAQSRHSQQSILIHFSHQ SYHTDHISTV
16227	46595	A	16322	227	3020	SCIKPRRKEMGRSNSRSHSSRSK SRSQS\SSRSRSRSHSRKKRYSS\ RSR\SRTYSRSRSRDRMYSRDY RRDYRNNRGMRRPYGYRGRG RGV/YYQGGGGRYHRGGYRPV WNRRHSRSPRR\GRSRSRSPKR RSVSSQRSRSRSRRSYRSSRSPR SSSSRSSSPYSKSPVSKRRGSQE KQTKKAEGEPQEESPLKSKSQE EPKDTFEHDPSESIDEFNKSSAT SGDIWPGLSAYDNSPRSPHSPSP IATPPSQSS
16228	46596	B	16323	258	3728	
16229	46597	B	16324	1	435	
16230	46598	A	16325	1120	1209	ASSDNPP*SEPRVSLTIEGQEIDF FLDTGTAFSVLSSCPGWLSSRS VTIRGILGQPVTRYFSHLL
16231	46599	A	16326	1291	1582	IHQSALCI*LKVCKHTNQQPVSS SGFVNAPIDTLYLATLVGPWRT LCVHTLYLVNLVGMWRTFVSS SGIVNAPISALSKQTTWLYQSA GCGWGQIRE

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16232	46600	A	16327	2	840	APAVATEVLPGAGLTAGVLLW SDPKEPSNPGSSHRVGASDLDN PAHPTLLSYTMQKLEEELDVVL FDRSGHRTKFTNVGRMLLERG RVLLQAADKLTTDAEALARGW ETHLTIVTEALVPTPAFFPLIDK LAAKANTQLAIIT*VLAGAWER LEQGRADIVIAPDMHFRSSSEIN SRKLYTLMNVYVAAPDHPIHQ EPEPLSEVTRVKYRGIAVADTA RERPVLTVQLLDKQPRLTVSTIE DKRQALLAGLGVATMPYPMVE KDIAEGRLRVVSPESTS
16233	46601	A	16328	3	923	RFLSDGTIISVDSAGKVQFWDS ATGTLVKSHLIANADVQSIAVA DFFPGHESRATEALCWAEGQR LFSAGLNGEIMEYDLQALNIKY AMDAFGGPIWSMAASPSGSQL LVGCEDGSVKLFQITPDKIQFER NFDRQKSRILSLSWHPSGTHIA AGSIDYISVFDVKSGSAVHKMI VDRQYMGVSKRKCIVWGVAFL SDGTIISVDSAGKVQFWDSATG TLVKSHLIANADVQSIAVADQR RQFRGGHSRGNSLPFSAGPC\AS NSS*EAVGADKTVPASHS*RAH CGPTAQQR*YLGGTDTHLVFRP
16234	46602	A	16329	2	1059	
16235	46603	A	16330	582	1540	
16236	46604	A	16331	1	720	
16237	46605	A	16332	1	477	
16238	46606	A	16333	1	540	
16239	46607	A	16334	1	261	
16240	46608	A	16335	964	1574	LRWCCGSQLFRGYWGGVTGR YLTVLPPHLAVGCMAPWGPFS VRIAAVVFIQIFAGEVFWCPVM CVRGLCTPVLTGVPGHGNSHIP AIVFTCSLQTLVGGTRRWWRC CAAGDVTKFPALVGVGGETPR PQLPIGVTTVILLQVLVWKFGR NVSMSVWALRVPGLAFQSRH/ ASWKFCRHSFLHCNAYIPLHTQ ECRSSHISFLDQ
16241	46609	A	16336	3	87	
16242	46610	A	16337	1	1398	

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16243	46611	A	16338	1596	2205	LRWCCGSQLFRGYWGGVTGR YLTVLPPHLAVGCMAPWGPFS VRIAAVVFIQIFAGEVFWCPVM CVRGLCTPVLTGVPGNGNSHIP AIVFTCSLQTLVGGTRRWWRC CAAGDVAKFPALVGVGGETPR PQLPIGVTTVILLQVLVWKFGR NVSMSVWALRVPGLAFQSRH/ ASWKFCRHSFLHCNAYIPLHTQ ECRSSHISFLDQ
16244	46612	B	16339	276	442	
16245	46613	A	16340	1	300	
16246	46614	B	16341	1	903	
16247	46615	A	16342	119	889	RQHILESHSRPILCTTWLPLLIIQ DPRTLQSAAMLLTQSLFGGIFT RTRMKFGAVTWIGGPPLGDQS P\SSCSLLREKDPPTTSGPQTHQ PKEHLTNFKSGVRPRRDACLGP SPLAASPAFLGKGQVPQPLISLC PDPLFPHPNLISLRPNPLCPHPD LVSLCPDPFPAFLEAHKNFQTPE PQQPGIPPEPPPPGACYKCQKSD HQAKECLQPRIPPKPCPICAGPH WKSDCSTHLAATPRAPGTLAE GSLTDSFSA
16248	46616	B	16343	1	498	
16249	46617	A	16344	3	903	
16250	46618	A	16345	1	684	
16251	46619	A	16346	2	1028	
16252	46620	A	16347	1	338	
16253	46621	A	16348	2	392	
16254	46622	A	16349	790	2184	
16255	46623	A	16350	773	890	
16256	46624	A	16351	467	606	
16257	46625	A	16352	1569	1841	
16258	46626	A	16353	430	980	LLTEDALDDLIPSFLLTGQQTPA FGRRVSGVIEIADGSRRRKAAA LTESNYRVLVGELDDEQMAAL SRLGNDYRPTSAYERGQRYASR LQNEFAGNISALADAENISRKII TRCINTAKLPKSVVALFSHPGE LSARSGDALQKAFTDKEELLKQ QASNLHEQKKAGVIFEAEEVIT LLTSVLKTSSASRTSLSSRHQFA PGATVLYKGDKMVLNLDRSR* RGIT*AAGI*PS*AEKSWGDI*S* RSYHSFNFCA

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16259	46627	A	16354	1	343	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGRDVKFTLEV\SGVI VLRRPLGYGQVMNVTRSCLLR THWMISSLLFY*LVNRHRRSVE EYLVS
16260	46628	A	16355	1	584	MLRDLLKNVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMVLKNVVRETDEVGKGQI RMRTVFEQAIDQRSSTDNEGAP VIPKHTLNTQPVEDTSLSTPAAP MVDSLIARVGVMARGNAITLP VCGRDVKFTLEV\SGVIVLRRPL GYGQVMNVTRSCLLRTHWMIS SLLFY*LVNRHRRSVEEYLVS
16261	46629	A	16356	62	350	SLPNLDNAAICSSSSSPTRTR*SL SVSAAALRRRLPSAISDHTREVF STLSPRSTSRVNFTSRPHTGKV MALPRAITPTRAINESTIGAAGV DNEV
16262	46630	A	16357	291	502	RLFEVHHHVHKHLLGDNRYPI WIMQPSAHHP/RSPTRTR*SLSV SAAALRRRLPSAISMTPDTLRP NAGVC
16263	46631	A	16358	1	378	
16264	46632	A	16359	159	433	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHP/RSPTRTR*SLSVS AAALRRRLPSAISMTPDTLRPN AGVC
16265	46633	B	16360	1	624	
16266	46634	A	16361	3	299	
16267	46635	A	16362	163	699	
16268	46636	A	16363	795	980	
16269	46637	A	16364	663	734	
16270	46638	A	16365	391	1248	
16271	46639	A	16366	1	1143	
16272	46640	A	16367	1	271	
16273	46641	A	16368	1	493	MSKRRWLTGNGSDRENIRLDL GFLVSDEEKRYKCEDCGKAFN RSSNLTTHKKIHTGEKPYKCEE CGKAFKRSSILTTHKRIHTGEKP YKCEECGKVFKYLSSLSTHKIIH TGEKPYKCEECGKAFNWSSHL TTHKRIH\MERNPTNVKNVAKA LSTPLPLLNIK
16274	46642	A	16369	728	1428	
16275	46643	A	16370	3689	3864	NYKSFFKWS/SQMQSMTKIYRG PLDHPDSPCSNVNDIEGTPPEEI STAQPLLHPRPAGSS

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16276	46644	A	16371	2	126	WPLLLLGCLSLTKEWGFQA*LE KHVKRVKFPSHNLVPGRSI
16277	46645	A	16372	728	2207	
16278	46646	C	16373	1	873	
16279	46647	A	16374	1220	2097	
16280	46648	A	16375	73	1438	QDLRLFYLKDTMFSKLAHLQR FAVLSRGVHSSVASATSVATKK TVQGPPTSDDIFEREYKYGAHN YHPLPVALERGKGIYLWDVEG RKYFDFLSSYSAVNQGHCHPKI VNAL\KSQVGQN*PLTSRAFYN NVLGEYEEY\ITKLF\NYHKVLP MNTGVEAGETA\CKLA\RKWG L/YTVKGIQKYK\AKIVFAAGNF WGRTLSAISSSTDPTSYDGFGPF MPGFDIIPYNDLPALERALQDP NVAAFMVEPIQGEAGVVVPDP GYLMGVRELCTRHQVLFIADEI QTGLARTGRWLAVDYENVRPD IVLLGKALSGGLYPVSAVLCDD DIMLTIKPGEHGSTYGGNPLGC RVAIAAL\EV\LEEENLAENADK LGIILRNELMKLPSDVVTAVRG KGLLNAIVIKETKDWDAWKVC LRLRDNGLLAKPTHGDIIRFAPP LVIKEDELRESIEIINKTILSF
16281	46649	A	16376	600	806	

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16282	46650	A	16377	1	2255	EPDVCAKMAGRSMQAARCPTD ELSLTNCSVVNEKDFQSGQHVI VRTSPNHRYTFTLKTHPSVVPG SIAFSLPQRKWAGLSIGQEIEVS LYTFDKAKQCIGTMTIEIDFLQK KSNDSNPYDTDKMAAEFIQQF NNQAYSVGQQLVFSFNEKLFG LLVKDIESMDPSILKGEPATGK RQKIEVGLVVGNSQVAFEKAE NSSLNLIGKAKTKENRQSIINPD WNFEKMGIGGLDKG\FSDIFRR AFASRVFPPQIVEQMGCKHVK GILLYGPPGCGKTLLARQIGKM LNAREPKVVNGPEILNKYVGES EANIRKLFADAEEEQRRLGANS GLHIIIFDEIDAICKQRGSMAGS TGVHDTVVNQLLSKIDGVEQL NNILVIGMTNRPDLIDEALLRPG RLEVKMEIGLPDEKGRLQILHIH TARMRGHQLLSADVDIKELAV ETKNFSGAELEGLVRAAQSTA MNRHIKASTKVEVDMEKAESL QVTRGDFLASLENDIKPAFGTN QEDYASYIMNGIIKWGDPVTRV LDDGELLVQQTKNSDRTPLVSV LLEGPPHSGKTALAAKIAEESN FPFIKICSPDKMIGFSETAKCQA MKKIFDDAYKSQLSCVVVDDIE RLLDYVPIGPRFSNLVLQALLV LLKKAPPQGRKLLIIGTTSRKDV LQEMEMLNAFSTTIHVPNIATG EQLLEALELLGNLKDKERTTIA
16283	46651	B	16378	1	2181	
16284	46652	A	16379	1	441	
16285	46653	B	16380	47	482	
16286	46654	A	16381	1	636	MRDPNTKRSRGFGFVTCATVE EVDAAMNARPCKVVGRTVEPK RAVSREDSQRPEDTEELHLRDY FEQYGKIEVIEIMTDQGSGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGSGNFGGGRGGGF GGNDNFGRGGNFSGHGGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVNYNNQSSHFGPM
16287	46655	A	16382	1	762	
16288	46656	B	16383	59	1042	
16289	46657	B	16384	76	848	
16290	46658	B	16385	179	400	

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16291	46659	A	16386	27	372	VGSLRRPGPPREETRRLRERRRS LEPWAFLLKEAKVG*QPSSLFQ WEGPMGLCSTPLVMNMGDSLI TK\HLFQVPPLTITSPGPRTRRPH S*YPSPSLATGVWAAVWCKQP HFPAK
16292	46660	B	16387	134	284	
16293	46661	A	16388	1	2013	
16294	46662	A	16389	313	770	IFGFVVAMHGAPGQAVLELLQ LTGDQSLGLSQRHMAALDALV HLLHGGLAVLTTAGAAPEHET RGIAGLREEQCRNPRCVKRGW AQEKQA*PGQRGGRKSSPFWSF TL/DSASAGPRAAHLHLPDVLS LQTLHHGLHRLLHPELLQLSHG
16295	46663	A	16390	1	2753	
16296	46664	A	16391	1	1363	
16297	46665	A	16392	26	181	
16298	46666	A	16393	1	867	
16299	46667	A	16394	1	1447	
16300	46668	A	16395	31	659	APALPGCEHMMAIRELKVCLL GDTGVGKSSIVCRFVQDHFDH NISPTIG\ASFMTKTVPCGNELH KFLIWDTAGQERFHSLLPLYL\R GSAAAVIVYDFTEAGFHFHPLK KWV\KRLKELGPE\NIVMAIAG NKCDLSDI\REVPPEGMLKEY\A ESIGAIVVETSAKNAINI\EELFQ GISRQIPPLDPHENGNNG\TIKVE KPTMQASRRCC
16301	46669	A	16396	1	1182	
16302	46670	A	16397	1	513	
16303	46671	A	16398	146	429	TFYTCFSPSVIPFSFSIHTKPYPG HHQSFYMTNVSSNNPTISPLTT RPPFSLISPALGSHAAPNPA*SSP EKHRPFSLHTTPQKFHRPNTSTL F
16304	46672	A	16399	1	435	
16305	46673	A	16400	56	477	ARAAKGESCEGPGVGRCFSFSS YRQTPPCCQRLVNVPKTR\RTF CKK\CGKH\RPHKVTQYKKGKD SFYA\QGRRRYDRKQSGYGGQT KPIFRKKAKTTKK\MGLRLECV EPNCRSKR\MLAIKRCKHFELG GDKKRKGQVIQF
16306	46674	A	16402	183	373	IHGSSENPTPERETLFWHAENG SALASC*KSGGQAPKRKVRTTL ILKAEILILGMLVLRSHGM

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16307	46675	A	16403	1	881	MPFKCKKQHTFNKTSPKEGAII FTHGCLCTSPFNSELSEHLGNL KLSSWEHLHHRSQQTLSVRLH VPTPQPVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPLWQL KYPKLILREASSVSEELHKEVQ EAFLTLHKHGCLFRDLVRIQGK DLLTPVSRILIGNPGCTYKYLNT RLFTVPWPVKGSNIKHTEAEIA AACETFLKLNDYLQIETIQALEE LAAKEKANEDAVPLCMSADFP RVGMGSSYNGQDEVDIKSRAA YNVTLLNFMDPQKMPYLKEEP YFGMGKMAVSWHHDENLVDR IQLQLWDPVDGTTASSAVPKQ GRDKRREVPNTLSQPNSQEGLI SAFHSRCVHAVFYKLTSAPKTT SLPDVPSDLLAEGLAASRAGQA LWRCDKKSLLTLVRKINLQGK RDGGRSATNQQSQPHLDNTGL ERQLEQKVGRCRSPWRGLGHL EGNAQKGHLLHGVNKNGQHL L*MPPSPLPGGQKGRLVGMLS WVLT*VYKIQH/GT/PAAVEG*D EAFLAVWLGEGVGDFSPLVPSL LWHS*RGCCSIHGIPELELNPVH QIFIM/SASSLPFSPCQNKVPLSG
16308	46676	A	16404	1	459	
16309	46677	A	16405	1	2025	
16310	46678	A	16406	1	816	
16311	46679	A	16407	1	217	
16312	46680	A	16408	3	135	
16313	46681	A	16409	21	218	
16314	46682	A	16410	392	3744	LNYKMLLKNLSPMSMLKAFSF AIPMQPPAQTNLPTAKPNGFQP LLLSQYNACPPPQ*EAG/QVDL CSTIPLNLLPDSLPLTVPTGPLPQ GSVGLVLGRASSSAKGITIHTGL INSDSVDEIKLITSAKVPVSILAG ESIAQLLLLPNIILNKGDKTRGP GMGSRGEKAAYWINVISKQRP TCTIHIQGRKFEGLVDTGADVS VISSSLWPSSWLKHPTNMGLVG VGKAEEVYGSTFILPCTGLDGQ KGTIQPYIM
16315	46683	A	16411	1	783	
16316	46684	A	16412	1	1911	

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16317	46685	A	16413	3	1381	KTPFVGYQHQRPKVDKTTKMG RNQSRKAENSKNQSTSSPPKDR SSLPATEQSWTENDFDELTEVG FRRSAITNFSELKEHVLTRRKEA KNLEKRLDEWLTRINSVEKTLN DLMELKTMAQELRDARTSFNS *FNQVEKRISVIEDQIDEIKQDD KAAETCNWRWVSESLRQLRAS VDAFHARASHYNAGECLHQLA ALNSRLNCAQEMARRDSIGEVP PVPWRTVVGSGIAGEAKLDHL RLVSLIGREVNKENSPAATRWL FSFQAGALAGGQIVLQAAKPN AHGQPVVATRNLLNPAGIVAV LKQRPRLVAAAVQAFYLRDPID LRACRVFKTFLPETRIMTSYYAI EWSLWTLVDVLHAENSESAHM SHNSYDPPSDVARHLTHLPMSP IPDYIIARFRYRHRSRVRLTARK LSPAFMRCSSEIQRYSTMLERG FNGGYCRSTTVRVVTEATRML
16318	46686	A	16414	1	1191	
16319	46687	A	16415	1	1909	
16320	46688	B	16416	1	1791	
16321	46689	A	16417	1	1818	
16322	46690	A	16418	1	1044	
16323	46691	B	16419	1	1140	
16324	46692	A	16420	1	1062	
16325	46693	B	16421	1	972	

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16326	46694	A	16422	1	1758	MDTFLQAERKDYMEAYELIEQ EEQGVKELNRPLTAPSALHPRD EAHLIMVDKLFDVLLDSVCQYF IEDFCIDVHHINSRWI/AVCQYFI EDFCIDVHHINSRWIKDLNVRP KTIKTLEENLGNTIQDIGMGKD FLSKTPKAMATKAKIDKWDLIK LNNFCTAKETTIRLPVPNPCGPV AETPLSRVFVLREARKTLKPHQ STCLSKGRDNSIDSWKTAARVL KTAISSTPTIPILKDQTQEWSVS ATFTSDGKIRLFYTDYSGKHYG KQSLTTAQVNVSKSDDTLKING VEDHKTIFDGDGKTYQNVQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTNFFRKESQK LQQSAKKRDAELANGALGIIEL NNDYTLKKVMKPLITSNTVTDE IERANVFKMNGKWYLGELGW RREWSSGDRKSLARLSKTGTLG LAALTYKCTRDQWTVYCRVIR EKNLCQDMRWYQRCCQTCRD FYANKMSPATAELVTRSPKGRS KLRLRYQLVFISLKGKPARKGK ASSGSKLSLLSSSKTVALAGMG RGDEFQMELESEDLTSERDGIL TPTSSNQKKSKAYGSLIRT
16327	46695	A	16423	1	4449	
16328	46696	A	16424	3	3859	QFLPNLDSTVLGENYFDGTYQ MLYLLVKGTIPVEIHTATVIFVS FQLSVATEDDFYTSHNLVKNLA LFLKIPSDKIRISKIRGKSLRRKR SMGFIIEIEIGDPPIQFISNGTTGQ MQLSELQEIAGSLGQAVILGNIS SILGFNISSMSITNPLPSPSDSGW IKVTAQPVERSAFPVHHVAFVS SLLVITQPVAAQPGQPFPQQPSV KATDSDGNCVSVGITALTLRAI LKDSNNNQVNGLSGNTTIPFSS CWAN

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16329	46697	A	16425	65	1905	RTSSRKTTNHCSEIKEDTNNWK NIPCSWIGRINIVKMAKLPKPPL VIPRQTGSGVDLQQTPTDLHLR VLTVRRKTNKQKGHPHQNPICT SPSSKTKVLEVLARAFRQEKEI KGIQVGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMTELPFTTASKRIKYLGIQLTR DVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFIELEKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYNYLIFDKPEKNKQWGKDS LFNIWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRSKTIK TLEENLGNTIQDIGMGKDFMSK TPKAMATKAKIDKWDLIKLKSF CTAKETTISVNRQPTEWEKIFAI YSSDKGLISRIYNELKQIYKKKT NNPIKKWVKDTNRHFSKEDIYA AKRHMTKCSSSLAVREMQIKT TMRYHLTPVEEVRAGEMAKTR RCQNVKGASEEGIRA/HCFVSH *PHCP/LWRATTLMETLKFKPIE VPCKPLEKSVSLLLL
16330	46698	B	16426	1	2348	
16331	46699	A	16427	1	660	MPNFFIDRPIFAWVIAIIIMLAGG LAILKLPVAQYPTIAPPAVTISA SYPGADAKTVQDTVTQVIEQN MNGIDNLMYMSSNSDSTGTVQ ITLTFESG\QVQNKLQLAMP/LL PQEVQQQGVSVEKSSSSFLMVV GVINTDGTMTQEDISDYVAAN MKDAISRTSGVGDVQLFGSQY AMRIWMNPNELNKVERNSRRQ DVGERDISSGSRKVNKESREDE EVT
16332	46700	A	16428	1	975	

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16333	46701	A	16429	1171	2007	AVDIVQGLVRGWGRQGWLLS GRGIPEGPLLLWGATVGSWRR LLPLTGVCGLPLGAVPVLIS*LL GGAQVQLLREEEAGHELVQQL VDGALVLLLDGRLPLHVVADE RCCVLQDLPVLVHKDEVRLAR GGTAALRVLLLVLVVDALDLV EQALGAQGLGVVLLEVHSLVV KGLEVRLLILLPPDLVEALLGLP PLLFLGLQSFQDNGDSGDRVLL EALDDLRGLVAIDAINGTALDH LRRASQGVVQPELLLVFRRHPR QLLLHTFQHTDCGQVRLQDIV
16334	46702	B	16430	1	768	
16335	46703	A	16431	1	2553	
16336	46704	A	16432	3	573	CEMHSVQKNEHDKTPEHSRKR SRPSLLRPVSAPAKKKMKLRGT KDLSIAAVGKYGTL/PGIFFL*Q GPPGAEEPGGV*KLPPLHRTLQ PGAGVWL*APAARQPISGVSS* LPRAP*GGSVPVNSIYLVFSYCF *AMIVLF*NPVY*LT*LI*LLIPM HL*GAIHHLGTLQLVPLPVTSV VSILTRIQWVLE
16337	46705	A	16433	110	1347	LTTATGMELSMGSTTWTSLCK AENAACQQEKPHIWLCSISSFL RLKRRRTTTKNTGTKKIASTVA VTIPPITPLPTAFCAPEPAPVLLT SGIPPRLNASENPQLLSGS/SSSD STGTVQITLTFESGTDADIAQVQ VQNKLQLAMPLLPQEVQQQGV SVEKSSSSFLMVVGVINTDGTM TQEDISDYVAANMKDAISRTSG VGDVQLFGSQYAMRIWMNPNE LNKFQLTPVDVITAIKAQNAQV AAGQLGGTPPVKGQQLNASIIA QTRLTSTEEFGKILLKVNQDGS RVLLRDVAKIELGGENYDIIAEF NGQPASGLGIKLATGANALDT AAAIRAELAKMEPFFPSGLKIG YPYDTTPVVNISIHEVGKTLVE ANNLVFLAMNLVLQEFPADVIS TIAGPPSLRSSRVPGL
16338	46706	B	16434	1	2550	
16339	46707	B	16435	1	630	
16340	46708	A	16436	270	455	
16341	46709	A	16437	174	492	GALQPPPCTVGAPFWAGQGWS PLPQLAGRCGGRGT\RGTGAAC GACGPAGVPGGLGLGGPRTRSS RPALLAPGNGGLSTRASGCGGC TESPSSGWPTSAALDFLPGP

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16342	46710	A	16438	3	413	
16343	46711	A	16439	31	507	
16344	46712	A	16440	1	537	
16345	46713	A	16441	152	247	
16346	46714	A	16442	44	208	EEMTSKMYKVIIRKTMKASVC TQVKHPAIASICKAVL*VGPWS GHFKYAGLPTL
16347	46715	A	16443	1	549	
16348	46716	B	16444	376	862	
16349	46717	A	16445	2	1603	TNVSTTIATVVLNALARATKLL PPGHRRSPNPATAAASSPPTTLA HCSLRSHHQPLRGEQQPQAIRT TAGRCKALSSCPSFFECGSRSSG APPGACGQIFRVSNAKLEPQAR PSSPVTGGPLDLMACRVVAAST REMAMLIAQALQTINYGRDDE NGHTHSACEVHHGGRVPELSV PSFSWRNRNNPSFIMGSITPTDY TLSKCYLPREDVVLIIYCGVSTN EQPDEEVPRTRFPTVAVSIGFAV RQELEFGVIYHCLE\YRLYTGRR GRGAFCNGQRLRVSGETASGM LPGIQQIHIQQEQNLQVGASTEL PCNLHTTRIRVASAPSSAPEDGT ESKTCNFRVTSSKGYCLALPRV PFPLTTGYKHLHKPPTGTHSTY HSMCLLNQPGWLRTISIILFLNN KICWQKKSGREIKIEDYFPEYA NYTVPEDGHLSAHLYILSGLCM WLQHSGQDSILYTDYRRGGEN SFVMVNSVALNGDGCGICSETE AELIEVSHRLNCSREVGEHLNA TGELGEERAHGRQQAACGFTIA
16350	46718	A	16446	1	648	

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16351	46719	A	16447	329	2497	GEGQAVLQGKMGGEEKPI\GA GEEKQKEG\GKKKNKE\GSGDG SRAELNPWPEYIYTRLEMYNIL KAEHDSILAEKAEKDSKPIKVT LPDGKQVDAESWKTTPYQIAC GISQGLADNTVIAKVNNVVWD LDRPLEEDCTLELLKFEDEEAQ AVYWHSSAHIMGEGMERVYG GCLCYGPPIENGFYYDMYLEEG GVSSNDFSSLEALCKKIIKEKQA FERLEVKKETLLAMFKYNKFK CRILNEKVNTPTTTVYRCGPLID LCRGPHVRHTGKIKALKIHKNS STYWEGKADMETLQRIYGISFP DPKMLKEWEKFQEEAKNRDHR KIGRDQELYFFHELSPGSCFFLP KGVYIYNALIEFIRSEYRKRGFQ EVVTPNIFNSRLWMTSGHWQH YSENMFSFEVEKELFALKPMNC PGHSLMFDHRPRSWRELPLRLA DFGGLHRNELSGALTGLTRVRR FQQDDAHIFCAMEQIEDEIKGC LDFLRTVYSVFGFSFKLNLSTRP EKFLGDIEVWDQAEKQLENSL NEFGEKWELNSGDGAFYGPKI DIQIKDAIGRYHQCATIQLDFQL PIRFNLTYVSHDGEDKKRPVIV HRAILGSVERMIAILTENYGGK LAPFWLSPRQVMVVPVGPTCD EYAQNVRQQFHDAKFMADIDL DPGCTLNKKIRNAQLAQYNFIL VVGEKEKITGTVNIRTRDNKVH
16352	46720	C	16449	189	456	
16353	46721	A	16450	3	1414	
16354	46722	A	16451	95	293	

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16355	46723	A	16452	1	1136	MKKRPGHSLFQFQFLMFRLFSE ARQPLSEEDVASLSWRPLHLPS ADWQRAALSLWTHRTFREVLK EEDVHLTYQDWLHLELEIQPEA \MLFQILNGRTSTSGRSMSTFSL SPRLQGAVTETCRLRVPFLSTH* WISTKAQGVMTTQKILIWSLVA AQEMRILFPDCRRW*LTWSCSK TS*CLSATPLPRSTSSLRFSADG SRL*QAGGAWLPAFRDRGSC*C TNGSSSACLRLSSAAAASRQNS PSLPDASSSSTWSTLR*ETSAPT EVP*HRTSLPTS\QGPPERLSAE QRPLPDGR/RSYWPSARRNA/RL ILT/FCSGVVAEPGACAALPVEE TLPEPAAPGTAEATRRPAVCQR VRVGAIGFPFLLLLDGPAVVTS DLK
16356	46724	A	16453	3003	3482	HRPRTRPCPWRRNHHLGHRAP L*PQRARR*SPNPPEDGSEDEHL *QLC
16357	46725	A	16454	598	759	KVILGLWTEEAQVGGQGLRAP TPRLLHHVLK*DIKR*AHRPDA VAHACNPNTLG
16358	46726	A	16455	1	1767	
16359	46727	A	16456	2	572	
16360	46728	A	16457	1	726	
16361	46729	A	16458	155	1334	HALGRRGGSQELSAAAGAASP SGSERRAPGALPCAWAAALLV LGAPPASRPGGFAAGKTMLLK E\YRI\CMPLTV\DEYKI\GQLYM ISKHSH\EQSDRGEGVEVVQKE PFEDPHHGNGQFTEKRVYLNSK LPSWARAVVPKIFYVTEKAWN YYPYTITEYTCSFLPKF\SIHIET KYEDNKGSNDTIFDNEAKDVE REVCFIDIACDEIPERYYKESED PKHFKSEKTGRGQLREGWRDS HQPIMCSYKLVTVKSEVWGLQ TRVEQFVHKVVRDILLIGHRQA FAWVDEWYDMTMDEVREFER ATQEATNKKIGIFPPAISISSIPLL PSSVRSAPSSAPSTPLSTDAPEFL SVPKDRPRKKSAPETLTLPDPE KKATLNLPGMHSSDKPCRPKSE
16362	46730	A	16459	26	355	
16363	46731	A	16460	86	489	
16364	46732	B	16461	1	201	
16365	46733	A	16462	3	367	

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16366	46734	A	16463	58	553	VARSAPPDGAVCAGPGSRRTE MAEQSDEAVKYYTLEEIQKHN HSKSTWLILHHKG\YDLTKFLE EHPGGEEVLREQA\GGD\ATENF EDVGHSTDAREMSKTFIIG\ELH PDDRPKLNKPPEP*RRCFKETLI TTIDSSSSWWTNWVIPAISAVA VALMYRLYMAED
16367	46735	A	16464	185	489	
16368	46736	A	16465	134	345	
16369	46737	A	16466	572	1017	
16370	46738	A	16467	911	1013	
16371	46739	A	16468	1	157	FGGNQKGERTGQKGKGERGAK RKDFPGAVCISALGLLAKGCG* SWRPSSSAN
16372	46740	A	16469	71	369	SCGLSLIKMTTSQKHRDFVAEP MGEKPVGSLAGIGEVLG\KKLE ERGFDKAYVVLGQFLVLKKDE DLF\REWLKDTCG/APNAKQSR DCF*CLREWCDAFL
16373	46741	A	16470	1	831	
16374	46742	A	16471	368	679	SSQLNKAPSLFNPVSEEFCLWL LLLQKELLTRITSLEKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK
16375	46743	A	16472	536	717	
16376	46744	A	16473	1	1632	
16377	46745	A	16474	1	651	
16378	46746	A	16475	1	903	GGGGRMKLIDYGLSGYQEESA E\VKAMDFITSTAILPLLFGCLG VFGLFRLLQWVRGKAYLRNAV VVITGATSGLGKECAKVFYAA GAKLVLCGRNGGALEELIRELT ASHATKVQTHKPYLVTFDLTDS GAIVAAAAEILQCFGYVDILVN NAGISYRGTIMDTTVDVDKRV METNYFGPVALTKALLPSMIKR RQGHIVAISSIQGKM\SIPFRSGI CQPSKHATQAF\FDCLAVPEM\E QFEIEVTVISPGYIHTNLSVNAIT ADGSRCGVMDTTTAQ\AEALW RWPRMFLLLWGRRRKM
16379	46747	A	16476	359	1094	
16380	46748	A	16477	1	906	
16381	46749	A	16478	1	371	
16382	46750	A	16479	11	257	
16383	46751	A	16480	2	419	
16384	46752	A	16481	1	2514	

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16385	46753	A	16482	262	822	AGCTRKTRIIDVVYNASNNELV RTKTLVKNCIVLIDSTPYRQWY ESHYALALGRKKGAKLVRVTS L*GLWGGQPDSSLLVMKTLSSS ATEGREMRAF*AEEGQHWGVQ GSRKLPGPAFLP*AHIFVSPFQT PEEEEILNKKRSKKIQKKYDER KKNAKISSLLEEQFQQGKLLGE KADELEVGSRRD
16386	46754	A	16483	2	799	SQWLKLPSPLPHAGISRY\NWD QAP*KTGGPRESPYHKKREVM KLGRPSCPN/NPKIGPPAGIQHSP VCRGG*QVNTRAPEVWTVGNF \SWGLICRCTP*NKDPSIVVLQC HLNNGAWFRTQGPWVEEFCIV ASSDQQQPYR\QWVRSPNLCAC PLGPAKKGEPKLDSLRKEEIFK QKNDLKKLRKEI*LKRKKNCQI PAVLPGREQFPARGKLSCRA/SR FQGPGQLWAEQDGFCA*EGQK SLEFLSFRKNPRPRKGQIKFLVF VFHPC
16387	46755	A	16484	1	681	
16388	46756	A	16485	287	694	HSSRPAPASAPRRWGLSWSWQ RCWC**TPSPSPRPRPAEG\CLR GRGRGAGGGLPFRPHGSLVHS GAQPPHFPHLPGGARQTCGAPP GSWSCVL/CRPAETGAAAAGSP AAAGSTRKRLGRAQGRGCRVA ALRLSPTH
16389	46757	A	16486	189	381	QGAGSVGRTGQQLLKPGPFFLE KLLSLGCT/LSG*ALRARACCSP CCRPGAGCQPQAPVAQAGHP

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16390	46758	A	16487	1	2388	QGRLVAKPPRPARSTAADSSTP RDMLGLRPPLLALVGLLSLGCV LSQECTKFKVSSCRECIESGPGC TWCQKLNFTGPGDPDSIRCDTR PQLLMRGCAADDIMDPTSLAET QEDHNGGQKQLSPQKVTLYLR PGQAAAFNVTFRRAKGYPIDLY YLMDLSYSMLDDLRNVKKLGG DLLRALNEITESGRIGFGSFVDK TVLPFVNTHPDKLRNPCPNKEK ECQPPFAFRHVLKLTNNSNQFQ TEVGKQLISGNLDAPEGGLDA MMQVAACPEEIGWRNVTRLLV FATDDGFHFAGDGKLGAILTPN DGRCHLEDNLYKRSNEFDYPS VGQLA\HKLAENNIQPIFAVTSR MVKTYEKLTEIIPKSAVGELSE DSSNVVHLIKNAYNK\LSSRVFL DHNALP\DTLKVTYDSFCSNGV THRNQ\PRGDC\DGVQINVPITF QVKVTATECIQEQSFVIRALGFT DIVTVQVLPQCECRCRDQSRDR SLCHGKGFLECGICRCDTGYIG KNCECQTQGRSSQELEGSCRKD NNSIICSGLGDCVCGQCLCHTS DVPGKLIYGQYCECDTINCERY NGQVCGGPGRGLCFCGKCRCH PGFEGSACQCERTTEGCLNPRR VECSGRGRCRCNVCECHSGYQ LPLCQECPGCPSPCGKYISCAEC LKFEKGPFGKNCSAACPGLQLS NNPVKGRTCKERDSEGCWVAY
16391	46759	A	16488	353	1205	
16392	46760	A	16489	11	440	FRALTEGDTQLNWNIVSFPVAE ELSHHENLVSFLETVNQPHHQN VSVPSNNVHAPYSSDKEHMCT VVYFDDCMSIHQCKISC\ESMG SHPNIRWVSLMACCECIGPECID YGSKTVKCMNCMF*RRQMQT KAT**NNRYKKLKK

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16393	46761	A	16490	515	1808	KRKQTGEFGFNSFE\WCDSDLC EMNAGMPKGNLNEQDPKHCPE SEKCLLSIEDEESQQSILSSLENH SQQSTQPEMHKYGQLVKVELE ENAEDDKTENQIPQRMTRNKA NTMANQSKQILASCTLLSEKDS ESSSPRGRIRLTEDDDPQIHHPR KRKVSRVPQPVQVSPSLLQAKE KTQQSLAAIVDSLKLDEIQPYSS ERANPYFEYLHIRKKIEEKRKLL CSVIPQAPQYYDEYVTFNGSYL LDGNPLSKICIPTITPPPSLSDPL KELFRQQEVVRMKLRLQHSIER EKLIVSNEQEVLRVHYRAARTL ANQTLPFSACTVLLDAEVYNVP LDSQSDDSKTSVRDRFNARQF MSWLQDVDDKFDKLKTCLLM RQQHEAAALNAVQRLEWQLK LQELDPATYKSISIYEIQEFYVPL VDVNDDFELTPI
16394	46762	A	16491	1	699	
16395	46763	B	16492	6	5954	
16396	46764	A	16493	22	585	
16397	46765	A	16494	1	837	
16398	46766	A	16495	1	1422	
16399	46767	A	16496	13	189	
16400	46768	A	16497	193	366	GRPGIFKSFCRWW*C*FHMEFI WKSSA*/WSGVWHAGNICLSIS NPEDLRASQFCSSG
16401	46769	A	16498	1	888	
16402	46770	A	16499	3	531	DAWADAWADAWADAWALQS RRRRRRTQLTLSSPHDCYRGLQ SLLLILCKMATLKEKLIAPVAEE \EA\TVPNN\RITVLGDGQVGMA CAISILGKSL\ADELALVDVLED KLKGGNDGSFQHG\SLFL\QTPK \IVGRIKDYSG\TAQF*RIVVGN WQGVRSARRGKVRSNLVQRN VNVFK
16403	46771	A	16500	2	406	
16404	46772	A	16501	2	394	
16405	46773	A	16502	1	399	
16406	46774	A	16503	74	464	FAFNMPEPAKSAPAPKKGSKK AVTKAQKKDGKKRKRSRKESY SVYVYKVLKQVHPDTGISSKA MGIMNSFVNDIFERIAGEASRL AHYNKRSTITSREIQTAVRLLLP G\EL\AKHAVSEGTK\AVTKYHQ
16407	46775	B	16504	84	832	
16408	46776	B	16505	201	829	
16409	46777	A	16506	1	804	

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16410	46778	A	16507	3	615	PECIIGIDILSSGQNPHIGSLTGR VRAIMVGKAKRKPLELPLPRKI LNQKQYRIAGGIEEISATIKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALGLLLGFGGN*TFDY
16411	46779	C	16508	25	153	
16412	46780	A	16509	1	1317	
16413	46781	A	16510	1	1557	QVPGCIIGIDILSSWQNPHIGSLT GRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIK DLKDTEAVTPTTSPFNSPIWPV QKTDGSWRMTVDYCKLNQVV TPIAAAVPDV/VSLLEQINTSPG TWFEWSPK\KALQQVQAAVQA ALPFGPYDPADPMVLEVSVAD RDAIWSLWNAAIGESQRRPLGF WSKALLSSADNYSPFERQLLAS YWALVETERLTVGHQVTLRPE LPIMNWVLSDPSSHKVSGAQQ HWKCAVHT/IIKWKWYIRDWA QAGLEGTS*LYWPRASRYQQG HQDLFILRSDLPSQVFIRDKLME RRNRRTGRTEKARIWEVTDRT VRTWIGEAVAAAAADGVTFSV PVTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRVQFAMPESDAVA MLKQLS
16414	46782	A	16511	41	428	
16415	46783	A	16512	1	1026	

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16416	46784	A	16513	648	1886	LDPEVAWAKWQHSTVKGPQK QFAFSWQGQQYTFTGLPQGYIN SLSLCYNLIPRDLDRFSLPQDIT LVHYIDDIMLTGSSEQELAYTL DLLVRRLCAKGWEINLTEIQEA STSVKFLRVQWCGACQDIPSK MKDKLLHLFPPTTKKKASLFGF RRQCIPHLECGPEQEKALQQAQ AAVQAAVPLERYDPADPMVL/ V/ELTWLWPLLSAQFASSGDQH *ALHMAPFLGVVSQLPGGKLIIL DIFHHGKGRVLFSLE*TLTPDM GLPILHIMLLPRLPSVNSQNALS TVMPGFTGPGIKGWKWHHSPS PLVIH*QNFCFLFP*HYVLLA*R S*FQRKEPCHQET*Q*FH*TGS* GCQLDTLGSCYF*VNKLRRELQ CWLG*LTQTIKMKSVYYSITEN CWMKRSPVKRRKILELEEA
16417	46785	A	16514	1	402	
16418	46786	A	16515	1	396	PTRPGERSVHVEIPRRVGSGAG HAQWAGPVRVARPQLNAQLE GWLSQVQSTKRPARAIIAPHAG YTYCGSCAAHAYKQVDPSIT\Q RFRYSYYDESQGEIYRSIEHLDK MGMSIIEQLDPVSFSNYLKKYH
16419	46787	A	16516	2	358	
16420	46788	A	16517	2	769	
16421	46789	A	16518	1	1017	
16422	46790	C	16519	54	294	
16423	46791	A	16520	159	245	GISVSCSMYL*PDRSAGYYGLF KDRKEK
16424	46792	A	16521	1	1227	
16425	46793	A	16522	1	2697	
16426	46794	A	16523	200	696	YGIVTGPSLCAGDKQPKKQEK NPVLVSPEFVDEALCACEEYLS NLAHMDID/IGPGGPAVPQPPRA GPSSSSVT\PSGPVSPLQLGLWA VGRCLGIDPFCLVQPLPLPQASR SFTPLFCSGTLEDSHCLRDRVW ATFLGSWHSIVTKSMDCATKW TAHYPKCVLCGC
16427	46795	B	16524	1	960	
16428	46796	B	16525	1	2183	
16429	46797	A	16526	306	1844	
16430	46798	A	16527	59	189	YNSGCLYGSQCSVCRCL*GVRN QVRSQQQAMMAMAILVNKKG G
16431	46799	A	16528	1	2034	
16432	46800	B	16529	1	855	
16433	46801	A	16530	1	834	

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16434	46802	A	16531	65	172	
16435	46803	A	16532	321	429	
16436	46804	A	16533	460	647	
16437	46805	C	16534	529	804	
16438	46806	A	16535	3	433	
16439	46807	A	16536	1	484	
16440	46808	A	16537	511	681	QQGYTPFQGSGRESFLASSSFW WL/PGLPWLAAA*LQALTPSSH SLLSYLCSLLFCHP
16441	46809	A	16538	51	634	PVPTFGLPARHTGAEKRRKNSG GEQLSKNNLYIRGLPPGGTDQD LIKLCQPYGKIVS\TRAFLDKTTI RCKGYGFVDFDSPAAAQKAVA SLKANGVQAQMAKLQERDPA\ GLSVSSLLL\SMYEQELENMLK PFGHVISTRILRDANGVSRGVG FARMESTEKCEVVIQHFNGKYL KTPPGIPAPSEPLLCKIADG
16442	46810	A	16539	1	759	
16443	46811	A	16540	74	352	
16444	46812	A	16541	1	747	GSAVYLCYKKSVAKTNTVSYK AGLICRYPQEDYESFSLPESVPL FCLPMGATIECWPSNSKYPLPV FSTFVLTGASAEKVYGAAIQFY EPYSEENLTEKQRLLLGLTSAD GKSDSSKTIHTNKCICLLSHWPF FD\AFRKFLTFLYR\YSISGAHVL PIEKHISHFMHKVPFPSPQRPRIL VQLSPHDNLILSQPVSSPLPLSG GKFSTLLQNLGPENAVTLLVFA VTEHKILIHSLRPSVLTSVTEAL
16445	46813	A	16542	319	969	
16446	46814	A	16543	131	342	NSDMGLNLGSALTG*PWVAIEF CCFGFFQIIIVFSCLLGWL*VAP HPNLPSSPAEYMDFREAQEGTD VIY
16447	46815	A	16544	1	1086	
16448	46816	A	16545	469	759	
16449	46817	A	16546	3	598	
16450	46818	A	16547	227	604	
16451	46819	A	16548	416	1814	
16452	46820	A	16549	763	867	
16453	46821	A	16550	1	1419	

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16454	46822	A	16551	915	3125	SLAGMRLTGTVSGGEVRV/TAK AGARVGPPELVGRPLEGECWY FSGVSRTQAQQLLLSPPNEPGA FLIRPSESSLGGYSLSVRAQAKV CHYRVSMAADGSLYLQKGRLF PGLEELLTYYKANWKLIQNPLL QPCMPQKAPRQDVWERPHSEF ALGRKLGEGYFGEVWEGLWL GSLPVAIKVIKSANMKLTDLAK EIQTLKGLRHERLIRLHAVCSG GEPVYIVTELMRKGNLQAFLGT PEGRALRLPPLLGFACQVAEGM SYLEEQRVVHRDLAARNVLVD DGLACKVADFGLARLLKDDIY SPSSSSKIPVKWTAPEAANYRV FSQKSDVWSFGVLLHEVFTYG QCPYEGMTNHETLQQIMRGWF FGCISRSEAVRRLQAEGNATGA FLIRVSEKPSADYVLSVRDTQA VRHYKIWRRAGGRLHLNEAVS FLSLPELVNYHRAQSLSHGLRL AAPCRKHEPEPLPHWDDWERP REEFTLCRKLGSGYFGEVFEGL WKDRVQVAIKVISRDNLLHQQ MLQSEIQAMKKLRHKHILALY AVVSVGDPVYIITELMAKGSLL ELLRDSDEKVLPVSELLDIAWQ VAEGMCYLESQNYIHRDLAAR NILVGENTLCKVGDFGLARLIK EDVYLSHDHNIPYKWTAPEALS RGHYSTKSDVWSFGILLHEMFS RGQVPYPGMSNHEAFLRVDAG
16455	46823	A	16552	1	990	
16456	46824	A	16553	1	2847	MTAREHSPRHGARARAMQRAS TIDVAADMLGLSLAGEPHRACT GLQTTGYPGL\DPSG*TRK*GRG MSALFL*TASAGA*LH*FSSLVA GAPPG*CGNVQVF/WLAHAQA MGTNNPIFLSSIAFFQDSLINQM TQVKLSVYDVKDRSQGTVKSA ESDRVGNITVIGWQMEEKSDQ RPPVTRSVDTVNGRLHPPAPTV MHSLSHRHSKKNSNFRALALM VLPVDESLTEALGIRSKYASLR KDTLLKSVFGGAICR
16457	46825	A	16554	1	327	
16458	46826	A	16555	259	3109	
16459	46827	A	16556	262	3159	
16460	46828	A	16557	1	1398	
16461	46829	A	16558	123	393	
16462	46830	A	16559	245	424	

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16463	46831	A	16560	1	531	
16464	46832	A	16561	2348	2775	
16465	46833	A	16562	373	555	LRIQVTFDDVAVEFTPEEWALL DTTQKYLYRDVML\ENYMNLA SVGKSNITLLGMVACTCS
16466	46834	A	16563	165	457	
16467	46835	A	16564	310	349	K*TMK*EMGKFK*FY/IYLEQED YANANALLSPAPALPKEKRTDS NGRVYFVNHNTRITQWEDPRS QGQLNEKPLPEGWEMRFTVDG IPYFVDHNRRTTTYIDPWSTRP
16468	46836	A	16565	1	2217	
16469	46837	A	16566	1402	1860	
16470	46838	A	16567	461	696	KRMCFCTSLSSARSSGSMYMSC RICCSMMPPFSSVFRSISSRYSR AAFW\AWTETRLCWQAAMPRQ QPPGLLHQWTTSP
16471	46839	A	16568	1	601	
16472	46840	A	16569	468	1213	
16473	46841	A	16570	2	365	EGCFQKIKLDHILSPPPMPFWK CSNPDVAFGPGKSLKYKRQLS* DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPWMNCPPIK
16474	46842	C	16571	220	408	
16475	46843	A	16572	840	1091	QSLQHDVTL*VPVLLSYPEPAPS GHGLLRGSAQIAL*TIPADPAGT YLKTREPTLGCQTVPLPAPHLS VDTVCRCLSSSVWPQ
16476	46844	A	16573	1	1356	
16477	46845	B	16574	1	1084	
16478	46846	A	16575	2	526	QPRGKKFSKNKPRKQNFPTPKH MRVVLPPF/PPLKFFIFPKGLKFL EGGCPNISPPQKKGSLPKIPR*V LIRPPIRKKLFPCTARVKLGPPQ GSFKTAAPSSSSP*SADPVYLAG K/PRQSSSPGGTGGLNPPPRRLQ PQPHPGPSWHSSSSRGPGGHPR RESAERSRCASGNPGGQ
16479	46847	A	16576	36	167	RQLFENTQSDETKQEQNKQNK K*STATESRKVPQTGKSKSYWP
16480	46848	A	16577	171	527	
16481	46849	B	16578	1	471	
16482	46850	A	16579	1	294	
16483	46851	A	16580	185	299	GLQYLKGKSGLKVKRGKVW*S ACCKKKGAALGTVASPL
16484	46852	A	16581	3	414	

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16485	46853	A	16582	462	928	WGVPGLPGRHLLPLPSQPPPSW LSILYVSWAALTCFLNSGESTA AKFFCPNLSAISYHTEAIPTTWQ GVHLSWAFGNGAPDIFSGPGGL L*PA/PQP/DLALGALFGAGVLV TTVVAGGITTLLLFIQHHTTQEI H*QIVQWIKTTL*ILATVSYVIG
16486	46854	A	16583	1	654	
16487	46855	A	16584	66	323	RVSLEIHVIQKRRPHHLSLLSFW TRMKTFRRRK/WGEAEESATDT TSETNKVGTGVFVLSLWVPVL VRNLAGPGVVLGNICKHFPVC
16488	46856	A	16585	1	1530	
16489	46857	A	16586	615	873	FVFLWSLMMVMYRWGFGVAV LSVC*FSF*QSGPSAAGLLEFAG GPFQTPFAWVSVVEAAEQRIML NSKRCCVIVPLVVSSQRGTRP
16490	46858	A	16587	286	626	PCKLFPCCNTCYS\RV*DFFRVA GKRSL\LNNYTSWVNTSMLVPR VAFACGFPLQQAAVLCVHLLG SPILGAADSSVTPPFCWMANAH ICGLQLQNTLSFAEPIYLGQEHA QLS
16491	46859	A	16588	226	489	PYLSVIFFFDYGINEEQCQRPIQ GDGQNFHRHNGWIKINPSCISF AIFFPFGAEKNMWSTPVTEAFN LLST*AF*LFGYKCTLVISSS
16492	46860	A	16589	1	1344	
16493	46861	A	16590	1	257	
16494	46862	A	16591	73	374	ESETEHKRPGKHSPKRSCNMCG QWAFHASLTVSYCLLTWCNET CSGDGCEGGMRIDIDPPVSQTR FFITLL*LC\FPGAGPQPAYFCTQ TQCHVETPRVSQ
16495	46863	A	16592	1	666	
16496	46864	A	16593	95	1840	
16497	46865	A	16594	1740	2026	
16498	46866	A	16595	39	487	SRLDPRVRLLFRQFCETRPGLEC YIQFLDSVAEYEVTPDEKLGEK GKEIMTKYLTPKSPVFIAQVGQ DLVSQTEEKLLQKPCKELFSAC AQSVHEYLRGEPFHEYLDSMFF DRFLQWKWLE/RVCACQVRAT GK\MYACSRLEKKRIQKRK
16499	46867	A	16596	1	591	

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16500	46868	A	16597	71	1994	EQEQRGRQGGLLAPPAPAAAA AARAAAAAAAAPQALTAPPAG SVADRRLSMELENIVANTVLLK AREGGGGKRKGKSKKWKEILK FPHISQCE\SLRRTIDRDYCRVC DKQPIG\RLLFRQFCETR\PGLEC YIQFLDSVAEYEVTPDEKLGEK GKEIMTKYLTPKSPVFIAQVGQ DLVSQTEEKLLQKPCKELFSAC AQSVHEYLRGEPFHEYLDSMFF DRFLQWKWLERQPVTKNTFRQ YRVLGKGGFGEVCACQVRATG KMYACKRLEKKRIKKRKGESM ALNEKQILEKVNSQFVVNLAY AYETKDALCLVLTIMNGGDLK FHIYNMGNPGFEEERALFYAAE ILCGLEDLHRENTVYRDLKPEN ILLDDYGHIRISDLGLAVKIPEG DLIRGRVGTVGYMAPEVLNNQ RYGLSPDYWGLGCLIYEMIEGQ SPFRGRKEKVKREEVDRRVLET EEVYSHKFSEEAKSICKMLLTK DAKQRLGCQEEGAAEVKRHPF FRNMNFKRLEAGMLDPPFVPD PRAVYCKDVLDIEQFSTVKGVN LDHTDDDFYSKFSTGSVSIPWQ NEMIETECFKELNVFGPNGTLP PDLNRNHPPEPPKKGLLQRLFK RQHQNNSKSSPSSKTSFNHHINS
16501	46869	A	16598	1	963	
16502	46870	A	16599	192	609	RPKGARELRLHPGPRYGRTSPQ NCPWARPGCLHEAL*G\WKICL HCKCPQEEHMVTVMPLEMEKT ISKLMFDFQRNSTSDDDSGCAL EEYAWVPPGLKPEQVHQYYSC LPEEKVPYVNSPGEKLRIKQLL HQLPPHDNEV
16503	46871	A	16600	1	915	
16504	46872	B	16601	30	820	
16505	46873	A	16602	99	248	RLEKHINCSRVI*SWAASPGLTA AAYRVTLNPPGTFLEGVAKVG QYTFT
16506	46874	A	16603	1	717	
16507	46875	A	16604	271	556	TAACLQSHHFKSSGQLSFERKW PKVGTITRSIASLLSGPVFGLHH LAFSAHVPREGPTTPWNYFPRV AAP/RRWTPGEHARTTTGLGAA PCVLLWA
16508	46876	C	16605	135	341	
16509	46877	A	16606	125	226	
16510	46878	A	16607	194	547	

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16511	46879	A	16608	2073	2338	
16512	46880	A	16609	1127	1282	
16513	46881	C	16610	1	2094	
16514	46882	A	16611	523	706	QHPLPNPCCHQPFHLCLRR*TL HCLRQQ*WPPLRQLPGKIMLIL LRSHPQHPCLLLDLQLD
16515	46883	B	16612	190	805	
16516	46884	B	16613	90	2812	
16517	46885	A	16614	44	216	RCRRRLIPHPRRLSPVVIRRIQVP Q/VQPGAGPSRPGHTRDPIGAA AAHCPCPGDSGAH
16518	46886	A	16615	1	1107	MTEEPLQALVLSAVLLYQEAY VRRSLTALGLDTFANFAHFSEM QPLSDAPCGLVTGVTRPLVAYS VEVGGFTIICGLSLASGNISGWC QLYLLLTQCRRGAATLWDSGM GGGRQSSRQTSVPRWTLDSKCI PGPKLTTRPQMDTKALGGQQA HVEHQTHEDIRPQVDTQAPGG HKALGEQQDPVGHQASVGYSP QVPQDSLGQALAGQATPEIPLG LQLHTVLVQEIQELIEAQTRAP GPCAEVRALPAPAAEPEPAWEE APPERALELEGAPAKDQTNEEL PEITA/PYC/EPLALTLELKAWLE RKVGGRG\DQHSPSQQLPCCP*S WARWQTCRQRAGHLAWPPVP RCREASLIH*NHSPAAAGPFILL
16519	46887	A	16616	1	792	
16520	46888	A	16617	1	963	
16521	46889	A	16618	1	378	
16522	46890	A	16619	1	494	MKPRTLAVSVTVLKGGVSRVC SFWCSDVFRVSSFWWVRGLAD SGVKLRTFAVSVTPLKAARLEL FVPPGGFVVSLASGVKLQPFEV SVTAHKGSVDPKSEKQQDLLQ RGKEQSYHTGEGHPSRLP/PAG SGSLLLFSYLAPPTSC*LVQPSG LF*QGADWCIYNP
16523	46891	A	16620	137	262	

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16524	46892	A	16621	1	2786	EVSLREATQRKLRRFSELRGKL VARGEFWDIVAITAADEKQELA YNQQLSEKLKRKELPLGVQYH VFVDPAGAKIGNGGSTLCALQC LEKLYGDKWNSFTILLIHSDEW KKKVSESYVITIERLEDDLPIKE KELTELRNIFGSDEAFSKVNLN YRTENGLSLLHLCCICGGKKSH IRTLMLKG\LRPSRLTRNGFTAL HLAVYKDNAELITSLLHSGADI QQVGYGGLTALHIATIAGHLEA ADVLLQHGANVN
16525	46893	A	16622	174	722	
16526	46894	A	16623	1	1554	
16527	46895	A	16624	1	843	
16528	46896	A	16625	2	745	ECWDGEHDIETPYGLLHVVIRG SPKGNRPAILTYHDVGLNHKLC FNTFFNFEDMQEITKHFVVCHV DAPGQQVGASQFPQGYQFPSM EQLAAMLPSVVQHFGFK\YVIGI GVGAGAYVLAKFALIFPDLVEG LVLVNIDPNGKGWIDWAATKL SGLTSTLPDTVLSHLFSQEELVN NTELVQSYRQQIGNVVNQANL QLFWNMYNSRRDLDINRPGTV PNAKTLRCPVMLVVGDNAPAE DGVVECNSK
16529	46897	A	16626	3	949	
16530	46898	A	16627	1	633	
16531	46899	A	16628	2	1324	
16532	46900	A	16631	1	591	
16533	46901	A	16632	138	832	
16534	46902	A	16633	55	586	IFVHPTPAASTMPSKFDPNEIKV VYLRCTGGEVGATSALAPKIGP LGLSPKKVGDDIAKATGDWKG LRITVKLTIQNRQAQIEVVPSAS ALIIKALK\EPPRDRKKQKNIKH SGNITFDEIVNIARQMRHRSLAR E\LSGTIKEILGTAQSVGCNVDG RHPHDIIDDINSGAVECPAS
16535	46903	A	16634	1	735	
16536	46904	A	16636	3	346	
16537	46905	A	16637	57	649	GPRRAYGGRMAGGGGDLSTRR LNECISPVANEMNHLPAHSHDL QRMFTEDQGVDDRLLYDIVFK HFQR\NKVEISNAIKKTFPFLEG LRDRDLITNKMFEDSQDSCRNL VPVQRVVYNVLSELEKTFNLPV LEALFSDVNMQEYPDLIHIYKG FENVIHDKLPLQESEEKEREERS GLQLSLEQGTGENSFRSLTWPP

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16538	46906	A	16638	1	1665	
16539	46907	A	16639	348	1534	
16540	46908	A	16640	1	627	
16541	46909	A	16641	1	1343	
16542	46910	A	16642	76	479	IRAVSRSRERPGSRSRYLQAC*G GGAFPGP*SAEISRLVRSHNLGG YSCT/EGGGGCRKGSCLLQHSC LLWHSCLLPASKNTVCSKDLG GCSCTQESRAPACSWSPRTQGG SASSHDLGSCRNAWETPSRQLG RSW
16543	46911	A	16643	130	675	
16544	46912	C	16644	118	420	
16545	46913	A	16645	1	987	
16546	46914	A	16646	1	494	
16547	46915	A	16647	360	1510	
16548	46916	A	16648	375	2187	VTAAAAATAMAESGESGGPPG SQDSAAGAEGAGAPAAAASAE PKIMKVTVKTPKEKEEFAVPEN SSVQQFKEEISKRFKSHTDQLV LIFA\GKILKDQDTLSQHGIHDG LTVHLVIKTQNRPQDHSAQQTN TAGSNVTTSSTPNSNSTSGSATS NPFGLGGLGGLAGLSSLGLNTT NFSELQSQMQRQLLSNPEMMV QIMENPFVQSMLSNPDLMRQLI MANPQMQQLIQRNPEISHMLN NPDIMRQTLELARNPAMMQEM MRNQDRALSNLESIPGGYNALR RMYTDIQEPMLSAAQEQFGGN PFASLVSNTSSGEGSQPSRTENR DPLPNPWAPQTSQSSSASSGTA STVGGTTGSTASGTSGQSTTAP NLVPGVGASMFNTPGMQSLLQ QITENPQLMQNMLSAPYMRSM MQSLSQNPDLAAQMMLNNPLF AGNPQLQEQMRQQLPTFLQQM QNPDTLSAMSNPRAMQALLQI QQGLQTLATEAPGLIPGFTPGL GALGSTGGSSGTNGSNATPSEN TSPTAGTTEPGHQQFIQQMLQA LAGVNPQLQNPEVRFQQQLEQ LSAMGFLNREANLQALIATGG DINAAIERLLGSQHHSSISVS
16549	46917	A	16649	269	440	
16550	46918	A	16650	469	746	RLNLPGPLCAGTSILFAVLMEAI GVSCIRQAGGGHVASHIY*GLM /PALAL*DTEPRNPSALPETCLC GSGPQSQMGHQTSHLLSSPGTG LSF
16551	46919	A	16651	1	1026	

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16552	46920	A	16652	719	906	
16553	46921	B	16653	1	1971	
16554	46922	A	16654	200	239	
16555	46923	A	16655	109	177	
16556	46924	A	16656	1	1542	
16557	46925	A	16657	1	453	
16558	46926	A	16658	2	487	
16559	46927	A	16659	1	1260	MEDAEGTVTLLAVTLVARDLN CIQPQTGPSGGIPEESIVIIGDVSS MHVIAPEDLPVGQDVEVEDSDI DDPDPVRALPLQIHACGRVGFE AHDDWSEGGDPAADTLIDPSQ DARYLKCEGMQAPHNSNPVAQ KTEISYHIWIARIPREKSGKVTG TLCDLLKDLTVIHSLIPKQGCSD GLGVLVQGTFQPQGNTDTCTC QVSAVEGKGEGLMQLASLSRR VTIWAYGDSQERDLKTQLEKIT AIKDMKEMQEKEYRIMEKAHS RQRKQHHKGPERKEQAAIFAV LQPPLVITRQTGSGVDPQKTPA DLQKRCRTVRRKTSQQKAVAS TLTKRITTQKLNAKDHNSSPTR EQNCTENEFDELTEVGFRRWVI TNSSELKEHVLTQCKEAKNFDK RLEELLIQITSLEKNISDLMEL*S FALSFCVVILFVNVDATAFCWL VFLLTVRHLFCRSAGVFWGSTP DPVCLVITSGGCRTAKIAACSFL SGPLWCCFLCLEWAFSIILYSFS CISFMSLIAVIFSNWVLRSLS
16560	46928	A	16660	1	799	
16561	46929	A	16661	1	969	MHVIAPEDLPVGQDVEVEDNDI DDPGQAKKTMEEQWTLVSLLS TSQQQGPVPPGSTASSATDKLS RWELTLLYSTTLFLAREAFRRA CLSGGTQRDWSQTLNLLWLTV PLGVFWSLFLGWIWLQLLEVPD PNVVPHYATGVVLFGLSAVVE LLGEPFWVLAQAHMFVKLKVI AESLSVILKSVLTAFLVLWLPH WGLYIFSLAQLFYTTVLGLCYV IYFTKLLGSPESTKLQTLPVSRIT DLLPNITRNGAFINWEEAKLAW GFFKQFFLKQI\LTEGGRYVGG HFLNVLNFGDQGVYDIMNNLG SLVARLIFQPIEESFIYS
16562	46930	A	16662	1	1665	

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16563	46931	A	16663	1	1521	MDVSSPPCVDGVSILPPLLIPRQ TGSGVDLQQNPTDLQLRVLTV KRKTNKQKGHPHQNSICTSPSS KTKEYTFFSVQHHTYSKIDHIV GSKAVLSKRKTIEIITNCLPDHS AIKLELRIKKLTQNHKTTWKQN NLLLNDYWVHNKMKAEIKMFF ETNKNKDTTYKNLWDTVKAV CRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKIHES RSWFFEKINKIDRPLAGLIKKKR EKSQKDAIKNDKLDITTDPTET QTTIRDYHKHLYAIKLENLEEM DKFLDTYTLPRLNQESLNRPITG SEIEAIINSLPTKKKYRTRRIHSR ILSEVQGGAVLEVLARAIRQEK EIKCIQLGKEEVKLSLFADDMIV YLENPTVSAQNLLKLISNFSKVS RYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLNEIKED/N KWKSIPCPRIGRINIM
16564	46932	A	16664	2	2315	
16565	46933	A	16665	1	912	
16566	46934	A	16666	1	912	
16567	46935	B	16667	199	619	
16568	46936	B	16668	64	1815	
16569	46937	A	16669	1	239	
16570	46938	A	16670	1	242	FREDGKTACGHEPSPVLLGLRL GLQPWG*GWGCSHGAGSAPDL VAGSAHSCGLWLPGSLHHHPA QCLPALLCGHLCLSVQDQQNG LLGR
16571	46939	A	16671	58	505	ASSRTRPSCTLARGRRWFPQPL SGRQRQRGGRRGSRVG/YGTA QNSTTLTSPAASASEATVSGHW PSTAPCCV\PAGAG\SATMWRSP A*AACGSAAWTSTWSRRSPGP GAAAGYGGVRTFCQPAGLTR/L ANRSTAGLCGWGLTLSCRETEL
16572	46940	A	16672	242	2952	
16573	46941	B	16673	474	2690	
16574	46942	A	16674	97	451	
16575	46943	A	16675	667	893	

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16576	46944	A	16676	3	639	RIRVHPTPAAFTMPPKFDPNEIK VGYLRCTGGEVGATSALAPKIG PLGLSPKKVGDDIAKATGDWK GLRITVKLTIHNRQAQIEVAPSA SALIIKALKEPPRDRKKLKILKL SGNITFDENGNICSTDMR/HRSL SRELSGTTKEILGTAQSVGCNV DGRHPHDIIDDINSENDKQPRKS KMRTSFSPQIPGHEHFHYLLLL QHVHCQLALTL
16577	46945	A	16677	350	984	VYLEVAPGGESRLPLSALGPQR IGPPGSCLPKKSWVNDICQRQP G\DWKGP*GLQVKLTHSRTGQ APDCTRVP/VLPSCP*FIQSPSRE PPKRPEKKPEKTFKHQLGIFTFL NEICSTLLRQMR\HRSLSPEKLS\ GTPLKEIPGGLPQSSWAGNV*W AAIPHDI\IDDIQQWVLWKCPAV SDIFIVTVGVKGGPPSVFTEISW EVLEMVTGGVG
16578	46946	A	16678	252	964	
16579	46947	A	16679	1	182	
16580	46948	A	16680	275	639	
16581	46949	A	16681	376	418	
16582	46950	A	16682	1135	1591	
16583	46951	A	16683	3	420	AAKEIEVGGGRKAI\KSFQKIQV RLVRELEKKFSGKHVVFIAQRR ILPKPTRKSRTKNKQKRPRSRTL TAVHDAILEDLVFPSEIVGKRIR VKLDGSRLIKVHLDKAQQNNV EHKVETFSGVYKKLTGKDVNF EFPEFQL
16584	46952	A	16684	1	879	
16585	46953	A	16685	2	691	HEEKAMFSSSAKIVKPNGEKP\ DEFESGHLPGLFLELE\MNSD\L KASAQGT*IITAS*RKLKVGGCS ESLFH*SFVPRSLKLKTFPQKNP KVRA*LRRIGKKKVPVGKAMS VLYPPSEGEFLPLSPTSEKARTK K*AKSRPPGARTLDKLVH\DAH PLRDFGPFPSGNFWAKRIPRSNL DGQPGSIKVPFWTKAQQNQCW NTRVETFFLVSYK\KLTGQGC*F LEFPRVFNC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16586	46954	A	16686	1	452	TLLVIPRKMRSAVELQQTSTDL QLRDLTVRKKTNKRKATASTS QKGHLHQNPICRSPTSKTKEVG FRRSVITNFSELKEDVRTYHKE AKNLENRLDEWLTRINSVEKTL NDLKELKTMARDLHDACTSFN RRFDQVEERVTVTEDQIN*QTE SNSINFTKRSSTPKPHL\RSPTSK TKEVGFRRSVITNFSELKEDVR TYHKEAKNLENRLDEWLTRINS VEKTLNDLKELKTMARDLHDA CTSFNRRFDQVEERVTVTEDQI
16587	46955	A	16687	1	618	
16588	46956	A	16688	280	353	SCNSIFARSVRACCS*VASSSFC C
16589	46957	A	16689	1	459	IKYSSPMKSTFVDPVDPVAVAV IYCLAAGLVIIRIPFFQLVPLKEE KMVLLNMDYYEMASLSLVTH RNEAPFSGRVRSSLPATEQSWM ENDFDKLTEVGFRRSVITNFSEL KEHVLTHHKEAKNLEKRLDKW QTRINSVEKTLNDLMELKTMA* EEKMVLLNMDYYEMASLSLVT HRNEAPFSGRVRSSLPATEQSW MENDFDKLTEVGFRRSVITNFS ELKEHVLTHHKEAKNLEKRLD KWQTRINSVEKTLNDLMELKT
16590	46958	A	16690	2	403	LALSGEMTLVLFMLLAGGWVT HDKPEPMPRAATSGGTRKGKT KAALKDLIATWKEVCVSSPATE QSWMENDFDELTEVGFRRSVIT NFFKLKEYVLTHHKEAKNLEK MLDEWLTRINSVEKTLNDLME LKNMA*ELTEVGFRRSVITNFF KLKEYVLTHHKEAKNLEKMLD EWLTRINSVEKTLNDLMELKN
16591	46959	A	16691	1	676	
16592	46960	A	16692	1	1965	
16593	46961	C	16693	1	3075	
16594	46962	A	16694	78	152	CAAGFGLPVFY*GFLHRCSLGIL V
16595	46963	B	16695	1	904	

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16596	46964	A	16696	1	2026	EQEASYGRDAFAKAIYERLFC WIVTRINDIIEVKNYDTTIHGKN TVIGVLDIYGFEIFDNNSFEQFCI NYCNEKLQQLFIQLVLKQEQEE YQREGIPWKHIDYFNNQIIVDL VEQQHKGIIAILDDACMNVGK VTDEMFLEALNSKLGKHAHFSS RKLCASDKILEFDRDFRIRHYA GDVVYSVIGFIDKNKDTLFQDF KRLMYNSSNPVLKNMWPEGKL SITEVTKRPLTAATLFKNSMIAL VDNLASKEPYYVRCIKPNDKKS PQIFDDERCRHQVEYLGLLENV RVRRAGFAFRQTYEKFLHRYK MISEFTWPNHDLPSDKEAVKKL IERCGFQDDVAYGKTKIFIRTPR TLFTLEELRAQMLIRIVLFLQKV WRGTLARMRYKRTKAALTIIR YYRRYKVKSYIHEVARRFHGV KTMRDYGKHVKWPSPPKVLRR FEEALQTIFNRWRASQLIKSIPA SDLPQVRAKVAAVEMLKGQRA DLGLQRAWEGNYLASKPDTPQ TSGTFVPVANELKRKDKYMNV LFSCHVRKVNRFSKVEDRAIFV TDRHLYKMDPTKQYKVMKTIP LLQLTCLN\VSNGKDQLVVFHT KDNKDLIVCLFSKQPTHESRIGE LVG\VLVNHFKSEKRHLQV\NV TNPVQCSLHG\KKCTVSVETRL NQPQPDFTKNRSGFILSVPGN
16597	46965	A	16697	1	1665	
16598	46966	A	16698	1727	1908	FLFFYIC*RELYFQLCGQFWNK CNVLLRRMYILLIWGGEFCRYQ LGLLGAELNSVPGYHC
16599	46967	A	16699	1	384	
16600	46968	A	16700	1	636	
16601	46969	A	16701	1744	2283	
16602	46970	A	16702	194	368	
16603	46971	C	16703	62	205	
16604	46972	B	16704	1	1257	
16605	46973	A	16705	1	1077	

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16606	46974	A	16706	1213	1228	AQN*QTQRTSTPKPHL\SSPSTK TKENDFDELREEGFRRSVITNFS KLKEDVRTHRKEAKNLEKRLD EWLTRINSVEKTLNDLMELKT MAQELRDTYTSFSSRFDQVEER VSVIEDQMNDMKREEKFREL/K RVQRNEQSLQEIWDYVKRTNL RLIGVPEKIQTTIREYYKHLYAN KLENLEEMDKFLDTYTCPRLN QEEVESLNRPVTGSEIEAIINSLP TKKVQDQADSQPNSTRVFKTV CISSLGHTTASADTQDVCQLPV TSLLEQGLSSKSAGFLDYAVQR LWLLGTEPL
16607	46975	A	16707	33	263	
16608	46976	A	16708	204	1756	
16609	46977	A	16709	760	821	TMRTHGHRKGNI*QR/R**PEST KNSNKFTRKNQTTPSKREWMK LETIILSKLSQGQKSKHRMFSLI SGN*TMRTHGHRKGNITHWGL LWG
16610	46978	A	16710	1	879	
16611	46979	A	16711	311	514	KNAHHQWPSKKCKSKLQ*DTIS HQLEWQSLKSQETTGTRMKME TITLSKLSQGQKSKHCMFSLIGG N
16612	46980	A	16712	24	1268	AGLCAARARMRLFRWLLKQPV PKQIERYSRFSPSPLSIKQFLDFG RDNACEKTSYMFLRKELPVRL ANTMREVNLLPDNLLNRPSVG LVQSWDMQSFLELL*YENKSPE DPQVLDNFLQVLIKVRDRHND VVPTMAQGVIEYKEKFGFDPFI STNIQYFLDRFYTNRISFRMLIN QHTLLFGGDTNPVHPKHIGSIDP TCNVADVVKDAYETAKMLCE QYYLVAPELEVEEFNAKAPDKP IQVVYVPSHLFHMLFELFKNSM RATVELYEDRKEGYPAVKTLV TLGKEDLSIKISDLGGGVPLRKI DRLFNYMYSTAPRPSLEPTRAA PLAGFGYGLPISRLYARYFQGD LKLYSMEGVGTDAVIYLKALSS ESFERLPVFNKSAWRHYKTTPE ADDWSNPSSEPRDASKYKAKQ
16613	46981	A	16713	175	465	
16614	46982	A	16714	240	381	FFLSFPPLCQSS*NQNLLPW/ICA KVCSFTPEVSKTTNPLEGRNSG HI
16615	46983	A	16715	268	1524	
16616	46984	A	16716	1	378	

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16617	46985	A	16717	708	987	IQLPGHRSQGQ\AGASHTDARQ QDPGNSHSDFVRHSHSLPCLER QDRRSAGHNGSATVPGTEACG RAYKAPAGHYHSGAGQSLPAA SHRSFSSP
16618	46986	A	16718	1	2052	
16619	46987	B	16719	1	606	
16620	46988	A	16720	1	541	QHQRKQKRQLRAQQNLSWEEI AKEYQNEEDSLGGSRVVVCDI NKEMLKVGKQKALAQGYRAG LAWVLGDAEELPFDDDKFDIYT IAFGIRNVTHIDQALQEAHRVL KPGGRFLCLEFSQVNNPLISRLY DLYSF\RVIPVLGEVIAGDWKSY QYLVE\SIRRFPSQE\KFKD\MIE DAGF\HKVTYESLTSG\IVAIHSG FKL*FLCLEFSQVNNPLISRLYD LYSFQGHPCPGRGHRWRLEVLS VPCREVSEGFRLRKEFKDHDRR CRLSTR
16621	46989	A	16721	526	933	
16622	46990	A	16722	191	468	
16623	46991	A	16723	2	677	GKVHVLERRGFHRTEMHLQKI LLLPVLSSSSSSDP/STLSVSALV RMFSSADE*SVSEASSSEPSSSFS RRSSCSFGSEPSFASFSFSSFPDL ASLSSVFLLFRAFS\SSHVM*WL PSSS*VGS/STSARAQLPSYVPSF SVKTKSGLKSALRFFPKAFCRL PSTMGPSSSSSPESDSALHRHLV ILDVWLQIKPRVRKPCCRRSHF RKRAQPAVRPLTFRSLLVVLR
16624	46992	A	16724	31	187	
16625	46993	A	16725	215	947	
16626	46994	A	16726	1	378	
16627	46995	A	16727	2	7567	GGGGARRQRRGDAGGGAETAP SEIILSPAAEERSGRSETLRRGT AAGRMATVVVEATE\PEPSGSI ANPAASTSPSLSHRFLDSKFYLL V\VVGEIVTEEHLRRAIGSIELGI RSWDTNLIECNL\DQELKLFVSR HSARFSPEVPG\QKIL\HHRSERF *ETV\VLIQ\PFLMEGSSGTEVRL MITDAARHKLLVLTGQCFENT GELILQSGSFSFQNFIEIFTDQEI GELLSTTHPANKASLTLFCPEE
16628	46996	A	16728	101	365	VITGQPNPTNPNLQATPDIQGTL ARLGPA/LHPRGIIPFIGHQSA/R PHAPAPANPNKRTLFRPPPLSPP SPEPPGSGQGAGLGARPALP

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16629	46997	A	16729	1170	2847	VASC*ENACKQNQRQKPCDYL NRCRKGLWQNSTTLHAKNSQ* TVLYKTIKFQLEKTTLKFIWNQ KRAHIAKSILSQKNKAVGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEIMPHIYNHLIF DKPDKNKKWGKDSLFNKWCW QNWLAICRKLKLDPFLTPYTKI NSRWIKDLHVRPKTIKTLEENL GNTIQDIGTGKDFMSKTPKAM ATKDKIDKWDLIKLKSFCTAKE TTIRVNRQPTKWEKIFTT
16630	46998	A	16730	79	536	
16631	46999	A	16731	232	771	
16632	47000	A	16732	3	339	
16633	47001	A	16733	279	416	
16634	47002	A	16734	1	1760	
16635	47003	A	16735	309	1718	
16636	47004	A	16736	10	417	IAIMNDTVAIRTRKFMTNRLLE RKQMVIDVLHPGKATVPKTEIL EKLAQMYKTTPDVIFVFGFRTH CGGGKTTGFGMIYDSLDYAEK NEPKHRLARHGLYEKKKTS*K QRQERTNRMKKVRGTAKANV VAG*KPNE
16637	47005	A	16737	96	609	EKFMT\NRLTSGETKWVI*CPFT PGRRTVP*AQKIR\EKLAQNVQ RPHPDVIFVFGFRTHFGGGKTT GFGMIYDSL\DYAKEKMNPKH RLA\RHGPGMEEGKRPSKKGN GKER\KNQN*RKVQGGLAKGP LLGAGQKEEMKCLGSELEIGSQ PKELKVLPMMLAVATVDFSQE
16638	47006	B	16738	1	1041	
16639	47007	A	16739	3	447	VSVPFIFIWLTCKSFLKFDLKSN TNVLQSL/GKFQSEVSKRQKLA TVFSSFTSTGLCQGSVAFISRCP PLASGSDSVWRGGSVFFSFRP* RLMISLLGSCVSHQFPEKLEF** KKMPYKIPTAHHQQQDDQQRG HEHKQSQPDAVPHLG
16640	47008	A	16740	1	2385	
16641	47009	A	16741	1	639	
16642	47010	A	16742	1	993	
16643	47011	A	16743	127	426	CTDKITLVFGV*MLTPKPDK/CD DSAV*ELLWLTNQLSACVVHP GLYHLHVRSIWIPYRCLFSTMC GVCQTCTVAMQLDCLADSFNA VFKLTEAAGHMAR

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16644	47012	A	16744	3	374	SLRLQFYYKISFQTQDQANKLS DSDASHLHPLAPCSEPTRTNVH TKLPRERPQSQIASPYPLPPCPE RLKKQTNKKKNW*EPSPHILPP RNAAAHTGQSRASKSLPAPPPT VSPRPRPGAPGT
16645	47013	A	16745	16	253	
16646	47014	A	16746	163	588	TFHAVLHIENAGYFNSIPFFRIL NHNPLTTVEDPYLFKLPALKYL *VL*YSHESRDDLYSF*IFHQRL SILHLG*NVII\KF*LSY*KKVIGE EKN*EDV*WSRQPAGEREQC*R THIDLE/PCRHMEEYYLTKKAK GKRCSLF
16647	47015	A	16747	2	363	GTSQTLLRSLASACIFQPKVRLL SREEIPLNLNY*SVSPNSNPNHL YSRHTILTAMLTLQLGTCVLLPI GLLVPYPNCPSPTGLQVTPFLPS PCGSGWPASFTYSSNRFTTNLL FCVFIL
16648	47016	A	16748	1028	1621	
16649	47017	A	16750	1	112	LGNTWG*QPCKRLKIWLSLEFT KINVIRHMWKKFKRL
16650	47018	A	16751	91	597	LKNRRRSRPSIRQSIGSTSVSRW LTSLFTYLDHTADVQ*V*REFIP LKPRQ*ED*MFQSWLHAWGDT LEEAFEQCAMAMFGYMTDTGT VEPLQTVEVETQGDDLQSLLFH FLDEWLYKFSADEFFIP\GWGEE FSLSKHPQGTEVKAITYSAMQV YNEENPEVFVIIDI
16651	47019	A	16752	226	668	IYFFRLHAWGDTLEEAFEQCA MA\MFGYMTDTGTVEPLQTSRS \KTQGDDLQSLLFHFLDEWLYK FSADEFFIPREVKVLSIDQRNFK LRFN\GWGEEFSLSKHPQGTEV KAITYSAMQVYNEENPGSFCD HWTFKTTQKIKRLPTGKK
16652	47020	A	16753	3	942	
16653	47021	A	16754	3	419	SLYHNSSQKRHWTFSSEEQLAR LRADANRKFRCKAVANGKVLP NDPVFLEPHEEMTLCKYYEKRL LEFCSVFKPAMPRSVV\LTCAFL ACKVDEFNVSNPQFVGNLRESP LGQEKALEQILEYELLLIQQLNF HLIVHN
16654	47022	A	16755	312	537	
16655	47023	B	16756	209	1381	
16656	47024	A	16757	1	927	
16657	47025	A	16758	1	3987	
16658	47026	A	16759	2	175	

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16659	47027	A	16760	2395	2700	
16660	47028	A	16761	2	1118	
16661	47029	A	16762	26	1205	
16662	47030	A	16763	1	1594	
16663	47031	A	16764	1	595	
16664	47032	A	16765	1	1029	
16665	47033	A	16766	1172	1364	
16666	47034	A	16767	253	389	
16667	47035	A	16768	489	855	
16668	47036	A	16769	2	401	
16669	47037	A	16770	415	694	EAKLHLNLCDMSWLCCPTKGK RKQALEVLNILGPFLAPFWIAK SYFFTSPKTQVSSL*FLRYKRIK LQCRPKTCTNPSRTRSCALPGR FIPPF
16670	47038	A	16771	1	765	
16671	47039	B	16772	1	1095	
16672	47040	A	16773	82	311	KANSDVPFGFGVNLEHLMEAC NS/GTNLLNSKRLNNDCICLASH TDVSIIARKCCLVVSCLLLLRGL SILRSKESHC
16673	47041	A	16774	2	683	
16674	47042	A	16775	1	2703	
16675	47043	A	16776	1	555	DHNSSPAREQ/SSMENKFHELT EVGFRKITSLEKNINDLMELKN TARELREAYTSIKSRIDQAKESI SEIEDQLNEIKCEDKVREKRMK SNKQNFQEIWDYVKRPNLRLT GVPESDRENGTKLENTLQEIIQE NFPNLARQANIQIQEIQRTAQR QSSSRATPIHIIVRFAKFEIKEKM LRAAREK
16676	47044	A	16777	1	839	
16677	47045	A	16778	1	504	
16678	47046	A	16779	1	2367	
16679	47047	A	16780	1	1566	
16680	47048	A	16781	146	464	VTGWTNYEGNGRWRERSRQLC GCCSRKSSSSWGISLMKGSGAP LRPGRMMWSGFRKCSDTQVM YS*R*LLETMTLASIMR*THTK* NALRKCSALKDCFLGKALTL
16681	47049	A	16782	1	1782	
16682	47050	B	16783	221	1075	
16683	47051	A	16784	1	627	
16684	47052	A	16785	1	1539	

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16685	47053	A	16786	1	1318	LSPVLSLSPDSMSFTTRSTFSTN YRSLGSVQAPSYGARPVSSAAS VYAGAGGLATGIAGGLAGMG GIQNEKETMQSLNDRLASYLDR VRSLETENRRLESKIREHLEKK GPQVRDWSHYFKIIEDLRAQIF ANTVDNARIVLQIDNA\RLAAD DF\RVKYETELAMRQS\VENDIH GLRKV\IDDTNITRLQLETEIEAL KEEL\LFMKKNHEE\EVKGLQA QIASS\GLTVEV\DAPKF\QDLRQ DSWADIR\AQY\DELARKEPRG A*TKYWFSADLRESTTV\VTTQ F\AEV\GAA*DDASQSWRTYSPS SLGDPTWGFPWRKS*RAS\LEN SLREG*RPAYALT/QMEQASTGI LACTFESELGTDPGAEGQRQAQ EY\EALLNIKVKLEAEI\ATYRRL \LEDGEDFNLGDALDSSNSMQT IQKTTTRRIVDGKVVSETNDTK
16686	47054	A	16787	1	253	RVRTLKTSTSTCLYWFENKDS/ DHPERSSP*YMSPSHRYGSLVK ASITKPAFLKTSGRLFTCSSQFC PLISKISDGFSHLPPFST
16687	47055	A	16788	1	276	AAAAGPPGPLVMFTYRERVSG LRSVHILRASHTDARLRQEEPT ERLQFHSSGLLIRFSRETEPIGV YIKED*EEWAYKMMVFAKSHD LPFAN
16688	47056	A	16789	1	203	LLHTSTKNELWQ*GKRDPLIVF YTQYLF*EKTTRK*NQRQAGSL ALGPKPGLRLPGLNPVVENQFI
16689	47057	A	16790	8	361	RGLDGQGGRDGSSSGGGGGGR RRRCLLLLAPAPAVIRASGRGP R*DCWRAGCA*AWRPC/RLAR RMWTLRSPLTRSLYVNMTSGP GGPAAAAGGRKENHQVARKR LNVCVFTRSVSETA
16690	47058	A	16791	674	1076	VQLFRSAGSRDHHRFLGRGRN KQTKTLYPTPIPCSLKYQRKQN GSLLWTSRMPSSVFPCTLTPSFS LPLRISQTTHPNLRGPSCPKGLG IALISLVRHWLKI*ATSQVQAL WSFSMWMIYFWLPVQKPHASR
16691	47059	B	16792	296	1470	
16692	47060	A	16793	1	334	
16693	47061	A	16794	718	2541	
16694	47062	A	16795	2	406	
16695	47063	A	16796	74	464	
16696	47064	A	16797	159	610	
16697	47065	A	16798	1	273	

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16698	47066	A	16799	1	543	
16699	47067	B	16800	1	873	
16700	47068	A	16801	1	558	
16701	47069	A	16802	27	136	
16702	47070	A	16803	89	363	
16703	47071	A	16804	579	994	
16704	47072	A	16805	129	362	PKIIQPRRATTRFTSIHGWRICPS IPCFPEATINRRRCVKVDSVTCH LLTQR*YKSSKVQERC*SCRIQG QKISDCY
16705	47073	A	16806	878	1811	
16706	47074	A	16807	1	843	
16707	47075	C	16808	19	231	
16708	47076	A	16809	1	1650	
16709	47077	A	16810	3	404	
16710	47078	A	16811	279	428	
16711	47079	A	16812	3	507	
16712	47080	A	16813	1	1128	
16713	47081	B	16814	1	567	
16714	47082	A	16815	3	1206	GSEGQGAGPGGAAATAAAME DEMPKTLYVGNLSRDVTEALIL QLFSQIGPCKNCKMIMDTAGN DPYCFVEFHEHRHAAAALAAM NGRKIMGKEVKVNWATTPSSQ KKDTSNHFHVFVGDLSPQITTE DIKAAFAPFGRISDARVVKDMA TGKSKGYGFVSFFNKWDAENA IQQMGGQWLGGRQIRTNWATR KPPAPKSTYESNTKQLSYDEVV NQSSPSNCTVYCGGVTSGLTEQ LMRQTFSPFG\QIM\EIRVFPDKG Y\SFVRFNS/HMESGRHMAIVSV NGTTIEGHVVKCYWGKETL\D MINPV\QQQNQIGYPQPYGQWG Q\WYGNAQQIGQYMPNGWQV P\AYGMYGQAWE/SSQGFNSDT VFLAPWDGDPNFGSCNRLQGQ NG\SLLPN\RPSGYRVAGYETQ
16715	47083	A	16816	1425	1564	
16716	47084	C	16817	151	339	
16717	47085	A	16818	67	373	FCDCHHFILMFKSPHIWPVGIFS SWLLCFFWACLHHSLSIALLSC TKRYSGLILYFLCSSFEITVSSKS SVSF*RRMVFRNQVLGSRCACC C*GVAAPRPFP

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16718	47086	A	16819	1	799	MGPHWLWLHLALVLLPPSALL LPSCEKGVLRVRFYHEKWIYV HKESTKERHGYCTLGEAFNRL DFSSAIQDIRRFNYVVKPLLPRY KFQRLNAITKDRQRSSSGVQLP HAGQPQGADPTQDERRQVAGD TPGDPRALAGGGVVDRTYPGS YEASGRPGLQLALAIEDLLRDS AIGCTFCDRCRPVGAQRLLAHS LALAAPGAEKREVVKLLLVAY VRRRPGKNLTTQNCQ\PAAGYI PPGHQ*AASAHARSWKNQQPP PRVLIGSA
16719	47087	B	16820	28	438	
16720	47088	A	16821	366	793	AWVEQSKVLIKEGGIQLLLTIV DTPGFGDAVDNSNCWQPGINYI DSKFEDYLNAESQVNRCQMPG NRVHCCLYFIAPSGHGPLHN*R LPPSGRIG*YMFVTTWHCLLLR LKPLDIEFTKHLHEKVNIIPLIAK ADTLMPEEC
16721	47089	C	16822	228	374	
16722	47090	A	16823	291	604	AWELEKSHLRRGLDPSHNINIR VEPKF*SKYGGVQLLLTIVDTP RFGDAVDNSNCWQPVINYIDIK FEDYLNAESRVNRCQMPGNRV Q**LYFIAPSGHGPLHN
16723	47091	A	16824	148	498	
16724	47092	A	16825	1	595	DRPRITGGGKSGTEYPENLPTL KATIENKNSVLNTATKMKDVQ TSTPAEQDLEMA\SEGEQKRLE EYENNQPQVKN\QIHSRDDLDD IIQSSQTVSEDGD\SLCCNCKNVI LLIDQHEMKCKDCVHLLKIKNT FCLWKRLIKLKDNHCEQLRVKI RKLKNKASVLQKRISEKEEIKS QLKHEILELEKELCSLRFAIQQE
16725	47093	A	16826	1	828	
16726	47094	A	16827	1	540	
16727	47095	A	16828	295	460	
16728	47096	A	16829	2	1355	
16729	47097	A	16830	650	1184	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16730	47098	A	16831	725	2368	AVDIIKEIKHPQKHKKLPAFQLR PFPLREETIPCNGVSFPRCEPPCL AEVYMCLNEMLKDEKKGCMN KSGAGENPQERTAQKRKFPSPP HSSNGHSPQDTSTSPIKKKKKP GLLNSNNKEQVKQPLECIETQS KAMTMLTIEQLSYLLKFAIQKM KQPGVRRKLKPVPLEQHPDYA EYIFHPMDLCTLEKVGLRQMY GCTEAFLADAKWILHNCIIYNG GEWLRTQIAKVVIKICEHEVCV SQVCPECYLAACQKRDNWFCE PCVSWIYD\SACQPV*WKLVIQ MFLPM/WKADIL/RGEEG*YTSE LIGWL*SLSCDCSAGTSISHPSD SD*RWLTEHEGRRVSWP\VNNC YLMSKEIPFSVKKTKSIFNSAM QEMEVYVENIRRKFGVFNYSPF RTPYTPNSQYQMLLDPTNPSAG TAKIDKQEKVKLNFDMTASPKI LMSKPVLSGGTGRRISLSDMPR SPMSTNSSVHTGSDVEQDAEK KATSSHFSASEESMDFLDKSTG QLRAGERGGGPLDTGVSHGCT LGGPKQVSIKQQASVLQDTMN
16731	47099	A	16832	2	164	PSTLRAEAWPP*NGSPVPLASS QASSSRSGPTSCIPRYPVASPSE RLPLPTAAA
16732	47100	A	16833	51	498	
16733	47101	A	16834	1	531	
16734	47102	C	16835	257	358	
16735	47103	A	16836	63	193	SGRLAPHTSRRTSANCSDDAKS SDSCSPSRKT*WSGRNTNRIH
16736	47104	A	16837	1	834	
16737	47105	A	16838	258	545	CQNPQILASPSTKDLMGLGRNT NKDTLKACLARVVKRRSECSQ KPAS*MCTERNPTSMREVHDLE RKYAVLYQPLFD*AVLKLLMQ FMNLRKEGM
16738	47106	A	16839	66	476	
16739	47107	A	16840	1	1362	
16740	47108	A	16841	1	747	
16741	47109	A	16842	522	687	
16742	47110	A	16843	112	861	
16743	47111	A	16844	87	472	TVTFSQCRFGKMLPLEKAFASP QELPSPAGSAHAGVSSRSSSRK NPRPSLRGPLLTLEFSRLRFREF VYP\EAAGPHHTLARLDELCRQ WLMPEARSKEQMLELLVLEQF L/SILPDKVRPWVVAQYPES
16744	47112	A	16845	1	393	

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16745	47113	A	16846	621	1099	
16746	47114	A	16847	1	453	
16747	47115	A	16848	209	1175	
16748	47116	A	16849	1	546	
16749	47117	A	16850	187	421	LGESSQ*GSP\PPPTGGCGPATG Q*PLGQSFQRKELAAIFAVSQY SLVVPPGMGETEATGIWSRPPA NGNSPTVEWHIK
16750	47118	A	16851	3	1654	
16751	47119	A	16852	166	465	
16752	47120	A	16853	1	558	
16753	47121	A	16854	51	380	RNNLLLLTHHFVLIIQFLIPRKET KYYLVITPYSLSINVLSNFFYYS PESLNDTNCYHHEEADTPWR*F LAIFEGLFNIAHQMQNMPFFLL WKQVPETLVIQQQLPRIN
16754	47122	A	16855	3	550	
16755	47123	A	16856	1	462	
16756	47124	B	16857	1	2811	
16757	47125	A	16858	3	514	ASGTAPEIQARPTRPRRKRRRK LLPL/TKAEAKAKALKAKKAVL KGVHSHKKKKIRTSPTFRRPKT LRLRRQPKYPRKSAPRRNKLDH YAIIKFPLTTESAMKKIEDNNTL VFIVDVKANKHQIKQAVKKLY DIDVAKVNTLIRPDGEKKAYVR LAPDYDALDVANKIGII
16758	47126	A	16859	73	396	FFQFSPKKNCSVWWNC\AEVLL KYKTGETNDFELLKNQLLDPDI KRLPWLNRSQTVVEEYLAFLG NLVSAQTVFLRPCLSMIASHFV PPRVIIKEGDVDVSDSDDEDD
16759	47127	A	16860	132	357	YVSKFAGRLSSSSSESETSTSPS LMITRGGTKWGSNHAETRSEE NSLC*YKITKKSQILFHYCFDFY STKAISI
16760	47128	A	16861	380	597	
16761	47129	A	16862	179	280	QRDIKSCVQILQWEGSTRPFTN E**YMANVRNS
16762	47130	A	16863	2	175	
16763	47131	A	16864	178	374	
16764	47132	A	16865	386	2120	
16765	47133	A	16866	887	1104	

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16766	47134	A	16867	1	708	MEVAALEHLDHRLREKVKQQN ALRHQVVLRQRRLEELQLQHS LRLLEMAEAQNRHTEVAKTMR NLENRLEKAQMKAQEAEHITS VYLQLKAYLMDESLNLENRLD SMEAEVVRTKHELEALHVVNQ EALNARDIAKNQLQYLEETLVR ERKKRERYISECKKRAEEKKLE NE/LHGAQADPGSDLNPRADPP RAPAATVRRHHPGQPACQGGG AAAALEHVPDGGDLWQGQGR HWH
16767	47135	A	16868	1	1327	
16768	47136	A	16869	1	1776	
16769	47137	A	16870	1	397	
16770	47138	A	16871	1	1974	
16771	47139	A	16872	1	336	
16772	47140	A	16873	3	661	GRGGHNFAPNLTARSAVTSGL GGPPAAVMVGSLNCIVAVSQN MGIGKNGDLPWPPLRNEFRYF QRMTTTSSVEGKQNLVIMG\KK TW\FSIPE/RRNRPFKG*EFNLVL SRELQGNLPQGAHFLSRSLDDA LKLTEQPELANKVGMVW\IVG GSSI\YKESMNHSSSLKLFVTRII QDFESDTFFPEIDLEKYKFLPEY PGVFFDVQEEKGIKYKFEVHEK
16773	47141	A	16874	38	755	ALKTCSVNQPDAKDNIAGSSGH LRTLSPVVSRSCLKEEERRRRR RMKRRQRSRRRRSRRRRMRRR RRSRSRRRRMKRRKRRRRMKR RSSFILMYFFMLLLSGIPLLYME VIMGQWLHVDNIRVWKQLVP WLCSMSY/SSQSVCASVSLYNS TIISWNFFYSFAHPLPWDHCPLV KNISVTDWAHQYFLYHTTLHA SDHSEEAAEALVPNRSLGCLLG RDHRDLDFKPEIRRGAHTGGAR
16774	47142	A	16875	1	1830	
16775	47143	A	16876	2	1142	
16776	47144	A	16877	1	435	
16777	47145	A	16878	1	963	
16778	47146	B	16879	247	1092	
16779	47147	A	16880	1	1653	
16780	47148	A	16881	1	2268	
16781	47149	A	16882	301	555	
16782	47150	A	16883	1	630	
16783	47151	A	16884	731	834	
16784	47152	A	16885	1	2277	
16785	47153	A	16886	45	2446	
16786	47154	B	16887	625	696	

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16787	47155	A	16888	193	315	WPGGGYSLLCFWCPLSFAGAA G/W*PPPGHH*PYSPKQEHYRT NSDTLIFLSSRTLVLQGS*GIKV AGSEGPKYNE*PRNPVLPSLCL HLFGC
16788	47156	A	16889	1	588	
16789	47157	A	16890	2	229	
16790	47158	A	16891	1	502	
16791	47159	A	16892	516	576	
16792	47160	A	16893	144	435	
16793	47161	C	16894	1	996	
16794	47162	A	16895	424	632	
16795	47163	B	16896	446	1944	
16796	47164	C	16897	207	470	
16797	47165	A	16898	1	396	
16798	47166	A	16902	1	585	
16799	47167	A	16903	141	906	
16800	47168	B	16904	99	276	
16801	47169	A	16905	1	756	
16802	47170	A	16906	1	383	
16803	47171	A	16907	1	582	
16804	47172	A	16908	3	615	PECIIGIDILSSGQNPHIGSLTGR VRAIMVGKAKRKPLELPLPRKI LNQKQYRIAGGIEEISATIKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALGLLLGFGGN*TFDY
16805	47173	A	16909	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVIFPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY
16806	47174	A	16910	232	633	
16807	47175	A	16911	1	1677	
16808	47176	A	16912	328	381	LLKLQH*MQSPYLVGPSQ
16809	47177	A	16913	3	811	
16810	47178	A	16914	1	1125	
16811	47179	A	16915	1	1191	
16812	47180	A	16916	113	485	
16813	47181	A	16917	1	357	
16814	47182	A	16918	12	398	
16815	47183	A	16919	498	595	TEMASTTTCT/RFHDEYQLFEEL *KGAFSVNGT
16816	47184	A	16920	5	367	

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16817	47185	A	16921	190	2005	VLYPLHLGTGTGKGAGGASSG EEGSEARRRRRIGGLWGRRPHA TLSGHLPSRPAPAHTPSRASYFR TRKVRAALGDSAAGPVPGLAA RLLASGPSRSQPGHSPGPEMAS TTTCTRFTDEYQLFEE\LGRGAF SVVRRCMKIPTGQGYAAKIINT KKLSARDHQKLEREARICRLLK HPNIVRLHDSISEEGFHYLVFDL VTGGELFEDIVAREYYSEADAS HCIQQILESVNHCHLNGIVHRD LKPENLLLASKSKGAAVKLADF GLAIEVQGDQQAWFGFAGTPG YLSPEVLRKDPYGKPVDMWAC GVILYILLVGYPPFWDEDQHRL YQQIKAGAYDFPSPEWDTVTPE AKDLINKMLTINPAKRITASEAL KHPWICQRSTVASMMHRQETV DCLKKFNARRKLKGAILTTML ATRNFSAAKSLLKKPDGVKEST ESSNTTIEDEDVKARKQEIIKVT EQLIEAINNGDFEAYTKICDPGL TAFEPEALGNLVEGMDFHRFYF ENALSKSNKPIHTIILNPHVHLV GDDAACIAYIRLTQYMDGSGM PKTMQSEETRVWHRRDGKWQ NVHFHRSGSPTVPIKPPCIPNGK ENFSGGTSLWQNI
16818	47186	A	16922	1	288	
16819	47187	A	16923	318	458	
16820	47188	A	16924	1	578	
16821	47189	A	16925	803	1068	
16822	47190	A	16926	1	660	
16823	47191	A	16927	2	325	TSSENNNGPKR*IHSTESLYLLQ GSVVADHDYIGLPEIPIGAYQA NILVEDATIGIVDNELLTSSKDR ELLEYRNTKISPLIDDHSSLEKQ TFSLLDSSNQVLEYLS
16824	47192	A	16928	156	573	
16825	47193	A	16929	405	599	GLEPPQKPGLVTSILQANPVPLP CGNSQSR*TSTRCWYEHLQCTQ SHLQMQQYHEAYQSACALA
16826	47194	B	16930	1	1676	
16827	47195	A	16931	1	1125	
16828	47196	A	16932	27	818	
16829	47197	A	16933	1	4986	
16830	47198	A	16934	1	4401	
16831	47199	A	16935	153	370	SVLETCMSTAFPVSCHSSFKTA VLRISLS*ISAQGGPIDLFSQCHP SSSTGVSS\NHRGSWDTPGQSL VVICL

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16832	47200	B	16936	47	501	
16833	47201	A	16937	49	1714	
16834	47202	A	16938	1	999	
16835	47203	A	16939	140	2029	FAARAGPGGSRRARRGNKWAR MPYEIKKVFASLPQVERGVSKII GGDPKGNNFLYTNGKCVILRNI DNPALADIYTEHAHQVVVAKY APSGFYIASGDVSGKLRIWDTT QKEHLLKYEYQPFAGKIKDIAW TEDSKRIAVVGEGREKFGAVFL WDSGSSVGEITGHNKVINSVDI KQSRPYRLATGSDDNCAAFFEG PPFKFKFTIGDHSRFVNCVRFSP DGNRFATASADGQIYIYDGKTG EKVCALGGSKAHDGGIYAISWS PDSTHLLSASGDKTSKIWDVSV NSVVSTFPMGSTVLDQQLGCL WQKDHLLSVSLSGYINYLDRN NPSKPLHVIKGHSKSIQCLTVH KNGGKSYIYSGSHDGHINYWD SETGENDSFAGKGHTNQVSRM TVDESGQLISCSMDDTVRYTSL MLRDYSGQGVVK\LD\VQPKC\ VAVGPGGYAVVVCIGQIVLLK DQRKCFSI\DNPGYEPEVVAVH PGG\DTVAIGGVDGNVALYSIL GTTL\KDEGKLLEAKGPVTDVA YSH\DGAFLAVCDASKVVTVFS VADGYSENNVFYGHHAKIVCL AWSPDNEHFASGGMDMMVYV WTLSDPETRVKIQDAHRLHHVS SLAWLDEHTLVTTSHDASVKE
16836	47204	A	16940	31	449	
16837	47205	A	16941	1	53	
16838	47206	A	16942	1	389	GMPTSTIASCSQDGRVFIWTCD DASSNTWSPKLLHKFNDVVWH VSWSITANILAVSGGDNKVTEG QQNEQ*QDRWGLAPHPPAPGL PLPGPTNQTTGKSPQLQQDYFP RRSYRCSHRLIICLNVIGNAL
16839	47207	A	16943	1	438	
16840	47208	B	16944	1	1267	
16841	47209	A	16945	635	808	

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16842	47210	A	16946	37	1319	QGEGHGRGLHGFLGRPESQIPS WSRSAPLHRLEIWGALAPSLAD HSEGSPEVSVINTVDTSHEYMI Y\DAQMDYYGHPPGQPASSDRS VKIF*CAQWEGRSLFADLQGS WRGPVWQVGWGFTPLLRATS WAFVASLLTGKFIYSWERGKT GTLGRRATSNAGTRLLKLNFGC CWAPHGLTVLHSWACWVVSD RGPSSL\LDFTPGEGQWEVKKIN NAHTIGCNAV\TWAPACCTWK PHRRPHRGQKPNYIKRFASGGC \DNLI\KLWKEEEDGQWKEEQK LE\GHSDWV\RDVAWAPSIGPA HQHHRPAAPRMGRVSIWTCDD ASSNTWSP*IV\DKFNDVVWHV S\WSITANILAVL\CGDNK\VPL WKESS*WAKWVVPSSDVKQRG PGLPYQPSSDQEGPARNEQVNK DQGGALAPPPAQLPGPAPSPGP
16843	47211	A	16947	1	1021	MSGEFIDHSHIARIIYPGIFGTDA GSCIDQRGITGKLQQPPEDRRL GEGKLTNTKDIHTKTPSVRHHH QRPKVDKTTKIGKKQSRKTGNS KNQSAPPPPKECSSSPAMEQSW TENDFDELREEGFRRSNYSELK EEFRTHGKEVKNLEKRLDEWL TRITNAEKSLKDLMELKTKARG LQRVSVMEDEMNEMKQEEKFR EKRIKRNKQSLQEIWDYVKRPN LRLIGVPESDGENGTKLENTLQ DIIQESFPNLARQANIQIQEIQR MPQRDSLRRATPRHIIVRFTKV EMKEKMLRAAREKA\HIALIPK LTT*LEVKLSSANVKEQKL*QT VFQTTVQSN
16844	47212	A	16948	1	393	
16845	47213	A	16949	1	2631	
16846	47214	A	16950	1	1155	
16847	47215	A	16951	1	1185	
16848	47216	A	16952	1	942	
16849	47217	A	16953	1	615	

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16850	47218	A	16954	474	2678	IKPQRWGKKQSRKTGNSKNQS ASPPPKERSSSPAMEQSWTEND FDELREDSFRRLVITNYSELKEE VRTNGKEVKNLEKKLDEWLTR ITNAEKSLKDLMELKTMAQELP DQCTSLSSRCDQLEERVSVMED EMNEMKCEEKFREKRIKRNEQ SLQEIWHYVKRPNLRLIGVPES DGENGTKLENTLQDIIQENFPN LARQANIQIQEIQRMPQRYSSR RATPRHIIVRFTKVEMKEKMLR VAREKGQVTHKGKPI\RLTADL LAETLQARREWG\PIFNILKEKN FQPRISYPAKLSFIDRSTRQKVN KDTQELNSALHQADLIDIYRTL HPKSTEYTFFSAPHHTYSKIDHI VGSKALLSKCKRTEIITNCLSDH SAIKLELRIKKLTRNHSTTWKL NNLLLNDYWVHNEMKAEIKM FFETNENKDKTYQNLWDTFKT VCRGKFIALNAHKRKQERSKID TLTSQLKGLEKQEQTHSKASRR QEITKIRAELKERVGRWRIGEA ADLVGVSSQAIRDAEKAGRLPH PDMEIRGRVEQRVGYTIEQINH MRDVFGTRLRRAEDVFPPVIGV AAHKGGVYKTSVSVHLAQDLA LKGLRVLLVEGNDPQGTASMY HGWVPDLHIHAEDTLLPFYLGE KDDVTYAIKPTCWPGLDIIPSCL ALHRIETELMGKFDEGKLPTDP HLMLRLAIETVAHDYDVIVIDS
16851	47219	A	16955	1	675	
16852	47220	A	16956	1	1032	
16853	47221	A	16957	3	978	HEAKHQMADDAGGSGGGPKA LVGPGMG\NPVAFRRGF\GIVIR GPGSRPGGRGRGR\GRGARGSK \AEDKDW\MPVTKLG/RALVKD H*RSKFPWKEIYLFSLPH*RNQR IIDF\FLGGLLSKDEGFE*LCPVQ EQDPCPASRTQASRPFVAIGGL QMAHVGLGC*VLPRKVATGHP VGAIILAKLS\IVPVRR\GYLGNK VLAKP\HTVP\CKV\TGRCGSVL VRLIPAP\RGLGMVSAPVA\KKL LMMAGIDDCYT\SARG\CTATL GQIWPRATL*LPFLRTYKLP*PP DLWKGRLYLPSFPIKEFT\DHLV KDPHPESSVQQDSELQLVATT
16854	47222	B	16958	124	274	

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16855	47223	A	16959	202	2264	KWPKMNPQQQRMAAIGTDKE LSDLLDFSAMFSPPVNSGKTRP TTLGSSQFSGSGIDERG\GTTSW GTSGQPSP\SYDSSRGFTDSPHY SDHLNDSRLGAHEGLSPTPFMN SNLMGKTSERGSFSLYSRDTGL PGCQSSLLRQDLGLGSPAQLSS SGKPGTAYYSFSATSSRRRPLH DSAALDPLQAKKVRKVPPGLPS SVYAPSPNSDDFNRESPSYPSPK PPTSMFASTFFMQDGTHNSSDL WSSSNGMSQPGFGGILGTSTSH MSQSSSYGNLHSHDRLSYPPHS VSPTDINTSLPPMSSFHRGSTSS SPYVAASHTPPINGSDSILGTRG NAAGSSQTGDALGKALASIYSP DHTSSSFPSNPSTPVGSPSPLTG TSQWPRPGGQAPSSPSYENSLH SLQSRMEDRLDRLDDAIHVLRN HAVGPSTSLPAGHSDIHSLLGPS HNAPIGSLNSNYGGSSLVASSR SASMVGTHREDSVSLNGNHSV LSSTVTTSSTDLNHKTQENYRG GLQSQSGTVVTTEIKTENKEKD ENLHEPPSSDDMKSDDESSQKD IKVSSRGRTSSTNEDEDLNPEQ KIEREKERRMANNARERLRVR DINEAFKELGRMCQLHLKSEKP QTKLLILHQAVAVILSLEQQVR ERNLNPKAACLKRREEEKVSA VSAEPPTTLPGTHPGLSETTNP
16856	47224	A	16960	1190	1327	
16857	47225	A	16961	386	554	ATISFRYSQCK*AEQGCDSELG LFTKIRKSGYWGV*ATISFRYSQ CKALEIHLTAPVVPSALRIWGF QIPGFNQLSFHPSPESKGSFLPC
16858	47226	B	16962	499	915	
16859	47227	A	16963	1	1785	
16860	47228	A	16964	1	3036	
16861	47229	A	16965	2	710	
16862	47230	A	16966	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGGLHDLKIVVL
16863	47231	A	16967	1	1335	
16864	47232	A	16968	83	426	
16865	47233	A	16969	93	345	APALCLQILLDCKSVRNRTSRF RPREVGIQQYKKGGGAAGKGG TGNAPGFLLFSKDS*KDPTPLPP PLLL*GQRDH*IQLHQE
16866	47234	A	16970	1	1302	
16867	47235	A	16971	1	1174	
16868	47236	A	16972	274	1428	

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16869	47237	A	16973	411	629	HCLSHFQNTGPRGDVDFQQEL\ FPVLMADIRKEERSHLCRSSRR TWTILDKS*IQGSRLSSKEQGW GWGTSRK
16870	47238	A	16974	618	1552	
16871	47239	A	16975	1	558	
16872	47240	A	16976	1	765	
16873	47241	A	16977	2	418	
16874	47242	A	16978	130	1965	
16875	47243	A	16979	1	1062	
16876	47244	A	16980	1	558	
16877	47245	A	16981	37	676	
16878	47246	A	16982	1	1014	
16879	47247	A	16983	1	2964	
16880	47248	B	16984	259	1751	
16881	47249	A	16985	1	987	
16882	47250	A	16986	1	1047	
16883	47251	A	16987	3	1413	GLHAARGPWVVQAWISITM\ER KEVCYGQLGCFSDEKPWAGTL QRPVKLLPWSPEDIDTRFLLYT NENPNNFQLITGTEPDTIEASNF QLDRKTRFIIHGFLDKAEDSWP SDMCKKMFEVEKVNCICVDWR HGSRAMYTQAVQNIRVVGAET AFLIQALSVKPCLGPVLWVGVR EGQGDAARGTALEDVHVIAHS LGAHT/AAEAGRSWGPRGRITD DLGTA*YKVDGMG*ERRGVRF SI*P*GGGV*AGFGGERFR*RKN VGKSTAGWRM\GLDPAGPCFQ DEPEEVRLDPSDAVFVDVIHTD SSPIVPSLGFGMSQKVGHLDFFP NGGKEMPGCKKNVLSTITDIDG IWEGIGGFVSCNHLRSFEYYSSS VLNPDGFLGYPCASYDEFQESK CFPCPAEGCPKMGHYADQFKG KTSAVEQTFFLNTGESGNFTSW RYKVSVTLSGKEKVNGYIRIAL YGSNENSKQYEIFK
16884	47252	B	16988	95	315	
16885	47253	C	16989	1	780	

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16886	47254	A	16990	2	1426	SGTLDRMLIFWTITLFLLGAAK GKEVCYEDLGCFSDTEPWGGT AIRPLKILPWSPEKIGTRFLLYT NENPNNFQILLLSDPSTIEASNF QMDRKTRFIIHGFIDKGDESWV TDMCKKLFEVEEVNCIFV\DWK KGSQATYTQAANNVRVVGAQ VAQMLDILLTEYSYPPSKVHLI GHSLGAHVAGEAGSKTPGLSK/ RLQGLDPVEASFESTPEEVRL\D PSDADFVDVIHTDAAPLIPFLGF GTNQQMGHLDFFPNGGESMPG CKKNALSQIVDLDGIWAGTRDF VACNHLRSYKYYLESILNPDGF AAYPCTSYKSFESDKCFPCPDQ GCPQMGHYADKFAGRTSEEQQ KFFLNTGEASNFARWRYGVSIT LSGRTATGQIKVALFGNKGNTH QYSIFRGILKPGSTHSYEFDAKL DVGTIEKVKFLWNNNVINPTLP KVGATKITVQKGEEKTVYNFCS EDTVREDTLLTLTPC
16887	47255	A	16991	1	1407	
16888	47256	A	16992	954	1663	EPSPDPAHAPSVALLHTGNQSK VLPWPRNPCMKRW*K*KMLKI SWVHEWVTSNWISTAVRSLRV FAPKNVFQ**ALGPSGWLVYC
16889	47257	A	16993	3	242	
16890	47258	A	16994	1	1815	
16891	47259	A	16995	1	375	
16892	47260	A	16996	3	2005	
16893	47261	A	16997	1	651	
16894	47262	A	16998	114	275	
16895	47263	A	16999	1	270	
16896	47264	A	17000	140	876	PPALVVGRRQKSWRMFEQMRA NVGKLLKGIDR\YNPENLATLE R\YVETQAKENAYDLEPNLAVP ESCTKFNP\AFFQTNGSTAQDSC *KALTN\LPHT\DFTL\CKC\MIRP GHIQE\ERPIPTDFCYLGGPGWE TWPFSRAFWESPGMKTVDLLW KV*LGF\EDSV\RKFI\CHVVG\IT YQHIDR\WLLAEMLGDLFGQAS *RCW\MSKYGWSADESGQIFIC SPRREHLTPRNIVEKIDFDSVSSI MASSQ

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16897	47265	A	17001	1	777	MSGENVTKVSTFILVGLPTAPG LQYLLFLLFLLTYLFVLVENLAI ILIVWSSTSLHRPMYYFLSSMSF LEIWYVSDITPKMLEGFLLQQK RISFVGCMTQLYFFSSLVCTEC VLLASMGYDRYVAICHPLRY\N LACTDFSTAELV/SFILAFIILVFP LLATILSYWHITLAVLRIPSATG CWRAFSTCASHLTVVTVFYTA LLFMYVRPQAIDSQSSNKLISA VYTVVTPIINPLIYCLRNKEFKD ALKKALGLGQTSH
16898	47266	A	17002	2	876	
16899	47267	A	17003	1	894	
16900	47268	A	17004	377	501	
16901	47269	A	17005	3	823	
16902	47270	A	17006	1	874	
16903	47271	C	17007	156	287	
16904	47272	A	17008	1	1140	
16905	47273	A	17009	1299	3135	ISGSVCILLWLQLLPAYNLIIHT WEHRHSPPGT/RMSRLAKRNA WEADR/YAEAKLAASRRGQPSS LMSSREGGWGEGSQSRNSSHG ALKEAQFIITNAEKSLKDLMEL KTMAQELRDECTSLSSRFDQLE EKVSVMEDEINEMKQEEKVRE KRIKRNEQSLQEIWDYVKRPNL HLIGVPESDRENGTKLENTLQDI IQENFPNLARQANIQIQEIQRMP QRYSSRRATPRHIIVRFTKVEM KEKMLRAAREKEIQTTIREYYK HLYTNKLENLEEMDKFLDTYS LPRLNQEEVESLKRPITGSEIGAI INSLPTKKSPGPDGFTAEFYQRY KKELVPFLLKLFQSTEKERILPN SFYEASIILIPKPGRDTTKKENFR PISLMNINAKILNKILANQIQQHI EKLIHHDQVGFIPGMQGWFNIR KSINVIQHINRTNEKNHMIISIDA EKAFDKIQQPFMLKTLNKLGID GTYLKIVRAIYDKLTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIRQEKEIKGIQLG KEQVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIK
16906	47274	C	17010	189	457	
16907	47275	A	17011	2	2600	
16908	47276	A	17012	107	1493	

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16909	47277	A	17013	3	2209	IHTKTPSVCHHHQRPKVDKTTK MGKKQSRNTGNSKNQSTSPPP KECSSAPAMEQSWMENDFDEL REEGFRRSNFSELTEEVRTHRK EAKNLEKKIRQM\VTRITNVEK SLNDLMELKNMARELRDKCTS FSSRFDQLEERVSVIEDQMNEM KQEEKFREKRVK\RNEQSLQEIR DYVKRP\NLRLIGIPESDEENGT KLENTLQDII\QENFPNLARQAN IQIKEIQRMPQRYSSRRATPRQI\ IVRFTEVEMREK\MLRAAREKG RVTHKGKTIRLTVDLSAETIQA RRESTRQKVNKDIQELNSAQHQ ADLTDNYRTLHPKSTEYTLFSA PHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELRIKKL TQNLSTTWKLNNLLLNDYWVH NEMKAEIKMLFETNENKDTTY QNLWDTFKAVCRGKYIALNAH KRKQERSKIDTLTSQLKELEKQ EQSHSKASRRQEITKIRAELKEI ETQKTLQKINESRDWFFEKINKI DRQLARLIKKKREKNQIDTIKN VLEFLAKAIRQDKEIKGIQLGKE EVKLFLFAEDMIVYLENPIVSA QNLLKLISNFSKVSGYKINVQK SQAFLYTNNRQTESQIMSELPFT IASKRIKYLGIQLTRDMKDLFK ENYKPLLNKIKEDTKKWKNIPC SWVGRINIMKMAILPKVIYRFN AIPIKLPMTFFTELEKTTLKFTW
16910	47278	A	17014	292	699	
16911	47279	A	17015	269	803	ALGPCSEALPTWVNENGEEMA QEIDLSALKELEREAILQVLYRD QAVQNTEEERTRAAGN*KHTC SISGGKGPKNTDWEHKEKCCA RCQQVLGFLLHRGAVCRGCSH RVCAQCRVFLRGTHAWKCTVC FEDRNVKIKTGEWFYEERAKKF PTGDNSV\RTSCTGKHETVGGQ LLQSYQK
16912	47280	A	17016	1	1173	
16913	47281	A	17017	349	718	AGPEGTTTAECP/I/CQQQRPILS LRYGTISWG/DQSATWWQVDY IRTLLSWKWQSASAKTTIHGLT KCLIHHDIPHSIASD*GTCFMAK EVWQWYCFSHSQDSRVQESRG GIGSCTTHHHPCSFPN

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16914	47282	A	17018	196	577	GSSGQSESAQPQGLWVLPSRTS LAILSTDVNV*QPCFPAGAHQG QPLAWPVPFLAWLSWQQKRC* KQQRSSRNLVDHRNPGWLHEE GDKTPFFHHPFPQLGQSLSQQS LLPAGRR*ARGPQQLPSPP
16915	47283	A	17019	1	2523	
16916	47284	A	17020	236	558	
16917	47285	A	17021	1610	2004	VTWSAQQMPWAIKNCPTHSPL GQGCLPQPKM*VVQNDFQ*G* WTHCRKGIKGGQRVGVWPWQ TQNRGKGTFLTPLHSAVADAM LYAL*RGSDLDAAQTLPTAAQ DALYAVVPGGEPTGQLQVRHN EFALGQ
16918	47286	A	17022	1	735	
16919	47287	A	17023	88	1871	
16920	47288	A	17024	1	1299	
16921	47289	A	17025	2	260	
16922	47290	A	17026	144	1737	
16923	47291	A	17027	1	1182	
16924	47292	A	17028	262	1132	
16925	47293	A	17029	1	484	
16926	47294	A	17030	3	382	LKGAPDLELDGESRRTWRERK GRKRKERALGRWQV*RSRCA* P/STPAALNAPLQGASHSPFRLR NCWKGRSVRASSLLRQLAKGG CAARRLSWNLCQIVQMYEGHS QQPGLQPRLQRWSSQTLRTA
16927	47295	A	17031	1	2022	
16928	47296	A	17032	209	403	
16929	47297	A	17033	213	1993	
16930	47298	A	17034	1	378	
16931	47299	A	17035	64	1180	SASHSGAPATSLYERGVCPPAL RRPPAVLVCRAAASCTLLAMS DLQEEGKNAINSPMSPALVDVH PEDTQLEENEERTMIDPTSKEDP KFKELGKVLLDWINDVLAEERI IVKQ\LEEDLYDGQVLQKLF/EK NLAGLQSLNVAEVTQSEIGQKQ KLQKVLEQLH\DLLRPRSWALR \WLGNSIHGKNLVGNPQLLVSL AMHFRAPIRLPEHVTVQVVVV RKREGLLHSSHISEELTTTTEM MMGRFERDAFDTLFDHAPDKL SVVKKSLITFVNKHLNKLNLEV TELETQFADGVYLVLLMGLLE DYFVPLHHFYLTPESFDQKVHN VSFAFELMLGRRPSRNPRLVLK TWLTWDLKSPLRVLYNLFTKY
16932	47300	A	17036	3	764	

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16933	47301	A	17037	1	1230	
16934	47302	A	17038	1	313	
16935	47303	A	17039	145	263	IFLLYLKNKVQNK*EIKQHFLG KIMSRDNNTYLTWGTEN
16936	47304	A	17040	5	982	PTFSRAVATMFSRAGVAGLSA WTLQPQWIQVRNMATLKDITR RLKSIKNIQKITKSMKMVAAAK YARAERELKPARIYGLGSLALY EKADIKGPEDKKKHLLIGVSSD RGLCGAIHSSIAKQMKSEVATL TAAGKEVMLVGIGDKIRGILYR THSDQFLVAFKEVGRKPPTFGD ASVIALELLNSGYEFDEGSIIFN KFRSVISYRTEEKP\IFSLNT\VAS ADQHGVSMTDIDADVAAKITQ EY/NIWANIILLTLWKESTTSGG RSARG*QPWDNGQARIAFWRM DLDNLDIWTF\NR\TRQAVITKE LIEIISGAASSVKKENSAS
16937	47305	A	17041	1334	1790	
16938	47306	A	17042	1	930	
16939	47307	A	17043	2	477	SGLGRLPGPWQEAGSSRGPSSG DMAGVKALVALSFSGAIGLTF/ LHMLGCALEDYGVYWPLFVLI F\HAISSIPHFIAKRVTYDSDAT\S SACRELAYFFTTGIVVSCLWISP VILARVALIK\WGACGL\VLA\G NAVIFPYNSRGFSLYLGRGDDF SW\EQW
16940	47308	A	17044	130	434	
16941	47309	A	17045	1	1365	
16942	47310	A	17046	656	839	
16943	47311	B	17047	16	149	

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16944	47312	A	17048	1	1317	MTLNEHAAFKHLFNKAHLAPP LIHLTLSGHSTCFREHRVGVICS HFAQDLWPEQGREDSFQKVILR RYEKCGHENLQLKIGCTNVDES LTYKRIHTGEKPCKCEECDKAF SKFSILTKHKVIHTGEKHYKCE ECGKAFTRSSSLIEHKRSHAGE KPYKCEECGKAFSKASTLTAHK TIHAGEKPYKCEECGKAFNRSS NLMEHKRIHTGEKPCKCEECG KAFGNFSTLTKHKVIHTGEKPY KCEECGKAFSWPSSLTEHKRIH AGDKPYKCEECGKTFKWSSTL TKHKIIHTGEKPYKCEECGKAF TTFSSLTKHKVIHTGEKHYKCE ECGKVFSWSSSLTTHKAIHAGE KLYKCEECGKAFKWSSRLSEH KRIHTGEKPYKCEECGKAFSW VSVLNKHKKIHAGKKFYKCEE CGKDFNQSSHLTTHKRIHTG\E KPYKCEECGKAFSKASTLTAHK TIHAGEKPYKCEECGKAFNRSS NLMEHKRIHTGEKPCKCEECG KAFGNFSTLTKHKVIHTGEKPY KCEECGKAFSWPSSLTEHKRIH AGDKPYKCEECGKTFKWSSTL TKHKIIHTGEKPYKCEECGKAF TTFSSLTKHKVIHTGEKHYKCE ECGKVFSWSSSLTTHKAIHAGE KLYKCEECGKAFKWSSRLSEH KRIHTGEKPYKCEECGKAFSW VSVLNKHKKIHAGKKFYKCEE
16945	47313	A	17049	2	2183	

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16946	47314	A	17050	3	1440	IKVLLGENRVPNTMAVWLAQ WLGKGASLTSFPPCPTASLLRR LGEHIQQFQESSAQGLGLSLGP GAAALPKVGWLEQLLDPFNVS DRRSHL\QRYWVNDQHWVGQ DGPIFLHLHLTSPPPTHTLFTGH PAALAPAWGALVISLEHRFYGL SIPAGGRLALSRLFNISSSSPWIC FGGSYAGSLPSHHAPTF\PRAQR IS*HFRIPSSAVRPQVVSRSLMS TAIGGSLE/CRRWGLVRGGLGG KRGLGCQGRGGPA*VLADIASC FPQCRAAVSVAFAEVERRLRSG GAAQAALRTELSACGPLGRAE NQAELLGALQALVGGVVQYD GQTGAPLSVRQLCGLLLGGGG NRRGGIYVLCMYIVP*IVLHSLG QKCLSFSRAETVAQLRSTEPQL SGVGEAPIYLAPSYPFFPGDTDP WHVLSVTQALGSSESTLLIRTG SHCLDMAPERPSDSPSLRLGRQ NIFQQLQTWLKLAKESQIKGEV
16947	47315	B	17051	41	2709	
16948	47316	A	17052	874	1024	
16949	47317	A	17053	1	1602	MDSLWGPGAGSHPFGVHNSRL SPDLCPGKIVLRALKESGAGMP EQDKDPRVQENPGDQRRVPEV TGDAPSAFRPLRDNGGLSPFVP GPGPLQTDLHAQRSEIRYDQSS QTSWTSSCTNRNAISSSYSSTGG LPGLKRRRGPASSHCQLTLSSS KTVSEDRPQAVSSGHTQCEKV AEKAPGQTLALRNDSSRSEASR PSTRKFPLLPHRRGEPLMLPPPV ELGYRVTAEDLDWEKEAAFQC IKSALQVEDKAISDCRPSRPSHT LSSLATGAS\DSAQVTSLIPAPFP AASMDAGMRRTRPGTSAPAAA AAAPPPSTLNRTLGSLLEWMEA LHISGPQPQLQQVPRGQNQRSQ TSRTSSCPK/LKCHLELLQLYGR PPGTKAEEAPASSHCQLTLSSSN TVSEDGPEAVSSGHTQCEKTAD TAPGQTLGPRGGSPRSQSSRPR RHKFPLLPRRRGEPLMLPPPLEL GYWVTAEDLDREKEAAFQRIN SALQVEDKAISDCRPSRPSHTLS SLATGASGLPAISKAPSMDAQQ ERHKS
16950	47318	A	17054	1	1155	

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16951	47319	A	17055	1	1237	MDSLWGPGAGSHPFGVHNTRL SPDLCPGKIVLRALKESGAGMP EQDKDPRVQENPGDQRRVPEV TGDAPSAFRPLRDNRGLSPFVP GPGPLQTDLHAQRSEIRYNQTS QISWTSSCTNRNAISSSYSSMGG LPGLKRRRGPASSHCQLTLSSS KTVSEDRPQAVSSGHTQCEKA ADIAPGQTLALRNDSSTSEASRP STHKFPLLPRRRGEPLML\PPSL EVGVPGSLVKELDREKEAAF\Q RINSALQVEDKAISDCRPSWPS HTLSSLATGTSGLPAISKAPSMD AQQETHKSQDCLGLLAPLASA AGVPSTAPMSGKKHRPPGPLFS SSDPLPATSSHSQDSAQVTSLIP APFPAASMDVGMRRTRRGEPL MLPPPLELGYRVTAEDLDQEKE AAFQRIKSALQVEDKAI
16952	47320	A	17056	132	835	
16953	47321	A	17057	1	2947	MPEQDKDPRVQENPDDQRRVP KVTGDARSAFRPLRDNGVLSPF VPRPGPLQTYLHAQRSEIRYNQ TSQNTWTSSCTNQNAISSSYSS VGGLLGLKWRRGPAGQESGAG MPEQDK\DPRV\QQNPDDHRTV PEVTGDARSAFWPLRDNGGLSP FVPRPGPLQTDLHAQSSEIRYN QTSQTSWTSSSTKRNAISSSYSS TGGLPGLKQRRGPASSRCQLTL SYSKTVSEDRPQAVSSGHTRCE KAADTAPGQTLAPR
16954	47322	C	17058	229	624	
16955	47323	A	17059	1	1011	MVSTPATLPSLPKPALMASWG VPYDQLTKEEKTRVWFTDGSA RYAGTTQKWTAVALQPLSRTS LKDSSEGKSSQWAELQAVYLV VHFAWKEKWPDVGLYTDSWA VANGLAGWSETWEKQDWKIG DKEIWGRGMWMDLSEWSKAV KIFVSHVSAHQRVTSAEEEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYSWAQQT\GLPFTKADL AMATAECPICQQQRPTLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFVLTVIDTYSRYRFAY PAHNASAKTTIHGLIECLIHCYG IPHSIASDQSIHF/TTKEVQ*WAH AHGIHWSYHVSHHPEAAGL
16956	47324	B	17060	10	597	
16957	47325	B	17061	6	297	

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16958	47326	B	17062	1	474	
16959	47327	A	17063	1	2712	
16960	47328	B	17064	1	738	
16961	47329	A	17065	3	772	DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLTM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWRWYIHYQA QAGPEGTSNLHEEVAQMPTVS TSATLPSLPEPTQMAL\WEVPY D\QFTEEEKTGAWFTDGSAHYT GTT*KWTVAALQPLSRTTLKDS CEGKSPHHPVIAQWAHEQSGH GGRDGGYLWAQQHGFPLTKA DLAMATAECPICQQQKRTLNP
16962	47330	A	17067	1667	2012	LSPHWPPGLPPSALIYAFLGRSS RNKRRLMKTMKVEACEDLSAP KYLRIQLPTGSPRRRSEAPEVCI FQGSS\FSLVHPPPLLSYPSARR* PQTPPRPPPRHPSLHPLHPPSAQ
16963	47331	A	17068	5	1074	RHSALGTGGSSSCRQQRPRDT WVPETTILTAWSS/RLQQLGPW LQVTVAGQVNTLAGIQKTIHAE HCNVTE\RPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCGYQL STAINRNQELCGRKPAVSPSR/G ISPGSPILRPAVHPGHYCLQQRL SGQKSNRRTTQKSFQKLHVDK RKPENFSKESDHLLIYSREGNPD VASLATPPGIWMMSATDLFYG DPFAFPGGGPFTLSLERGPSVIL GTDASEELLFTKASLAVSTSVF QFSTGKIYTEWVWQKNKSFLSP HFPTKPMASPVKGKHSTSLLQR LNYRDRWQCLQEGAGLALLSA HMKVPTGSKEPQQAGKLPSKP RKQTTPTFKD
16964	47332	A	17069	2	699	CSACPVSHPWLLPWQSGSAFSL P*RALQRPPQHGHRLSKPMQSP RLSVLLRPWPRRPLPTDLLY*PS TRGHIHLHDRHHGAPSVSRRW GDKASPPQFPRYSRDSK/RRPPQ HGEVGTVFTNNKGGQS/PATST WEVQSAECQKAPEAGPTPPSTA GDAEGANALRQESEGNWGSEA KSPHVAEAGSWRPQQGSCHHL HPPDKTKDAARKTHSPGDNGC QPRPPRPCKTLWSLSRI
16965	47333	A	17070	223	1611	
16966	47334	A	17071	12	310	

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16967	47335	A	17072	31	430	LQAVRLFTLPTTSSGL*KLRTVP TWPSPPSCFPHFQSGPRTTRAPT PSTI\PGYSGSYSSGPPSLCPRTS RRAPPRHRVPAGRERLHIRVPP YPRPERHLLRVSRRGILGNNRV GRLPESRAIAGRKEEKTDTK
16968	47336	A	17073	1	474	
16969	47337	A	17074	153	1224	RVFSESVCSPVRNLEFLWRFAF PLAPAGRCPPGVPLQTSPRDTD AHRSSPLPPARASPGQVAAAYR WARCPGCGGRKPRSSGSWQLC RCPTLPPPPRGSRSSGRC/RTWP SPPSCFPHFQSGPRTTRAPTPSTI\ PGYSGSYSSGPGR*GLSPLHAA/ VSPPLPPGGP*GSWARAGLGSI ASAHSPCPLCRSLIRSRS*QTCT RSPT*NCEVPPSAP*AASPLRTM FALVRTAGLKVHLLPLGYCTT MS*SSSMPQTVPVVVKVSNIPS VHPP*PCCKDCTISRSRSIFTRSPI CNPPGFLLPFCSPSTGQ*SL*KEP PLASWTHFRSDVLLLFSVSMNG STLSLGCPSQKAVIALVQVT
16970	47338	A	17075	215	1246	
16971	47339	A	17076	566	675	QPCRQQ/CLQPGSPPRFHARTLT VTLVHTRTHTHAHAH
16972	47340	A	17077	184	584	
16973	47341	A	17078	1	1167	
16974	47342	A	17079	849	2266	
16975	47343	A	17080	1505	1891	DAEKAFDEIQQ/PFMIKILSRISI QGTYLNVIKTIYDKPTANTILN VEKLKTFPLRTGTRQGCPLSAL LFNMVLEVIARAIRQEKGIKGIQ ISKKEVKLSLFADDMIVHIENPK DSSRKLLELIKEFSKV
16976	47344	A	17081	1	842	
16977	47345	A	17082	155	531	GNLWSVDLRPGTPLRQNFRGTI RQQHSRFTKNHCSQTPLLIPRQ TGSGVDLSKLQQTCS*GSCLVC TIDLANAFFSIPVHKA/HQKQFA FSWQ\YTFTVLPRLTWLQPC*V PNLPAAETNTEPSNGT
16978	47346	A	17083	1	1773	
16979	47347	B	17084	598	1428	
16980	47348	A	17085	3	227	
16981	47349	A	17086	1	207	

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16982	47350	A	17087	1	789	RDLQPFTSVTVHCRKGNDQTF GGPLDAGSELTLIPGDPKHHCG PPVKVGAYGGQVINGVLA\HPL IWLVQKTDGS/WRMTVDYCKL NQVVIPIAAAVSDVVSLLEQINT SPGTWYAAIDLANAFFSIPVHK AQQKQFAFSWQGQQYTFTVLP QWYINSPALCHNLIRRDLDCFS LPLDITLVHYIDDIMLIGSSEQE VANTLDLFVRHLRARGWEINPT KIQGPSTSVKFLGFQWCGACQA IPSKMRDKLLHLVPPTTKKEAQ
16983	47351	A	17088	1	435	
16984	47352	A	17089	2	808	PLIWLVQKTDGS/WRMTVDYC KLNQVVIPIAAAVSDVVSLLEQI NTSPGTWYAAIDLANAFFSIPV HKAQQKQFAFSWQGQQYTFTV LPQWYINSPALCHNLIRRDLDC FSLPLDITLVHYIDDIMLIGSSEQ EVANTLDLFVRHLRARGWEINP TKIQGPSTSVKFLGFQWCGACQ AIPSKMRDKLLHLVPPTTKKEA QCL\QLLACY/WALVETEHLTIS HQVTMRPELPIMNWVLFDPSSH KVGCAQQHSIIKWKWYVHDW ARAGPEGT
16985	47353	A	17090	2	544	
16986	47354	A	17091	1	633	MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAF\LPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTLDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLPWEQVPSS GDIKEYFPNAFVLLTTASLQGQ DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
16987	47355	A	17092	1	3228	MVTSSLTVAITSLVVVITSLVVII TSFVVVTTSLVVVITSLVVVITSI AIAIATLVVVLTFTVVVLTSLV VVTTSLVMVITPPFAVITSLGVV ITSLVVIITCLVLVITALGVVITS LGVVVTSLVMVITPLVAVITPL GVVITSLVVVITSLVMVITSLTV VITSSIVVITPLVMVITSLTVIITS LFVVITPLVMVITFLIVVNTSLV VVLITLIVSPPPSLCSLVVVITFL VVAITSLVVVITSLVVVITSL
16988	47356	A	17093	1	471	
16989	47357	A	17094	1	1590	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16990	47358	A	17095	332	1704	RGYVFCSWKKTDGS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQGQQYTF TVLPQWYINSPALCHNLIRRDL DCFSLPLDITLVHYIDDIMLIG\P RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVLFDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTTPVISQWPHEQCGHG GRDGGYAWAQQCRLPLTKAD LNTATAKRPICQQQRPTLSPQY GTIPQGDQPATWWWVDYMGS LPSWKGQRFVLTGIDTYSGYGF AYPACNASAKTAICGLTECLIH HHDIPHSIASDQGTHFMAKEVR QWAHDHGIHWSYHVSHHPEA AGLIEWWNGLLKSQLQCQLGD NTWQGWGKVLQKVVYALNQH PIYGTVSPIAKIHRRVADSLKGG SGSWVWGFSTLAALDNDLGTF RKVRAPSTN
16991	47359	B	17096	1	2061	
16992	47360	A	17097	1	1623	
16993	47361	A	17098	1	741	
16994	47362	A	17099	213	679	
16995	47363	A	17100	33	853	
16996	47364	A	17101	3	1249	
16997	47365	A	17102	17	770	
16998	47366	A	17103	130	469	
16999	47367	A	17104	1	1425	
17000	47368	A	17105	1	882	

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17001	47369	A	17106	227	1519	VTLIKMNAMLETPTLS\AVSDG VKLSAVAAVLYVIVRCMNLKS ATAAPDLYLQDSGLSRFLLKSC PLLTKEYIPPLIWGKSGHIQTAL YGKMGRVRSPHPYGHRKFITM SDGATSTFDLFEPLAEHCVGDD ITMVICPGIANHSEKQYIRTFVD YAQKNGYRCAVLNHLGALPNI ELTSPRMFTYGCTWEFGAMVN YIKKTYPLTQLVVVGFSLGGNI VCKYLGETQANQEKVLCCVSV CQGYSALRAQETFMQWDQCRR FYNFLMADNMKKIILSHRQALF GDHVKKPQSLEDTDLSRLYTAT SLMQIDDNVMRKFHGYNSLKE YYEEESCMRYLHRIYVPLMLV NAADDPLVHESLLTIPKSLSEKR ENVMFVLPLHGGHLGFFEGSVL FPEPLTWMDKLVVEYANAICQ WERNKLQCSDTEQVEADLE
17002	47370	A	17107	21	385	SRSSSVVRQEPGRADGQRRRRR GGPGLRSPGERQQPRPARPCRR AHHPGDPAGAQ/PPPKTGKTCG APKATTRSTRCSISR*PPFPRSSC PTSPRATPSSSASSTAAMRRWL VTCRMPNWRA
17003	47371	A	17108	158	423	
17004	47372	A	17109	1	1851	
17005	47373	A	17110	1	1104	
17006	47374	A	17111	66	432	
17007	47375	A	17112	103	3531	
17008	47376	A	17113	1	1311	
17009	47377	A	17114	1	750	
17010	47378	A	17115	183	373	QPQATTLVHPVHVA*LF*VHW QNRYRAPDNQGYRHWRCLLPA LPDAGR/VRLSASC*KPPNSRG
17011	47379	A	17116	344	480	SPKDQEPSISKKV***TSLPTSSR SLCLPPARMHFWVLAALLSFA
17012	47380	A	17117	3	3565	HEARRGLKMAACGRVRRMFRL SAALHLLLLFAAGA\RNSPARA SHSQGQGPGANFVSFVGQAGG GGPAGQQLPQLPQSSQLQQQQ QQQQQQQQPQPPQPPFPAGGPP ARRGGAGAGGGWKLAEEESCR EDVTRVCPKHTWSNNLAVLEC LQDVREPENEISSDCNHLLWNY KLNLTTDPKFESVAREVCKSTIT EIKECADEPVGKGYMVSCLVD HRGNITEYQCHQYITKMTAIIFS DYRLICGFMDDCKNDIN

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17013	47381	A	17118	1	495	PDRRRGCPALSGS*SGPAPRL/C LCNPTLTFHPGSVIGVCL*RHW LCRANTRHPSYRGRLSSR
17014	47382	A	17119	1	1479	
17015	47383	B	17120	67	8652	
17016	47384	B	17121	67	9183	
17017	47385	A	17122	1	1440	
17018	47386	A	17123	1	422	FRWKELLDRPLEPSPETAQPPPP WLQK/NPTAVERANLLNMAKL SIKGLIESALSFGRTLDSDYPPL QQFFVVMEHCLKHGLKVRKSF LSYNKTIWGPLELVEKLYPEAE EIGASVRDLPGLNEFYEYHALM MEEEGAVIVG
17019	47387	A	17124	2	587	WMGSCGLHRAWLQMRWWPE SAWKELLDRPREPPPETAQPPPP WLQK/NPTAVERANLLNMAKL SIKGLIESALSFGRTLDSDYPPL QQFFVVMEHCLKHGLKVRKSF LSYNKTIWGPLELVEKLYPEAE EIGASVRDLPGLKTPLGRARAW LRLALMQKKMADYLRCLIIQR DLLSEFYEYHALMMEEEGAVI
17020	47388	A	17125	312	493	
17021	47389	C	17126	102	278	
17022	47390	A	17127	2	140	KAHNCSGLERPPLDNPSVSNRL FASFLSPRDLKGR\ICSD*SQVL
17023	47391	A	17128	1	2051	
17024	47392	A	17129	1	498	
17025	47393	A	17130	2	340	
17026	47394	A	17131	140	396	
17027	47395	A	17132	703	912	
17028	47396	B	17133	201	912	
17029	47397	A	17134	1	1382	
17030	47398	A	17135	2	431	
17031	47399	B	17136	99	1151	
17032	47400	A	17137	1	891	
17033	47401	A	17138	15	2722	

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17034	47402	A	17139	476	2934	TEPKTKTT*LSQ*MQKKPLTKF NNPSC*KLSIN/IVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLRFIWNQKRARIAKAI LSQKNKAVGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITPLIYNYQIFDKPEKNKQ WGKDSLFNKWCWDNWLAICR KLKLDPFLTPYTKINSRWIKAL NLRPKTIKTLEENLGITIQDIGTG KDFMTKTPKAMATKDKIDKW DLIKLKSFCTAKETTIRVNRLPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWEKDMNR HFSKDDILAAKKHMKKCSSLAI REMQIKTTMRYHLTPVRMAIIK KPGNNSQKDIPDWRNGPKRKD RQITTFRGPTKLQVVVPTLGAA PGRGCPWPRRPRCPGREGEELH PALGGERGQRQAAGSGGARRL APSAGDGLCVGPVEDTGETQT WKTGQPGLREPWWGWRPTEPP PAPSSHSEEWPRRPPVRRAPRP AGEHAGEGGAAVADTTAFSPW LPRVGGWHLQVHRGGRSCAGA RRFGGSRGWDLGDLSSAPVASL
17035	47403	A	17140	1	2298	
17036	47404	A	17141	3	482	
17037	47405	A	17142	1	1026	
17038	47406	A	17143	1	623	
17039	47407	A	17144	25	392	ESLKGADPKFLRNMRFANKHN KKGLKKMQANSARATSARAD AIKALVKPKEGKPDIPKGVSRK LDPLAYIAHP\RLGKCAHSCIAK GLKLCRLQAKDKDQTKAQAA APA*APKGARTPTKASE
17040	47408	A	17145	1	507	

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17041	47409	A	17146	2	811	YRFSGPTIRSIQNHTTHNQGRK WHKKGIKKPRAQRYESLKGPE V*PSGQGVTCLLRADWLSPLLG SGTY\VGPKFLRNTRFAKKHNK KGLKKMQANNAKAMSAR\AE A\IKALVKPKEVKPKIPKGG\SR KLRSTLPDIVHP\KLGKSARAPY LPRGFRLCLPNANAKSISSQGQ GQGQGQGSNQGPGFKPQLQVP ASGVPNVPRALTKGFQSRYSLA QHEGQERTWVRPPTPRPWGYH FAWGWGSPVAICTNKPEAGKR RNEKEKLCQGDGY
17042	47410	A	17147	1	636	
17043	47411	A	17148	169	410	
17044	47412	A	17149	385	1359	QTNSPNCVRGRVSPPVLPGSSS MDVLASYSIFQELQLVHDTGYF SALPSLEETWQQTCLELERYLQ TEPRRISETF\GEDLD\CFL\HAFP SPCIEESFRRLDPLLLPVEAAICE KSSAVDILLSRDKLLSETCLSLQ PASSSLDSYTAVNQAQLNAVTS LTPPSSPELSRHLVKTSQTLSAV DGTVTLKLVAKKAALSSVKVG GVATAAAAVTAAGAVKSGQS DSDQGGLGAEACPENKKRVHR CQFNGCRKVYTKSSHLKAHQR THTGEKPYKCSWEGCEWRFAR SDELTRHYRKHTGAKPFKCNH CDRCFSRSDHLALHMKRHI
17045	47413	A	17150	1	948	
17046	47414	A	17151	400	446	PSFLR*PSFWSREFH
17047	47415	A	17152	7212	10914	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQRGRFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSAFFLVN DWLSVETEANGGLVEKEVLAA SDAALLRFRRLLVAELQRGFFD KHIWLSIWDRPPRSRFTRIQRAT CCVLLICLFLGANAVWYGAVG DSAYSTGHVSRLSPLSV
17048	47416	B	17153	1	14934	

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17049	47417	A	17154	999	3009	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQRGRFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSAFFLVN DWLSVETEANGGLVEKEVLAA SDAALLRFRRLLVAELQRGFFD KHIWLSIWDRPPRSRFTRIQRAT CCVLLICLFLGANAVWYGAVG DSAYSTGHVSRLSPLSVDTVAV GLVSSVVVYPVYLAILFLFRMS RSKVAGSPSPTPAGQQVLDIDS CLDSSVLDSSFLTFSGLHAEVRT LLGVLGWAGGPAALAQLGLKT LCTSQQAFVGQMKSDLFLDDS KSLVCWPSGEGTLSWPDLLSDP SIVGSNLRQLARGQAGHGLGPE EDGFSLASPYSPAKSFSASDEDL IQQVLAEGVSSPAPTQDTHMET DLLSSLCAEVHTALPLHCSCLQ DSVQWHAVQGLPAFCRGDPVT QEAQETARPAAQNLVLIPLHAA PHQAVAEIDALYDVYLDVIDK WGTDDMLFLGDFNADCSYVR AQDWAAIRLRSSEVFKWLIPDS ADTTVGNSDCAYDRIVACGAR LRRSLKPQSATVHDFQEEFGLD QTQASGPWGGAGLGSPPPGRT QAAGRALAISDHFPVEVTLKFH
17050	47418	A	17155	242	363	TKRQENGRKKQDRTPTEQQLR VK*KSRSTKKRRKQSRSES
17051	47419	B	17156	1	12879	
17052	47420	A	17157	3	596	NLLFPVRSERGPHRPTPLSWLW LRPCELNKLAAGGLAAGSSRA GALYLLIYIPRRPARAAPLCPAA ATGAPGASAGSASPASARPPGL ARAAPGPLRGRRPRSPRTPFCV/ WLGVSLLLS\YQHYFAEPFESFQ VCCRHCGILCLTIRVHFPCLSAN PFHFSQLHLGPRPGKACHSVGL QIYNSQAHSHPSQQERQLFC
17053	47421	A	17158	1	235	FFFVLYNLFLFVITSIPLQKVSIL TQRQLVAEENVKCCTV\PEPQ** *LSNYPIFVEMGFCHVGPGWSR TPTPKSVSR

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17054	47422	A	17159	256	4064	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQRGRFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSAFFLVN DWLSVETEANGGLVEKEVLAA SDAALLRFRRLLVAELQRGFFD KHIWLSIWDRPPRSRFTRIQRAT CCVLLICLFLGANAVWYGAVG DSAYSTGHVSRLSPLSV
17055	47423	A	17160	2	347	LTSRGP/LCCVLLICLFLGANAV WYGAVGDSAYSTG/LCVQAEP AERRHSRCWPGVQRGCLSRLP GHPLSLPDVPEQGGWEPEPHTC RAAGAGRRQLPGLNPCWTAPS SRSEASTLR
17056	47424	A	17161	9415	9994	ADSGCKL/PSSC*HVLCA/WVTY MVMAAILHKLDQLDASRGRAI PFCGQRGRFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGH RHLDGDRAFHRNSLDIFRIATP HSLGSVWKIRVWHDNKGLSPA WFLQHVIVRDLQTARSAFFLVN DWLSVETEANGGLVEKEVLAA SKASFRVPTPSRSPVALPAPAGG
17057	47425	A	17162	1030	1222	
17058	47426	A	17163	2	2762	
17059	47427	A	17164	25	115	
17060	47428	A	17165	1	383	
17061	47429	A	17166	120	596	IKAPCASFPTSGFPGQRRSFVGR SSSTPEECGHSELGRNEDKASR GRIRQQ/PFAVLKYLLFCSLRW* YPGKQGLEWTSSKLQQTCRKY RERHKDTPQEEQLQDT*LSG/V TK/G*NEGKNVKGSQRERSGYS QREAHQTNSRSLGRNSTSQKRV GASIQRS

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17062	47430	A	17167	1	2236	RPSGPQPLPGSVRHPRPVLRRPL PRAQGSSSSFRPRPPFAPDTMD KFWWHAAWGLCLVPLSLAQID LNITCR\FAGVFHVEKNGRYSIS RTEAA\NLCKAFNSTLPTMAQM EKALSIGFETCRYGFIEGHVVIP RIHPNSICAANNTGVYILTSNTS QYDTYCFNASAPPEEDCTSVTD LPNAFDGPITITIVNRDGTRYVQ KGEYRTNPEDIYPSNPTDDDVS SGSSSERSSTSGGYIFYTFSTVH PIPDEDSPWITDSTDRIPATSTSS NTISAGWEPNEENEDERDRHLS FSGSGIDDDEDFISSTISTTPRAF DHTKQNQ\DW\TQW\NPSH\SNP EVLL\Q\TTTRMTDVDRNGTTA YEGNWNPEAHPPLIHHEHHEEE ETPHSTSTIQATPSSTTEETATQ KEQWFGNRWHEGYRQTPREDS HSTTGTAAASAHTSHPMQGRT TPSPEDSSWTDFFNPISHPMGRG HQAGRRMDMDSSHSTTLQPTA NPNTGLVEDLDRTGPLSMTTQ QSNSQSFSTSHEGLEEDKDHPT TSTLTSSNRNDVTGGRRDPNHS EGSTTLLEGYTSHYPHTKESRT FIPVTSAKTGSFGVTAVTVGDS NSNVNRSLSGDQDTFHPSGGSH TTHGSESDGHSHGSQEGGANTT SGPIRTPQIPEWLIILASLLALALI LAVCIAVNSRRRCGQKKKLVIN SGNGAVEDRKPSGLNGEASKS
17063	47431	A	17168	1	1980	

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17064	47432	A	17169	362	2551	EDFSTSATTPSSSPRELPSGQGL WLCWLELLPSFTRNGVVHTGP C*GLC*RWQLSPQPSLPSNFGM KISDMATLITTVPAA/FSSSSDW NTPAPTQSPEEVRRLHLCTSFM DMLKVGGQGEGAAAGLVQNP SGHALGCLDSAASGISDPSVAV LLENVPNQRGESLRCVPVYLGQ WNCSKETGMDSGQFGEEKGAH DPSPTYYHACLSTQWWPSPESP YPQPSGPQVKEPRNPGKSISML CLWIRYHAADSGSSRAKLPLEE RLRPFSPTHDCLAFPLPLEKRPE GNVGSRCPSGTKLPEEGSGSNI CCSAIFPVLQPPLVIPRQTRSGV DLQQTPTDLQLRDLTDRSSLPA MEQSWIENDFDELNRSRLQKA NKLENLEETDKFLDTYTLPRLN QEETESLNRPITGSEIEAIINNVP TKKSPGPDGVTAKFYQRYKEE LRTVNKNHMIISIDAEKAFDNIQ QPFMLKTLNKLGIDATYLKIIRA IDDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI NNFSKVSGYKINVQKSQEFLYN NNRQTENQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYNPLL NEIKKDTNKWKNIPCSWIGRINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPEEAAEQQILPN
17065	47433	A	17170	1	483	
17066	47434	A	17171	52	321	
17067	47435	A	17172	274	393	
17068	47436	A	17173	304	415	
17069	47437	A	17174	321	796	
17070	47438	A	17175	1	198	
17071	47439	A	17176	2	454	CRPVPAATNGRCFPATPRDPGP RMRRACAWGRSKGAGRCLRR ATRRDKMAKKESILDLSK\YID\ KTIRVKFQGGRK\ASGILKGFEP NLL\NLVLTVTI*YMRDPDDQY KLTED\TRQLG\LVVFRG\TSLVL \ICPQDGMEAIP\NPFIQQQDA
17072	47440	A	17177	1	1806	
17073	47441	A	17178	1215	2065	
17074	47442	A	17179	217	441	
17075	47443	A	17180	117	296	DWSDIQKLG*SLSLSKEIFQL*IV SPPALHPAKLLHRSA*LSVPQIG RECQGCGWTAMC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17076	47444	A	17181	2	138	LRTAPEFPGRRFRGCAAAAAES VAALL*STPPCRSGDSLCGKSR
17077	47445	A	17182	222	760	
17078	47446	A	17183	192	244	YIQPVF*GWTLGCCQFF
17079	47447	A	17184	1	990	
17080	47448	A	17185	1	2196	
17081	47449	A	17186	459	1387	
17082	47450	A	17187	2	454	
17083	47451	A	17188	1	957	
17084	47452	A	17189	398	553	
17085	47453	A	17190	2	293	
17086	47454	B	17191	53	182	
17087	47455	A	17192	3	1114	
17088	47456	A	17193	1	1024	SVVEFIPSCAVVLWSSVLLSPVR LLSYLSGVPPGHPMEDSMDMD MSPLRPHNYLFGCELKAGQDY HFKVDNDENEHQLSLRTVSLG\ AGAKDELH\IVEAEAMYYEGSP IKV/THLATLKMSVQPT\VSLGG \FEITPPVV\LRLKCGSGPVHISG QHLVAV\EEDAESEDEEEEDVK/ LSLSISGKRSAP\GGGSKVPQKE RKTCMLMKDDDD\DDEEDGYD EDD\DDDDDDF\DDEEAEEKAP SERNLYRDTP\AKNAQKSNQNG KDSKPSSTPRSKGQESF\KKQEK TPKTPKGPSSVEDIKAKMQASI A/EKGGSLPKVEAKFINYVKNC FPMTDQDAIQDLWQWRKSL
17089	47457	A	17194	2	291	
17090	47458	A	17195	185	307	
17091	47459	A	17196	3	392	VRGGQAFRQRPAPPLPVTRSAH RGRRPTRASQPSLFHLLLREGK MSESSSKSSQPLASKQEKDGTE KRGRGRPRKQP\PVSPGTALVG SQKEPSEVPTPKRPRGRPKGSK/ NKLEKEEEEGISQESSEEEQ
17092	47460	C	17197	76	378	
17093	47461	B	17198	1803	1905	
17094	47462	A	17199	1	416	
17095	47463	A	17200	30	407	
17096	47464	A	17201	1	993	
17097	47465	A	17202	1	1287	
17098	47466	A	17203	1	2004	
17099	47467	A	17204	1	1368	
17100	47468	B	17205	1	3035	
17101	47469	B	17206	1	981	
17102	47470	A	17207	1	2017	
17103	47471	A	17208	1	1069	
17104	47472	A	17209	1	2463	
17105	47473	A	17210	1	324	

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17106	47474	A	17211	51	1528	GREASKMAQTQGTRRKVCYY YDGDVGNYY*G\QGHPMKP\HR IRMTHNLLLNYGLYRKMEIYRP HKANADEMTKYHSDDYIKFLR SI/RVPDNIVGSTSKQMQRFNVG EDFPSIPMACFEFCQLSTGGSVA KCL*NFNKQQTDIAVNWAGGL HHAKKSEASGFCYVNDIVLAIL ELLKYHQRVLYIDIDIHHGDGV EEAFYTTDRVMTVSFHKYGEY FPGTGDLRDIGAGKGKYYAVN YPLRDGIDDESYEAIFKPVMSK VMEMFQPSAVVLQCGSDSLSG DRLGCFNLTIKGHAKCVEFVKS FNLPMLMLGGGGYTIRNVARC WTYETAVALDTEIPNELPYNDY FEYFGPDFKLHISPSNMTNQNT NEYLEKIKQRLFENLRMLPHAP GVQMQAIPEDAIPEESGDEDED DPDKRISICSSDKRIACEEEFSDS EEEGEGGRKNSSNFKKAKRVK TEDEKEKDPEEKKEVTEEEKTK EEKPEAKGVKEEVKLA
17107	47475	A	17212	1	492	
17108	47476	A	17213	1	1851	
17109	47477	A	17214	1	753	
17110	47478	B	17215	427	614	
17111	47479	B	17216	1	711	
17112	47480	A	17217	750	1173	
17113	47481	A	17218	1	1224	
17114	47482	A	17219	1242	1743	
17115	47483	A	17220	423	1739	
17116	47484	A	17221	117	1183	
17117	47485	A	17222	1	377	FRRGAW/VPLLTRWGFRPRGGC ISNDSPRRS/IHYRETKPEPPVRV CARGLQRTPSAGHRAVLRMPR RGRTRPGAPQGGAALGGPARD RECACAGRGAQTFALRKNCVC KMPSGRGRTCSKNFSYFPS
17118	47486	A	17223	331	1134	
17119	47487	A	17224	178	1200	
17120	47488	A	17225	1	367	
17121	47489	A	17226	85	3360	
17122	47490	A	17227	8	930	
17123	47491	A	17228	1	765	
17124	47492	B	17229	120	509	
17125	47493	A	17230	232	3187	
17126	47494	A	17231	1	999	
17127	47495	A	17232	1	325	
17128	47496	B	17233	1	535	
17129	47497	A	17234	271	634	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17130	47498	B	17235	301	523	
17131	47499	A	17236	1	1185	
17132	47500	A	17237	178	497	LPVPAYELNGSQQLPLLLGAAA IGYLAYKRFYVKDHRNKAMIN LHIQKDNPKIRHAFDME\DLGD KAV\YCRCWRSKKFPFCDGAHT KHNKE\TGDNVGPLIIKKKET
17133	47501	B	17238	184	395	
17134	47502	A	17239	1	103	PAWHEGQPQPESECPPQRQCIC SHGRGTPARCGVSY*ART/PAG ESP*TQQDLRAS*LGTRANHSQ RASARHKDSASAVTGAGHQRD AE
17135	47503	A	17240	447	667	HRPRRRFQIKPQSQVPEHAPLPL PTASDPP/AHSPRCPSESRLSPGG QRLGFPSSVLNCSKCSWQLAAC MGFSF
17136	47504	A	17241	265	890	
17137	47505	A	17242	1	1374	
17138	47506	A	17243	1	6189	
17139	47507	A	17244	1	8277	
17140	47508	A	17245	178	1177	
17141	47509	A	17246	1	447	
17142	47510	A	17247	1	465	
17143	47511	A	17248	3	3910	
17144	47512	A	17249	2	1871	
17145	47513	A	17250	1	666	
17146	47514	A	17251	1	635	FPGRRFRRAVWCTHCCAPTPSG PVLPHSAAMSFLKSFPPPGPAE GLLRQQPDTEAVLNGKGLGTG TLYIAESRLSWLDGSGLGFSLE YPTISLHALSRDRSDCLGEHLY VMVNAKFEEESKEPVADEEEE DSDDDVEPITEFRFVPSDKSAF* FPCSVEAMFTAMCECQALHPD PEDEDSDDYDGEEYDVEAHEQ GQGDIPTFYTYEEGLS
17147	47515	A	17252	1	2796	

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17148	47516	A	17253	1	2393	MEIRGALDLRKRQVLIFLVLLG LSRAGTESAHYSVAEETEIGSFV ANLARDLGLGVEELSSREARV VSDDNKKYLHLDLLTGNLLLN EKLDRDELCGSTEPCVLHFQVV LENPLQFFRFELCVKDINDHSPT FLDKEILIKISEGTTVGATFLME SAQDLDVGSNSLQNYTISPNSH FYIKIPDSSDRKIYPELVLDRAL DYEQEAELRLTLTAVDGGSPPK SGTTLVLIKVLDINDNAPEFPQS LYEVQVPEDRPLGSWIATISAK DLDAGNYGKISYTFFHASEDIR KTFEINPISGEVNLRSPLDFEVIQ SYTINIQATDGGGLSGKCTLLV KVMDINDNPPEVTISSITKRIPE NASETLVALFSILDQDSGDNGR MICSIQDNLPFFLKPTFKNFFTL VSEKALDRESQAEYNITITVTDL GTPRLKTEYNITVLLSDVNDNA PTFTQTSYTLFVRENNSPALHIG SVSATDRDSGTNAQVNYSLLPP QDRHLPLASLVSINADNGHLFA LRSLDYEALQEFEFRVGATDRG SPALSSEALVRVLVLDANDNL\ PFVLYPLQNGSAPCTELVPRAA EPGYLVTKVVAVDGDSGQNA WLSYQLLKATEPGLFGVWAHN GEVRTARLLSERDAAKHRLVV LVKDNGEPPRSATATLHVLLVD GFSQPYLPLPEAAPAQAQADLL TVYLVVALASVSSLFLLSVLLF
17149	47517	A	17254	89	1283	
17150	47518	A	17255	1	276	
17151	47519	A	17256	2	259	WQGGILGSDPTPPLTSPNLLQT ACFREERDV/RRERGQPLGDHS ALCLPRRGVPVPCDGLLCWWG PPDAAEPLRGPSPARAGPVLPG
17152	47520	A	17257	624	4055	
17153	47521	A	17258	3	1784	
17154	47522	A	17259	1	1272	
17155	47523	A	17260	3	576	
17156	47524	A	17261	1	1017	
17157	47525	A	17262	1	1107	
17158	47526	A	17263	256	634	
17159	47527	B	17264	76	1340	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17160	47528	A	17265	1659	2107	NLLCCTCSPFSSPVSAPQTCTSN CIALLVHQQQWLVSSHLQKHF LHLHIFLA\LIVFNFSLHSF*IFDF DPWKLPP*PISPTLSSLPSNRHIA LILPCSCMTEDFDFKMPPAVAR YMTSPQAVHIIAVCPFKASRKV SHSSLKIWLFKSV
17161	47529	A	17266	248	540	KFFSLRMLNINPHCLLACRVSA ERSAVSLMGFPLCISRPFSLAAL NIFSFISTLVNLMIISLGVALLEE YLCGILCIS*IGMLACLARLGKF SWIIR
17162	47530	A	17267	4880	5121	
17163	47531	A	17268	468	602	CLQLCSFGLGLTW*CGLFFYST *TLK*FFPIL*RMMVVF*WGLH
17164	47532	A	17269	359	462	
17165	47533	A	17270	457	600	LWWFNALFLCWLTSFLTTTLLE LHECLPVWRD*TRRHLTGWSK GSCTN
17166	47534	A	17271	2405	2830	TPVFRFIALSYTFADSDGEYF*IL LSENPQRFFKCCFNMRSNKIPW DTFANSIKGAEFSGKHFITEFISS SESESESESTRFRDFRGLETSSSL SLDSFSLLGDDFLSFLLSFTIDA VSSKRLSKEIRKARLCWRFPRI
17167	47535	A	17272	1	2172	
17168	47536	B	17273	446	625	
17169	47537	B	17274	1	2604	
17170	47538	A	17275	1	3039	
17171	47539	B	17276	1	1383	
17172	47540	A	17277	1	993	

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17173	47541	A	17278	3	2494	RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTYSKIDHIVGSKTLLSKCKRTE IITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNLLLNDYWVHNE MKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAYKR KQERSKIDTLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKNKREKNQIDTIKNDK GDITTNPTEIQTTIREYYKHLYA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLKLFQSIEKEGILPNSFYE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIHKSI NVIQHINRAKDKNHMIISIDEEK AFDKIQQPFMLKTLNKL\G/DKI PRNPTYKGCEGPLQGELQTTAQ GNKRGHKQMEEHSMLMGRKN QYHENGHTAQG/IL*IQCHPHQ ATNDFLHRIGKNYFKVHMEPK KSPHRQVNPKPKEQSWRHHTT *LQTILQGYSNQNSMVLVPKQR YRSMEQNRALRNNAAYLQLSD L*QP*EKQAMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RFKR*T*NHKNPRRKP RHYHSGHRHGQGLHVQNTKSN
17174	47542	A	17279	285	502	
17175	47543	A	17280	1	3189	
17176	47544	B	17281	1	1235	
17177	47545	A	17282	1	3139	
17178	47546	B	17283	1	1779	
17179	47547	B	17284	1	3127	
17180	47548	A	17285	1	3325	
17181	47549	A	17286	1	3145	
17182	47550	A	17287	1	1095	MIMGDFNTPLSTLDRSTRQKVN KDIQELNSALHQADLIDIYRTLH PKSTEYTFFSASHLTYSKIDHIV GSKALLSNCKRTEIITNYLSDHS AIKLELKIKKLTPNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAEC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEMETQK\TLQK\INE SRG/WKKFLEKLCFIELS*ARRI

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17183	47551	A	17288	1	3229	
17184	47552	A	17289	1	1205	
17185	47553	A	17290	1	986	
17186	47554	A	17291	1	3170	MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDGS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVPNEMKAEIKMFF ET\NENKDTTYQNLWDTFKAV CRGKFIALNAHKRKQERPKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKIN*S QSWFFERVKKIDRPLARLIKKK REKNQIDTIKND
17187	47555	B	17292	1	2148	
17188	47556	A	17293	1	1416	
17189	47557	A	17294	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
17190	47558	A	17295	1	3345	
17191	47559	B	17296	1	3122	
17192	47560	A	17297	1	2118	
17193	47561	A	17298	965	4091	
17194	47562	B	17299	15	2762	
17195	47563	A	17300	1	3049	MTVKVRITVTSGKKPPWLIPRQ TGYGVDLWQTPTDLQLRVLTV RRKTNKQKGHPHQNPICTSPSS KTKDRSTRQKVNKDIQELNSAL HQEDLIDIYRTLHPKSTEYTFFS APHHTYSKIDHIVGSKALLSKW KRTEITANCLSDHSAIKLELRIK KLTQNWSATWKLNNLLLNDC WVHKEMKAEIKMFFETK\ENK\ DTTYQNLWDAFKA\VCRGKFIA LNAHKRKQERSKIDTLTSQLKE LEKQEQTHSKASRR

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17196	47564	A	17301	3	4101	PLSTLDRSTRQKVNKDIQELNS ALHQVDLIDIYRTLHPKSTEYTF FSVPHHNYSKIDHIVGSKALLS KCKRTEIITNCLSDYNAIKLELR TEKLTQNRSTTWKLNNPLLND YWVHKEMKAEIKMFFETNENK DTTYQNLWDAFKAVCRGKFIA LNAHKRKQERSKIDTLTSQLKE LEKQEQTHSKATRRQEITKTRA ELKKIETQKTLQKINESRSWFFE KTNKIDRLLATLIKKKREKNQI GARKNDEGAITTN
17197	47565	A	17302	1	3234	MANKNNQCREVLKGPDELKT MAREPHDKCTSFSSQFDQLEER VSAMEDQMNEMKREEKFREK RIKRNEQRLQEIWDYVKRPNLC LIGVPESDGENGTKLENTLQDII QENFPNLARQANIQIQEIQRMP QRYSLRRTTPRHIIVRFTKVEM KEKMLRAAREKGRVTHKGKPI RLTADLSAETLQARRESTRQKV NKDIQELNSAQHQADLTDNYR TLHPKSTEYTLFSAPHHTYSKID HIVGSKALLSKCKRTEI
17198	47566	A	17303	1	3390	MLTLNHNRLTDAILNISTCLSR HLDLNTGGKKRISYKRNYLME EHLEGLCSNEFTWENSTIMTDS QMLMHREEPGSLPNIPILSIVFT NNRSKRQKVNKDIQELNSALH QADLIDIYRTLHPKSTEYTFFSA PHHTYSKTDRIVGSKALLSKCK RTEIITNCLSDHSAIKLELRIKKL TQNCSTTWKLNNLLLNDYWV HNEMKAEIKMFFETNENKDTT YQNLWDTFKAVCRGKFIALNA HKRKQERSKIDTLTS
17199	47567	B	17304	1	2427	
17200	47568	A	17305	1	4257	
17201	47569	A	17306	1	3726	MVVKTNARELRDECTSLSSPFN QLEERVSVMENQMNKMKQEE KFREKRIKRNEQSLQEIWDYVK RPNLCLIGVTESDGENGTKLEN TLQDITQENFPNLARKANIQIQE TQRTPQRYSSRRATLRHIIVRFT KVEMKEKMLRAAREKDFTPTK IKRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFIKQVLSDLQ RDLDSHTLIMGDFNTSLLTLDR SMRQKVNKDTQELNSSLHQAD LIDIYRTLHPKSIE
17202	47570	A	17307	1	1059	

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17203	47571	A	17308	130	1092	
17204	47572	A	17309	1	924	
17205	47573	A	17310	1	1206	
17206	47574	B	17311	1	1257	
17207	47575	A	17312	1	685	MEIILRICKLTISKELLDSGSSRL TMTHYKHRYFSHSAEEQIISEEL NESEMICQHHHTAENDFDELRE EGFRRSVITNFSKLKEDVQTHF KEAKNLEKRLDEWLTRINSVEK TLNDLM*LKTVA*ELRDTYTSF NSRFDQVEERVSVIEDQMNEM EREEKFREKRV*RNEQS/LQEIW NYVKRPNLHLIGVSEIDRENGT KLENTLQDIFQENFTYLARQAN IQIQEI
17208	47576	B	17313	70	1227	
17209	47577	B	17314	640	751	
17210	47578	A	17315	1	2328	MGVSGAQPGRSCWHRSSTGSQ GLGPVPEPADCGGEAAGRARE EGTVSLTMGTADSDEMAPEAP QHTHIDVHIHQESALAKLLLTC CSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDY TLLVTSGAAIWTGAVAVLAGA AAFIYEKRGGTYWALLRTLLTL AAFSTAIAALKLWNEDFRYGYS YYNSACRISSSSDWNTPAPTQSP EEVRRLHLCTSFMDMLKVGGQ GEGAAAGLVQNPSGHALGCLD SAASGISDPSVAVLLENVPNQR GESLRCVPVYLGQWNCSKETG MDSGQFGEEKGAHDPSPTYYH ACLSTQWWPSPESPYPQPSGPQ VKEPRNPGKSISMLCLWIRYHA ADSGSSRAKLPLEERLRPFSPTH DCLAFPLPLEKRPEGNVGSRCP SGTKLPEEGSGSNICCSAIFPVL QPPLVIPRQTRSGVDLQQTPTD LQLRDLTVRRKTNKQKGHPHQ NPMCTSPSSKTKELKEDVRTHH KEAKNLEKRLDKM\VNRINSVE KTLNDPMELKT\QARELHDKCT SFSSRFDQLEERVSVTEDQMNE MKREEKFREKRVK\RNEQSLQE IRDYVKRPNLCLTGVPESDGEN ETKLENTLQDNIQENFPNLARQ ANIQIQEIQRTPQRYSSRRATPR HIIVRFTKVEMKEKMLRAAGE KGQVTHKGKPITLTADLLAETL
17211	47579	A	17316	508	666	
17212	47580	A	17317	622	780	

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17213	47581	B	17318	1	777	
17214	47582	A	17319	1	508	MSGFEKQYKKIRLDKTLDSENE GLELPVPAKRSNLGVRLYACC GLLLCPAYPQHFAHGYVDKIPG YPGRAGTLTGLHPMQVCRCRR QAPCLKSNNALIVILGTVTLDA VGIGLVMPVLPGLLRDIVHSDSI ASHYGVLLALYALMQF\LCAPK YKLPSENTTNTSMQIN
17215	47583	B	17320	310	1047	
17216	47584	A	17321	1	1101	
17217	47585	A	17322	577	735	
17218	47586	A	17323	337	642	
17219	47587	A	17324	2	653	
17220	47588	A	17325	2	935	
17221	47589	A	17326	532	729	
17222	47590	A	17327	1	675	
17223	47591	A	17328	1	684	
17224	47592	A	17329	2	641	
17225	47593	A	17330	1	808	
17226	47594	A	17331	562	675	
17227	47595	A	17332	2	1687	DTGNNEWKQQEGLSHNNWLG LGCLFGPETPIFYPATLGHTSSIY YERKKEDKNGMKEEHDTSVA MFFTLFNFQISVENIRKGPMVV GESIAQSYLNVVQEIFRSRNHQ LLQDLTRDLCDNLKTCHTSHGS VMAETAVINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKQRSNLGVRLYAC CGLLLCPAYPQHFAHGYVDKIP GYPGRAGTLTGLHPMQVCRCR RQAPCMKSNNALIVILGTVTLD AVGIGLVMPVLPGLLRDIVH\SD SIASHYGVLLALYALMQFLCAP VLGALSDRFGRRPVLLASLLGA TIDYAIMATTPVRGHSVLKGKQ HKSVENLQPDNVIEKKIPFSGEK FKPAAEICKSNRELNVNHQDNG ENVSRACQRPLLQPLPSQAWRF RRKNWFCGPGPWSPFSVQSRD LVPCVPAAPALTKRGQGTAQA VASEGGSPKPWQLPHGVEPAG AQKSRAEVWEPPPRFQKM
17228	47596	B	17333	12	60	
17229	47597	B	17334	253	2103	

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17230	47598	A	17335	469	2512	PTSAYERGQRFASRLQMNLLEY FLRWLMAKIFPQAPCMKSNNA LIVILGTVTLD\AVGIGLVMPVL PGLLRDIVHSDSIASHYGVLLAL YALMQFLCAPVLGALSDRFGR RPVLLASLLGATIDYAIMATTP VLWIYPLVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYLVFEANTGTENGYQGEE SLFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGIIELN NDYTLKKVMKPLITSNTVTDEI ERANVFKMNGKWYLFTDSRGS KMTIDGIKLNDIYMLGFVSNSL TGPYKPLNKTGLVLQMVLDPN DVTFTNFYLPGPQAKANMWLL QAHDKKSFSRIKGTFGPAL
17231	47599	A	17336	2393	2945	
17232	47600	A	17337	980	1732	

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17233	47601	A	17338	1	2400	GRPFPRPPRLCQRRLRGGGRMK MTGDFEECLKDSPRFRAALEEV EGDVAELELKLDKLVKLGIAMI DTGKAFCVANKQFMNGIRDLA QYSSNDAVVETSLTKFSDSLQE MINFHTIL/L*PNSEINLRHSFSN FVKEDLRKFKDAKKQFEKVSE EKENALVKNAQVQRNKQHEVE EATNILTATRKCFRHIALDYVL QINVLQSKRRSEILKSMLSFMY AHLAFFHQGYDLFSELGPYMK DLGAQLDRLVGDAAKEKREME QKHSTIQQKDFSRDDSKLKYNV DAANGIVMEGYLFKRASNAFK TWNRRWFSIQNNQVVYQKKFK DNPTVVVEDLRLCTVKHCEDIE RRFCFEVVSPTKSCMLQADSEK LRQAWIKAVQTSIATAYREKG DESEKLDKKSSPSTGSLDSGNE SKEKLLKGESALQRVQCIPGNA SCCDCGLADPRWASINLGITLCI ECSGIHRSLGVHFSKVRSLTLDT WEPELLKLMCELGNDVINRVY EANVEKMGIKKPQPGQRQEKE AYIRAKYVERKFVDKYSISLSPP EQQKKFVSKSSEEKRLSISKFGP GDQVRASAQSSVRSNDSGIQQS SDDGRESLPSTVSANSLYEPEG ERQDSSMFLDSKHLNPGLQLYR ASYEKNLPKMAEALAHGADVN WANSEENKATPLIQAVLGGSLV TCEFLLQNGANVNQRDVQGRG
17234	47602	A	17339	1	782	
17235	47603	A	17340	1	475	
17236	47604	A	17341	1	852	
17237	47605	A	17342	432	696	
17238	47606	A	17343	3	296	ETEIEALKEELLFLKKNQEEEV KGLQAQIAISGLTVEVDVPKSQ DLAKIMADIWAQ*DELEDGEDF SLRDALDSSNSMQTIRKTTTRPI VSGWQSGV
17239	47607	A	17344	2	292	SQKKGLVGALTLNPPHFCPCHL *EVKGLQAQIASS\GLTVEVDAP KSQDLAKIMADIRAQYDELAR KNREELDKYWSQQVREGKGM GCQGVGGRQTE
17240	47608	A	17345	1	908	

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17241	47609	A	17346	1	1452	TGPEFHDRLRVRRRPQSLSPVL LLSSPDSMSFTTRSTFSTNYRSL GSVQAPSYGAGPRRAARPASY AGAGGSGSRISVSRSTSFRGGM GSGSL\ATG\IAGG\LAGMG\GIQ NEKETMQSLNDRLASYLDRVR SLET\ENRRL\ESKIRE\HLEKKG PQ\VRDWSHYFKI\IEDLRA\QIF\ ANTV\DNARIVL\QI\DNAPSCVR DDFR\VKY\ETELA\MRQSCWRT DIHGAPQGPFDDTNYHTDLQL/ EKTEIRGSSRRELLFQ*RRNHEE /EKLKGLQAQIAQFLGLTRGRL DCPQIFRDLRQDSWADIRGPIID ELASEEPRGSLDKY\WSQQI\EE STTVVTTQF\AEVEAAETT\LTE LRRTVQSLEI\DLDSMRNLKAS\ LENSLREG*RPAYALQ\MEQLN G\LLHLESELAQTRAEGQRQA QEYEALLNIKVKLEAEIATYRR LLEDGEDFNLGDALDSSNSMQ TIQKTTTRRIVDGKVVSETNDT
17242	47610	A	17347	467	843	
17243	47611	A	17348	114	1363	
17244	47612	A	17349	2	281	
17245	47613	A	17350	1	588	
17246	47614	A	17351	184	354	
17247	47615	C	17352	391	657	
17248	47616	A	17353	1	2010	
17249	47617	A	17354	2	443	VPDLPPSHRGFRAAQGGLPPKN KVAALPSWGSANQNSSARWEL VSPPIHRGGS*GPGETGDLDGSS IQRAVELRLVQAFVVPKSSLRD PSREGRGGWAG*VQTKGA*AR PTLLWAPKR/DRGGKAAPTSTW NSPKAGCPSARSSPAPP
17250	47618	A	17355	1	1359	
17251	47619	A	17356	260	380	
17252	47620	A	17357	153	273	
17253	47621	A	17358	270	484	AKYRGTGSSRKALGAHWVPKQ PIPAWQHKDPSGGRPEEQGVKL YREKEFSS*TL*/RI*TGPDAWA YAWADAW
17254	47622	A	17359	2	941	
17255	47623	A	17360	1	615	
17256	47624	A	17361	911	1472	
17257	47625	A	17362	2	442	
17258	47626	B	17363	76	235	
17259	47627	A	17364	38	190	
17260	47628	A	17365	134	523	
17261	47629	B	17366	1	1776	

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17262	47630	A	17367	394	554	
17263	47631	A	17368	22	831	
17264	47632	C	17369	1	1191	
17265	47633	A	17370	199	647	PSVPTEGSRNRTTAVAVEERQS DGSGSLSPGKLQTTTTGII\PALL HITGAPVSSDFRLDWLIERPKG GRRAELSIRSLALPLPQHCGSD NDWIPLQLRLLSRASFHSDDDL GFGAYRRLALHILCIHSSKEALE LNTFQPVTFLNAFSK
17266	47634	A	17371	1	2697	
17267	47635	B	17372	25	1698	
17268	47636	A	17373	2	218	ASLRSSPFSRSLRCQGKNTPERS GLPKALFCTKPSR\ADLGPAGH RRPLPSVQPG*AIPGRVSRGEKN LTNR
17269	47637	A	17374	2	2543	
17270	47638	A	17375	198	403	PQALREHSPSV*TGRQDRQLLF KDCTCQRQRRDVDSVQGKRRL HISSPQGLNSFPAVSLKLEHNV KAE
17271	47639	A	17376	58	543	VLYRSSRMCRKIRVLISRPFSIV KICERVLSQTSQGRHDYAAAA VSKTGQKRIHSSGTRGSGAPHS PGWWEPSPDRVGVSICFLFSLK YRLFSSCLVQPCLGPVLGNNSC SPEGPREPSPPSHGLGFPKMCT* TQVPASTTQSDNGQNHPNPGCP MPISPDS
17272	47640	A	17377	14	701	
17273	47641	A	17378	91	309	GRKQFPHLATGKEGCVGGQRL PCVTVELIFPAPAGAAVPRRP*L PRTAPS*LHCLPVCRMPGEAPT ARHAAWV
17274	47642	A	17379	2	2625	
17275	47643	A	17380	1	1752	
17276	47644	A	17381	3257	3412	
17277	47645	A	17382	1	1091	
17278	47646	A	17383	233	1148	
17279	47647	A	17384	1	1716	
17280	47648	C	17385	162	356	

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17281	47649	A	17386	836	2106	AKKFRKRWPLEEQEQNVPDGG AAPVTALRKRVTSQRCSLEFLE DAVGCAPAQRYTPPSAPSSTTP LGLPLT/TCGARGSWEEKSDLC PLPCRTKHTSGSPRHKGLKKTH FIKNMRQYDTRNSRIVLICAKR SLCAAFSVLPYGEGLRISDLRV DSQKQRHPSGGVSVSSEMVFEL EGVELGADGKVVSYAKFLYPT NALVTHKSDSHGLLPTPRPSVP RTLPGSRHKPAPTKSAPASTEL GSDVGDTLEYNPNLLDDPQWP CGKHKRVLIFASYMTTVIEYVK PSDLKKDMNETFREKFPHVKLT LSKIRSLKREMRSLSEECSLEPV TVAMAYVYFEKLVLQGKLIKQ NRKLCAGACVLLAAKISSDLRK SGVTQLIDKLEERFRFNRRDLIG FEFTVLVALELALYLPENQVLP
17282	47650	A	17387	1	2531	
17283	47651	A	17388	1	1506	
17284	47652	A	17389	34	576	
17285	47653	A	17390	112	1840	EELRVREHVTGGICGGSQMMV DLLGATTLELVAVAPWVMSAA AGGKNLKSPHKVEVDIIDDNFI LRWNRSDESVGNVTFSFDYQK TGMDNWIKLSGCQNITSTKCNF SSLKLNVYEEIKLRIRAEKENTS SWYEV\DSFTPFRKAQIGPPEVH LEAEDKAIVIHISPGTKDSVMW ALDGLSFTYSLLIWKNSSGVEE RIENIYSRHKIYKLSPETTYCLK VKAALLTSWKIGVYSPVHCIKT TVENELPPPENIEVSVQNQNYV LKWDYTYANMTFQVQWLHAF LKRNPGNHLYKWKQIPDCENV KTTQCVFPQNVFQKGIYLLRVQ ASDGNNTSFWSEEIKFDTEIQAF LLPPVFNIRSLSDSFHIYIGAPKQ SGNTPVIQDYPLIYEIIFWENTS NAERKIIEKKTDVTVPNLKPLT VYCVKARAHTMDEKLNKSSVF SDAVCEKTKPGNTSKIWLIVGI CIALFALPFVIYAAKVFLRCINY VFFPSLKPSSSIDEYFSEQPLKNL LLSTSEEQIEKCFIIENISTIATVE ETNQTDEDHKKYSSQTSQDSG NYSNEDESESKTSEELQQDFV
17286	47654	A	17391	3	373	

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17287	47655	A	17392	1	432	LPRFVGQQPRPLGPLRGSGSEG CRAPGEAVRAPDYAFPIPGTRA S/PLNRFPLGGTAWPQAHPTNP KPAPAPGAQLDDPPRYSRHGLS RWGLPLQSLVLLPPLQRPMLPQ AAAPNTPWWPWTLRAGRREN AHAQRKLHLWAGKVE
17288	47656	A	17393	98	376	
17289	47657	A	17394	1	364	
17290	47658	A	17395	1	1230	
17291	47659	A	17396	892	2004	RRMSFMSSEVLVGELMSPFDQS GLGA\EESLGLLDDYL\EVAKHF KPHGFSSDKAKAGLLPNGLAV\ DGLVSPSNNSKE\DAF\SGTDW DVGRKWVLKEFDFGCPCLGIE* PWETIARLTFLTTFGIDICDSLLP P*FQGRLIKAAPPRRLNPIG\HLP QKFLTKPRPGLAPFTF\LQPL\PL SPGVL\SSTPDSFPFSFRSWGS*K WDIH*KGD*/RKPDYTAYVA\MI PQCIKE\EDTPSD\ND\SGI\CMSP ES\YLGSPQHSPST\RGSPNRSLP SPGVLCGSARPKPYDPPGEKMV AAKVKGEKLDKKLKKMEQNK TAATRYRQKKRAEQEALTGEC KELEKKNEALKERADSLAKEIQ YLKDLIEEVRKARGKKRVP
17292	47660	A	17397	43	1300	DSCCIQGTMRLSRTQQRPGVEG SLKQHQRLHSNFSSINESVFIVS FSLNTIGSGGRGAEGEP/GREPL SRPQPPAGPLGGALPAPP\SLMP QL*SE*GRLLQLLYLLLQ/PAVC SCSRCSAPRSRCVARPAARTGL PTPAPASSP/CSRSLSSSRSLSSSC RVSCCHSLSSCCRSLSCSRSSST SSRSSSTSSSSLSLSSSLSCSSCRL SCSNSFSTSSSSLSLSSSLSCSSC CLSCSNSFSTSSSSLSLSSSLSCS SCRLSCSNSFSTSSSSLSCPGSFS CSHSLSSCSRSLSSCSHSLSSCSR SLSSCSHSLSSCSRSLSSCSHSLS SCSRSLSSCSHSLSSCSRSLSSCS CSLSSCSRSLSSCSHSLSSCSHSL SSCSRSLSSCSCSLSSCSRCLSSC SCSLSSCSRSLSSCLLFRRLNI
17293	47661	A	17398	288	574	

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17294	47662	A	17399	230	648	VIAPGLWMMAADIPRVTTPLSS LVQVPQEEDRQEEEVTTMILED DSWVQEAVLQEDGPESEPFPQS AGKGGPQEEVTRGPQGALGRL RELCRRWLRPEVHTKEQMLTM LPKEIQAWLQEHRPESSEEAAA LVEDLTQTL*DSWVQEAVLQE DGPESEPFPQSAGKGGPQEEVT RGPQGALGRLRELCRRWLRPE VHTKEQMLTMLPKEIQAWLQE HRPESSEEAAALVEDLTQTL
17295	47663	A	17400	105	381	SSGFWPLRFPLDVIKAVSTIAVH EKEESLWPRVAVFSTLAP/ESPP WGEAPQSAGR*SGVPEDHVHL RYRGTLSLACCSSRHHPPAQLS HYKN
17296	47664	A	17401	1023	1915	
17297	47665	A	17402	3	277	QVLLQGALLLLITVAQAGRVLK LGVSREFQDLLILWGKETFRR/C PGPCSPALHLQPGSSIP/SSQQLL *YLAAEQPQLHRGPPRTPAPVS GAE
17298	47666	A	17403	3	299	
17299	47667	C	17404	46	398	
17300	47668	A	17405	171	403	GKNSTLQQFNNLLHYSSITVAV NNPTLGNSVSVFPLYILFTGIHQ LVKVILRKLGK*RFGLELASLSL LFLPPVSLF
17301	47669	A	17406	291	467	
17302	47670	A	17407	2	395	DHAYVFLGRTACYLMKAYRK VNPRVIFSSNTIETHPKDLLHSC DHPFAEKTQFTVSTLDDVKNSG SIRDNYCRTSEISAVHIDTECVS VMLQAGTPPLQVK*RKNFQQR KQG*KMKWDPSDISNSMAEVL
17303	47671	A	17408	1	149	EKEIPGPWLLGAMRFRFCGDLD CPDWVLAEISTLAK\IPL*SCGCS AARY
17304	47672	A	17409	555	1156	QFYNKTPSRSECPNLLHHMRTE GPPGGVDQPDGHQAGWPPPEP AGQQRGRQSGCHLLQGGASPR PSCGTVHARACTPPASCPPCHR YRSHLQRGKWWPK/GLPQHTR LDHTEVLGAAEGSTVSAVPSAT RAARDHVRRLQTRKCFCKGAL LLLITAARAGRVLFGQPQLLQF TGQGFAIDTVLGRTGEDETQHC HCGLHIA
17305	47673	A	17410	3	366	
17306	47674	A	17411	408	1702	
17307	47675	A	17412	1	2661	

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17308	47676	A	17413	2	2288	
17309	47677	A	17414	1	1992	MGDFNTPLSTLDRSMRQKVNK DIQELNSAVHQVDLIDIYRTLHP KSTEYTFFLAPHRTYSKIDHIVG SKALLSKCKRTEIIRNCLSDHSA IKLELRINKLTQNCSTTWKLNN MLLNDYWVHNEMKAEIKMFF ETNENKDTTYKNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQFKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFEMISKIDRPLARLIKKKRE KNQIDTIKNDKGDIITDPTEIQTT IREYYKHLYAIKLENLEEMDKF PYTNTLPRLNEEEIESLNRTITGS EIEAIIKSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKP/DVGSSS QGNQAGERNKGYSFRKRGSQI VPVCR*YDCTFRKSHFLSPKSP* ADKQLQQSLRIQNQCAKITSIPI HHQQTNREPNHE*TPIHNCFKE NKIPRNPTYKGCEGPLQGELQT TAQ*NKKGHKQMEEHSMLMD RKNQYRENGHTAQGNLQIQCH PHQATNDFLHRIGKNYFKVHM EPKKSPHCQDTPKQKE*SWRH HAT*LQTILQGYSNQNSMVLVP KQRYRPMEQNRALRNNTTHLQ QSDL*QT*QKEEMGKGFPI**M VLGKLASHM*KAETGSLLYIL
17310	47678	A	17415	1	1677	

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17311	47679	A	17416	1	2178	MGDFNTPLSTLGRSTRQKVNK DTQELNSALHQADLIDIYGTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNCLSDHR AIKLELRIKKLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKEKRE KNQIDATKNDKGDITTDPTEIQ TTIREYYKTLYANKLENLEEMD KLLDTYTLPRLNQEEVESLNRPI TGSEVVAIINSLPTKNSPGPDGF TAKYYQRYKEELVPFLLKLFQS TEKEGILPNSFYEASIILIPKPGR DTTKKENFRPISLMNVDAKILN KILANRIQQHIKKLIHHDQVGFI PGMQGWFNICKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQPF MLKTLNKLVLEVLARAIRQEKE IKGIQLGKEEVKLSLFADDMIV YLENPIISAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLNEIKEDTN KWKNIPCSWIGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARITKSILSQKNK AGGITLPDLKLYYKAIVTKTA WYCYQNRDIDQWNRTEPSEIM
17312	47680	A	17417	1	1770	
17313	47681	A	17418	1	1101	
17314	47682	A	17419	1	1614	

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17315	47683	A	17420	1	1878	MVLALTGNKADLASKRPLEFQ EAQAYADDDSWLFMETSAKG AMNVNEIFMAIAEKLPKNKPQ NAAGAPDRNQGYLSACEFSGR KLPKQTTKHIKQSLRTKLCGAS YASSNLIPRKLYEPPLVIPRKTG SGVDLQQTPTDLQLWVLTVRR KSNKQKGYPHQNPICMLPSSKT KDFKPTKIKRDKDGHYIMVKG SIQQEELTVLNINAPNTGAPRFI KQALRDLQRDLDSHTIIMGDFN TPLSTLDRSTRQKVNKDIQELN SALHQADLIDIYRTLHPRSKDY TFFSAPHHTYSKIDHIVGSKALL AKCKRTEITRNCLSDHSAIKLEL RIKKLTQKCSTTWKLNNLLLND YWVHNEMKAEIKMFFETNENQ DTTYQNLWDTFKAVCRGKFIA LNAHKRKQERSKIDILTSQLKE LEKQEQTHSKASRRQEITKIRVE LKEIKTQKTLQKINESRSWLFE KINKIDRQLARLIKKKREKNQID AIKNDKGDITTDPTEIQTTIREY YKHLYAKKLENLEEMDKFLDT YTLPRLNQEEVESLNRPITGSEI EAIIKSLPAKKSPGPDGFTAEFY QRCEKELAQFLLRLFKSTEKEGI LPNSFYEDSIIL/ILPKPGRDTTK KENFRPISL
17316	47684	A	17421	1	1761	
17317	47685	A	17422	1	1875	
17318	47686	A	17423	1	1611	
17319	47687	A	17424	1	4539	
17320	47688	B	17425	1	6294	
17321	47689	A	17426	2	1913	
17322	47690	A	17427	1	1026	
17323	47691	A	17428	1	2112	

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17324	47692	A	17429	1	1884	MENGFDELREEGFRRSNYSELQ EEIQTKGKEVKNIEKNLDECITR IPNTEKCLKKLMELKTKARELR EECISLRSRCDQLEESVSVMED EMHEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPED RSMRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTYSKIDHIVGSKALLSKCKRT EIITNYLSDHSAIKLELKIKKLTQ NFSTTWKLNNLLLNDYWVHN KMKAEIKMFFETNENKDTTYQ NLWDTFKAVCRGKFIALNAYK RKQERSKIDTLTSQLKELEKQE QTHSKASRRQEITKIRAELKEIE TQKTLQKINESRSWFFERINKID RPLARLIKKKREKNQIDAIKND KGDITTDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYTLPRL NQEEVESLNRPITGSEIVAIIHSL PTKKSPGPDGFTAQFYQRYKEE L/RNKIPRNPTYKGCEGPLQGEL QTTAQGNKRGDKQMEEHSML MGRKNQYRENGHTAQGNLQIQ CHPHQATNDFLHRIGKNYFKV HMEPKKSPHRQVNPKPKEQSW RHHAT*FQIILQGYSNQNSMVL VPKQRYRSMEQNRALRNNATY LQLSDL*QT*EKQAI
17325	47693	A	17430	1	1695	
17326	47694	A	17431	1	3779	MELKTKARELREECRSLRSRRN QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTPQRYSSRRATPRHIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE
17327	47695	A	17432	1	735	
17328	47696	A	17433	1	2541	
17329	47697	A	17434	1	1461	

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17330	47698	A	17435	2	429	AACAAAMSLVIPEKFQHILRVL NTNIDGRRKIAFAITASSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSVNLLSNGLYL/VKG VGRRYAHVVLRKADIDLTKRA GELTEDEVERVITIMQNPRQYKI PDWFL
17331	47699	A	17436	1	615	
17332	47700	B	17437	264	556	
17333	47701	A	17438	1	406	FFFFFLQKVGIYLHIKTFQQHRL WVTSAAFLSLSSMAAVGTSSSL SENSGPGHGGKQTF*GP/EGTDI PEGRHHFSAQAFSVVAGRGTA AALLHGSHVPQGR\SRIGSRSGG PPSHPDTCSGSSHSAGRSCPHSC TG
17334	47702	A	17439	3	3484	
17335	47703	B	17440	42	367	
17336	47704	B	17441	203	382	
17337	47705	A	17442	22	266	YRDLPHFLLNSDLIFNMSTSLRE TMILIRTLSRVPL/PLHGVIQPIS KIQGLVLNALNQVQESIFQVSF NLFPDAFQHVIRA
17338	47706	A	17443	1	1137	
17339	47707	A	17444	1218	1482	QSPWPSLLRGDVSITPNLIFSCL SIGWPFCLV/SFC*PKK*TFQGV GSEVYDVKHFASCVLCHKQMN KLNLYFRNTYFVALLSTELFEN
17340	47708	A	17445	2	377	
17341	47709	A	17446	1	211	
17342	47710	A	17447	2	732	CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVVPNPYTL LSQIPEEAESFTVLDLKDAFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPQGFRDSPHLFGQAQAQ DLVHFSSPGTLVVQYMDDLLL ATSSEASCQQATLDLLNFLANQ GCKRVGIALGVLTQTHGTTPQP VAYLSKETDVAAKGPLTAILLL LAFGPCIFNLLVKLVSSRIDAIK LQMVLQMEPQMSSTNNFYRGP

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17343	47711	A	17448	1	3003	MPGAQDLQPTMPEPPHPQWAP TWPEPPRRVPPPAPRRPVPLTA QGLSVDQSRLGKFSDDPDRYID VLQGLGQTFDLTWRDVMLLLD QTLAFNEKNAALAAAREFKDT WYLSQVNDRMTAEERDKFPSG QQAVPSMDPHWDLDSDYGDW SHKYLLTCVLEGLRRIRKKPMN YSMMSTITQGKEENPAFLEQL WEALRKYIPLSPKSLEGQLILKD KFITQSAADIRGKLQKQSLVPE QNLEALLNLATSVFYNRDQ
17344	47712	A	17449	5	624	IQPILAYPHPKTLKQLWGFLGIT /GFCPVWIPRCSKIAKSLYTLIKE TQRANTHLVEWEPEAETAFKT LKQALVQAPTLSLPTGENFSLY VTERAGIALGVLTQTRGTTPQP VTYLKDGEPMKCDCQQIIVQTY ATQDDLLEVPLANPDLNLYTD GSSFVENGIRRAGYAIVSDVTIL ESKPLPPGTSAQLAELVALTRA LELGKGKE
17345	47713	A	17450	636	2628	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKD
17346	47714	A	17451	2	568	CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVVPNPYTL LSQIPEEAESFTVLDLKDAFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPQGFRDSPHLFGQAQAQ DLVHFSSPGTLVVQYMDDLLL ATSSEASCQQATLDLLNFLANQ GCKRVGIALGVLTQTHGTTPQP VAYLSKETDVAAK

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17347	47715	A	17452	254	849	LQPESLEIAGILVQ*MIE*QPKK GTNSIPVSKPSP/GVQKPNGQW RQVQDLRLISDAVIPLYPAVSNP YTLLSQILEEAEWFTVLDLKDA FFCIPLRSDSQFLLAFEDPTDHT SQLTWTVFTQGFMDTPHLFGQ SLAQDLGHFSSPGTLVLQYVDD LLLAKQQATLDLLNFLANQGY KLSKLKAQLCELLVFSSCARMH
17348	47716	A	17453	1	369	
17349	47717	A	17454	1	1632	
17350	47718	A	17455	636	1837	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKDAFFCIPLHSDSQFLF AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQAQDLGHFSSPG TLVLQYSEIAKTLYTLIKEMER ANTHLVEWEPEAETAFETLKQ ALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTTPQPVAY
17351	47719	A	17456	2	52	EISFVENGIQRAGYAIVSDVTVL ESKPLLPGTSAQLAELVALTRA FELGKGKRINANTDSKYAYLIL HALAAIWKEREFLISGGTPIKYH KEIMELLHAMQKPKEVAVLHC QSHQKG*EWDTKGRLCHS
17352	47720	A	17457	1625	2505	PGVQKP/GQWRLVQDLRLINEA VIPLYPVVPKPYTLFSQIPKEAE SFTVLDLKDAFFCIPLHSDSQFL FAFEDPTDHTSQLTWTVLPQRF RDSPHLFGQALVQDLGHFSSPG TLVLQFVDDLLLAASSEASCQQ ATRDLLNFLANQGYKASKSKA QLCLQQVKYLGLILARGTRALS KKRIQPILAYPRPKTLKQLRGFL GITSFCRLQIPGYSKMARPLYTL IKETQRANTHLVEWEPEAETAF KSLKQALVQAPALSLPTRQNFS LYVRERAGIALEVLTQTHGTTL QPVAKG
17353	47721	A	17458	1	2415	

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17354	47722	A	17459	2646	5167	KNSGHILGTCPGYRYAKGKET GKEIIKGPQNPPGYRLCPLQAV GGGEFGPTQVHVPFSLSDLKQI RVDLGKFSDDPDRQYPLRPEAH EGLQDILRYLKVQGLVRKCSSP CNTRILGVQKPKGQWRLVQDL RFINEAVIPLHSVVPNSYTLLSQI PEEVEWFTVLDLKDAFFCIPLH SVCQFLFAFEDPTDHTSQFTWT VLPQGFRDSPHLFGQILAQDLG HFSSPGTLVLQYVDDLLLATSL EASCQQATLDLLNLLANQGYK ASKPKAQLCLQQVKYLDLSLA RVTRALSKERIQPILACPRPKTL KQLRGFLGITNFCQLWIPGYSE MARPLYTLIKETQRANSHLVER EREAETAFKTLKQALVQALALS LPTGQNFSLYARERAGIALGILT QTHGTTPQPVTYLRKLIYSFVE NGMRRAGYAIVSDVTVPESKPL PPGTSTQLAELVVLTQALELRK KKRINVNTDSKYAYLILHAHAA IWKEREFLTSGGTPNKYHKEIM ELLHAVQKPKEVAVIPCQSHQK GEEK/EAEGNRRADAE\AKIAA RRNLPTEIPMEGPLVWNNPVQE IKPQYSLTKTEWGLSQGHSFLP LGWLTTLEGKAGRATPNPRNV YFPLHLRGLRTGRLPLSQSTRA QEMTLVRPRPSSSPPPEKAAEG RGRRCSSETKLRHRRLFRPLRTP LCATAPLAASVAAVLAAAPAA
17355	47723	B	17460	1	2208	
17356	47724	A	17461	2	168	
17357	47725	A	17462	890	1034	
17358	47726	A	17463	386	619	TFITGDCLGTKN/HIFDGCGVLS EVGLVLDCSNQRFKAGPA*LCQ SPFKNIL*ESLPMCMCRQLEKH AHPQGLCHTQVT

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17359	47727	A	17464	123	2169	DLGHRGSREMASVA\LEDVAV NFTREEWALLGPCQKNLYKDV MQETIRNLDCVGMKWKDQNIE DQYRYPRKNLRCRMLERFVES KDGTQCGETSSQIQDSIVTKNT LPGS/VGPYESRMSGEVIMGHSS LNCYIRVGAGHKPHEYHECGE KPDTHKQRGKAFSYHNSFQTH ERLHTGKKPYDCKECGKSFSSL GNLQRHMAVQRGDGPYKCKL CGKAFFWPSLLHMHERTHTGE KPYECKQCSKAFSFYSSYLRHE RTHTGEKPYECKQCSKAFPFYS SYLRHERTHTGEKPYKCKQCS KAFPDSSSCLIHERTHTGEKPYT CKQCGKAFSVSGSLQRHETTHS AEKPYACQQCGKAFHHLGSFQ RHMIRHTGNGPHKCKICGKGF DCPSSLQSHERTHTGEKPYECK QCGKALSHRSSFRSHMIMHTG DGPHKCKVCGKAFVYPSVFQR HERTHTAEKPYKCKQCGKAYR ISSSLRRHETTHTGEKPYKCTLG KAFIDFCSFQNHKTTHTGEKPY ECKECGKAFSRFRYLSRHKRTH TGEKPYECKTCRKAFGHYDNL KVHERIHSGEKPYECKECGKAF SWLTCFLRHERIHMREKSYECP QCGKAFTHSRFLQGHEKTHTG ENPYECKECGKAFASLSSLHRH KKTHWKKTHTGENPYECKECG KAFASLSSLHRHKKTHWKKTH
17360	47728	A	17465	1	1317	
17361	47729	A	17466	1	336	
17362	47730	C	17467	51	353	
17363	47731	A	17468	190	348	YAIHIMDVHTVRSLYYFNCFRY *ACYCCHYLTDIPEITKLSGCSY GGTSLIWG
17364	47732	A	17469	1	1716	
17365	47733	A	17470	1	840	
17366	47734	A	17471	699	1283	LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFSICFVI C/FKNVDLKGFEPDVRILLTKYS NSNGSQSPWMEEQIRDAGERV HSAFSLNWGKPLVFEKDRPYSV SVFIGLFLPMAEKTGPLKGNPG GEFLLFLRQIQLVWLPAAGIMT EHYFPITATQALEINNAISTIMEI FPTVSFASQWITASFSV
17367	47735	A	17472	300	461	
17368	47736	A	17473	1	2451	

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17369	47737	A	17474	2	3542	
17370	47738	A	17475	1	1156	
17371	47739	A	17476	1	1176	
17372	47740	A	17477	1	257	
17373	47741	A	17478	295	1353	
17374	47742	A	17479	3	1772	
17375	47743	A	17480	2	284	
17376	47744	A	17481	1	141	
17377	47745	A	17482	1	506	PHSPLWKTLCSPSSGVCCGFVT LFCNDRFACLFQLTPPPSPAWM TAAASLLASLLPALPPLNLQDA KFVEERRKQLQNYLRTVMNKV IQMVPEFAASPKKETLIQLMPFF VMGLQVGMYGLFHFGVMMDQ PQPSLTRADESPCDRVLSPCAA HRKQRDCCLSWKAEPE*FLVK* KTLCSPSSGVCCGFVTLFCNDR FACLFQLTPPPSPAWMTAAASL LASLLPALPPLNLQDAKFVEER RKQLQNYLRTVMNKVIQMVPE FAASPKKETLIQLMPFFVMGLQ VGMYGLFHFGVMMDQPQPSLT RADESPCDRVLSPCAAHRKQR DCCLSWKAEPE
17378	47746	A	17483	1	741	
17379	47747	A	17484	1	993	
17380	47748	B	17485	277	416	

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17381	47749	A	17486	686	2400	TGMSVDEKPDSP\MYVYESTVH CTNILLGLNDQRKKDILCDVTLI VERKEFRAHRAVLAACSEYFW QALVGQTKNDLVVSLPEEVTA RGFGPLLQFAYTAK\LLLSRENI REVIRCAEFLRMHNLEDSCFSF LQTQLLNSEDGLFVCRKDAAC QRPHEDCENSAGEEEDEEEETM DSETAKMACPRDQMLPEPISFE AAAIPVAEKEEALLPEPDVPTD TKESSEKDALTQYPRYKKYQL ACTKNVYNASSHSTSGFASTFR EDNSSNSLKPGLARGQIKSEPPS EENEEESITLCLSGDEPDAKDR AGDVEMDRKQPSPAPTPTAPA GLCLERSRS/GNYGQPH/VGQK EVSNFTMGS/PLRGPGLEALCK QEGELDRRSVIFSSSACDQVSTS VHSYSGGARFLATEHQEPGLM GDGMYNQVRPQIKCEQSYGTN SSDESGSFSEADSESCPVQDRG QETGSTSDLRLSTKLQSCSGPM FKGPTATVAATESWGTVLQNIP LGCAGTGEEVTYTNPPPRGRAA LVPRSPLTVYSSSLPEHQTSLKQ CAQAGPGVCLLVHNHWQLLEG
17382	47750	A	17487	1	1089	
17383	47751	C	17488	295	348	
17384	47752	A	17489	1	711	
17385	47753	A	17490	1	1248	
17386	47754	A	17491	135	259	
17387	47755	A	17492	434	506	
17388	47756	A	17493	3	227	
17389	47757	C	17494	3	236	
17390	47758	C	17495	25	153	

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17391	47759	A	17496	1	1557	MASPEAVASQDNDGFSQKPPPT PLFASRSVNRLKSQRTPRGEVE SVTDGEKTDGSWRMTVDYCKL NQVVTPIAAAVPDVVSLLEQIN TSPDITLVHYIDDIMLNGSSEQE VTNTLDLLVRHLCATGWEINPT KIQGSSTSVKFLGVQWCGDCR DVPSKVKDKLLHLAPPTTKKEA QHLTGLFGFRRKYIPYLGVLLC PIYQVTRKAASFQWRPEQEKAL QQVQAAMQAALPLGPYDPAGP MVLEIAVADTEAVWGH/WHSA SFPSHPCHCPMGP*TKWP*WQG WRLCMGSATWTSTHEG*PGYG HQ*VPNLPAAETNTEPAI*HHS/ SRRSASYLVAG*LYWTSCIMER AE\HLLWIWVCLSCMQCFCQD YHPWTHGMPYPPLWYSTQLCL *PRHSLYH*RSVAVGSCSWNSL VLPCSPSS*SSRVDRTVERPFEIT TTMPTSQESRVQESRGGSGSGT THHHP**STSNIFASCFYGITFC WSRGLSSRGRNAATRRQNNSIK L*VKIATWTLWAPPTSKL
17392	47760	A	17497	2	1120	PSKVKEKLLHLAPPTIKKEAQR LVGQLGFWRQHIPHLGALLWLI YQATQKAASFEWGPEQEKALQ QVQVAVQAALPLGPYDPADPM VLEVSVADRDAVWSLWQAPIG ESQQRPLGFWSKALPSSTDNYS/ CFRCAIIY*FMGCCQ*FGWIVRD LEEA*LENW*QRNLGKRYVDG PL*VVKNWKDICIPCECSPTGDL SRGGF**SSG*DDPFCGHHSASF PSHPCCRPMGP*TKWPWWQE* RLCMDSATWTSTHQS*PDYSH C*VPNLPAAETNTETSIWHHFS G*SASYLLAG*LH*TSSIMEKAE VSPHWNKHSLWIWVCLSSMQC FCQDYHPWTHSMPYPLSWYST QHCLSLQRERHSLYR*RSAAVG ACS
17393	47761	A	17498	1	1908	
17394	47762	A	17499	1	915	
17395	47763	A	17500	2	670	
17396	47764	A	17501	1	1332	
17397	47765	A	17503	151	674	
17398	47766	A	17504	1	825	
17399	47767	A	17505	134	447	
17400	47768	A	17506	98	778	

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17401	47769	A	17507	1	830	MHCFFIFSAAWFCLWSISLHLV ERPDMAVLLFPFGLRLGLMLQ CPRGYWPVLLGAEWLLIYWLT QAVGLTHFPLLMIGSLLTLLPV ALISRYRHQRDWRTLLLQGAA LTAAALLQSLPWLRHGKESWN ALLLTLTG/EPDAGPDMSGVLA LSRQ*HLAAARSVTGFSANQLA RATSGLVLAAVCYQSLAPVGIA GRTVALYAILSGAADYRAGLA LWLARGADCDVDERHRADRH QSWRDLPWTYCSGDCDSRHGA QGQKARAPPKHDQFPHAIFRG
17402	47770	A	17508	2252	2772	RSKTTAFTPLRVRTSAHARPAG PAPIIATFLPVCFTPDISGRQPISN ALSLI*RSMLPMVTAPNSSFRV QEPS/SQTVLRADSSANFRQGV GLVRQFRRFKNTPLVGELQPVR DVVVYRAFPLAVWVAARQAA VSLRFGLAFGKRLVNFNKLNFA DLQRFLWRINALQVDKLITF
17403	47771	A	17509	539	1077	
17404	47772	C	17510	192	396	
17405	47773	C	17511	10	294	
17406	47774	A	17512	2	379	KRPGSGITEATSSRRQRPTRRLQ GQLPGQEKRVLKATEGIANPS WGWGGAVSPLRASLTSLRHKI NNHYNTENWKLPIKDS\HLIPSP QAPSMPFPLANPPW\APHPREK MWNPQIQGTNCIWVCGP
17407	47775	A	17513	291	590	
17408	47776	A	17514	187	589	VLSFLIHRWEGDKDSLLGPNFS QTPQPSRRFICAFPWENPS*EPS YPSISDPGFLILLPSKGDVWIHL GPIFSKKPLYS*SSFLVIFYPVTP SFLFLGYKFPLAHAVFRVEPTLS LLIQNSHCHGCYTYPDGPE
17409	47777	A	17515	1509	1748	IGVVREGIPVLCLFSKGMLPVF AHSV*YWLWVCHR*LLLF*DTS HQYLIY*EFLA*SVVDFCQRPFL HLVLDFFWLVSY
17410	47778	A	17516	152	568	CQLELSCMKCPSTPVGRSLPVG CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQGDGSFV CKHPTGAVTFPSGMPLGSMTIF KILILPIHEHGMFFSLSVSSFVSL

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17411	47779	A	17517	152	568	CQLELSCMKCPSTPVGRSLPVG CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQGDGSFV CKHPTGAVTFPSGMPLGSMTIF KILILPIHEHGMFFSLSVSSFVSL
17412	47780	A	17518	152	479	CQLELSCMKCPSTPVGRSLPVG CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NP LKLLPQLPLPPDALSQGDGSFV CKHPTGAVTFPSGCPTHTLQA
17413	47781	A	17519	1	474	
17414	47782	A	17520	1326	1712	FLYVIKALGKKQLQFGQQILIPS IELLDYLINPGSGCVSLWKLNK PQYCYLIHFSGLTELSWKVHTIL LEGHYEFLEYAADR*PICLFSW KERQLVSFLDYSLHHLLGSFYV VFFFFLYLLVRLCWDL
17415	47783	A	17521	18	236	
17416	47784	A	17522	281	1005	TGWSPLQLSKATVARLPLWIPP LWAGHLGELWLASGEYPSGLK LPEEGTGSNLRCSAASAGDTQA NRVWSGPAANFSRPAAEGPAF HALRGPSVHCSPLCVHEFSSFSS LISENMQYLVFCSGVRFLRIMVI SSIHILCLVPKRTRVLGRLSLTC FRFLRGPKEPRITIPHSSAPPLGH VIAIPLP*SFMKPSPEADAPMTG SFLKSPSEADTGATLPVQSVVPI PLSILPILEVGGVLFT
17417	47785	A	17523	1	1524	
17418	47786	A	17524	881	1108	SRKMGAPNA**SAWSWSREGL AAP*SMFSSLSADSSADCKLPE GKVQPASSTGLTARASKDLYFC CCFSISARAS
17419	47787	C	17525	1	867	
17420	47788	A	17526	203	514	SSSTARPSQTSSAEESPTSWYRG DNPSKPMDPLVAGVFGAIVGA ASVLGNAPLDGIETGCGAWSST NAEHTGLWLQILRKEGLKDL*N GTVPRLGRWTASPWM

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17421	47789	A	17527	1	1578	MAKKEQLLSAAPSKTNAEGQEI PSGVYTTRALGFKHKTGQPFGQ TPSYPQEFILYTNDTWNASKTE PFTPLERGLKPGSQESSGWHLV GTPLGRSFQRKEQAAIFAVLQP PLVIPRQTGSGVDLQQTPTDLQ KRVLTVRRKTNSININKKDDHA KTTSKGHQQQRPKVDKSTKMR KNQCKKATNSKNQNVSSPPKD HNSSTAKEQNWMENEFDKLTE VGFRSSQFDQVEERISDIEDKLN EIKHEDKIREKRMKKKEQSLQE IWEYVKRPNLRLIGVPESDGEN GTKLENTLQDTIQENFPNLARQ ANIQIQEIQRTPQRYSSRRATPR HII/E*IHQG*NEGKTVKGSQRE K*GQEIPSGVYTTRALGFKHKT GQPFGQTPSYPQEFILYTNDTW NASKTEPFTPLERGLKPGSQESS GWHLVGTPLGRSFQRKEQAAIF AVLQPPLVIPRQTGSGVDLQQT PTDLQKRVLTVRRKTNSININK KDDHAKTTSKGHQQQRPKVDK STKMRKNQCKKATNSKNQNVS SPPKDHNSSTAKEQNWMENEF DKLTEVGFRSSQFDQVEERISDI EDKLNEIKHEDKIREKRMKKKE QSLQEIWEYVKRPNLRLIGVPE SDGENGTKLENTLQDTIQENFP NLARQANIQIQEIQRTPQRYSSR RATPRHIIGRFTKVEMKEKRLR AVREKSRVTHKGKLIRLTADLS
17422	47790	A	17528	738	1323	ATGGHSNQRQRS*KLSKKFRR MYN*NNQYREVLKGADGAEN QGSRTTETLCM*RMRQSLQF\D SDLVRHQRKHSGEKPYECCEC GKAFRGSSELIRHRRIHTGEKPY ECGEYKSYECIACGKAFGRSST LIENQRIHTGEKPYECNECGKSF NQSSALTQHQRIHTGEKPYECS ECRKTFRHRSGLMQHQRTHTR
17423	47791	A	17529	1	656	MAGKPEYDKTISTSIVLNALNA LGVSAEASGRNDLVVKTVEGD RKVSGSAYRETKDRGFHHGTL LLNADLSRLANYLNPDKKKLA AKGITSVRSRVTNLTELLPGITH EQVCEAITEAFFAHYGERVEAE IISPNKTPDLPNFAETFARQSSW EWNFGQAPAFSHLLDERFTWG GVELHFDV/GKRPYHPRPGVYR QPQPRAAGSPRRTTARLPFLSL

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17424	47792	A	17530	1046	1401	LLDIRMLCHGKGVIIHVLRLQF LLGRPAPHRLHAALQLPGLSLH GTLALGLWLQLRQLLLLGQPF GISGCGSGCDPEQDCV/DCGRG CWPRKCPQGSHSAPRSRGAPHR PRPQQRAAGRQ
17425	47793	A	17531	112	1170	YPFFHLIDSTIDTCVCFTKFLCC VFQLHQVIYVLL*TGYSLIFDAD DLWMGFLRGHPFC*CYCFLFVS FPSNSQAPLLQVCWSLLEVHSR PCSPGYHQRRLQNSKDCCLLLP LEALSQSGTHQMPAGALLYEM SVNPCWEEHQTDQLFTHESTFI RSKTQKKVPDKLLDSSTVTPLF KITENIGCVMTGMTADSRSQVQ RARYEAANWKYKYGYEIPVD MLCKRIADISQVYTRNAEMRPL GCCMILIGIDEEQGPQVCKCDP AGYYCGCKATAVGVKQTESTS FLEKKVKKKFDWTFEQTLETAI TCLSTVLSIDFKPSEIEVGVVTV ENPKFRILTEAEIDAHLVALAER
17426	47794	A	17532	2244	2432	DGQQLIALHRLALRELQQAVH AGIAPAGENPV*WWFRNRQNP LIALRSLPAFQSGNLSCQLH
17427	47795	A	17533	251	546	SSISDILSSA*SIRLLILVYAS*SS RAVFFSTIRSFIFFSKLVILVSPSC NLLSRFLASFHWVRTCSFSSKEF VIITHLLPTSVNSSYSSLFSFVHF G
17428	47796	A	17534	597	1092	FTNQKESRTRWIHSRILPEVQG GTGTIPSETIPINRKRGNPP*LIL* GQRHSDTKAG\RDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIR K/CNKCNPAYKQSQRQK/HT*L SQ*MQKKPLTKFNNPSC*KLSIN *VLVGRISK
17429	47797	A	17535	1	2153	
17430	47798	A	17536	2164	2427	
17431	47799	A	17537	1	322	GPRWGPRVHRAPDPVRIPSSGP LLPPRFYPRYVLP\PPSASTSRPC QRTSASGRCPCPMH/DTVKATM PIWV/DPPVPDHYEGEAEHQGIL VTHPHHQRCPAGHRHRVVF
17432	47800	A	17538	1	627	

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17433	47801	A	17539	583	1145	GNGRTVDTQVCQAPITSQSLER PADPNP\GEQDAEAGPASRRDT EAERLRFRQFQYHVASGPHLA VGQLWTLCRQWLRPEARSKEQ MLEVLVLEQFLGALPSKMRTW VQSQGPRSCREAASLVEDLTQ MCQQEGLAAHPSHDTAIRGIPR LAASWETASAMEATADARQKR THTEKEAWLLEAPHELA
17434	47802	A	17540	1	1301	
17435	47803	A	17541	1	1232	
17436	47804	A	17542	1	549	MNTANVEKPYVQKYQTAFVLV MKHRQCQLASHLVQNYRS/IQL WAWE\KIQDPGTTCPSFNTITQG SKKPYPDFVARLRDAAQNSITD ENARKVIVELMAYGNANPECQ SATKPLKGKVPTGSDVISDQKA VGVQAAKRRNRTDTGLGRSAR KSGKGVTRMLPKHASMILDGG GPATSPSCCRFL
17437	47805	A	17543	146	510	SPYWNKGKSPGWLAES\FKRPV FRQGAK\EPYPDFAASLQDAAQ KSITNENARKVIVELMAYENAN PECQSAIKPLKGKVPVGSDVISR GFQGQQPPLSQVLQGMGQLPQ YSNCPRPQAAVQQ
17438	47806	A	17544	2	828	
17439	47807	A	17545	1	420	
17440	47808	A	17546	1	1947	
17441	47809	A	17547	1	399	PLKVNIYPDSKYAFHILHHHER GFLTTQGSSIINASLIKTLLKAA LLPKEARVIHCKGHQRASDPIA QDNAHTDKIAKKAASIPTYTPH FQFFSFSS\ATPTYSPAETSTYQS LPTQGKWFLDKETYFLPASQ
17442	47810	A	17548	1	2382	

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17443	47811	A	17549	1	2194	MAPEQGRVSILQTLFIEYHGYSI FVVKGDLPDCEADQLLQMIRV QQMHRPKLIGEELAQLKEQRV HKTDLERVLEANDGSGMLDED EEDLQRALALSRQEIDMEDEEA DLRRAIQLSMQGSSRNISQDMT QTSGTNLTSEELRKRREAYFEK QQQKQQQQQQQQQQGDLSGQ SSHPCERPATSSGALGSDLALLL TQSLFGSLFTWTRVTFGAEDPG QEDSFRRRVPCPCPHSVRRSTY DLGSSDQPAQGTSHEFQIGLLL TRLSQVPILPQPPVPHPIILLSPPP HTVSGLQFLSVTSPPLPAQQFLL KEVAGAEGIAKVIPTCPVPLLG QDILTKLSASLIIPGLQPHLIATL LPNPKPPSPLPLVSPNLNPQVW DTSTPSLATDQTPITIPLKPNHP YLAQCHYSIPQLALRGLKPVIT RLLQHGLLKPINSSYNSPILPVQ KPDKSYRLPQDLDLINQIVLPIH PVASPHIIPDTTPDPHDCISLIHL AFTPFPHTSFFPIPHPDHTWFID GSSTWPNRHSPAKVGYAIVVSS TSILEATALPPSTTSQQAELIALT RALALAKGLHVNIYTDSKYAF HILHHNAVIWAERGFLSTQRSSI IIASLIKTLLKAALLPKEAGVIH CKGHQKASDPIAQGNAYADKS DNGLAFTSQI/I/HKQFLRLLVFS GTFIPLTVLNLQERTGQYFYLLP FTELEPVLEKLQGTVHLNFYMD
17444	47812	A	17550	1	355	
17445	47813	C	17551	99	335	
17446	47814	A	17552	21	447	LGPLPFSLSPCCLHCQGKRLCG HHEEARRRKNVSIPRKEAGIIHC KGHQK/A/SDPIAQGNAYADKT KFLDLAFPPLRLSFTCQITQAVS QALGIQWNLHTLTILNLQKRIR ACPQDATGYSPFELLYGCSFLL GPSLIPDTSPT
17447	47815	A	17553	119	239	TQKGQRAALFLICILSPSPLPTL GKNFKN*IPALKPHNRI
17448	47816	A	17554	1	798	
17449	47817	B	17555	460	1059	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17450	47818	A	17556	3	1476	IPTCPVPLLGQDILTKLSASLIIP GLQPHLIATLLPNPKPPSPLPLV SPNLNPQVWDTSTPSLATDQTP ITIPLKPNHPYLAQCHYSIPQLA LRGLKPVITRLLQHGLLKPINSS YNSPILPVQKPDKSYRLPQDLD LINQIVLPIHPVASPHIIPDTTPDP HDCISLIHLAFTPFPHTSFFPIPHP DHTWFIDGSSTWPNRHSPAKV GYAIVVSSTSILEATALPPSTTS QQAELIALTRALALAKGLHVNI YTDSKYAFHILHHNAVIWAER GFLSTQRSSIIIASLIKTLLKAAL LPKEAGVIHCKGHQK\ASDPIA QDNAYADKLAKKAASVPTSVP HGISQAPPPLPTHQARYWQIDF THMPRVRKLKYLLVWVDTFTG WVEAFPTGSKKATAVISSLLSDI IPQFSLPTSIHSDSRLAFISQITQA VSQALGIQWNLHISYRPQSSGK VEQTNGLLKTHLTKLSLQLKK DWTVLLPLALLRIRACP
17451	47819	A	17557	24	594	VGSGDLPWEGNPLSSCSLLHEK DPPTTSGPQTDQPKEHLTNFKS GCSSPGPARSQFFLSLRSSTL*SF YHLPSSHLVCLTVSFRD*PSPTC PAIDS*KGG/CELKA/RVKEHFC HDLPASSMQSNYPVHDSGHLT TGPSLFKPTLNIEYSTGHAPYHV RSACFPFAFCHDCQFPEASPEAE AAAILSVQPAEP
17452	47820	A	17558	1	1152	
17453	47821	C	17559	301	462	
17454	47822	A	17560	1	423	
17455	47823	A	17561	421	856	KLINLFSNFCSYSRQFLSFSSTL YFVWVFCYNRCCFSK*RMIVHI TNRDINCQIAYARIEGDMIVCA AYAHELPKYGVKVGLTNYAAT YCTGLLLAHRLLNRFGMDKIC YLDAGLARTTTGNKVFGDLDG GLSIPQSTK*FPGYD

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17456	47824	A	17562	3	1082	GPLCIALALQEFGTRRRWACRS LSSSGRRSLFRRMGSVKAVKNK AYFKRYQVKFRRRREGKT\DYY ARKR\LVIQDKNKYNTPKY\RMI V\RVTNRDI\ICQMLYA/RRIEGD MIVCAAYCTPNLPKIWV*RVGL TNY\AAAY\CTGLLL\ARRLLP*/ RFGMDKIYEGQV\ELTGDEYNV ESIDGQPGCLPPAYL\DAGPCSE PTHWPLKFFGAPEGKLWMGGL SIPSQYPNRFP\GYDSEKQRNFN AE\VHRKAHSWGQNCCRFTWR YF\MEED\EDAYKK\QFS\QYIK\ NSVT\PDMM\EEMY\KKAHAAI RENPVLWKRRPK\KEV\KKKRW NRPKMS\LAQ\KKDRVAQKKAS FLQSSRSGLLESLTPAIFP
17457	47825	A	17563	2	4967	
17458	47826	A	17564	56	284	RQTRRAAGIVRGDCPASSPTNC DLGQC/NSTS/LEPRFVQTVHLL CPWT/GGSSPLLAARGSLPVSLL GPLKPMVSCAGR
17459	47827	A	17565	1	3525	
17460	47828	B	17566	35	3691	
17461	47829	B	17567	80	3787	
17462	47830	A	17568	225	507	
17463	47831	A	17569	2	2621	
17464	47832	A	17570	14	1658	
17465	47833	A	17571	1	3654	
17466	47834	B	17572	1	3570	
17467	47835	A	17573	1	3663	

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17468	47836	A	17574	485	2347	TEPKTKTT*LSQ*MQKRPLTKF NNTSC*KLSIN/IVLEVLARAIRQ EKEIKGIQLGKEEVKVSLFADD MIVYLENPTVSAQNLLKLIGNF SKVSGYKINVQKSQAFLYTNNR QTERQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENNKPLLKEV KEDTNEWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRACIAKSI FSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIAQWNRT EPSEIMLHIYNYLIFDKPEKNKQ WGKDSLFNKWCWENWLAICR KVKLDPFLTPYTKMNSRWIKD LNVRPKTIKTLEENLGITIQDIG VGKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRQ PTTWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDV NRHFSKEDIYAAKKHMKKCSS SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRKIQ/GGIWCDRIL* R*TTCRVAKEIQSL*RRI/WKRL QRTLSIPVLDAV*PPMF*ASVID TMTI*CFEARDTCFTLTLESFWD MHRCLAASKGIGLLLC*PLIWH MSLMGVKSPPFVFSCLWTSAV
17469	47837	B	17575	1	3354	
17470	47838	A	17576	1	3297	

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17471	47839	A	17577	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
17472	47840	A	17578	1	3514	MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFFSAPHHTYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRIKNLTKSRSTTW KLNNLLLNDYW
17473	47841	A	17579	1	3693	

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17474	47842	A	17580	1577	3354	TEPKTKTT*LSQ*MQKRPLTKF NNLSC*KLSIN/IVLEVLARAIRQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELGKTALKFIWNQKRARITKSI LSQKNKAGGITLPDFQLYCKAT VTKTAWFPSGDVGLEADFSPSH TLKTQFFSCLAEFAAASCFFQR MNGFGMAMTTTYSTGAAESPL PSCSIDQGDDTKLHRARSPGRT FPAAAGIPAAAAPDGPPLSLLH KLWFPVELGGRALPRAEESHGE VAALGVMVVAQGGKNQGEEA RSTPWLRPTSHLPPCSSSSAWW TEQTDAHPLLFLLCLGIYLLNA LSNLSMVALVRSDGALRSPMY YFLGHLSLVDVCFTTVTVPRLL AGLLHPGQAISFQACFAEMYFF VALGITESYLPAAMSYDRATAA CRPLRYGALVTPWALRLAARY DRLASVVYAVITPTLNPFINSLR NKEVKGALKRGLRWRAAPQE
17475	47843	A	17581	1	3042	
17476	47844	B	17582	1	3384	
17477	47845	B	17583	1	3264	
17478	47846	A	17584	1	3780	
17479	47847	A	17585	1	3165	
17480	47848	A	17586	1	3894	
17481	47849	A	17587	1	3345	
17482	47850	A	17588	523	3981	
17483	47851	A	17589	1	3429	
17484	47852	A	17590	1	3921	
17485	47853	B	17591	1	4797	
17486	47854	A	17592	1	6499	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ

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17487	47855	A	17593	1359	2520	IQCHPHQATNYFLHRIGKNYFK LHMEPNKSLHSQDNPKQKGTK LEV/CTLPDFKLYYKATVTKTA LYLYQ/NQRCRSMEQNRALRN NATYIYNYLIFDKPEKNKQWG KDTLFNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNTIQDIGMGKD FMSKTPKATATKAKIDKWDLIQ LKSFCTAKETTIRVNRQPTEWE KIFGIYSSDKGLISRIYNELQQIY KKKTNNPIKKWVKDMNRYFSK EDIYAAKRHMKKCSSSLAIREM QIKTTMRYYLTPLRMAIIKKFG NNRQETVREMACLLSGTMDFR HRACFVLSKPDFSTRWPGADA QRPPVLVVVALDSSLPFPQASG QRPPSLEDVDGGAGALVAPC
17488	47856	A	17594	1	1227	
17489	47857	A	17595	2	2774	NLCSLIIPLREVTIVEKADSSSVL PSPLSISTRNRMTFLFANLKDRD FLVQRISDFLQQTTSKIYSDKEF AGSYNSSDDEVYSRPSSLVSSSP QRSTSSDADGERQFNLNGNSVP TATQTLMTMYRRRSPEEFNPKL AKEFLKEQAWKIHFAEYGQGIC MYRTEKTRELVLKGIPESMRGE LWLLLSGAINEKATHPGYYEDL VEKSMGKYNLATEEIERDLHRS LPEHPAFQNEMGIAALRRVLTA YAFRNPNI
17490	47858	A	17596	1	3472	
17491	47859	A	17597	1	900	
17492	47860	A	17598	1	1290	
17493	47861	A	17599	153	3834	
17494	47862	A	17600	299	1184	
17495	47863	A	17601	1	729	
17496	47864	A	17602	1	2232	
17497	47865	A	17603	36	224	TQWGPSVCWCLIPWPSFPDQ*P GF*AVLLPWRCQGFWPLLLAC APAGPATAAEPAVSSPAEP
17498	47866	A	17604	1	624	
17499	47867	A	17605	1	578	RDLDLFSLPQDITL\VHYVDGIM LIGSSEQEVASTLDLLVRHLHA RGWEINLTKIQGLATSVKFLGV QWYGACRDIPSKVKDKLLHLA PPTTKKEAQHLAASFEWGPEQ KGLQQVQVAVQAALPLGLYDP ADPMVLEVSVADRDAVWSLW QAPIGESQWRPLGFQNKALPSA DNYSPFERQLLACYWALVETE

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17500	47868	A	17606	1	282	PIYRVSRKAANFEWSPEQEKAL QQVQAAVQAAWPLGPYDPAD PMVLEVSVADRDADWSCWQA SI/GHKVGHAQQHSIIKWKWYI RDWARADPEGT
17501	47869	A	17607	1	338	SIYLVTQKAA/SSEWGPEQEKA LQEVQAAVQAALILEPYDPAGP VVLEVSLADRDAVWSLWQAPI GESQQRPLGFWSKALPSSA/DH KACHAQQHSIIKWKWYIHDRA RAGPEGT
17502	47870	A	17608	1	757	
17503	47871	A	17609	1	1317	
17504	47872	A	17610	2	24	LCQRLLLAEPNEKPGSLGNVM AVARIEIGICEYYHEKTTEKALD SHGVLAGSTIKGVRSFQRNLEL KLPATERATANAIELLTVLDQA YENFAPQILPSTGSPTSQETAQF KANQNKPLVRGKGSPHEAIRYI SAAHREWKPAILTSAIRSFCST WLVFTSKNFPKLVTQHGSTIAG NGQSSDETQVQGAAWKSDSRG TKRQIPTWILAEGNNAGAQLDI PGPTIPAPNCSLKVPQSWSTTPS MPSSLGKAYWLLACYWALVET E/RLAMGHQVTM\KPELPVMN WVLSDPSSHKVGGAQQHSINK WKWYIRNRARAGPEGTS*LPAP LIG
17505	47873	A	17611	1	1815	
17506	47874	A	17612	875	1916	PGKQGLEWTPRKLQQTCKRGA GQLEEKLANRKQ*HQH*QKG*P /PQKLNAKDHNSSPTREQNWTE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNFDKRLEEL LIQITSLEKNISDLMELKNTARE/ LLEAYTSINSQIDQAEMDR*PD* **RRKERRIK*HNKK**RGYHN*S \QEIQTTIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVEP LNRPITSSEIEAVINSLPNQKSPG QTNSQLTSTRDAEKAFNKIQHP FMLKTLNKLDIDGTYLKITRAI/ S*QTHSQCHTEWAKAGSIPFEN RHKTRMPSLTTPIQYSIGNSGQ GNQEFWKLHLVEREW
17507	47875	B	17613	1	1158	

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17508	47876	A	17614	851	1344	IILKPSPSPLYPWKNCLPRNPSL VPKRQTGSGVDIWQTAADLQQ RGLLEGKLTNRKE*YQHQQKR CPHQNPI*RSPTSNTKARE/QNW TENEFDELTEVGFRRWIITNSSQ LKEHLLTQCKEAKNLEKRLEEL LTRITSLEKNINDPMELKNTAEE PHEAYTSINS
17509	47877	B	17615	99	716	
17510	47878	A	17616	1	588	
17511	47879	A	17617	1	1140	
17512	47880	A	17618	1	774	
17513	47881	A	17619	3	527	AENSKKQNASSPPND/RNSS/EA QNWTENEFDELTEVGFRRWIV TNSSKLKEHVLTQCKEAKNLD KRLQELLTRITSLEKNINDLMEL KNTARELREAFTSFCVNCEAVS LITSLREDSHWLEDSKGHRM/R RHQE*KCEYFHPPHPGLQFYQL PESDSHSDPLWPHGGSFLSSVV
17514	47882	A	17620	1	1383	
17515	47883	A	17621	1	990	
17516	47884	B	17622	337	1515	
17517	47885	A	17623	153	474	QTKSNNVNIKKQDVHTKTPSEG HQHQRPK\DHNSLPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLEKRLQEL LTRITSLEKNINDLMELKNTA
17518	47886	A	17624	1	771	MPFSDTERVITGPSTKVHSYPG GLQALLLQLRLHSLMWRWSAA VAIGVHVRCDLLAVHPVLWAV PQWQEPIEKMLTLIPGPRITATII GLYQHEGIRAYCDSRVYYIKPS SGIESVLTRPSTQDHNSSPAREQ NWTENEFDELTEVGFKKWVIT NSFELKEHVLTQWKEAKNLEK RLANLLTRITSLENINDLMELK NTAQELHEAYASINSRINQSEER ISEIEDQLTEIEQVDKIREKRIK/R RNEQSL*EIWDYV

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17519	47887	A	17625	53	814	PGKQGLEWTPRKLQQTCKRGA GQLEEKLANRKQ*HQH*QKG*P /PQKLNAKDHNSSPTREQNWTE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNFDKRLEEL LIQITSLEKNISDLMELKNTARE/ LLEAYTSINSQIDQAEMDR*PD* *RRKERRIK*HNKK**RKEQAAI FAVLQPPLVITRQTGSGVDPQK TPADLQKRCRTVRRKTSQQKA VASTLTKRITTQKLNAKDHNSS PTREQNCTENEFDELTEVGFRR WVITNSSELKEHVLTQCKEAKN FDKRLEELLIQITSLEKNISDLM ELKNTARERWKHTQVSIAKSIK QKWTASQTNKEEKREESNSTIK NDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEVEPLNRPITSSEIEAVI NSLPNQKSPGQTNSQLTSTR
17520	47888	A	17626	1	1566	
17521	47889	B	17627	1	1005	
17522	47890	A	17628	1	2172	
17523	47891	A	17629	1	504	
17524	47892	A	17630	2	1601	
17525	47893	C	17631	132	278	
17526	47894	A	17632	380	828	EVLRVMIELNAVIYPYPKDTGC QPLV*HAAASLNSPEVMGATQ LKPLRPCKKCPKI\LEGGH*EW MEARHRNLGTLHGLPCSRTHF* TTTAQGEWLCCLCHCGEHPQG GRHPCIC*HCYSCHTLAPPVQW TPNVAEPDNKAGAQYKSPRV
17527	47895	A	17633	1	963	
17528	47896	A	17634	2	368	EFSDPIHHTFDHMWRTKEHNE AGWLLLSSVDKVMKENDELGD SISQLQKQILSLKSAKIALSESLI SCRERTEIVEK*T*ALIMLVADL Q*KVHAQPHHAQPRQVSTVKV RALIVLQEVTDP
17529	47897	A	17635	1	1881	
17530	47898	A	17636	755	939	ARKNTRIIYSYGVCKNVETWR* MFCTLLGRQQGCATVGKGDRC GPLRYYASWRKGDVLQGD
17531	47899	A	17637	367	423	
17532	47900	A	17638	3	1925	
17533	47901	A	17639	1	1137	

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17534	47902	A	17640	153	474	QTKSNNVNIKKQDVHTKTPSEG HQHQRPK\DHNSLPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLEKRLQEL LTRITSLEKNINDLMELKNTA
17535	47903	A	17641	1	1068	
17536	47904	B	17642	1	717	
17537	47905	A	17643	585	2302	VLQLLRQERLELFVPPGELVVS LASGVKLQTFAGGKAWLLQTH SDLGEQKLTTFIPISLSLKVIFWC NWPEAKTAAYDGEQATCEPVL KAMFLADTHLLREFLGHWLDK LRREWQVERAFQTALWLLQPE VVFILEDVFDEGKWSTSEAWV DDVEQFRKMFRHPSHVQLKVV AGNHDTGFHYETNTYEVERWR NRNNPSFIMGSITPTDYALSKCH LPPEDVVLIIYCGVKLPDRIVDS KAGLLKLPVLKNVISTQLQFPSI MDQLLVYNLFNETSPLVMCLD VMAMSNRGNHHLAATRLRKV LDHNSLPAREQNWTENEFDELT EVVFRRWVITSSSELKEC/DVLT QWKEAKNLEKRLDELLTRITSL QKNINDLIELKNTAQELHEAYT SINSQIDQVEERISEIEDQLNEIK CEDKIREKRMKRNKQTLQETW DYVKRPNPCWIGVPESDGENG TKLENTLQDII\QENFPNLARQA NIQIQEIQRTPQRYSSRRATPRHI IVRFTKVEMKEKMLRAAGEKE DETDNNEFFLWSQKGKRAGTL NDHVEESCPPTKNACLGTPIHC
17538	47906	A	17644	1	282	PIYRVSRKAANFEWSPEQEKAL QQVQAAVQAAWPLGPYDPAD PMVLEVSVADRDADWSCWQA SI/GHKVGHAQQHSIIKWKWYI RDWARADPEGT
17539	47907	A	17645	3	903	
17540	47908	A	17646	1	349	
17541	47909	A	17647	1	489	
17542	47910	A	17648	1	352	
17543	47911	A	17649	1	505	KTDGSWRMTVDYHKLNQVAT PVAAAVPDVVSLLEQINTSLDT WYAAIDLGNVFFSIPVHKVHQK KFAFSWQGQQYTFTVLPQGYIN SPALCRHFVRRHLD/RFSLPQDI TVVHYIDDIMLVG\PLIYRMTR KAAIFEWGPEQKALQQVQAAV QAALPLGPYDPADPMRLR

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17544	47912	A	17650	1	1557	MASPEAVASQDNDGFSQKPPPT PLFASRSVNRLKSQRTPRGEVE SVTDGEKTDGSWRMTVDYCKL NQVVTPIAAAVPDVVSLLEQIN TSPDITLVHYIDDIMLNGSSEQE VTNTLDLLVRHLCATGWEINPT KIQGSSTSVKFLGVQWCGDCR DVPSKVKDKLLHLAPPTTKKEA QHLTGLFGFRRKYIPYLGVLLC PIYQVTRKAASFQWRPEQEKAL QQVQAAMQAALPLGPYDPAGP MVLEIAVADTEAVWGH/WHSA SFPSHPCHCPMGP*TKWP*WQG WRLCMGSATWTSTHEG*PGYG HQ*VPNLPAAETNTEPAI*HHS/ SRRSASYLVAG*LYWTSCIMER AE\HLLWIWVCLSCMQCFCQD YHPWTHGMPYPPLWYSTQLCL *PRHSLYH*RSVAVGSCSWNSL VLPCSPSS*SSRVDRTVERPFEIT TTMPTSQESRVQESRGGSGSGT THHHP**STSNIFASCFYGITFC WSRGLSSRGRNAATRRQNNSIK L*VKIATWTLWAPPTSKL
17545	47913	B	17651	47	838	
17546	47914	A	17652	1	1566	
17547	47915	A	17653	1	981	MVAIAKVLIAYKEDSDSHNQPN TRMTVSKGPVSAVEGGRRGQD SDDCVEENDAVRTWPPSRILRT ESHPSPHTCSWRRHLLSSCPYT GMSFPIPSSGNISSTHAVISFPPL SEEMNPMLPKATVMTSLEAAA RQNLKSRQAPRCEVESVTHEEV YYTRKELFEFSNLYRKKSGEQI REWILRKTDGSWRITVDYRKL NQMVTPIAAAVPDV/VVSLLEQ INTSPGTW\LCHNLIWRDLDCFL LPQNITLVHYTDDIMQIGSSEQE VANTLDLLPALMASW/ENSP*SI DRGRED*SLVHKWFCTICRHHP KVDSCSTTAPF*DIPEGQQL
17548	47916	B	17654	179	1219	
17549	47917	A	17655	1	2655	

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17550	47918	A	17656	1	942	MVGKAKWKPLELPLPRKIVNQ KQHHIPEGIAEIAATIKDLKDAG VVIPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHQKPFAFSW QG/QQYTFTVLPQDYINSLAL*H NLIWRDLDYF\LLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSII KWKLYIHDQAQTGPEGTTTSVI AQWAHEQSGPGSRDGGYAWA QQHGLPLTKADLATTTAECPVC QQQRPTLSPRYGTIPSLPLTKAL TLQLKKCSSGPMLMEFTGLAM FPIILKQLD
17551	47919	A	17657	1	868	
17552	47920	A	17658	83	346	
17553	47921	A	17659	1	643	MVGKAKWKPLELPLPRKIVNQ KQHHIPEGIAEIAATIKDLKDAG VVIPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAV PDVVSFLEEINTSLGTWYAAID LANAFFSIPVHKVHQKPFAFSW QG/QQYTFTVLPQDYINSLAL*H NLIWRDLDYF\LLLQDITLVHYI DDIMLIGSNDHKVGGAQQHSII KWKLYIHDQAQTGPEGT
17554	47922	C	17660	38	202	
17555	47923	A	17661	3	410	LKSRQAPRCEVESVTHEEVYYT RKELFEFSNLYRKKSGEQIREWI LRKTDGSWRITVDYRKLNQMV TPIAAAVPDV/VVSLLEQINTSP GTW\LCHNLIWRDLDCFLLPQN ITLVHYTDDIMQIGSSEQEVAN TLDLL
17556	47924	A	17662	2	526	
17557	47925	A	17663	2	431	
17558	47926	B	17664	55	1506	
17559	47927	A	17665	1	753	
17560	47928	A	17666	73	310	QLAEPPHWLPD*KGAGFEWGP EQKKALQ*VQAAVQAALPLGP YDPADPMVLVVSVADKDAVWI FHLSGSDRWRRTYRCL
17561	47929	A	17667	323	687	KTDGSWR/TVDYRKLNQVVTPI AAAVPDVVSLLEHINISPGIW/H HQKQFAFS*QGQQFT/FTVL/PH GYINSLALCHNLIRRDLDHFSLP QDITLVHYIDDIVLTGSSEQEVA GS\LESTCRHTKV
17562	47930	A	17668	3	1363	
17563	47931	A	17669	1	1203	

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17564	47932	B	17670	130	1374	
17565	47933	A	17671	1	1063	
17566	47934	A	17672	3	239	
17567	47935	A	17673	231	368	NKHQEDSLKPPIPGPSSWTAF/P KPTLGQKGTCCTEKKKKKKKK GRI
17568	47936	A	17674	1	1270	
17569	47937	C	17675	100	270	
17570	47938	A	17676	459	1978	
17571	47939	A	17677	35	347	VVRAWYPGWGQGSEKEWQW DQQEALGRVRGSKVTGEWEGR AGPEGTGQNGEGPRGILEVGGT TAPFCLAEGEWGPGGHPHHLLF PPSPPRPPPQPPPTPPEPPS*PPSP PRPPPQPPPTPPEPPS
17572	47940	A	17678	236	397	NWLQPCG*AHPTGSGFPAPKLC PASPGAPFSNE\ILSEPGPTLAPM PT/GAPCRSHGAGHSGDPGWPS SSPTGEDTNSAGPGAARVQMG CGHCVSLVPR*/CCWTPGGA
17573	47941	A	17679	132	492	TDHRDRKDKHPPALPASAMDK KNA/GQEGRPGASRGSSPMATA TTGPQGVMPGYH*CSLRPKGSS VGLW*MLPGLGLTLQDSGLPS GPRQVQNYCPGAKALNQGPQE PA*CKASNQRPSVYLPTREYPS EQIIVTEKTNILLRYLHQQWTK RTLPRRKTRSKQRKLTYGYCH YRSTGSNARLPLMFIKTQGFFS RLVVDAAWPGTHPSGQWAPF WPKAGPELLSRSQGFESGTSRA RLMFYPTMAAPVPK
17574	47942	A	17680	618	755	
17575	47943	A	17681	796	1092	
17576	47944	A	17682	1	391	
17577	47945	A	17683	1	697	
17578	47946	A	17684	1	888	
17579	47947	A	17685	749	1667	
17580	47948	A	17686	1	2088	
17581	47949	A	17687	189	438	
17582	47950	A	17688	387	497	

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17583	47951	A	17689	1	728	MAQEIEGDRLFRARLTRRVQG KGPCGPLKAPLGMVPECHSVK PSRDTFDSTKSFKALLLSFLKIP AIDVHKPIDHPINFTFPDPGHRA PARHRHSTAAAVTMSPSGP/PA AAPSPCSPIPRHG*GPLRATSYC PVSWKQKQNSVSNKQTNEQTK TAKAEGARSRGPRNKIPGLPPG PRSGLRIWLPPPREGSGFQTPAR GHPQPPCSGKGTECQSIAQNLA SRISPVGTSCGRTSRQTIRVRK
17584	47952	A	17690	1	819	
17585	47953	A	17691	1	2115	MSGSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKQPLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPPSRWDDGIS GIIADYSITAQTRHEENGGDDS NEISGNGTVGVNLGPWRMRAD WQTNYQHTRTQLALGEDYLNS DIFDGLNYVGGSVSTDDQMLPP HLRGYAPDISGVAHTTAK
17586	47954	A	17692	1	1080	
17587	47955	A	17693	1	253	
17588	47956	B	17694	1	1069	
17589	47957	A	17695	1	764	
17590	47958	C	17696	136	990	
17591	47959	A	17697	1	1422	
17592	47960	A	17698	547	1017	
17593	47961	A	17699	176	431	
17594	47962	A	17700	1	846	
17595	47963	A	17701	1	1815	
17596	47964	A	17702	1	1578	
17597	47965	A	17703	1	1149	
17598	47966	A	17704	22	441	
17599	47967	A	17705	828	920	
17600	47968	A	17706	1	231	MESKRLDNA/CAGGGD*PQLH QCPR*TAVD*RRNQTAFA*RDA STYRHESGGNASPECHGLYQR QKNADGGGGQRRI
17601	47969	A	17707	1	563	
17602	47970	A	17708	19	372	
17603	47971	A	17709	134	491	
17604	47972	A	17710	1	969	
17605	47973	A	17711	59	839	
17606	47974	A	17712	186	725	
17607	47975	A	17713	1	251	
17608	47976	A	17714	1381	2217	
17609	47977	A	17715	357	804	

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17610	47978	B	17716	1	2361	
17611	47979	A	17717	1	2832	
17612	47980	A	17718	1	3477	
17613	47981	B	17719	143	3122	
17614	47982	A	17720	1	3018	
17615	47983	A	17721	1	4371	
17616	47984	B	17722	1	2010	
17617	47985	A	17723	1	2168	
17618	47986	A	17724	1	2067	MKEIEIQKSLPKINESRSWFFEKI HKIDRLLARLIKKKREKNQIDTI KNDKGDITANPTAIQTTIREYY KHLYANKLENLEEMDKFLDTY TLPRLNQEEAESLNTPITGSDIE AIINSLPTKKSPGPDGLTAEFYQ RYKEELKKEGILLSSFYEASILLI PKPGRDTTKKENFRPISLMNID AKILNKILANRIQQHIKKLIHHD QVGFIPGMQGWFNICKSINVIQ HINRTKDKNHTIISIDAEKAFDK IQQPFMLKTLNKLGIDGTYLKII RAIYDKPTANIILNGQKLEAFPL KTGTRQGCPVSPVVFNTVLEVL AREIRQEKEIKGIQLGKEEVKRS LFADDMIVYLENPIVSAQNLLK LISNFSKVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIAPKR IKYLRIQLTRDVKDLFKENYKL LLNEIKEDTNKWKNIPCSWVGR INIVKMAILPKGIHRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAR IAKSILSRKYKAGGSMLPDFKL CYKATVTKKAWYWYQNRDID QWNRTEPSEIMPHIYNYLIFDKP EKNKQWGKDSLFNKWCWENW LTICRKLKLDPFLTPYTEINSRW IKDLNVRPKTIKTLEENLGNTIQ DIGMGKDFMSKTPKAMATKAK IDEWDLLKLK\SFCTAKETTVR VNRQPTEWETIFAIYSS
17619	47987	A	17725	1	3457	
17620	47988	A	17726	1	3630	
17621	47989	B	17727	1	3384	
17622	47990	B	17728	1	2199	
17623	47991	A	17729	1	3924	
17624	47992	A	17730	1	3345	
17625	47993	A	17731	1	2382	
17626	47994	A	17732	1	3720	
17627	47995	A	17733	1	3894	

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17628	47996	A	17734	1	2427	MGCVRQIIPLGTHPVVHQLTSIP QNCQSPQKTRKDREIGQPRGAY GDMRSKCNVMLMMESWNRKR TLEIQTTIREYYKHLYTNKLENL EEMDKFLDTYTLPRLNQEEVES LNRPITHSDIVTIINSLPTKK\SPG PDRFTAKFYQRYKEELVPFLLK LFQSIEK/EGILPNSFYEASIILIPK LGRDTTKKENFRPISLMNTDAK ILNKILANRIQQHIKKLIQHDQV GFIPGMQGWFNIRKSINIIQHIN RIKDKNHMIISIDAEKAFDKIQQ PFMLKTLNKLGIDGTYLKIIRAI YDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEALAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTS NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWIGRINIV KMAILHKALYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLPDFKLHY KATVTKTAWYWYQNRDIDQW NRTEPSEIIPPIYNYLIFDKLDKN KKWGKDCLFNKWCWQNWLAI CRKLKLDPLLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQDI GMGKDFMSKTPKAMATKDKID KWDLIKLKSFCTAKETTIRVNR QPTKWEKIFVTYSSDKGLISRIY
17629	47997	A	17735	1	3780	
17630	47998	A	17736	1	2808	
17631	47999	A	17737	1	4842	
17632	48000	B	17738	331	3282	
17633	48001	A	17739	1	2880	
17634	48002	A	17740	1	3213	

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17635	48003	A	17741	1	2561	MKAEIKTFFETNKNKDTTYQNL WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT YSKASRRQEITKIRAELKEIETQ KTLQKINESRSWFFEKINKIDRP LTRLIKKKREKNQIDSIKNDKG DITTDPTEIQTTIREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITGSEIEAIINSLPT KKSPGPDGFTAEFYQRYKEELV PFLLKLFQSIEKEGILPNSFYEAS IILITKPGRHTTKKNFRPISLMNI GAKILNKILANRIQQHIKKLIHH DQVGFIPGMQGWFNIRKSINVI QHINITNDKNHMIISIDAENAFD KIQQRFMLKTLNKLGIDGMYL KIIRAIYDKPTATQNLLKLIGNF SKVSGYKINVQKSQAFLYTNNS QTESQIMTELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLSEIK EDTKKGKNIPCSWVGRINIMK MDILPKVIYTFNAIPIKLPMTFFT EVEKTTLKFICNQKRARIAKSFL SQKNKAGGITPPDFKLYYKATV TKTACYWYQNRDIDQWNRTEP SEIMQHIYNYLIFDKPDKNKQW GKDSLFNKWCWENWLAICRKL KLDSFLTPYTKINSRWIKDLNIR PKTIKTLEENLGSIIQDIGMGKD FMSKTPKAMATKAIIDEWDLIK LKSFCTAKETTMRVNRQPTEW EKIFATYSSDIGLISRIYNELKQI
17636	48004	A	17742	1	5042	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNL
17637	48005	A	17743	101	471	MLSRILASRNRMRFAVEVVRA VRE/RVGNDFIIIYRLSMLDLVE DGGTFAETVELAQAVEAAGATI INTGIGWHEARIPTIATPVPRGA FSWVTRKLKGHVSLPLVTTNRI NDPQVADDILSSTH
17638	48006	A	17744	161	311	

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17639	48007	A	17745	221	799	
17640	48008	A	17746	20	346	
17641	48009	A	17747	431	1578	
17642	48010	A	17748	1	771	
17643	48011	A	17749	3	863	AVLRREMRQMEGAWLGSDLV DQGKERLNRLGFFETVDTDTQ RV/PGSPDQVDVVYK\IVSLGGR LFYNDFQADDADLSDYTNKKIE IIDSHADYFHIDIMDGHFVPNLT LSPFFVSQVKKLATKPLDCHLM VTRPQDYIAQLARAGADFITLH PETINGQAFRLIDEIRRHDMKV GLILNPETPVEAMKYYIHKADK ITVMTVDPGFAGQPFIPEMLDK LAELKAWREREGLEYEIEVDGS CNQATYEKLMAAGADVFIVGT SGLFNHAENIDEAWRVMTAQIL AAKSE
17644	48012	A	17750	2	893	
17645	48013	A	17751	139	2057	
17646	48014	A	17752	2	361	
17647	48015	A	17753	497	897	PRSASFSAWLAFCST/TKDSHPL LAQLLDGVENLDHRQHLLFTA GHGARPLIRAHADVEENCDHPF ILIVHPSIHPIIYLSIHPSTIRGERL MTQIPLIKHFLAGVTGLKLTQQ MRFCENVCLPLIATAGNRQTH
17648	48016	A	17754	83	1038	PSRAGHLPPKIKSSMAGTTPCLS IMVRQRK/PLVPAPLYQGMRDG KIVRFEEITRTPLEVQDCLLASA LALGLALMGNAQAVTTIPFWH SMEGELGKEVDSLAQRFNAEN PDYKIVPTYKGNYEQNLSAGIA AFRTGNAPTYFAGHIMQACGV ALSATIYFIRRKVVSLSDQKLNI AMTFVGSMSGALLVQYVQAD VLRQILPILVICIGLYFLLMPKLG EEDRQRRMYGLPFALIAGGCV GFYDGFFGPAAGSFYALAFVTL CGFNLAKATAHAKLLNATSNIG GLLLFILGGKVIWATGFVMLVG QFLGAPHGVPTCV
17649	48017	A	17755	571	1728	
17650	48018	A	17756	332	511	
17651	48019	A	17757	581	637	RALR*SLQDGSAKRGASVS
17652	48020	A	17758	1	1098	
17653	48021	A	17759	1	366	

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17654	48022	A	17760	321	611	GEGENYCDSVVMTWVAI*QN WQCHCCSLRCASLRQG*RQDV TDTRGETIKREMARNWV/WRA RVINAGFSRGSLLRGPISDHRRK RLSASIRQFYPRP
17655	48023	B	17761	95	645	
17656	48024	B	17762	1	3978	
17657	48025	A	17763	1	328	MLIAEGLMTAKNITVITNSLPA AFALSENKDITLVVCGGTVRHK TRSMHGSIAERSLQDINADLMF VGADGIDAVNGITTFNEGYSIS GAMVTAANKVIAVLDSSKFNR RGFNQVLPIEKIDIIITDDAVSEV DKLALQKTRDTSLVYVLSLADF FRTASTIGERDGTQVEMILFAGF VYLVISLSASLLVLTDCSTEVK KGEVVVVCGPSGSGKSTLIKTV NGLEPVQQGEITVDGIVVNDKK TDLAKLRSRVGMVFQHFELFPH LSIIENLTLAQVKVLKRDKAPA REKALKLLERVGLSAHANKFP AHYSGGQQQRVAIARALCMDP IAMLFDEPTSALDPEMINEVLD VMVELANEGMTMMVVTHEM GFAVKWRIGSTQQGAQLHCNR WLHVRKHLLVAYYNLVGIKPG KESYMRLNEKALDDFCQSLVD YLSAGHFSIYERILHKLEGNGQ LARAAKIWPQLEANTQQIMDY YDSSLETAIDHDNYLEFQQVLS DIGEALEAAFVLEDKLILLVLD AAR*NLLKLKVIIMIDGGFQTGI VVIHNLLSIGFELRPNLRGAREL PVAFQLMKNALINTEMSGRQVI DQALTKIIKGFFV
17658	48026	A	17764	216	473	DALRVASGNGCYSALLPLFCRL L*AESA*VPVQRPCGETLMRSS VVCLGGTAPECSSLGCAEKSGR SWPRKVAHTLGSWTVPRES
17659	48027	B	17765	1	1570	
17660	48028	A	17766	1580	1764	PASSLVMR*CLNRIA\SRAHQPA VRAY*SASAPGIA*KENA*G*RL HHR*NPAGKPDPGLL
17661	48029	A	17767	1	1827	
17662	48030	B	17768	1	1281	
17663	48031	B	17769	72	1169	

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17664	48032	A	17770	20	552	SAGDA*DWFWHGGVAGGNG*RSP*A/VTSSALKCIHRALVRAWLLRMKKV*ATCA*CVTMRLKCCIK*/CPDNSLRMVQLFFPDPWHKARHNKRRIVQVPFAELVKSKLQLGGVFHMATDWEPYAEHMLEVMSSIDGYKNLSESNDYVPRPASRPVTKFEQRGHRLGHGVWDLMFERVK
17665	48033	A	17771	3287	3568	CAFQRNIWHAKLNASPTPVFVP**LLASLTIPMKPAAMPGGKMDWWRVCRASASRPCQK*SLCQTPASVNTLLTVTAVCCASMASTTTRLWKI
17666	48034	A	17772	1	3126	
17667	48035	A	17773	249	3943	
17668	48036	B	17774	1	2178	
17669	48037	A	17775	263	434	
17670	48038	A	17776	619	1184	MRTSCGSFIKRRVMRRIASGMVAENRAV**PSGICAIMVSTSSMKPMRSISSASSRTRPLSL/AEVQSATFQVVQQTARSTDNDLRPLTQGA*LHVITLAAVQS/IPHLRRACV*RNPSLLQQPVPPVRGSVPAPESVVLSAQDQDSATEVKRMLQFFRSPSGPYPERRGHSADVEYTLPELEMVFRNPDR
17671	48039	A	17777	1	1485	
17672	48040	A	17778	497	1838	
17673	48041	A	17779	534	922	
17674	48042	A	17780	1	458	MQQLEEALKQLAQGSGSSQALTQVRRWDSACQKLPDANLALISVAGEYAAELANQALDRNLNVMMFSDNVTLEDEIQLKTRAREKGLLVMGPDC/WYVDDCRHTAGFC*RDAGRQYWRHWRFRYRDSGAVFADCAGRGGNYSRDWPWRARPQP
17675	48043	A	17781	2	270	QAGKYYGGAVFAPVFGAIMGGVLRTMNIEPDALTSVDKNEFVINHGEGTGGRS*FARPSCSVGARRTFASTARDDTRQPCGCGGRSLCS
17676	48044	A	17782	1	1437	
17677	48045	B	17783	63	201	
17678	48046	A	17784	1016	1263	
17679	48047	A	17785	1	933	
17680	48048	B	17786	1	1888	
17681	48049	A	17787	845	2220	
17682	48050	A	17788	110	581	
17683	48051	A	17789	696	989	

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17684	48052	A	17790	199	573	
17685	48053	A	17791	1	3270	
17686	48054	A	17792	1	3018	
17687	48055	B	17793	1	708	
17688	48056	A	17794	264	512	FLAQWLPELPLSRHLRQCTWCR RHRNRW*VRSLHRCWLADCRC PELRIRSHDL*SLAQRSLYDRTR TPDRRQLRTVLHWLLC
17689	48057	A	17795	1	2109	
17690	48058	A	17796	1239	1854	YHDDRNQPDAGNPSNADSGPQ I*QATGSPRRLVRR\RWKRVNR LLAGKLAIVIDDFGYRPHNENQ VLAMPSAISVAVLPDSPHAREM ATKAHNSGHEVLIHLPMAPLSK Q/TAGEKYATPGDEQRRN*AHY S*\WVNNVPYAVGINNHMGSK MTSNLFGMQKVMQALERYNL YFLDSVTIGNTQAMRAAQGTG VKVITRKVFLDGFAK
17691	48059	B	17797	1	2243	
17692	48060	A	17798	74	295	TISVLWLMLSLNTSKKRLA*TG SIGFFGLHSFTPRNGLRGASGTA FFGGVEVSTCGSFSKLLAFTSV MSGGRL
17693	48061	A	17799	1	1872	MLRIHCMQHWYNLSDGAMED ALYEIASMRLFARLSLDSALPD RTTIMNFRHLLEQHQLARQLFK TINRWLAEAGVMMTQGTLVD ATIIEAPSSTKNKEQQRDPEMH QTKKGNQWHFGMKAHIGVDA KSGLTHSLVTTAANEHDLNQL GNLLHGEEQFVSADAGYQGAP QREELAEVDVDWLIAERPGKV RTLKQHPRKNRTGISIAYMTGSI RARVEHPFRIIKRQFGFVTARYR GCLNTITNGDVFPLATWFGG
17694	48062	A	17800	1	1269	

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17695	48063	A	17801	1	1988	MNDSEFHRLADQLWLTIEERLD DWDGDSDIDCEINGGVLTITFE NGSKIIINRQEPLHQVWLATKQ GGYHFDLKGDEWICDRSGETF WDLLEQAATQQAGETITGFRV YTLQLNAQLRLGFLRLPYSVNL ATEYKSLTHYTKVPEATNPSLE SSVDVKLSANRLKYPMMRKRL MKMWREAKALHSDPVEAWAS IIEDADKAKSFKQARGRGGFVR SSWQEVNELIAASNVYTIKNYG PDRVAGFSPIPAMSMVSYASGA RYLSLIGGTCLSFYDWYCDLPP ASPQTWGEQTDVPESADWYNS SYIIAWGSNVPQTRTPDAHFFTE VRYKGTKTVAVTPDYAEIAKL CDLWLAPKQGTDAAMALAMG HVMLREFHLDNPSQYFTDYVR RYTDMPMLVMLEERDGYYAA GRMLRAADLVDALGQENNPE WKTVAFNTNGEMVAPNGSIGF RWGEKGKWNLESIA\RIENPHF RSVKHNPVLVRQLPVKNLTLV DGNTCPVVSVYDLVLANYGLD RGLEDENSAKDYAEIKPYTPA WGEQITRVPRQYIETIAREFADT AHKTHGRSMIILGAGVNHWYH MDMNYRGMINMLIFCGCVGQS GGGWAHYVGQEKLRPQTGWL PLAFALDWNRPPRQMNSTSFFY NHSSQWRYEKVSAQELLSPLA
17696	48064	A	17802	3854	5726	
17697	48065	B	17803	1	1869	
17698	48066	A	17804	391	1246	
17699	48067	A	17805	58	1353	
17700	48068	A	17806	872	2123	
17701	48069	A	17807	1	1422	
17702	48070	A	17808	217	509	
17703	48071	A	17809	76	422	
17704	48072	A	17810	2	288	
17705	48073	A	17811	1	1626	
17706	48074	A	17812	779	832	
17707	48075	A	17813	1	1818	
17708	48076	A	17814	1	645	
17709	48077	A	17815	157	293	ALVCSSPWPSEKCKSKPQ*DTIS HQLEWQSLKSQETTGAGEDVE K
17710	48078	A	17816	1	1446	
17711	48079	A	17817	1	306	

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17712	48080	A	17818	71	513	TIRSGLGWSQMEMRNMLGTGA KKYKLPSENTINTSTQIN*KI*K KRINSSTHTLSQD*TRKKLNL*I DQ*QELKLWQ*SIAYQPKRVQD QMDSQ/REFYQRYKEELHINRA KDKNHMIISIDAEKAFDKIQQRF MLKTLNEVLMGRISK
17713	48081	A	17819	1	828	
17714	48082	B	17820	1	567	
17715	48083	A	17821	1	1224	
17716	48084	A	17822	1	897	
17717	48085	A	17823	207	547	NHFLQGLGPLLQFPTSSSSPSET TSAWTLCPHHYQAFGQSHSTSL *EV/HKLSHIFMSSSEPSKLFQPL PVTQFQSRFHIFRYLFSSIPLYW CQFTVLVHFPAADKDISVTTIP
17718	48086	B	17824	1	1128	
17719	48087	A	17825	1	765	
17720	48088	A	17826	1	952	
17721	48089	A	17827	1570	2176	FLQSTHLTKG*YPESTMNSNKF TRKKQPNQRAKDMKRPFSKED IDAANKHMKKCSSSLAIREMQI KTTMRYHFTPVRMAIIKKSGNN RCWRGCGEIGTLLHCWWDCKL IQPLWKSMWRFLKDLELEIPFD PAIPLLGIYPKDYKSCCYKDTCT HMFIAALFTIAKTWNQPKCPTM IDWIKKMWHIYTMEYYGAIKR MSSCPL
17722	48090	A	17828	1	531	
17723	48091	A	17829	1	462	
17724	48092	A	17830	876	1111	
17725	48093	A	17831	2	276	LLPGFFCSNLAPVPPSGGHQHD LPYPSSA*NPGASGTGQARMGQ SHQWAFLWRKDAHVRKESGY MYSLYDRAYGERTTGRRGRGR GPIPRP
17726	48094	A	17832	1	1290	
17727	48095	A	17833	1293	1863	RSTPSMKE/QLATALPRHMTAE RMIRIANTEFRKVPALGNCDTM SFVSAIVQCPQLGLEPGSASGH AYLLPFGNKNEKSGKKNVQLII GYRGMIDLARRSGQIASLSARV VREGDEFSFEFGLDEKLIHRPGE NEDAPVTHVYAVARLKDGGTQ FEVMTRKQIELVRSLSKADTD* PWMCPCPMKRKSAT
17728	48096	C	17834	1	786	

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17730	48097	A	17835	2	654	FCRQRQCQVYRRGRFTHAAFT GTHRDNVLQVQSKLRADGCAL EDYFSQSEQVLPSELAFDEAPQ DVVNKVFNITLRTIMEGQSIVN VDEIHRAARFFYQARQRDLYG AGGSNAICADVQHKFLRIGVRC QAYPDAHIMMMSASLLQEGDV VLVVTHSGRTSDVKAAVELAK KNGAKIICITHSYHSPIAKLADY IICSPAPETPLLGRNASARILQLT LLDAFFVSVAQLNIEQANINMQ KTGAM*KRP*NWQKRTGQRLF V*PIATIHR*RNWPIILFAHQPRK RRY*VVMPRQEYYN
17731	48098	A	17836	1	4806	
17732	48099	A	17837	1	466	
17732	48100	B	17838	193	1045	
17733	48101	A	17839	1196	2732	
17734	48102	B	17840	1	732	
17735	48103	A	17841	290	664	
17736	48104	A	17842	302	1716	
17737	48105	A	17843	249	909	
17738	48106	A	17844	36	340	
17739	48107	A	17845	902	1455	RRCVLRP/GLDIMRNRLNIRQQ QRLEQAAYEMTALRAATIELGP LVRGLPHLRTIHRQLYQDIFDW AGQRRITLINHGFVPKSTTVVET NGPSDQSIAMRRPGQTISRIHQV QKKLGIELTNCYEHSGLPDIKN VTGILICRQTHARPARLARLIFT ANKTNTINALVDIEVDDFFTDA CQIDCCFETGSHSVLARLGGAS AQDLQLDATSASHGSK
17740	48108	A	17846	1	1668	
17741	48109	A	17847	1	1080	
17742	48110	A	17848	1	907	MRAGFTSNVLTFLTCTSHFLNT FRAADVANVQTATSNFRQIQVF EDIITQYNGKYILAVEGNPPLGE QGMFCISSGRPFIEKLKRAAAG ASAIIAWGTCASWGCVQAARP NPTQATPIDKVITDKPIIKVPGCP PIPDVMSAIITYMVTFDRLPDVD RMGRPLMFYGQRIHDKCYRRA HFDAGEFVQSWDDDAA\PKVT ACTKWAAKGLPPITPVPHTLE* WVWSRLLAGGNGLDRGRFSGV DSSWISYLSSAISVTMAPATTLN QTSKAALAACAISTLCNGWPA VILAQHRWMKWSGLAS
17743	48111	A	17849	239	899	

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17744	48112	A	17850	155	249	CMRRKTALTGGEPDR*TAMR*HNKSPALTGS
17745	48113	A	17851	1	1326	
17746	48114	A	17852	1	1394	
17747	48115	A	17853	46	705	
17748	48116	A	17854	2	488	
17749	48117	A	17855	563	687	LLARTSRQ*KTSLNCVNKL*MPSGQWAVLLLPVCRCWWLRT
17750	48118	A	17856	1	1429	
17751	48119	A	17857	1	1037	
17752	48120	A	17858	2	276	LLPGFFCSNLAPVPPSGGHQHDLPYPSSA*NPGASGTGQARMGQSHQWAFLWRKDAHVRKESGYMYSLYDRAYGERTTGRRGRGRGPIPRP
17753	48121	A	17859	1	1290	
17754	48122	A	17860	1293	1863	RSTPSMKE/QLATALPRHMTAERMIRIANTEFRKVPALGNCDTMSFVSAIVQCPQLGLEPGSASGHAYLLPFGNKNEKSGKKNVQLIIGYRGMIDLARRSGQIASLSARVVREGDEFSFEFGLDEKLIHRPGENEDAPVTHVYAVARLKDGGTQFEVMTRKQIELVRSLSKADTD*PWMCPCPMKRKSAT
17755	48123	A	17861	207	210	QLSLLLNLPLDSIHHRLASSALKRVNDQVGAAPPRHQSPPPRNAVSLAPRPVPVEWSCAKLLCLSCRVNCQD*GNKALTSIHFVWGEGIVGKMWLFYCTEAHFVRDPSGYSN
17756	48124	A	17862	2	654	FCRQRQCQVYRRGRFTHAAFTGTHRDNVLQVQSKLRADGCALEDYFSQSEQVLPSELAFDEAPQDVVNKVFNITLRTIMEGQSIVNVDEIHRAARFFYQARQRDLYGAGGSNAICADVQHKFLRIGVRCQAYPDAHIMMMSASLLQEGDVVLVVTHSGRTSDVKAAVELAKKNGAKIICITHSYHSPIAKLADYIICSPAPETPLLGRNASARILQLTLLDAFFVSVAQLNIEQANINMQKTGAM*KRP*NWQKRTGQRLFV*PIATIHR*RNWPIILFAHQPRKRRY*VVMPRQEYYN
17757	48125	A	17863	1	4806	
17758	48126	A	17864	1	466	
17759	48127	A	17865	214	907	
17760	48128	A	17866	1288	2757	
17761	48129	A	17867	705	839	AGRSRENRRYRAKQPRCGKR*F*CVYRFYPSGRYAEPSSAPNYT

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17762	48130	A	17868	199	1628	
17763	48131	A	17869	746	1013	TRARRRFITALRFSSLVSASPCC NWAAAFSS\YFCQQIVR*PHFDR QEKRSVQNQPDGCSSSASQSVR QRPKSPQQPVQSANPSLLLCR
17764	48132	A	17870	2	331	
17765	48133	A	17871	1	591	
17766	48134	A	17872	1	1197	
17767	48135	A	17873	45	3402	NRFSHISVTSACGWYHIPVEE/Q PEY/PGNLELERRIRSAIRWNAI MTVLRASKKDLELGGHMASFQ SSATIYDVCFNHFFRARNEQDG GDLVYFQGHISPGVYARAFLEG RLTQEQLDNFRQEVHGNGLSS YPHPKLMPEFWQFPTVSMGLG PIGAIYQAKFLKYLEHRGLKDT SKQTVYAFLGDGEMDEPESKG AITIATREKLD/NLVFVINCNLQ RLDSP\RWDELLRKDTSGKLIQL MNETVDGDYQTFK
17768	48136	A	17874	452	1395	LAGATGTAIRLILHAPLLLPIKM RLP/TVSEGKPDSIPAAEKFAAE NKNTYGALASLELAQQFVDKN ELEKAAAQLQQGLADTSDENL KAVINLRLARVQVQLKQADAA LKTLDTIKGEGWAAIVADLRGE ALLSKGDKQGKHQRAENCEIQ GYIDMIKHLVAPLVFTSLILTGC QSPQGKFTPEQVAAMQSYGFT ESAGDWSLGLSDAILFAKNDY KLLPESQQQIQTMAAKLASTGL THARMDGHTDNYGEDSYNEGL SLKRANVVADAWAMGGQIPRS NLTTQGLGKKYPIASNKTAQGR AENRRVAVVITTP
17769	48137	B	17875	1	1579	
17770	48138	A	17876	182	2069	

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17771	48139	A	17877	1	2017	MESGVATRPIADFDVYIDKLTE FVYKTNLFMKPIFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILIGRPNVIEMRIQKLGLQI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVTQEQAQRALIS NPTVIGAIMVQRGEADAMICGT VGDYHEHFSVVKNVFGYRDGV HTAGAMNALLLPSGNTFIADTY VNDEPDAEELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTVGPVLMGVAKP VHVLTPIASVRRIVNMVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRYQHGVVTLRFSG CFFAFHRHINAVFFRFNIQAVFV ALRPEVIAIMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIYQH VLQAEGFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTRPLWAWLKLLW QRIDEDNMTTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFIFANFLPATGDVIQRYIE QFVANSNKMTAVGA\ASLAISS YLLSLIANVLMLMS*SVLRMS WNPKWAWSSIWYS
17772	48140	A	17878	31	312	RGTGHCALYRRAAARCAKITL TTFISLFSSYFVIYNILLLIYLIFA ASFCLLVV*CIITVFITVCSAGD VSGMSATWCAFVAISVDHFTG FNRF
17773	48141	A	17879	1	1098	
17774	48142	A	17880	1	1015	
17775	48143	B	17881	1	1917	
17776	48144	A	17882	931	1773	
17777	48145	A	17883	785	956	KKWMHSAV*WRKRSIRRVSSL GY*TQAKDRRFALPELRRIVCS TVRRYVRRWRTNRT
17778	48146	A	17884	221	367	
17779	48147	B	17885	1	1318	

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17780	48148	A	17886	1190	1634	APSQTVSLPEVASSMSGVMAG VEAVSSPGPYAVCAGSLLPSGW LCVKTSVIAMIASAWSAPGAVS IKRSSAVSVRIWALCGA\QPECA VRSLPSYPAFRQVLAPVTHAL* PRRSSGCP*CDYSLQLLLQ*PAH *HLQGLLRKQLSCQR
17781	48149	A	17887	1	2499	
17782	48150	A	17888	454	1698	
17783	48151	A	17889	635	1665	KSIFWRAPADCEP/QVRQSAKV QFGDYQANGMMAVAKKLGM APRQLAEQVLTHLDLNGIASKV EIAGPGFINIFLDPAFLAEHVQQ ALASDRLGVATPEKQTIVVDYS APNRGFFGGGAPLGTTLQDLTR PTKEDGLQAKPISFWASFALQF VNVKIILYGVTALSTFVLPQTQ ALSWVVGVSVLLAMIGTFGNV CWALAGHLFQRLFRQYGRQLN IVLALLLVYCAAFSKGTSDNVA LLFRSQRVKANCITGYTDGQLR IFFRMLNCIFQSFATQNVNVQV LTTFNANFWFHFYWNFTVFNV TQFAYCNHFIFCITCFCNDATPF AFFAVQQPERVHRKTAILL
17784	48152	A	17890	73	212	
17785	48153	A	17891	2049	2445	VFPVFLRIYVFWKKPGMKVTN ARNWQLKPLFTELPVILPDTQL HYVAWMELYSPAE*ERIQA*FV VWSWNIWLY*A*RLIQK*IIALT PVVRTGKTKLMSAILFNITIHR MKAMNLSSPKRRLPPRNCGKK
17786	48154	A	17892	1	1476	
17787	48155	A	17893	332	572	RGGA*RQKHRRTSALSLLSLP* NMATAVHLHRFSTRRAVTSSS ARKWTNSGAMSGLNRASA\AV LRV*QSPEDGCCARIR
17788	48156	A	17894	80	405	PRNLRKSGPPISDAISPTSKP*TI TEPISAPSLLATYKAAGCGGTT QCTAINAVHSGMASFNNEVLV FLAIEKARGINSTTPTSTNSVMP QIRPTSTIMTSTESQRQR
17789	48157	A	17895	1	1392	
17790	48158	A	17896	1	1374	
17791	48159	A	17897	1971	2306	
17792	48160	A	17898	209	449	
17793	48161	A	17899	1	240	
17794	48162	A	17900	1	456	
17795	48163	B	17901	222	3807	
17796	48164	A	17902	3140	3219	
17797	48165	A	17903	240	298	

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17798	48166	A	17904	1902	2047	NQPVYRSNGD/RIWRTGKLFPT TVFRLIRTLSPRAFPPFTSYRRCS VAY
17799	48167	B	17905	1	1994	
17800	48168	A	17906	1	2151	
17801	48169	A	17907	3	1127	GTPYASQPVIRPVEGSKPLIKQV LDIGAHGTDKTIAQKLARVAR MHFARQRLAAVATFACSAQNA IALMEEIAANFSYEMIRLTECIL GFTWNRLYQGINVHNAERVRQ LAHDGHELVYVPCHRSHMDYL LLSYVLYHQGLVPPHIAAGINL NFWPAGPIFRRLGAFFIRRTFKG NKLYSTVFREYLGELFSRGYSV EYFVEGGRSR/TGRLLDPKTG\M LRGGTRPITLIPIYIGYEHVMEV GTYAKELRGATKEKESLPQML RGLSKLRNLGQGYVNFGEPMP LMTYLNQHVPDWRESIDPIEAV RPAWLTPTVNNIAADLMVRIN NAGAANAMNLCCTALLASRQR SLTREQLTEQLNCYLDLMRNVP
17802	48170	A	17908	192	486	PVLVYLWVSFSWLCGRSLVCD AFGCVLCVLCFWCGVCWGWF SRCLVLVRVLDCVAVAWVCPL GVGIGLWV/RVLPTGLVSAVPC CCDVLARFRVDLCWG

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17803	48171	A	17909	1	2470	MFQPSDSGKSFIFNMSVGYNLE GIKQPPMQQFIDNMMDASDHP KFAQYRDTLNKLLQDDAFLAR HGLQEKRESLQALPARIPTSMV HGVTLSTMHGCPPHEIEAICRY MLEEKGLNTFVKLNPTLLGYA RVREILDVCGFGYIGLKEESFD HDLKLTQALEMLERLMALAKE KSLGFGVKLTNTLGTINNKGAL PGDSTSGVLRTYERLLTAWML TCPCADEHQRGESVKLATALT WWLRGSQNRDEITKDGFQSNH AGGILGGISSGQQIIAHMALKPT SSIDVPGRTINRFGEEVEMITKG RHDPCVGIRAVPIAEAMLAIVL MDHLLRQRAQNADVKTDIPRC AQSIGSFSNGCIVGADTLPIQSE HYQVMRTDQRRYFGHPDLVM FIQRLSSQVSNLGMGTVLIGDM GMPAGGRFNGGHASHQTGLDV DIFLQLPKTRWTSAQLLRPQAL DLVSRDGKHVVSTLWKPEIFSL IKLAAQDKDVTRIFVNPAIKQQ LCLDAGTIATGCAKCDPGVSIG AYAYLLTLRAQCLAHDLPDPLE PLEIDGTLLPRYVFIHGGPRVFT YYTPKEESIKLFHDYLDLHRSN PNLDVQMVPVSVMFGRAPGRE KGEVNPPLRMLNGVQKFFAVL WLGRDSFVRFSPSVSLRRMADE HGTDKTIAQKL\ARVARM\HFA RQRLAAVGPRLPARQDLFNKL
17804	48172	A	17910	1	734	
17805	48173	A	17911	1	962	
17806	48174	A	17912	1630	2633	
17807	48175	A	17913	1360	1600	HSTGRWATTINVPITCGTKARH STSSICKTGMILLWANALKQHC LLSRNLP*KGESINVANSLLSYF NLRPQCNQTRTQD
17808	48176	A	17914	1	816	
17809	48177	A	17915	703	1546	
17810	48178	A	17916	209	485	QVIRPTFIPSTSSNGAISLPASTR RDS*MANAS*RCSLA*RATMFP A*SATSIFHARPGVEGT*IVRIV VIMLRLLSRRKVRGIRLPAAVLI
17811	48179	A	17917	619	1167	

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17812	48180	A	17918	1	764	DSGQQLDDVQLARYLLSGQNQ PKSDRPYRVR*LTGAMLKLILT L/VIEGNVTLGHRVKIGTGCVIK NSGDWR*LRNQSVYRCGRCES GSGLYHWARLPVCVLVLSCWK VLTSSLVPPD
17813	48181	A	17919	3	1462	
17814	48182	A	17920	122	983	
17815	48183	B	17921	1	1287	
17816	48184	A	17922	289	958	
17817	48185	A	17923	1	5079	
17818	48186	A	17924	1	255	
17819	48187	A	17925	1892	2448	TESRCADGAGSVDVGTEPVVP RVELVAKWPGSRAGGTGLGCS PWVGAGCVGGLGPQARLSGPT ASTEASAKAASTLASLMWLRV RL*GACPFARTGATAPSSSKGP ELGVSGLRKATWMGRGSGCCT RGLGAGEWRAVPESCGLDESS EDSDDRDHAVPFSSSSCRRSML RPRRVARGLCRRRGV
17820	48188	B	17926	52	888	
17821	48189	A	17927	929	1148	TVWNGTCGLPFSSLMKCMVIM IMRAIQKKMMSKPDTITLVGW N*RRASVFSGQPRVEKVHSAEE NQVSRTSSS
17822	48190	A	17928	125	937	RISMVFPWCFCSCSRTLATTPAP TVRPPSRIAKRRPSSIAIGWIRVT TILMLSPGITISTPSGSSMVPVTS VVRK*NCGR*PLKNGV*RPPSS LDRMYTSDSNLHGLRPAVSPVT NTPA/SDGYYSHDGSLAQVDLS ANYHEGQYTSAGLSLQGGATL TTHGGALHRTQNMGGTRLLID ADGVADVPVEGNGAAVYTNM FGKAVVSDVNNYYRNQAYIDL NKLPENAEATQSVVQATLTEG AIGYRKFAVISGQKAMAVVNF AEGKVSLAVV
17823	48191	A	17929	3992	4213	VPAIQQKFPRSWKLGGERPPKA FRLRLSAA*RKSVP*AQRSLAD/ SGMPLRLEKCLDTF*TQIV*SAF KIQREGS
17824	48192	A	17930	1	1636	
17825	48193	A	17931	1	900	
17826	48194	A	17932	1	939	
17827	48195	A	17933	427	1250	

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17828	48196	A	17934	521	805	LCPSNTSPLSCLLCDLVASTEM APMRVFQPAPKVNA**LFATIEP PYSVNKLLKPY**PAWTKSLCL LAPSIWLRPAAKSYFDTPGCSIF GTAA
17829	48197	A	17935	1	2052	
17830	48198	B	17936	1	573	
17831	48199	A	17937	1	1278	
17832	48200	A	17938	161	659	
17833	48201	A	17939	1	588	
17834	48202	A	17940	695	1281	KLKPYSWAFSRQSGRSVILTPPR VTVVVVAGFGPIPVFGTVMVRP GWAAP*FLPVASVYFP*AGLAG FLKKNRGCCANPAPPPIRRPIMY PP/MQRLQEPPADWWACAWFS GKD*\WKKSPPNCTRCA
17835	48203	A	17941	261	2045	
17836	48204	A	17942	1	637	
17837	48205	A	17943	31	280	
17838	48206	A	17944	1	582	
17839	48207	A	17945	1	2496	
17840	48208	A	17946	330	507	
17841	48209	A	17947	1087	1875	
17842	48210	A	17948	1	476	
17843	48211	A	17949	1	537	
17844	48212	A	17950	2	492	
17845	48213	A	17951	1	1101	
17846	48214	A	17952	2538	2833	TRRNWRPIQSSEESWRAAGSST PLTTQNRQQTAGIY*RSR*TAA RR*SPALPRRNPRLATAG\WQY ATQTRQQ\RVPQL*LSAPATRK NRLLANAWLTM
17847	48215	A	17953	125	1831	
17848	48216	A	17954	2	825	
17849	48217	A	17955	1	840	
17850	48218	A	17956	1	1725	
17851	48219	A	17957	463	1824	
17852	48220	A	17958	2	117	
17853	48221	A	17959	1	2640	
17854	48222	B	17960	223	1560	
17855	48223	A	17961	638	746	RIP*MT*WS*KPWHKNYMMHA QASVDNLIKWKKGYQ
17856	48224	A	17962	385	514	
17857	48225	A	17963	17	225	SSPSKFTVAFFASLVMASAVSL ALSLRSLTTLSI/CGLVLQEERT DDALVEQFSPIRRARGHAPQQE ATEM

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17858	48226	A	17964	1	521	LVFLVLFVGFLSCFKSTYTLTY GDSPSLCDGLLII*IISRIDTNKPA DNSISGIRDVGWVAKSYQVA/V GERLHNRTPGTSHQSDTRFDF* LC*PGSACPNLVSEHERPQANM LVEASGRLAA*YQNALSCSFGY GVGLVRRQDFSSLGRFLQSAFA SNRY*QVVWVFEFQQVS
17859	48227	A	17965	267	554	LRFRFTRAVGRIFHRLDLLVLL GCNRYGRRGGDHGLCSVLVPR SLRLGRLPGGDSAAADAQSRH REKCR*DGVLVCDDQNRQTPV WKPHQEDVQV
17860	48228	A	17966	1	915	
17861	48229	A	17967	1226	1399	SDSNISICTCAQIH*KHFRII*NCT L*EVEP*RLS*M*LQRKCVQGEP SKVHSLWGI
17862	48230	A	17968	828	1070	SFFDYQTSALEHARR*LHCRT* NAGWLPHRTDRSSGYHGRTCS AAGRCSSGDHSSYQQQNPAEK LPAGHPQRSGSPERTG
17863	48231	A	17969	45	1198	
17864	48232	A	17970	348	508	RLFRWCPM*S\WASYFPPESQSL PDSYWLF*ECNLPTAYNSQNAII RESHAIYS
17865	48233	A	17971	251	601	MAKKMSLSIAVFWRRLYAY\Y PHLR*KS*TNW/QWWRSALS*A V*PNRS/IDSRWSIIWSVLFGML V/AT/ALAPAFWLRY*KKSFSA WNPTKSPRCLSNARPCCSLSKK ASLPWTIAARSR
17866	48234	A	17972	1	2121	
17867	48235	C	17973	1	1710	
17868	48236	A	17974	1	1335	
17869	48237	A	17975	1	1497	
17870	48238	A	17976	2	824	
17871	48239	A	17977	1	1965	
17872	48240	A	17978	1	3555	
17873	48241	B	17979	197	2021	
17874	48242	A	17980	1	348	
17875	48243	A	17981	1	891	
17876	48244	A	17982	1	679	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17877	48245	A	17983	3	2502	EAIREVSNPI\PQEEIWTHREAVP PVQLLTGWCVTAKAPPDISAIS ALTAVKHGNCSSLTPLLNPPGS DVIVCAEMDEQWGYVGAKSR QRWLFYAYDSLRKTVVAHVFG ERTMATLGRLMSLLSPFDVVIW MTDGWPLYESRLKGKLHAILV TFEEKFQEEPVKKQIIMVSISVS DTGGKKEKPKLINLSSKTNGLQ NTTEAQLCETKSDFELSFSGFNP ISIDTEDMKTGCCFQEQSVRRA YFKATSSPRRGLIITKLTTRVDG YVADDPSRRYSGHGDLLWPNA GNSCVETTVGSLLCEVQAAPTP HTLEGKHGCRNKEKKRLTHSG ACTYTFSELGLELWAWNCGKT EVNLGAVGKGVGGDRGFKKIH AKSQFTCSVLYTFTIKQGISLTL WSKVMHILEHLKENSKQLTSIC TRYQRVFGPTWLHETIFCKVAL TATLLAELEKTSTLQTFLDKIWI LGAQQHTGSQEPSQALLTCDPA WKKALRKVTQKGGAFFGVDN LGSSLSPTTDLLYEEQRLTSLSG SWFPICVMVELTLRAGSSPGGR LYVEFDQAVTKEPRFLQYKHY WDGAVAGSSILRQDSFVAEAST TITRIESPSVPSRSSTFLDDFSITQ QHRRHAGLSVMLSLIISPPVRGL CQERTLRRDFRERLMYLDLEY QSGYCRLRTAGSEMQMVPDVL IFAHRSGLAGLFPGLDRRLVNA
17878	48246	A	17984	10	211	GSQSTIFTFAARW\NLWANENT DTSISPLGVGEQRHCSSP*RFPD SDRCSPWSPRSQGQNQSPQTW Q
17879	48247	A	17985	1	1725	
17880	48248	A	17986	1	379	
17881	48249	A	17987	3	273	
17882	48250	A	17988	3	1157	
17883	48251	A	17989	76	378	
17884	48252	A	17990	1527	2005	
17885	48253	A	17991	578	1312	
17886	48254	A	17992	1	1758	
17887	48255	A	17993	1	2433	

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17888	48256	A	17994	1	537	SQEELLQQALVAQLA/HSEQLE GVQLPEPDEPSARHALPANEPRI VLNNGVVSYNDRPILNNLSWQ HIGYVSSSLHLDYRVSTTVRNV ILSGYFDSIGIYQAVSDRQQKLV QQWLDILGIDKRTADAPFHSLS WGQQRLALIVRALVKHPTLLIL DEPLQGLDPLNRQLIRRFVDVLI
17889	48257	A	17995	1	536	
17890	48258	A	17996	1	1319	
17891	48259	C	17997	74	341	
17892	48260	A	17998	3	103	
17893	48261	A	17999	1	745	
17894	48262	A	18000	1	663	
17895	48263	A	18001	2	297	
17896	48264	A	18002	8	340	VPANSLSAIALFRRESVTPLAAL AASPVCAGRFVLLKNHRRDLP* ISVPVNSSSNSARSLVWHSGRQ QIAPDWSSKDDFMRLGKPNRFS VLLLATWIR*STVIRRSPFTS

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17897	48265	A	18003	1	1341	MVHRFGIRVRFVALGFYQDVIL PVRAHRHEWGHYVHLCASIQR QIDVSFARDATSHSSCPVTGVR FWGYPFAANKVVIAGFELEGET MTRPGLICAEGGLLVMIVSLRS ELYDSYHEFTRQRVTEIVEKAA NHLPAVVEMMTLHRCAINRHN FVRRVGPAGISTFFASSPDGVN AGFSTFRVVFTCQRSRPLQRHS HADVQTATLLLNTVNLEQKQA NAILSGLSDMIPNSSPESAPEIQL LQSRMILGKTIAELNLRDIVEQK YFPIVGRGWARLTKEKPGELAI SWMHIPQLNGQDQQLTLTVGE NGHYTLEGEEFTVNGMVGQRL EKDGVALTIADIKAKPGTQFVL SQRTELEAINALQETFTVSERSK ESGMLELTMTGDDPQLITRILN SIANNYLQQNIARQAAQDSQSL EFLQRQLP*TLSKNRPTPFSAA*/ DDMIPNSSPESAPEIQLLQSRMI LGKTIAELNLRDIVEQKYFPI/D GSRLGEINQRKTR*AGDQLDAY STTEWSGSATDT\QVGENGHYT LEGEEFTVNG/NGRPASGKRWR CADYRGH*GQDQQLTLTVGEN GHYTLEGEEFTVNGMVGQRLE KDGVALTIADIKAKPGTQFVLS QRTELEAINALQETFTVSERSKE SGMLELTMTGDDPQLITRILNSI ANNYLQQNIARQAAQDSQSLE FLQRQLPEVRSELDQRKKNSTFI
17898	48266	A	18004	414	893	VFAQHGLTVAAIAAHARDRWF VGRTAHANPPVRCSTDGSGRVP VTRYSGFVAAAVILLTASPRGG ECSREAPLCSVSEYLLLQSAGE YAPAPRCVLRCVPSVDEDFVPV VPD*APPVEVALFLLRLTPVAR PADGGWLLAAIRPDALTSLAIV VLAAAR
17899	48267	A	18005	432	1108	
17900	48268	B	18006	1	753	
17901	48269	A	18007	46	282	
17902	48270	A	18008	1	1201	
17903	48271	A	18009	1	618	

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17904	48272	A	18010	1	1045	MLCTKWDKLGLEKNAGKNKN AYKWYGWPANAPDEPHIEQLV GECRVMRQLKRLISRIAPSPSSV MVVGESGTAIPVVSHAEFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDFGYLEFEGGANFSWGEM YGFFDWENFYNGRHNKPGSEQ RYTFKNTNRIYLGDTGFNLYLH AYGTYGSANRVNFHDDM\FLA GFGFQF*PAGGW/WGSNPFFAK\ RYTRSKPYYT\GDNGYV\AGWV AGYNFMLGSEKFTLTNWNEYE FDRDATYAADFLPLYDVDCQD NGNLEYDTYSQPEWKHNLFDH YLAVLYRFKDESGKEQFSGAV VKTREATPGKEIEAITRRMLDFS PRLKKLA
17905	48273	A	18011	228	430	YPRQHRQRADGSDRHR**/CWS A*IWANPTSNLPPCRFALTKRK RPILCAPPSRQSYAAWCRWEIRI A
17906	48274	A	18012	296	1178	
17907	48275	A	18013	1	1395	MPSDISLASCRLRATSRLFTDHR RQSDCMTAINRIPIVDDEDNVR RFETHCANNVRTALHLFADIHP DVVLMDIRMPEMDGIKALKEM RSHETRTPVILMTAYAEVETAV EALRCGAFDYVIKPFDLDELNLI VQRALQLQSMKKEIRHLHQAL STSWQWGHILTNSPAMMDICK DTAKIALSQASVLISGESGTGKE LIARAIHYNSRRAKGAFIKVNC AALRESLLESELFGHEKGLFER ANEGTLLLDEIGRM/PLVLQAIL RILQEREFERIG/GHQTIK/VDIAS LLAPTRLQAMVKEGTFREDLFY RLNVIHLILPPLRDRREDISLLA NHFLQKFSSENQRDIIDIDPMA MSLLTAWSWPGNIRELSNVIER AVVMNSGPIIFSEDLPPQIRQPV CNAGEVKTAPVGERNLKEEIKR VEKRIIMEVLEQQEGNRTRTAL MLGISRRALMYKLQEYGIDPAD
17908	48276	A	18014	1	771	
17909	48277	A	18015	1	2154	
17910	48278	A	18016	859	1014	IKTGETHPGIGPSVM*RHSKAD LTHRHCGGIPEPQSVSFGSSQH GGGQFPPL

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17911	48279	A	18017	1224	1520	SPLVNQ*GA*KFFSRGNLFPQG ETH*KTKGVPCWTRYPDLKRS DSAEIFKTPANASGRTSGSLGC AAQLEKVADGRDLDEKLAEAG IGGSNKTSVWQG
17912	48280	B	18018	182	2392	
17913	48281	A	18019	72	266	
17914	48282	A	18020	600	914	PYRGSPRNGHQLCDHCSHRLSE DPFVRYSNHCQSISNYRCDKPP VRPLSPLHQKTDRKHHQRPDRP FQWSAAPAHGRWRSGDS*ETP LHYAQPAGKLRWLWVNY
17915	48283	A	18021	1102	1171	LLGYGQQPPASNLLSEG*RSVV L*ISALRM*ALPPQKSSDAPNG WLPNRWPISSTHMIR
17916	48284	A	18022	1	1279	
17917	48285	A	18023	1329	1403	
17918	48286	A	18024	442	918	
17919	48287	A	18025	3	1345	
17920	48288	B	18026	436	988	
17921	48289	A	18027	637	1086	
17922	48290	A	18028	1	321	
17923	48291	A	18029	1	845	
17924	48292	A	18030	298	581	GARAEARAGSGQGAGLGVSSP VRWRGWSDKGAERPGGPLSPL REVSRAGPSG/HAARGQQPGRP RFPPPGPRPPRRRCPCTRARPGG AAGGGPCL
17925	48293	C	18031	450	604	
17926	48294	A	18032	1279	2253	

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17927	48295	A	18033	1	1957	MAQFHVSHPPAEWPRHVLLLM ADSKNELQNMNTGQTCGTRQT LKSKLQGWNKPGIQSDPGSQG HPRCLKTFPLVAQSSTQERNHV MEKAVLKSQNWAIIEEFITKIG WFPDYSGKVKYLSSPKSSCTTV LQVTHFSLFFHPNPDELVSKIKV WSKHRLYQNNSEAFLEVQIPEP KCEVYSMRTMGRRQPGTAMD LNAGGSICNVPRTLLHLTGESTF RDRQRVGAYLDIRGWYILVLV VDKEKLGIPGQKQNSSKILFGSE KLKQWVYVKNHAKESITQEAM GIWVGQQRKRQPLGYEERKLT NRKDIHIKNPSVCHHHQRPKVD KTTKMGKKQSRKTGNSKNQST SPTLKESSSSPATEQSWTENDFD ELREEGFRRSDYSELQEEVQNN GKEVKNFGKKLDEWITRITNAK KSLKDLMELKTKARELCDERTS LSSQCNQLEERVSVMEDEMNEI KQEEKFREKRIKRNEQSLQEIW DYMKRPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLARQANI QIQEIQRTPQRYSLRRATPRHIIV RFTKVEMKEKMLRVAREKGRV THKGKPVRLTADLLAETLQAR RQDTHRLKIK\DGGRFTKQMEN RKRQGLQS*SQIKQNLNQQRSK ETKKAIT*W*RDQFNKKS
17928	48296	A	18034	1	2838	
17929	48297	A	18035	1	897	
17930	48298	A	18036	26	308	
17931	48299	A	18037	749	1020	
17932	48300	A	18038	1	1773	
17933	48301	A	18039	1	1890	
17934	48302	A	18040	1	756	
17935	48303	A	18041	399	660	CPPEAVMPRRHEPVWEMTGFF LPDVLLSDSSDTSEGFRLHLET WAPFLCRCLSLRLIS*HHHQTT GNSSPPVSASQHQSVDRDSLN
17936	48304	A	18042	909	2005	
17937	48305	A	18043	1	490	
17938	48306	A	18044	104	775	
17939	48307	A	18045	170	451	
17940	48308	A	18046	1	207	

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17941	48309	A	18047	146	678	LGFLLRLSEMPRKQGDYRTRIW KFEDGLSNVLVIQLNKLIICVM CLVRDCDVLKTYFHR*SGLLPI KDTS/RPFTRVTVQWGKKNDQ TFQGLLDTGSELTLIPEDPKRHC GPPVKVGAYGGQVLHSKWAPI YHFLSSHNCNGFCYISIANLPKK FGQNIKECLTNNRIVPFNCVQD
17942	48310	A	18048	270	1444	
17943	48311	A	18049	700	1062	
17944	48312	A	18050	3	1096	
17945	48313	A	18051	1	1500	
17946	48314	A	18052	1	6215	MEDNLISINKIKILLAVSDGEIDE TFSLKQLMFNSVPVQNEDGSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRIKMFMPRGVRIESN GDKNGVRVEYEVQQAVDGGSF ETVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKA
17947	48315	A	18053	1325	1417	
17948	48316	A	18054	1	4971	
17949	48317	A	18055	251	1091	
17950	48318	A	18056	1	2277	
17951	48319	A	18057	2	448	KNDKGDIIVTTKSGGRGTSTVS FKLLKPEKI/GSKFSQKDLEMLF HGMRADFTSENFSAAWYLIEN HSNTSFEQLKMAVTNLKRQAN KKSEGSLAYVKGGLSTFFEAQD ALSAIHQKLEADGTEKVEGSMT QKLENVLNRASNTADTVYE
17952	48320	A	18058	124	984	

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17953	48321	A	18059	142	1393	DKKPGMVPPPPGEESQTVILPP GWQSYLSPQGRRYYVNTTTNE TTWERPSSSPGIPASPGSHRSSLP PTVNGYHASGTPAHPPETAHM SGRKSTG\DSQNLGSSSPSKKQS KENTITINCVTFPHPDTMPEQQL LKPTEWSYCDYFWADKKDPQG NGTVAGFELLLQKQLKGKQMQ KEMSEFIRERIKIEEDYAKNLAK LSQNSLASQEEGSLGEAWAQV KKSLADEAEVHLKFSAKLHSEV EKPLMNFRENFKKDMKKCDHH IADLRKQLASRYASVEKARKAL TERQRDLEMKTQQLEIKLSNKT EEDIKKARRKSTQAGDDLMRC VDLYNQAQSKWFEEMVTTTLE LERLEVERVEMIRQHLCQYTQL RHETDMFNQSTVEPVDQLLRK VDPAKDRELWVREHKTGNIRP VDMEI
17954	48322	A	18060	1	435	
17955	48323	A	18061	3	926	
17956	48324	A	18062	3	693	RPPLAYLRDGDARAGLNGLQL AVLAMLSSRKMFCKKSGQSYS PSRVLITENDVKEGLQRSHILYD RAGEEHYNCISALHKSMRGSD QNASLYWLARMLEGGEDPLYV ARRLVRFA\SEDIGLADPSALTQ AVAAYQGCHFICMPECEELLA QCVVYFARAPKSIEVYSAYNN VKACLRNHQGPLPPVPLHLRN APTRLMKDLGYGKGYKYNPM YSEPVDQEYLPEELRGVD
17957	48325	B	18063	1	2020	
17958	48326	A	18064	19	404	
17959	48327	A	18065	1	407	FRATITSAKMGAYKYIQELWR KKQADVMRFLLRVRCWQYRQ LYALHRAPRPTRADKARRLGY NDKQGYVIYRIRVRRGGRKRPD PKGATYGKPVHHGDNQLKIAR SLQSDAEEPAGRHCGALREQSS Y*VGEHST
17960	48328	A	18066	53	431	AKKGAYNYIQELWRKKRADV MRFLLRVRCWQYRQLSALHRA PRPTRPDKARRLGYKAKQGYVI YKIRVRRGGRKRPVPKGATYG KPVHHGANQLKSAQSLQTGVQ ERPGHP*YAMRVLKAYRARPD
17961	48329	A	18067	5	328	

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17962	48330	A	18068	93	836	AKMGAY\KYIHELWRKKQSDV MRFLLRARCWQYPALHRAGTE WQLSALHRAPRPTRPDKARRL GYKQ\AKQGYVIYRIRVRRYI*D SCSPWWLKTAQFPKGCNFTGK PVHSWVFNQLKSFASKAFQFR WQEGGEAWDGTCGGLLEEFLN FFNWVWV/GKIST*QNFFEGLIL I/VIPFHKS*SEENPDTQWDQPN QSHKHR\EMRG\LTSARPEKSRG L/GKKGHKFHHTIGG/SLRRAT WRRRNTLQAPPLPLI
17963	48331	A	18069	1495	2055	
17964	48332	B	18070	125	2530	
17965	48333	A	18071	345	800	RWRLQNLSFCSSCSGSGSEGAT CFARGR*RPPGNSLNVSRMGTR SSYSCRRHSPAFLSWGKGRCHL CNKAHLLAGA*HYSFLSGSAPY *N*VNGQI**R*TAHRSTPDAPT GH*NCCS*L*CHSY*QRA*PGY RHD*CRMCC*CADCSHAC
17966	48334	A	18072	181	1687	
17967	48335	A	18074	205	1734	
17968	48336	A	18075	1	705	
17969	48337	A	18076	590	685	
17970	48338	B	18077	1	881	
17971	48339	A	18078	1043	1248	ITLGIMAIFTVLILPIHEHGMVFH LFVSSFISLSSGL*FSLKRSFTSL VSWIPKYFILFEAVVNGSSL
17972	48340	B	18079	1	1977	
17973	48341	A	18080	805	1153	AWKVLPFFVSFCF\LSSGL*FSL KRSFTSLVSWIPRYFILFEAIVN GSSLMIWLSVCLLLVYKNACDF CTLILYPETLLKLLISLRRFELLF LSMFSASFRSSCKAGLVVAESL
17974	48342	A	18081	471	1442	IWSFHIVPYFLEALFV*GVRKGS SFSFLHMAGQFSQHHLLSRESF PHCLFFSGLSKTR
17975	48343	A	18082	188	355	
17976	48344	B	18083	1	1677	
17977	48345	C	18084	35	1816	
17978	48346	A	18085	557	724	
17979	48347	A	18086	179	346	

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17980	48348	A	18087	135	1461	INRIYILLSTTSHLFQN*PHSWK* STPQQM*KNRNYNKLSLRPQC NQTRTQDEETHSKSLNYMETE QPAPE*LLGT*QNEGRNKDVL* NQREQRHNIPESLGHI*SNC*QD **RRKERRIK*MQ*KC*RCNKN AKGVITTDPTEIQTTIREYHKHL YANKLENLEDTDKFLDTYTLPR LNQEEVESLNRPITGSEIEAIINS LPTKKRPGPDGFTAEFYQRYKE EQRIKYLGIQLTRDVKDLFKEN YKPLLNEIKEDTNKWKNIPCSW IGRINIMKMAILPKVIYGFNAIPI KLPRTFFTELEKITLKFIRNQKR ARIAKTILSKKNIAGGIMLPDFK LYYKATVTKTAWYWFQNRDID QWNRTEASEITPHIYNHLIFDKP EKNKKWGKDSLFNKWCWENW LAICRKLKLDPFLIPYTKINSRW IKDLNVRPKTIKSLEENLGIPFR
17981	48349	B	18088	1	2016	
17982	48350	A	18089	659	826	
17983	48351	A	18090	3531	3878	
17984	48352	C	18091	1	2793	
17985	48353	A	18092	1607	1774	
17986	48354	B	18093	1	1666	
17987	48355	A	18094	1	1068	
17988	48356	B	18095	1	1549	
17989	48357	A	18096	557	623	KKWINYWTHTPSQD*TRKKLN P
17990	48358	B	18097	1	1231	
17991	48359	A	18098	263	1461	GGSSCYPSWEATIRTAKMVTLR K\RTLKVLTFLVLFIFLTSFFLNY SHTM\VATTWFPKQMVLELSEN LKRLIKHRPCTCTHCIGQRKLS AWFDERFNQTMQPLLTAQNAL LEDDTYRWWLSLESVMFSVTM GFCLQRPFGDKQGTTQPVYINQ TGRDLTQQQRLQREKKPNNLN DTIKELFRVVPGNVDPMLEKRS VGCRRCAVVGNSGNLRESFYG PEIDSHDFVLRMNKAPTAGFEA DVGTKTTHHLVYPESFRELGDN VSMILVPFKTIDLEWVVSAITTG TISHTYIPVPAKIRVKQDKILIYH PAFIKYVFDNWLQGHGRYPST GILSVIFSMHVCDEVDLYGFGA DSKGNWHHYWENNPSAGAFR KTGVHDADFESNVTATLASINK IRIFKGR
17992	48360	B	18099	1	4855	

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17993	48361	A	18100	571	4189	FSLKRSSTSLVSWIPRYFILFEAI VNGSSLMIWLSV*AKILVQRA* VLAFHPS*LRFVKDQVVVDMW HYF
17994	48362	A	18101	7449	7626	SFRSRLFSFHVVELF*VSFLILSS SLIALWSERQSVIISVLLYFLRS AFLPTMWSILE
17995	48363	A	18102	63	329	SGQRRKEVPSPTLPAPPFILKKK EWPDPPRSFFSGGHWAKSSCPS DCSSQLMAC*/CKNAKHQKDN SCLI/STHMKGNSERK*NSGYQ GLG
17996	48364	A	18103	2	618	GAFLLEVATAAGLSAGLTRLGS QVGGAMRRSKADVERYIASVQ GSTPSTLQKSMKGFYFAKLYYE AKEYDLAKKYICTYINVQERDP KAHRFLGLLYELEENTEKAVEC YRRSVELNPTQKDLVLKIAKLL CKNDVTDGRAKYWVERAAKL FPGSPAIYKLKN/DGWVRGQM VPKPDDEGVQVRGRSGRPDAG WRLNRRSSVGGSAW
17997	48365	A	18104	1	995	
17998	48366	A	18105	1	513	
17999	48367	A	18106	62	521	
18000	48368	A	18107	1	375	
18001	48369	A	18108	76	480	LVKVCHCTYHHFLTGVVSLPR DGGKGAPCWGRARSPKSALLP YLAPGRG*VGTYEVQN/PNGTS PVQSPATDVGRSPALGNQEP/G T*SPGPQIGRGVTGTARPHTGV SRDSWRRPPSFILNAVANIPKGN APIPKE
18002	48370	A	18109	445	1128	
18003	48371	A	18110	784	1189	IPLGKLLLKPVGAPQIERFPFQIP VPLCSLSFPSHSPSSSSARS*VRQ ES*LGTPGSAPTGSP/TSHHPSAS SPPHPSAKAAFLSFVCFLCS*PPP SSCHPCGLGPGPDPSQKMMICT VAHLNQSLIFTVVKVHLL
18004	48372	A	18111	1	2088	
18005	48373	C	18112	169	213	
18006	48374	A	18113	1145	1229	
18007	48375	A	18114	1	975	
18008	48376	A	18115	1	750	
18009	48377	A	18116	288	368	
18010	48378	A	18117	34	168	
18011	48379	A	18118	479	1579	
18012	48380	A	18119	2279	2398	SDCSCPGL*GPPGRWHKRRKSG SPHLSTPEGTPALTSQA
18013	48381	A	18120	21	190	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18014	48382	A	18121	1	1773	
18015	48383	A	18122	18	290	VAGTWPNFLKKVGIVGKYGTR YGASLRKMVKKIEISQHAKYTC SFCGITKMKRRAVGIWHCGSC MKTVAGGAWTYK*V*FLVVFG SVWTT
18016	48384	C	18123	325	486	
18017	48385	A	18124	1	498	
18018	48386	A	18125	3	306	RQEIDSIHQVGVYCLALVPANT LPKTPLGGIHISQTKQLFLEGSL HPCNILMCPHTCVTNLPKPRQK QP/WCRPCFRDGWESGCWKTY STSCWKGSGTNRRE
18019	48387	A	18126	1	1197	
18020	48388	A	18127	1	390	NSRVDDFVAPGLSEAGKLLGLE FPERQRLAAAVG/CSPMSGVIS MSAPFFLGKIIDAIYTNPTVDYS DNLTRLCLGLSGVFLCGAAAN AIRVYLMQTSRQRVVKRLRTSL FSSILGQEVAFSDKAGTGELI
18021	48389	A	18128	1	695	SGFMDHLEEKADLSELVEKEEL GFFQYYRERCHQKVYHPITKPG GSAKDAAPGGGHHQAGPGQG GDEGIRMMFCVSPNRATFVVS VVPLVSIIDVIYGRYLRKLTKVT QDSLAQATQLAEERIGNVK\TV RAFGKEMTEIEKYPSKVDHVM QKARKEAFARAEGVILNEKSFQ GALEFKNVHFAYPARPEVPIFQ DFSLSIPSGSVTALVGPSGSGKS TVLSLLLRLYDPAS
18022	48390	A	18129	1	2136	
18023	48391	A	18130	1	822	
18024	48392	A	18131	257	388	
18025	48393	A	18132	1	765	MVNALSLAARIHAEVPADESPE MTEGYEGFYHLASMKGTVERA DMHYIIRDFDRKQFEARKRKM MEIAKKVGKGLHPDCYIELVIE DSYYNMREKVVEHPHILDIAQQ AMRDCDIEPELKPIRGGTDGAQ LSFMGLPCPNLFTGGYNYHA/P SPKFSAVSAMLLASASSAGRCG ESIFSPLAYTSSPIESDSCGPAL* RFLRH*P/EIFLTQPVF/SENEAID IWN\SPTASVSPLMPSRQNAVRE LFLLTVRRPTGTD

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18026	48394	A	18133	1	1166	LTHWVYHLYGIQRILIHIPSTSQ PNRVRGDIPPLQRIVVPVTVIVQ PRLLIMLLPWQTVRLVQVMRV LLIKLVAPFIILPAPRRIAVFADE RQRQAPVVAVVKMNFSRRCVF RLHLSGQLLHRQPALRKPRPAF TAHAVCPDFFLQPVQQPHQFSR EHHAVAVLTPFLLERLCQAAPL RFFPLAVLCLDPDERREASRLV YRLDTCGVSLHRRQPVSVPAIS LALPMLAILVVQTIFMALYAIF VTWRMMGKNYDAAVLAAGH CGFGLGATPTAIANMQAITERF GPSHMAFLVVPMVGAFFIDIVN ALVIKLYLMLPIFAG*PMKRR* K/SPPQQRQMPDTLRLSSVPSPA SSVLSGLLPVVGNVREYGVPGA ELPGSSPDRAVNPPL
18027	48395	A	18134	48	314	LVPMTWVIEASYSIMRKKVGE HPHFLDIAHQAMRDCDIEPELN PIRGGTDGAQLSFMGLPCPNLF TGGYN\IMVSMSL*LWKVWKK RCR
18028	48396	B	18135	83	3044	
18029	48397	A	18136	1	1080	
18030	48398	A	18137	3	979	DAWADAWSKKADVKVENP\D TKEKKPEAKK\VDAGGKVKKG NLKA\KKPKKGKP\HCS\RNPCP CKKEIGRNSRSGMYSRK\AMYK RK\YSAAKSK\VEKKK\KEKVLA T\VTKPVG\GDKNRR*PGVVKLP QKCPRYYP/SLEDVPRKACLSH GKKTPLVQHVEKNCEASIYPRG PF*FILTG\RHRGK\RVGFPESSL AKLAYLLC*LGPLVLKSEVPL\R RTHQKFCHLPLSTKI\DISN\VKI PKHLTGCLLSRRKKLRK\PR\HQ EG\EIFDTEKEKYEI\TEQRKIDQ KAVDSQILPKIKAIPQLQGYLRS VFALTNGIYPHKLVVLNCLKNP
18031	48399	A	18138	858	1418	
18032	48400	A	18139	97	516	
18033	48401	A	18140	1	219	

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18034	48402	A	18141	110	768	NLFSGCVESTFRKQPAHQRRSR ARAETMQRRLVQQWSVAVFLL SYAVPSCGRSVEGLSRR/LLKP MRPKNVHVPTKVTTYKRAVSE HQLLHDKGKSIQDLRRRFFLHH LIAEIHTAEIRATSEVSPNSKPSP NTKNHPVRFGSDDEGRYLTQE TNKVETYKEQPLKTPGKKKKG KPGKRKEQEKKRRTRSAWLD SGVTGSGLEGDHLSDTSTTSLE
18035	48403	A	18142	338	661	
18036	48404	A	18143	443	661	
18037	48405	A	18144	474	531	
18038	48406	A	18145	208	317	
18039	48407	A	18146	1	807	
18040	48408	A	18147	1	1122	
18041	48409	A	18148	283	2204	ASPMAPTSLCVPTLLPSLNQTSS SSTAPTGKASWGWPMLRLPGL TTPWSLSLTLW*SRPTFPTSSPC SFVVLASPSTSLKCWPLSEGA
18042	48410	A	18149	208	1212	
18043	48411	A	18150	202	1677	
18044	48412	A	18151	1	3285	
18045	48413	A	18152	3	2206	
18046	48414	A	18153	1	1041	
18047	48415	A	18154	2	1460	
18048	48416	A	18155	1	792	
18049	48417	A	18156	51	362	AHGAAWPSHRKDRESADLGSD GQNGQDLDWGGGCRRCC*RC DVLCWGAPHTFRHSYAMHML YAGIPLKVLQSLLLGQAPCRCG LGQNVGTALPLVSGGPMLFP
18050	48418	A	18157	609	690	
18051	48419	A	18158	1	2055	
18052	48420	A	18159	3	2236	
18053	48421	B	18160	406	454	
18054	48422	A	18161	1	2151	
18055	48423	B	18162	1	1215	
18056	48424	A	18163	1	594	
18057	48425	B	18164	1	1380	
18058	48426	A	18165	441	692	

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18059	48427	A	18166	2	1311	QHVRSTVTELWTGNFVNSIQTA FAAGIGWLITFCSKGGDCLTSQ TRLRLSGMLFLNSLDAKEIYLE VIHNLPDFELLSANTLEDRLAH HRWLLFFHFGKNENSNDPELK KLKTLLKNDHIQVDRFGCSSAP DICSNLYVFQPSLAVFKGQGTK EYEIHHGKKILYDILAFAKESVN SHVTTLGPQNFPANDKEPWLV DFFAPWCPPCRALLPELRRASN LLYGQLKFGTLDCTVHEGLCN MYNIQAYPTTVVFNQSNIHEYE GHHSAEQILEFIKDLMNPSGGS LTPTTFIELVTQRKHTEVRI/V*F HCPGWPPWPRLWPMAKKPRNL LP*SSRPLNT*SSLFCSSNQPDLR GPLLHRPLSLPRRYRGAQVPNP DFGHYSVSPSLIHGLHQCSHLFS HSPPPRVLRPPRILTTSTGLPPSP RRSATDVHTAYPPTAD
18060	48428	A	18167	1	924	
18061	48429	A	18168	10	1254	
18062	48430	A	18169	1	618	
18063	48431	A	18170	1	460	MAAPMTPAARPEDYEAALNAA LADVPELARLLEIDPYLKPYAV DFQRRMFWMFLPFFTLAFSPSV LVRFHAADKDIPETGQFTKGRG LLDLQFQVAEDASQSWQKLYL LPNCSGQPHQKLVPTAQKFYIT VEWGTFFSVPGQVVGSEGSQM SVTVEGSEESEDDKMYMTCSS ALLDSFALC**RHT*DWAIYKR KRFIGLTVP/MWLRMPRNHGRS CISCLIALANHTKNWFPQRRSFI SQWNGVLFSQCLAKLWALKEV RCQ
18064	48432	A	18171	1	582	
18065	48433	A	18172	1	1578	
18066	48434	A	18173	1	1293	

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18067	48435	A	18174	344	1358	EAQSVTNHKRNSDCTFKEDNSL PVRKPSFLITNPGSNQGPRFAGS PLGHEFTSLVLALLWTGGHPSK EAQSLLEQIRHIDGDFEFETYYS LSCHNCPDVVQALNLMSVLNP RIKHTAIDGGTFQNEITDRNVM GVPAVFVNGKEFGQGRMTLTEI VAKIDTGAEKRAAEESARKGIR TGLMGERFGGQILDTVDIENYIS VPKTEGQKLAGALKVHVDEYD VDVIDSTGTRSS/AISGFFHTYDS NSPTARCAPT*QNCAPSPSGEY APGEKAMRRTILVWRHCDY/PL CNAGNFVSMISRATSNTIATMII *GVCTDNTRLCLYALNCSGDIL SRTSCD
18068	48436	A	18175	1	1561	
18069	48437	A	18176	884	1171	PRRLNNEDHKRLMSWLHCLVP HHAKWLQRWQWQSAKVV*FA *IRAVNFVTAYRAIIYQQSRKQ HRYLRSACHGRSIITVITQSPTK SSATKMPEN
18070	48438	A	18177	274	416	QADDDADNQSGDTDAAFGALI Y/CESDDLC*LPLPALKPLCVM WYQTM
18071	48439	C	18178	24	509	
18072	48440	A	18179	1	1932	
18073	48441	A	18180	1	2583	
18074	48442	A	18181	1	495	
18075	48443	A	18182	36	798	KQRHSCFWSCWFSRAG*LGEL V*NPEIA*RPPRPQQQTVSGNG AWSGKAPRRRHSWHY/YTISFQ KLPLVECTNAGPIF*VAKAGRK CSIKPPLTSRSYIT\D*PVSLSRSQ LTGR/AGNFVTGW/QQLDEEIR YTMRTTVNAQTRDRRKGVQPP TTWIFNDTKDQLERRIARLETG MAWAEEPPSRTRHLISNCQISET DIPNVFAVRVNYLLYRAQKER DETFYVGTRFDKVRRLEDDTG ASWNGNRTGSAGIISIT
18076	48444	A	18183	114	724	ARTRVPHFPGHETAGGAAAHP HLSLLGQDPGNQTQLPGGRGGI PGGRGGGRGGGGGGDDGRRR ALRRQQVPVLCVQRAGPAMDA AAPRHSSPDRERPKDQEVLHRL PGHASHSPHLGRHAGQPAGPA GLWQAPGLRHHLHAGIQPPE/V TNTTLTALT*TRRCPAFSSGTVK PLIFIWNLAAGPPLLRKGAASIW ICSCSIFQR

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18077	48445	A	18184	1	2130	
18078	48446	A	18185	2	433	EMTLDSRVAAAGDLFVAVVGH QADGRRYIPQAIAQGVAAIIAE AKDEATDGEIREMHGVPVIYLS QLNERLSALAGRFYHEPSDNLR LVGVTGTNGKTTTTQLLAQWS QLL/GRNQRGNGHRW*RPAGES DPDRKYNRFGSRCSA
18079	48447	A	18186	114	586	SYITALGQFSRSGIQLLDRLGNF GTGWPNFDRKRFGSTMRTTVN GQTR/GPPQRRPAADNLDF**H QRPAGAANRPSGNGHGLGRRA AVTHPSLNQQLPDKRNRHPKRI CCAGKLSALSGTKRSAMKHSM LERVSTKFAVWKMTTGACWN GISSWIKR
18080	48448	B	18187	1	3577	
18081	48449	A	18188	2	861	YHSINAASACSALHPVAFLTILT CRTCSSSLVATTSTMRLPNTLP DLIISPVESILSTSFCAVPAFIREE PVTTSAPTIGVMANSAVVETAL PGLQEIPTVRQPSWRAYSSPAIT YGVRPLAAMP/SHHILCR*INIF QIINTAFPAIFRAFHRVLNGIFSA SNQTNHQTRFHAVCGRTFGDV GWVAKSYQVAEERGSITEHQV QGHQSDDTEHFHGGEIERQQQ HYHRQRGDPVGEIGEPELSISRD RHHVCHTGYNPAEPVSPAGEIS NGTANGNKLNMSVCEIAP
18082	48450	A	18189	560	2021	
18083	48451	A	18190	525	804	GG*CRNWCDHYANGCRDTSGT LYDKLAELGPQGLSPR*NNWQ TARRNQSSGRNSCHLRREVE*R RLDKALRRIRQFSAPDEGAKCP WPGIIDCSNHFARLRCQYGRFL EVTSAGDEKPYPLYDHHVGLV VEQLRCIITAKVRTRHFYYVLK SIHPAVAGLPALRDCGELFNSV YCRKPATGPELQADVMVVVAY GLILRKQCWRCRVLAVSTFMFT AATLARCCTNPTLTRAGDAET GVTIMQMDVEIPVVRCTTSWQ SLAHKAYHHVETTGRRHGETR VQDETLVTYAEKLSKEERVLTG HFRQHSLNAALRFQSMANELA
18084	48452	A	18191	1	266	SQYPLVAGHEVIGRVVALGSA AQDKGLQVGQRVGIGWTARSC G/QLRRLY*R*SDQLRARCGAD DYESRWLCREVACGLAMGDST ARKY

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18085	48453	A	18192	5	385	
18086	48454	A	18193	330	598	VMRFAIVVTGPAYGTQQASSAF QFAQALIADGHELSSVFFYREG VYNANQLTSPASDEFDLVRA/S ATTECATWCGAEYLRSGSITPW RC
18087	48455	A	18194	1	2652	
18088	48456	A	18195	1171	2091	
18089	48457	A	18196	486	837	
18090	48458	A	18197	1	2943	MAIYKQSQHMTEVVRRCPHHE RCSDSDGLAPPQHLIRVEGNLR VEYLDDRNTFRHSVVVPYEPPE VGSDCTTIHYNYMCNSSCMGG MNRRPILTIITLEDSSGNLLGRN SFEVRVCACPGRDRRTEEENLR KKGEPHHELPPGSTKRALPNNT SSSPQPKKKPLDGEYFTLQIRGR ERFEMFRELNEALELKDAQAG KEPGGSRAHSSHLKSKKGQSRL GTRFLCQPAVTVIPVKIVRVTG DTVIRPHAEGAVRVQLRVGQA VTCRVCGIRDADIQIRCGGVNA GQPAGGAVAVTPGLARAADAD EFAVVVPGQPFHGGQAVRYTA VRQPLRVGRMSGLMLAKTCFR LQVMHRLTLTVFSQKVFTESIE VVEALKVNLMRVFLRRMDLRQ HRKMIMIDNYIAYTGSMNMVD PRYFLRDALPHCPNPLTGPTFA VLEKLGYPHTFVSTDFNTVALD VKTFGIKANDDKAKLKALGEIA HACVDATIIYCKSPTVAGLVAR ELIKLGHGTPTENPHVYWSPLE TVLACILARYRGHCSNTLATNS MLENCAFCSAPPRSLKESTLSL NTVVIYDNRDGTRSIDKFNRFCI HAFPKIIRNAIYEVEQHT*RACR YQ*DVGWFNIYQPGISLAASKH CSTSSR*RWI*LDWI/CASASLL DEATAAAEAMAMAKRVSKLK NANRFFVASDVHPQTLDLMSY
18091	48459	A	18198	643	776	
18092	48460	A	18199	1	1257	
18093	48461	A	18200	3	346	
18094	48462	A	18201	1120	1335	
18095	48463	A	18202	312	1108	
18096	48464	A	18203	1	744	

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18097	48465	A	18204	381	1112	GVEPSPPTNPPPATAIPRATCVA AARAASPSPS*SHQPHPPPLAYD RCST*PTPTTTAGQDHDHGRR WRSAPAPRSDHLSDMLQE/RSM SLLPLILSSTRSGSNPLRSTFLSR SRSISKNCSAEV*SNNSAGVGTI STS/RSTYDINRADTQVRRAVN NYDIIVMSNSFNGQSEHQVWIG GQF/ILHQICPLTQFQYGAEPDR KE*CQAPASKWALLHK*HRPFP QDRKAGECLLHEYEDLYPSVIH
18098	48466	A	18205	2	307	HPARHKFVKGSSEHRKSPVKPP PIPSH*PP*PENTNPMRPLAPTDP VTNLRSLMTGRQRFTPYNNVS RSDPSTTARSSSADRVNASEYP TSSEETSGRSSR
18099	48467	B	18206	1	723	
18100	48468	C	18207	127	1410	
18101	48469	A	18208	1	1773	MGKKQSRKTGNSKNQSASPPP KERSSSPAMEQSWTDNDFDEL REEGFRRSNY\SSY*EEIRT*WQ TSLKALKRN*MMM/ILLASPSR TPISGPNGDPAGPKFVKAAATT GKARQRFHPATTTFHGRTPAPP LAHPAPTVSTPASTQHPARRHQ VARPDRSSTPLPARIALRVFCPT PSTAPPEHPRQNPNPAPQTDSA LPGADDVRVSTTDPERRHPHPT NTTTPGPGRVLRKELNRPRRPI HHRRRRFHVQRAWQLPVPHRH HHLDHTSHTRRRLRMTDVRLD RPQPQRPPRITITTVGGDQRLRL DRSYQPESPCDGDLRQLQMAG RAPCSPLSMLVLEKCDNLKTCH TSHGSVMAETAVINHKKRKNS PRIVQSNDLTEAAYSLSRDQKR MLYLFVDQIRKSDGTLQEHDGI CEIHVAKYAEIFGLTSAEASKDI RQALKSFAGKEVVFYRPEEDA GDEKQNAKNEHGTTSSLPTQFK TDHMESQKDHPHKEETSPKVP HLVQESQKDHLHKEATNLKVP HPHPGKPQGPPPQEGNKPQRPP PPGRPQGPPPPGGNPQQPLPPPA GKPQGPPPPPQGGRPHRPPQGQ

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18102	48470	A	18209	944	1577	RLCCLEISSTGYPKSSISSSKYPQ IPRAGAQCSQAV*SGSNPLRSTF LSRSRSISKNCSAEV*SNNSAGV GTISTS/GSTYDINRADTQVRRA VNNYDIIVMCNSFNGQSEHQV WIGGQF/ILHQICPLTQFQYGAE PDRKE*CQAPASKWALLHK*H RPFPQDRKAGECLLHEYEDLVP IRDTLRLFPGGRYLPRAKHVAP SEPDPTHHAYD
18103	48471	A	18210	3	634	DRVFDSGSKWRSEQDWAAAK AVGQCSENGDWRCCGNGRYP ARGPAVPA*PSLCLHHPR*RCT CCMPVYR
18104	48472	A	18211	3	255	
18105	48473	A	18212	101	547	TSVELMDLCPIRLCRTFSGIPAY SMCIA*EWRNVCGVTGTENVT PSAAAAATASPIQVLTVLSVTS QIRAFSVLPVRRLRRSMSLSRIN TCRTEYPRCAVVCLLWKDAVS CLSTTFCARLCGQNTWLPRPCR HVNRAASDASVSLSTVT
18106	48474	B	18213	1	1113	
18107	48475	B	18214	220	1173	
18108	48476	A	18215	1	509	MPNHKAILIKFKKTEIIPITLLDH STIKIEINIKKIAQNHTITWKLNN LLLNYFWPLTVSLCEMCKDFYS LGIEFSRFPLQELQNKDCALEK/ HSHWAQMWP*YPCPAKHWWS CRREHVLVVN/DCSTS*NSYWH FSD*LRAMKRRNEQCKR*AIRS LSRSLPARQDLKLLS
18109	48477	A	18216	3	281	
18110	48478	A	18217	878	1135	
18111	48479	C	18218	1	1602	
18112	48480	A	18219	33	608	VDSLRFQSPSCSVYSTDTR*ISE T**NKL*PPKPVIACPKMWIQV GQKFRQKAAATP*KAR*SPRPIP SH*QP*PKIQTRCGPQPPQIRSPT QKPHDRQTALSHRTTTFHGPTP APPLAHPAPTVSTPASTQHPAR RHQVARPDRSSTPLPARIALRVF CPTPSTAPPEHPRQNPNPAPQTD SALPGAVRG

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18113	48481	A	18220	3	893	NPRKRTEQGKAQNKVQWWLT RTPVMVQKRPTIVSLKSSPDSPL ETYSMFLFLGMWVGVGVEM/C SVKLEEQVNTYHYQRILLGISS DNAILLEEESEEGRPMHISTIKE PSPDSPILYLTLNLKLLTSLILFH YGESWNLLRADQRLIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEAVAAAA ADGVTFSVPVTPHTFRHSYAM HMLYAGIPLKVLQSLMGHKSIS STEVYTKVFALDVAARHRVQF AMPESDAVAMLKQLS
18114	48482	A	18221	1	327	LISLRQRQQRTPGKPGKGPRPIP SPWPP*PENTNPMRPPSPTRSGH QPRSLMTGRQRFHTAQQRFTV RPQHHRSLIQRRPCQRQRVPNI QRGDIRSLVQIGHQRRCLRG
18115	48483	B	18222	1	1419	
18116	48484	A	18223	1	2784	
18117	48485	A	18224	936	1157	RTSTGLSGCIRCG\CASEGGQAV FV/WPRGPPETPCSRCPAAEGSP G*SPPREDPSSGSPGKRQTCTQT SARSPS
18118	48486	B	18225	67	1314	
18119	48487	A	18226	302	1423	CRWRFRFIMPFVMASMSAECL MNYNSTAMSGKTGLQNDTTLI ARPWVKPYLGLEIMRIVGN*PH LTWCFPCTMYIPLFSQLLCCPVS FGQCGAFRNPGHPPSPNPEFFLG PRRCNPSLGHKALVQEAASDTP GKS\PGKSPPGPIPKPIGPP*PGK HKPDAAPSPHRSGSPNPEAS*PE DSAFTPHNNVFTVRPQHHRSLI QRRPCQRQRVPNIQRGDIRSLRF GCFARHHPRHHRNIHDRTRTRP RRLTRHSRGLFEDDVRVSTTDP ERRHPHPTNTTTPGPGRVLRKE LNRPRRPIHLRRRRFHVQRAWQ LPVPHRHHHLDHTSHTRRRLR MTDVRLDRPQPQRPARITITAV GGDQRLRLDRITKPRARPN
18120	48488	A	18227	1731	2392	
18121	48489	B	18228	1	1422	
18122	48490	B	18229	298	1464	
18123	48491	B	18230	1	1800	

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18124	48492	A	18231	745	1250	HTQNQRSGRSQNDF*RRRKNIS ERSAVYR*RQLYIRRQPYAERP SLR*RQRP*IPCIRSQHGNRKRIP RRRIFI*QSVLRRRHELLP*RKPE ASAERHKTRC*VSERRPRYHRV KYDYH*KSIYSR*AHGAA*PSH RKDRESADLGSDGQNGQDLDC RGGCQPLLLTV
18125	48493	A	18232	1	1661	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFD DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS YAAKEVVLYRPEEDAGDEEGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRM PDFRRRFLQCINAGHEMTKAIAI AQFNDDSPEARKITRRWRIGEA ADLVGVSSQAIRDAEKAGRLPH PDMEIRGRVEQRVGYTIEQINH MRDVFGTRLRRAEDVFPPVIGV AAHKGGVYKTSVSVHLAQDLA LKGLRVLLVEGNDPQGTASMY HGWVPDLHIHAEDTLLPFYLGE KDDVTYAIKPTCWPGLDIIPSCL ALHRIETELMGKFDEGKLPTDP HLMLRLAIETVAHDYDVIVIDS APNLGIGTINVVCAADVLIVPTP AELFDYTSALQFFDMLRDLLKN VDLKGFEPDVFIRDKLMERRNR RTGRTEKARIWEVTDRTVRTWI GEAVAAAAADGVTFSVPVTPH TFRHSYAMHMLYAGIPLKVLQ SLMG*YVHCKALWMDCAHV** TKEKIHSLLHRRHPLQGDKEPL PSPRNSSMPAVYPYWLPQRSIRI FQHI
18126	48494	A	18233	162	446	
18127	48495	B	18234	144	2537	
18128	48496	C	18235	1	873	
18129	48497	A	18236	700	1198	PFFGTDFFPWARWCIQLRHKFW SKGKQRTTKKAPVKPPGPSPAI DHP*PGKHKPDAAPSPHRSGHQ PKTSMTGRQRFHTAQQPFHGPT PAPPLAHPAPTVSTPASTQHPA RRHQVARPDRSSTPLPARIALR VFCPTPSTAPPEHPRQNPNPAPQ TDSALPGAVRG

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18130	48498	A	18237	363	940	LQTVLQGYSNENSMFVKQKGS PPGKPGKKKPCFWGAPKNGAD IPSQSWRPSGNPGTTPPLPKPPSF FPGAPRMGQSQAWGHKGFWF KKGKPTEPPGKKARVKKPPGG QSPKAIGPTRGPGKPPKPDMRA PKPPTDSGHQTQKPS*PADSAFT PHINVSRSDPRTTARSSSADRVN ASEYPTSSEETSGRSSR
18131	48499	A	18238	861	1517	SLRPHLSGFYQARTL*DQRS*A DHE/DISKNCSAEV*SNNSAGV GTISTS/RSTYDINRADTQVRRA VNNYDIIVMSNSFNGQSEHQV WIGGQF/ILHQICPLTQFQYGAE PDRKE*CQAPASKWALLHK*H RPFPQDRKAGECLLHEYEDLVP IRDTLRLFPGGRYLPRAKHVAP SEPDPEQDEQKLRFCKRHLYGQ QPRSPVEIRLQHVAIAYQTHHA
18132	48500	B	18239	1014	2337	
18133	48501	A	18240	1495	1947	IVTLCFPSYCLHCEAGP/LPCGH PWLWLC*VLGSPG*TQRTGSW AMPGVQASKPACG*KVAPAAR RVPHPLHMLPHSGHSAASGGA SCPLCRG*ATGSDQVLKHAFRK GRSSNCASNGTPPPNADFLGQD VHPARHKLRQKSASEPRKKAR
18134	48502	B	18241	1	2055	
18135	48503	A	18242	1	909	
18136	48504	B	18243	184	395	
18137	48505	A	18244	447	667	HRPRRRFQIKPQSQVPEHAPLPL PTASDPP/AHSPRCPSESRLSPGG QRLGFPSSVLNCSKCSWQLAAC MGFSF
18138	48506	A	18245	265	890	
18139	48507	B	18246	1	551	
18140	48508	A	18247	407	636	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR */ERDYISIMPKPDGLTAAKNLA EAFEHYNECIRI
18141	48509	A	18248	1	1448	
18142	48510	A	18249	817	930	
18143	48511	B	18250	303	461	
18144	48512	A	18251	612	3359	
18145	48513	A	18252	1	462	

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18146	48514	A	18253	268	749	RGGIEYLLLVVFILTRTRFIQAV EHRRNGRRVAEKIVPELITHFM AEIRDLLQRTGVAL/W*HQSAA YLPG*QICALA**IHPGVAAGEY QRRSIQENGGKVQESGQTAS*M RG*MSVESRSGIAARCPESDAQ SGVVHRSRWNQSLPARFGAGR DYREAS
18147	48515	A	18254	1793	2193	TQRIPAAQKQGSRCIVDSSAEA LSAALAIGNIELVKPSRTMS/DK AAQEIVNSGKAKRVVVSLGPQ GALGVDSENCIQVVPPPVKSQS TVGAGDSMVGAMTLKLAENA SLEEMVRFGVAAGSAATLNQG TRLCSH
18148	48516	B	18255	1	1557	
18149	48517	A	18256	606	1123	QRDNPSGTDGGRNRAFGAGNI HTRGAAQAVERLVDSFPAQEK DPGESTGRTDSLPSSRPQKVAY PVHRNDRR/ERLWFAAPSSPSN ATWGNAEWTLNFSSSDSVTGA SSER*NLLFRLATVRCTLPSSVS ADGAIVAALATHIGEAELTLES QCGAWRATFSSTCSSLPLNPN
18150	48518	A	18257	110	318	TALKLPLPMSTKVTRCLSNLLK PKFNLPPLVQPPKKMLPRHLSR *APNTKTSRVLKKN*PIPIPTRR KT
18151	48519	A	18258	2	3062	
18152	48520	A	18259	4435	4954	
18153	48521	A	18260	1	1959	
18154	48522	A	18261	2	715	
18155	48523	A	18262	1	756	MIRRVSVASGNEYPMRPASYIR TAPTVYPSSSPAGTWFAGNAPA SSCGFRDRYLIVCSHQTPHVPG KREEVNYETGIYWLRHYGYTD YSRNAKQRLQRNNLAPILFTTT VPLGGRQYNNSQHLPQRQSLE RIRHHTQAFTALIPHGAAGQGC GSGDLHYLSLEDVAVSSKATPD GSGVTRKASANLRVTIQIGGFQ LRTCGFGPSCRGCHPALQISRAL AVAAHQQAADNNMEFANYGP FELLQ\ARQLIES
18156	48524	A	18263	1	799	
18157	48525	A	18264	1	270	
18158	48526	A	18265	2	188	LGFFFQRPLGFGQELSKL*EQVL LAPEEVGHLGEHLLFRHASEWP APRVQLLLLVRVQDLQE

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18159	48527	A	18266	2791	3274	SKIFPRHDDLLLWRSHRNGDDL RTAGMNAFKQRLTLLGFKITIL TANDYLFADGQ/RSVRKKYPQ AQVSRVAGADLWEELMARAG KE/GTPVFLVGGEPEVLAQTEA KLVRSSSATSAIAWPLLIPCAISS WIRSTAFCCCSWVSEGKPADRS PAPSRTWLRC
18160	48528	A	18267	202	627	
18161	48529	A	18268	1	2390	
18162	48530	A	18269	1081	1911	
18163	48531	A	18270	86	272	
18164	48532	A	18271	674	2808	FILKLRTRRR*RHRLIRPWELFQ TARNAEVMKA/LVRHLWLEVK GVDLGRFPERRYGSDKPDLRNP MELTDVADLLKSVEFAVFAGP ANDPKGRVAALRVPGGASLTR KQIDEYGNFVKIYGAKGLAYIK VNERAKGLEGINSPVAKFLNAE IIEDILDRTAAQDGDMIFFGADN KKIVADAMGALRLKVGKDLGL TDESKWAPLWVIDFPMFEDDG EGGLTAMHHPFTSPKDMTAAE LKAAPENAVATLGDPLESPDDG LHNRISTHGCFYVLCGISTNIGV ESTARNAWELGFNLVIAEDACS AASAEQHNNSINHIYPRIARRG RDPQRVMIYIGLPQWSHPKWV RLGITSLEEYARHFNCVEGNTT LYALPKPEVVLRWREQTTDDF RFCFKFPATISHQAALRHCDDL VTEFLTRMSPLAPRIGQYWLQL PATFGPRELPALWHFLDSLPGE FNYGVEVRHPQFFAKGEEEQTL NRGLHQRGVNRVILDSHPVHA ARPHRKLGGTAVWEWEPEGA HWVGDEPGWFSSGDLSKAEY WAQKAADSGDADACALLAQIK ITNPVSLDYPQAKVLAEKAAQA GSKEGEVTLAHILVNTQAGKPD YPKAISLLENASEDLENDSAVD AQMLLGLIYANGVGIKADDDK ATWYFKRSSAISRTGYSEYWA GMMFLNGEEGFIEKNKQKALH
18165	48533	A	18272	532	2103	
18166	48534	B	18273	1	4401	
18167	48535	A	18274	343	765	
18168	48536	A	18275	447	709	

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18169	48537	A	18276	1	1571	MIEVKHLKTLQALRNCGSLAA AAATLHQTQSALSHQFSDLEQR LGFRLFVRKSQPLRFTPQGEILL QLANQVLPQISQALQACNEPQQ TRLRIAIECHSCIQWLTPALENF HKNWPQYSVIFKSGVTFDPHFF FQQGELDPERAFDDFGIKPMAS ASIAQVHSARFNSNGHEVVIKV IRAETLPVIKADLKLIYRLARW DAAFAAGWSPPAANLSCAGST KIHRLMNRTCCRNLPTPFSFGA KPGLYLVEAMVGGYRATTVVF VSDTVALSKVSGIELLVWGAG KKQGEANAGSEILWTDGLGVM TRGVTDDSGTLQLQHISPERSYI LGTLAMVQLREDMAKRQAAGI IAPRSGRRMHRTQHKPPMTTE MGPRAVLREDTIPFLEALKASG KQRILLTNAHPHNLAVKLEHTG LDAHLDLLLSTHTFGYPKEDQR LWHAVAEATGLKAERTLFIDDS EGDAMKEKPAVEVRLDKWLW AAR/SL*NPRAGP*ND*RR*GAL QRAAHEAEQNRRAECHAHSAP
18170	48538	A	18277	2080	2274	RFQVVYFDHEKPSLRHE*FALE EYTGTRN*GCVNLLDR*KPFPF KFMERWLAFSPPGLTLESSRG
18171	48539	B	18278	1	3126	
18172	48540	A	18279	1	341	MLDRLESEILADRVSEESRRWL ASCGLTVEQMQNQMDPVYTPA RKIHLYHCDHRGLPLALISKEG TTEWCAEYD/GMGQPAE*REPA SAAAAYPPAGAAV**GVRPVL QPPPLL
18173	48541	A	18280	945	1484	
18174	48542	A	18281	965	1403	
18175	48543	A	18282	703	1149	
18176	48544	A	18283	161	476	LLPWRSCILRSDPLAAHPVI/LV P*ACIFIARNCYPRPSCDSACKL RRESCG*FG*TRMVSAQATFSIQ ITSA/LPFCEHLPGKRSGDFDTG EDNALSGQRPEFRHG
18177	48545	A	18284	1	443	MLSEPALRELATAIAGVRKGEN DIAVENIIGANIFNIVIVLGLPALI TPGEIDPLAYSRDYSVMLLQAG KEVLAIERECLAELDQYINQNF TLACEKMFWCKGKVVVMGMG KS/RAILGEKWPRNVCQHRIAN HENRDSIRKICCYHR
18178	48546	A	18285	3	550	

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18179	48547	A	18286	2157	2504	LVSLAGAAYRSPQDPVPYMPIS PGLDWVRQIVCCVMASDAD** RVPRQNALLLPVCTSGPYHALA TGCGFRRGQMLKTTVLPRHYK LYLGASSGMRYSTPATALMPLP LPHLAER
18180	48548	A	18287	1	621	
18181	48549	A	18288	1	423	
18182	48550	B	18289	1	1551	
18183	48551	A	18290	1171	2757	
18184	48552	A	18291	347	690	
18185	48553	B	18292	1	528	
18186	48554	A	18293	1	1417	
18187	48555	A	18294	292	699	
18188	48556	A	18295	859	1377	
18189	48557	A	18296	1	3036	
18190	48558	A	18297	1	942	
18191	48559	A	18298	1	2124	
18192	48560	A	18299	1955	2797	GGISIDRSGDH*GRGAVYHVAG R*NAGRTAELYFASRPTCG/RW LVAAVQGAATARISTIEMSVW AQL*QMCRGKIRAT/ISLPEATA QVISSGSGATKVEDGLGDLNKP VSNQNLVTGIDTPVYNAPSAGS APFGVLADNMRYPILHKLKDR LNQTWYQIRIGDRLAYISALDA QPDNGLSVLTYHHILRDEENTR FRHTSTTTSVRAFNNQMAWLR DRGYATLSMVQLEGYVKNKIN LPARAVVITFDDGLKSVSRYAY PVLKQYGMKATAFIVTTRIKRV
18193	48561	A	18300	1	1191	
18194	48562	A	18301	1	298	MPVVFTVFFLWFPSGLVLYYIV SNLPRYAEYLTVKDADGSVLD QGIALWFP\GPNSFTGEDVLELQ GHGGPVILDLLLIRILTVCGLRI ARPACSPRSL
18195	48563	A	18302	1	1011	
18196	48564	A	18303	1	1845	
18197	48565	A	18304	1	755	MSPVIDKMYVDAYQPFSEEKIS MQEALEKGAQPLREFMLRQTR EADLGLFARLANTGPLQGPEAV PMRILLPAYVTSELKTAFQIGFT IFIPFLIIDLVIASVLMALGMMM VPPATIALPFKLMLFVLVDGWQ LLVALVTGLIISILQAATQINEM TLSFIPKIIAVFIAIIIAGPWMLNL LLDYVRTLFTNLPYIIGRTMLQ VTSEQ/CAILVKPVLLAVTARA GADLHRADSERTQRTKTGGGF CRYWAG

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18198	48566	A	18305	1	1977	
18199	48567	A	18306	1	630	
18200	48568	A	18307	1715	1996	LFRLLKTLTGRRKRSNKSWITT CRGFWGTWCAGWSRP*VVQK CRIYTMWR*WQHAQR*VSPAT LNGLMLITISRKNPHTRKGAGK HCPFSGPS
18201	48569	A	18308	517	675	
18202	48570	A	18309	480	626	
18203	48571	A	18310	757	1146	
18204	48572	A	18311	318	724	
18205	48573	A	18312	1	1743	
18206	48574	A	18313	1	1197	
18207	48575	A	18314	161	613	LLRQGFIVISAGGKRVEGQIKLV FPAKFEAGFRHGVIANLRLYPF PEEKIGEMATAPLSTSGDCRT* YALIGIQ/PTDGDARGSPRYKPA LALLPACVGSAKSTPHGRTPIPA IYVPSSPT*FRALASDSVAQT*Y CRPASQTRRASPARSL
18208	48576	A	18315	177	425	SRYFSATSTWPLVMSIPVTCPFS PASWLST*QSLPLPLPRSKIQQF CRCSGITRPQP*YPDPKSSSFVD AQGSPDHSHNILGLLLRVHFAR LPECAWGPAWLW
18209	48577	A	18316	1	576	ADSSKKIADIISVIDGIAFQTNIL ALNAAVEAARAGEQGRGFAVV AGEVRNLASRSAQAAKEIKALI EDSVSRVDTGSVLVESAGETM NNIVNAVTRVTDIMGEIASASD EQSRGIDQVALAVSEMDRVTQ QNASLVQESAAAAAALEEQAS RLTQAV\PRSVWQPAHSPINRK HHPVLPIATGALMPGCGS
18210	48578	A	18317	121	1819	
18211	48579	A	18318	1	2151	

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18212	48580	A	18319	3	1127	GTPYASQPVIRPVEGSKPLIKQV LDIGAHGTDKTIAQKLARVAR MHFARQRLAAVATFACSAQNA IALMEEIAANFSYEMIRLTECIL GFTWNRLYQGINVHNAERVRQ LAHDGHELVYVPCHRSHMDYL LLSYVLYHQGLVPPHIAAGINL NFWPAGPIFRRLGAFFIRRTFKG NKLYSTVFREYLGELFSRGYSV EYFVEGGRSR/TGRLLDPKTG\M LRGGTRPITLIPIYIGYEHVMEV GTYAKELRGATKEKESLPQML RGLSKLRNLGQGYVNFGEPMP LMTYLNQHVPDWRESIDPIEAV RPAWLTPTVNNIAADLMVRIN NAGAANAMNLCCTALLASRQR SLTREQLTEQLNCYLDLMRNVP
18213	48581	A	18320	1	2470	MFQPSDSGKSFIFNMSVGYNLE GIKQPPMQQFIDNMMDASDHP KFAQYRDTLNKLLQDDAFLAR HGLQEKRESLQALPARIPTSMV HGVTLSTMHGCPPHEIEAICRY MLEEKGLNTFVKLNPTLLGYA RVREILDVCGFGYIGLKEESFD HDLKLTQALEMLERLMALAKE KSLGFGVKLTNTLGTINNKGAL PGDSTSGVLRTYERLLTAWML TCPCADEHQRGESVKLATALT WWLRGSQNRDEITKDGFQSNH AGGILGGISSGQQIIAHMALKPT SSIDVPGRTINRFGEEVEMITKG RHDPCVGIRAVPIAEAMLAIVL MDHLLRQRAQNADVKTDIPRC AQSIGSFSNGCIVGADTLPIQSE HYQVMRTDQRRYFGHPDLVM FIQRLSSQVSNLGMGTVLIGDM GMPAGGRFNGGHASHQTGLDV DIFLQLPKTRWTSAQLLRPQAL DLVSRDGKHVVSTLWKPEIFSL IKLAAQDKDVTRIFVNPAIKQQ LCLDAGTIATGCAKCDPGVSIG AYAYLLTLRAQCLAHDLPDPLE PLEIDGTLLPRYVFIHGGPRVFT YYTPKEESIKLFHDYLDLHRSN PNLDVQMVPVSVMFGRAPGRE KGEVNPPLRMLNGVQKFFAVL WLGRDSFVRFSPSVSLRRMADE HGTDKTIAQKL\ARVARM\HFA RQRLAAVGPRLPARQDLFNKL
18214	48582	B	18321	1	1460	
18215	48583	A	18322	2	234	

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18216	48584	A	18323	282	422	
18217	48585	A	18324	1	1974	
18218	48586	A	18325	154	1944	
18219	48587	A	18326	18	386	KACEAVF*DQGLPLGPKVQGQ WDWFPGPGALRHQQSVAHQA GGFRSLWGYSGVSGQCRRHSD *SRPGREARRRRSVAG**SHAL HRQTALFGARSDADLPAAAPR YLLYRGLSAAHFRPQAG
18220	48588	A	18327	181	655	KARSPEDQGFRPRVHIDGGVW HLDVGSSHPGAEVGPKGMAVR HLKWYASWV*NVVRQFGPYLP WALEN/WRGAAPSTRGHGVC/G ITVFGKSDGTT/SHDQY*TAPYG SPHPPGRWSLRHRYPAHLTSSA LAFSDARRNAARQPRRWNPLS GYSQVICLPAW
18221	48589	A	18328	1	658	MDDGTSIAPDGDLWAFIGDELK MGIPENDRIREQKQKYLRNKSY LHDVTLRAEPYMYWIAGQVKK RNMPMELVLLPIVESAFDPHAT SGANAAGIWQIIPSTGRNYGLK QTRNYDARRDVVASTTAALNM MQRLNKMFDGDWLLTVAAYN SGEGRVMKAIKTNKARGKSTD FWSLPLPQETKQYVPKMLALS DILKNSKRYGVRLPTTDESRAL ARVHLISPVKCARFSRFVFCPA VCRDSGGADERRTDSDGCQYA GGVKPESVMGAEIVEGFSHISV TSAWSRGDNSPAPMAFSRLWL TVFSMVFKRRETVRSLSAVGA GELRGAAPSTRGPEWTHHWCS GCHANGTARSAVVPPDPMPNS EVKRRSADGSVGSP*RLITAAK VGS*RQLKRTKRVGNPRTSGRY RCRRKRSSTCLKCWH*VIFSKT ASVMAYVCQRPMKAVLWRVC
18222	48590	A	18329	642	1343	LCLHLPLPTRFPRLQL*EEGGPV QPAAMPQWRTLPGPGPRPALPL PRRLRGSSLRARPGRLRGPRLR* RRHVCGGRRRAPLLLRAGLRRP RLPRARGPVRRAPLCSRRPLLR PLLRPRLRLRSRLHGSAV*VPSA PRRRKRLARGPAGPQARGPSAL PFASGSGTARGRGRGRRCALA GPRAPPWPLPGCWVSLAGWDP GAVSPRTPGCTQQPKDAGGFR GWSEAGVHDAQTV
18223	48591	A	18330	1	810	

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18224	48592	A	18331	236	717	ALPVGAAFSSTTGFGSGFGAGG ASTFGLGGSTGFGFGGATGAGS GSNSVLLAAIVAGSSDGAAASP ARTSSAAPSGGCD/QERRIVDFK RNKDGIPAVVERLEYDPNRSAN IALVLYKDGERRYILAPKGLKA GDQIQSGVDAAIKPGNTRLSYG QHREAWR
18225	48593	A	18332	49	291	
18226	48594	A	18333	75	839	
18227	48595	A	18334	1	579	
18228	48596	A	18335	223	563	
18229	48597	A	18336	1	1219	
18230	48598	A	18337	157	864	RGNRQLQQFPRHWRSNRLDGL LLQIQLQILGGHTVERHLVVQI ALVVNGHPGHADGMWILCIRV LLSLQQNGFRRVPSIGHWTGH* AATDQARLMLGGHINAQFAGI QRLEDLGTQLLHTTNGLVEVE ARRQILQLGLPLFLLLNQTDVW AIPGVHVLRFDVVGRDPS/EVLI DPRQNAGLLWKVFATFRPEPTR PAVCCPRGGQSGDDRRAGCAC NHVELVARHRRSCPWHSDRH
18231	48599	A	18338	1	219	
18232	48600	A	18339	1	2226	
18233	48601	A	18340	46	228	
18234	48602	A	18341	382	1431	
18235	48603	B	18342	1	2400	
18236	48604	B	18343	1	912	
18237	48605	A	18344	2267	2539	
18238	48606	B	18345	1797	3411	
18239	48607	A	18346	1842	2560	
18240	48608	A	18347	1	1284	
18241	48609	A	18348	1	792	
18242	48610	A	18349	1	978	
18243	48611	A	18350	757	1011	LFGRFSNGFLIVVCQRLRQAVV NEQFLPETATLTHRGELLFHSP A*LPGVFRYLAQM*RHAVIQVF RATGVPEPERCRQRRPHER
18244	48612	A	18351	148	679	RMSDDKFDAIVVGAGVAGSVA ALVMARAGLDVLVIERGDSAG CKNMT\GGRLYAHTLEAIIPGFA VSAPVERKVTREKISFLTEESAV TLDFHREQPDVPQHASYTVLRN RLDPWLMEQAEQAGAQFIPGV RVDALVREGNKVTGVQAGDDI LEANVVILADGVNSMLGRSLG MVPAS
18245	48613	A	18352	1168	2241	
18246	48614	A	18353	1	1344	

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18247	48615	A	18354	440	886	
18248	48616	A	18355	1	2876	MAGVPGFEPGNAGIKNRCLTA WRYPIRTTLSGEWCGRRDLNSQ EATLQQPLLQAIDLKKHYPVKK GMFAPERLVKALDGVSFNLER GKTLAVVGESGCGVLACTLFA WNRNYFVLLFVGVFLSSFGSTA NPQMFALAREHADKTGREAV MFSSFLRAQVSLAWVIGPPLAY ALAMGFSFTVMYLSAAVAFIV CGVMVWLFLPSMRKELPLATG TIEAPRRNRRDTLLLFVICTLM WGSNSLYIINMPLFIINELH
18249	48617	A	18356	606	726	
18250	48618	A	18357	1271	1726	
18251	48619	B	18358	1	1633	
18252	48620	A	18359	1	407	
18253	48621	A	18360	427	2307	
18254	48622	A	18361	120	694	
18255	48623	A	18362	804	1087	KRQHLCTHSGAIRLRIAGVGSW KG/GRPNWRKMAVRWRVPASA VVSGWLRRWHCWPVAMPSAE SPRIRCGAGCCICRLPLFRCGCC TPARLTISH
18256	48624	A	18363	216	436	
18257	48625	A	18364	476	577	FRRWYWGCCSTTRLSHCLTR* M*CMRWSLAVCC
18258	48626	A	18365	1159	3744	
18259	48627	B	18366	169	743	
18260	48628	A	18367	2811	3513	SLPRGWFQPEYGNLEIMEKTYN PQDIEQPLYEHLGFPRVGLRRE LKKAQESYWAGNSTREELLAV GRELRARH\WDQQKQAGIDLLP VGDFAWYDHVLTTSLLLGNVP ARHQNKDGSVDIDTLFRIGRGR APTGEPAAAAEMTKWFNTNYH YMVPEFVKGQQFKLTWTQLLD EVDEALALGHKVKPVLAGPGT WLWLGKVKSEQFYRLSLLNDI LAGYQQGLAETGVGPDDIVTA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18261	48629	A	18368	1	2810	MKQTVYIASPESQQIHVWNLN HEGALTLTQVVDVPGQVQPMV VSPDKRYLYVGVRPEFRVLAY RIAPDDGALTFAAESALPGSPT HISTDHQGQFVFVGSYNAGNVS VTRLEDGLPVGVVHVVDGLDR LARQLIKNLATLKAGNARVVN SNAMSFLAQKGTPHNIVFVDPP FRRGLLEETINLLEDNGWLADE ALIYVESEVENGLPTVPANWSL HREKVAAFAGAEPYHYLNHTL GFPRVGLRRELKKAQDSYW
18262	48630	A	18369	2279	2563	MNFGASLNSPTPRSYLSLGGEK KAPVWEHTLGVPSRRPAAGKL KKAPERYWGGEHPPVKKWLG G*ARKCRPRPWETL*KSHLRRR PSLGPWAGGL
18263	48631	A	18370	481	1020	
18264	48632	A	18371	1	998	MNENFGTQICVNNRLSFTDCSG YVTRYDHDRFGQVTAVHREEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNAAGDLTTVIAPDGS RNGTQYDAWGKAICTTQGGLT RSMEYDAAGRVIRLTSENGSHT TFRYDVLDRLIQETGFDGRTQR YHHDLTGKLIRSEDEGLVTHW HYDEADRLTHRTVNGETAERW QYDERGWLTDISHISERHRVTV HYGYDSKGRLASEHLTVHHPQ TNELLWQHETRLAYKRTGLAN RCIPDTCPPVNAYLGTACCQHE ICDTPWLSYRDPFTGKSWLSGR YELHKRIYGITAKERKDVDVW HPDVRFFELYDENNELRGSFYL DLYARENKRGGAWMDDCVGQ MRKADGSLQKPVAYLTCNFNR PVNGKPALFTHDEVITLFHEFG HGLHHMLTRIETAGVSGISGVP WDAVELPSQFMENWCWEPEA LAFISGHYETGEPLPKELLDKM LAAKNYQAALFILRQLEFGLFD FRLHAEFRPDQGAKILETLAEIK KLVAVVPSPSWGRFPHAFSHIF AGGYAAGYYSYLWADVLAAD AFSRFEEEGIFNRETGQSFLDNI LSRGGSEEPMDLFKRFRGREPQ L*HTVVELPRPFHREILAFRPL*I TQAYLRHHR*RA*RC*CLASGC

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18265	48633	A	18372	409	533	TGNDAPVPAQSAQYRYLQ*SV RNFCRLSFRLGINLSLPYPHVDD VIPLMAEGKILPYLDIPLQHASP RILKLMKRPG
18266	48634	A	18373	222	659	SAGSVKTQRSGANKQRRTRSRL ASFC/ETLSSVSFPAWRKISFLIP VGLPISNNYVCSLNPVWCAMR LNMPPMSKSICWQKHWKSTVS RWITTRHSFVQTLISTACWRRSP VTQSSWRSTFACSTGLLSHAPP LPIRHCTNITNVWY
18267	48635	B	18374	1	1527	
18268	48636	A	18375	1	1005	
18269	48637	A	18376	2	314	WVSYCSGSTTL/LLRALQECQR QQGPWASAGDPGEGAGERERL PQALASPPLQVKPARQ/RDPGL RTPDPGDTASPALNGHIFALPA GTAGDCFPRPPRGRKNSGT
18270	48638	A	18377	3	576	
18271	48639	A	18378	189	563	QGRGSSRPGCGHLDPGGEEWL PQRPGLQHLC\PSAYILIFAGVL VMVTGFLGFGAILWERKGCLS TTTGDRFWKDRQPWTCR/WQT SHRNQSGAGGQWDRFRSHQGH RDHEGRTSNWGSGFPREVA
18272	48640	A	18379	1	531	
18273	48641	A	18380	1385	1673	AASTDRAAETG**KTR/HRWFL SVKLRTSTPTAVSPKK*KRLAW TRCMTPPSKR*KKRVITPSSSPT SLTSTLPGATVATSPVMPRVWN CSTAVCRS
18274	48642	A	18381	1	921	
18275	48643	A	18382	1	2115	
18276	48644	A	18383	2	149	ARRNESRRGGR*HPCRPIT*TGT VNQRPAGFRRFAGPFRYSGKPG RERL
18277	48645	A	18384	482	1655	
18278	48646	A	18385	1	776	MENACVLLMGVLSTFLVSWLG KDAMAGVGLADNFNMVIMAF FAAIDLGTTVPGAFSLCKRDRR QARVATRQSLVIMTFLPVLLAP LIHHFGEQIIDFVAGDATTEVKA LALTYLELTVLSYPAAAITLIGS GALRGAGNTKIPLLINGQVAML MQAPYYFQEAQIEAAIAAMDV APEYADIRQVESSTAVLYLFSE RFMTYGKAYGLCEWFEGSRLSI AHIPVTDNDNETQYHFFRQSCQ HC/DRCSVHRRLPDGGVVA

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18279	48647	A	18386	1017	9228	FGRCAGVCQ*RGRDGQRRDEA GDGRLRARL*\ALYQTITHDLR YRHKNLYRRKLASQRVTEHVN RAGLRYSYQYEKDCITITDSLA HNKVLHTQGEAGLKRVVKKK HADGSVTQSQFDAVGRLRAQT DAAGRTTEYSPDVVTGLITRITT PDGRASAFYYNHHNQLTSATG PDGLELRREYDELGRLIQETAP DGDITRYRYDNPHSDLPCATED ATGSRKTMTWSRYGQLLSFTD CSGYVTRYDHDRFGQMTAV
18280	48648	B	18387	1	1431	
18281	48649	A	18388	575	835	RQKPERYLTAFISTTLPLRWMT LVRVMRPIVTCRRSRSILLRSIS HLCKWRVSTKSPVILWTILSN* RLFWKSWR*NGLQSKYQDG
18282	48650	A	18389	1207	2465	ASTAQQHQLLSPAKEETTGWRI FHPSDPWALGRSQGGAGLIQPP EVQKGSVRYRARFALLGPAMV AHRHTGRPEIRYRYDSDGRVTE QLNPAGLSYTYQYEKDRITITD SLDRREVLHTQGEAGLKRVVK KEH\ADGSVTQSQFDAVGRLRA QTDAAGRTTEYSPDVVTGLITR ITTPDGRASAFYYNHHNQLTSA TGPDGLELRREYDELGRLIQET APDGDITRYRYDNPHSDL\PCA TEDATGSRKTMTWSRYGQLLS FTDCSGYVTRYDHDRFGQMTA VHREEGLSQYRAYDSRGQLIGV KDTQGHETRFEYNIAGDLDGGI APEGG/RNG/TQYDAWGRRRTT /QGGDADDRSAGGTRARKGHT SFRSVGDRT\VSRHGYPGRNLR RMVRSSVPLYRLTASIAPVPQE YRFPPHQSEEVY
18283	48651	B	18390	1	2604	
18284	48652	A	18391	1	2640	
18285	48653	A	18392	1	549	
18286	48654	A	18393	290	389	HLCGPRTAR*ARFWHL*RAYG L*SGECRRAGSV
18287	48655	A	18394	1095	1268	HLCGPRTAR*ARFWHL*RAYG L*SGECRRAGSVAENARSACRC RRSAHAGRFLQTAS
18288	48656	A	18395	1056	2178	
18289	48657	A	18396	1	669	
18290	48658	A	18397	1628	1856	
18291	48659	A	18398	227	668	
18292	48660	A	18399	1	3186	
18293	48661	A	18400	291	631	

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18294	48662	A	18401	1	1437	
18295	48663	A	18402	345	727	
18296	48664	A	18403	870	1043	
18297	48665	A	18404	1	2175	
18298	48666	A	18405	1	1332	
18299	48667	A	18406	1	1566	
18300	48668	B	18407	1	921	
18301	48669	B	18408	1	2487	
18302	48670	B	18409	1	2919	
18303	48671	B	18410	1	2214	
18304	48672	A	18411	1714	1979	RLAWRLAGRWWAGSWRTSTIP PAAACSRLRCSPPSKFCSAWCR WCSTRACSSCCRSTSSPMPAWR PSAGS*LSTARRRAPPSALVLRI
18305	48673	A	18412	1201	2118	PSRQADKENRPHPGRGYPARM MSGLTGTITTVSTGWCTTRGHN MKSRWSKVAIFTTRWGRRVAK RVWRRERDLTGWMSLSRKPQV TWYGWDGDRLTTIQNDRTRIQ TIYQPGSFTPLIRRIPVLGGGDTT MDCLRTSIRLNAASVTCAYRRD QISMPGSRKEVVNAREEGVEFQ FNFQPQYIACDEDGRLTAVGLI RTAMGEPGPDGRRRPPPVAGSE FELPADVLIMAFGFQAHAMPW LQGSGIKLDKWGLIQTGDVGY LPTQTHLKKVFAGGDAVHGAD LVVTAMAAGRQAARDMLTLF DTK*PGTAGTATG*PQYRTTEP ASRRFISRGASRHSSEGS/SVLG GGDTT/MGLFADFHPPQCRQRD L\PYRRDQISMPGSRKEVVNAR EEGVEFQFNFQPQYIACDEDGR LTAVGLIRTAMGEPGPDGRRRP PPVAGSEFELPADVLIMAFGFQ AHAMPWLQGSGIKLDKWGLIQ TGDVGYLPTQTHLKKVFAGGD AVHGADLVVTAMAAGRQAAR DMLTLFDTKAS
18306	48674	B	18413	1615	1656	
18307	48675	A	18414	1287	5056	
18308	48676	A	18415	1	271	
18309	48677	A	18416	1	588	
18310	48678	A	18417	2150	2332	
18311	48679	A	18418	1	238	LEELGVIGAVLVGFSL*VLWAP LQLPKAGGRVKVAGIQLGEVEF WKVS\KSCSSPDPPPGVMAAKIS ISQALQPPQSTR
18312	48680	B	18419	1	2721	

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18313	48681	A	18420	712	1031	PVMRQRGVFRSVILIKIRSARCC QMIQPRVISHAMYSLSPFFALR RSTKSPKRFSMNNS*ASRSSGST SRDTSAIS*ARRSISSRTSRLLIRS LISLISSLLVNVV
18314	48682	A	18421	1	1779	
18315	48683	A	18422	693	921	
18316	48684	A	18423	758	1183	ALTAASRSECAVIMMTGRTSCC DIVEKWIPARCCQMIQPRVISH AMYSLSPFFALRRSTKSPKRFS MNNS*ASRSSGSTSRDTSAIS*A RRSISSRTSRLLIGWRSLWYTILI NSIPPTNRAKSMKPEPSPNACSK VKRCC
18317	48685	B	18424	1	708	
18318	48686	A	18425	1	2436	
18319	48687	A	18426	1382	1813	
18320	48688	A	18427	900	1028	AGYAAPGRTDRRSSPSG*GYRY SGCYQICRQPGRLGSRKSPV
18321	48689	A	18428	1	881	MTPSRFAKKNGSLVKRCPMGI DAEVTMIKPIAARPKVSHSKVR SYMIRLSVSFSREPITQPFSAVEI QTRIRYGVSGFFLRRVDTEHHP DRHAARALQYHITGSNRCDAIN AVQFDTAGGECTNRRMAEDHG RNVAVIQMLIRLVIKQAFREVP SELWTNRKQACPFLDFDCGENS AIAANNYDWFGNMNVLTFLRD IGKHFSVNQMINKEAVKQRLN REDQGISFTEFSYNLLQGYDFA CLNKQYGVVLQIGGSDQWGNI TSGIDL/NPSSASESGVWPDRSA DH*SRWHQIW
18322	48690	A	18429	1	3270	
18323	48691	A	18430	1	374	MKTCWQILEIESTTQIDIIRQAY LARLPLCHPETDPQGFKALRQA YEEALRLAVNPVEEADDEEKD AAAEHEILRAFRT/FTGFRK*SFS AFRLAEIYSAIKYLEHGGCRSIT LAAVCNRHRSAI

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18324	48692	A	18431	63	1272	LRRSCNAVYCW*CVATCPS\GE EDGIVLIDQDKCRGWRMCITGC PYKKIYFNWKSGKSEKCIFCYP RIEAGQPTVCSETCVGRIRYLG VLLYDADAIERAASTENEKDLY QRQLDVFLDPNDPKVIEQAIKD GIPLSVIEAAQQSPVYKMAME WKLALPLHPEYRTLPMVWYVP PLSPIQSAADAGELGSNGILPDV ESLRIPVQYLANLLTAGDTKPV LRALKRMLAMRHYQRAETVD GKVDTRALEEVGLTEAQAQEM YRYLAIANYEDRFVVPSSHREL AREAFPEKNGCGFTFGDGCHGS DTKFNLFNSRRIDAIDHQQEMF EAIAASKNLPKEDAHALGIFLR DLTTMDPLDAQAQYSELFDRG RATSLLLFEHVHGESRDRGQA MVDLLAQYEQHGLQ
18325	48693	A	18432	2	859	WPLRRSPYSIINGSGKSAASGSV MQVAQFNSHYQYDPKFERGM YLYEHRRCFNNIIDYCNSLCYH AWLVAHKDDIERNYRGPLVQV VGWCDAIFGAEELGISRAQFDQ FLRMMQGGAQFGGGYQQQTG GGGRPGGHFFEKRRLLRMVDR LNARFTGGVLVSFKGPLLEGFG PWQGLSPWVIGPDLGLPG/CLG AWGAVSVCHCPWVCKTGSPFR WVPHRRFHPPPG*KFPENWMG FCSSRTCSGLFSHPHSPTMAFKN FELGHGTPPRGTRNRPTMSSNT YRPHRFQ
18326	48694	A	18433	479	601	CWRPLPAEKRWWYLAANWW RLAARFVFPMLCVRQ*PSSMIW TTPDADIAIGTWRSCCAVLRGR KMPVSSITMRRRCY*CWRPLPA EKRWWYLAANWWRLAARFVF PMLCVRQAAPYTK
18327	48695	A	18434	69	194	ATYENMLANPRN*KHDANRHY PPGLSCSLTVVSSRNRSARV
18328	48696	A	18435	173	298	ATYENMLANPRN*KHDANRHY PPGLSCSLTVVSSRNRSARV
18329	48697	A	18436	1	1734	

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18330	48698	A	18437	851	2202	RQKRLIFCCVKGKNWPP*WRW LNEKLPCSLMLLPTLPPSVLGIR LQNQLQRQFVRQGGVWMPGD EVKKVTCKNGVVNEIWTRNHA DIPLRPRFAVLASGSFFSGGLVA ERNGIREPILGLDVLQTATRGE WYKGDFFAPQPWQQFGVTTDE TYARHRQGKPLKTCLPSVRCW ADLIPSPRDAAAVFVPSVLYMP LNRLPNAQEANNE
18331	48699	B	18438	1	5301	
18332	48700	A	18439	710	889	
18333	48701	A	18440	1622	2615	
18334	48702	A	18441	1	1309	
18335	48703	A	18442	1	266	PRQCGFMKKRLENGDDYFAVN PRGRCLHCCWMTVLC*RKRSD YAVSCRQRPRPPVLAPVNSISRS VSPYTPEEYKPTVRAQLEKNCN M
18336	48704	A	18443	267	395	
18337	48705	A	18444	1	3807	
18338	48706	A	18445	1	2193	
18339	48707	A	18446	1278	1846	SCRSAPRNRHQIPGTYRSRLPRH TTPPGYDHNRKNPNLYISTRQK RDAFFAVQYHSLLYYRQTLLPN DHNQSVDR*FVFRL*NQNGYNS GRHLYWRYHSYNAWL*LCHR HPVYYRLYYIFLQPVQMQMPQ CPSPLMPECSFSFSFLILINA/SNI QRESPVENRKVFNLRLLKIYYR LIIFLKCGNLLNL
18340	48708	A	18447	1	2106	
18341	48709	A	18448	881	1401	
18342	48710	A	18449	1	233	MMGFDGTVQYMASLGAPMPM LAA/MYCGSYGSARRDINRAW LFHPSAGGAVYFLHAGYGGDW SPLLGYDRRCGWAKYD
18343	48711	A	18450	1	1960	
18344	48712	A	18451	563	928	FSAIKSSPKAQALWHVLHY*AV N*TNIFKTEKPIFNRGKRFRPTP TRQLRECWIVWGSASCQLTKQ AVVARWTIILMRRRKGWHGRA IILMPGGPRLKQVPRQFCKPPA AAARLSKSMGRC
18345	48713	A	18452	1	828	

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18346	48714	A	18453	1	1327	MMQKPATVDEEESPRETHRYS VRRRGELIVEAGGRAENTVVT GAGWLKVATGGIAKCTQYGN NGTLSVSDGAIATDIVQSEGGAI SLSTLATVNGRHPEGEFSVDKG YACGLLLENGGNLRVLEGHRA EKIILDQEGGLLVNGTTSAVVV DEGGELLVYPGGEASNCEINQG GVFMLAGKASDTLLAGGTMN NLGGEDSDTIVENGSIYRLGTD GLQLYSSGKTQNLSVNVGGRA EVHAGEVTGDIHVEITDASRQT LCNALKLQPDEGGSSRVIPTCK ASRLRIDANFKRFVDEEVLPGT GLDAAAFWRNFDEIVHDLAPE NRQLLAERDRIQAALDEWHRS NPGPVKDKAAYKSFLRELGYL VPQPERVTVETTGIDSEITSQAG PQLVVPAMNARYALNAANAR WGSLYDALYGSDIIP\QEGAMV SGYDPQREAMECP
18347	48715	B	18454	71	4995	
18348	48716	A	18455	1	3572	MARKRKSRNNSKIGHGAISRIG RPNNPFEPCRNRYAQKYLTLAL MGGAAFFVLKGCSDSSDVDND GDGTFYATVQDCIDDGNNADI CARGWNNAKTAFYADVPKNM TQQNCQSKYENCYYDNVEQS WIPVVSGFLLSRVIRKDRDEPFV YNSGGSSFASRPVWVPSSIVIMS YGLASYVIAVAFLERDRIQAAL DEWHRSNPGPVKDKAAYKSFL RELGYLVPQPERVTVETTGIDS EITSQAGPQLVVPAMNAR
18349	48717	A	18456	485	1999	
18350	48718	A	18457	44	270	
18351	48719	A	18458	1	2223	
18352	48720	A	18459	290	756	
18353	48721	A	18460	8	314	
18354	48722	A	18461	2	686	
18355	48723	A	18462	1	732	
18356	48724	A	18463	1	780	
18357	48725	A	18464	101	435	
18358	48726	A	18465	805	993	
18359	48727	A	18466	452	2180	
18360	48728	A	18467	691	1443	
18361	48729	A	18468	1	320	DPRDCRLKVGKEMFTLFGPQF VRELQQRGFDIFLDLKFHDIPNT AAHAVAAAADLGVWMVNVH ASGGARMMTAAREALVPFRPD APLLIAVPV*RSIKASDLVVPL

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18362	48730	A	18469	632	796	
18363	48731	A	18470	129	425	TDIITRQNGTGANIDAIEIIATKA STGLFVYQPRFARCPRVMSSGY HTATRGSSGTRTVRARVCHTA AGVYGSSKQTQF*NRFCQRKCR RYPDGCRRA
18364	48732	A	18471	1	1062	
18365	48733	A	18472	1	996	
18366	48734	A	18473	1	1004	MLRVYHSNRLDVLEALMEFIV ERERLDDPFEPEMILVQSTGMA QWLQMTLSQKFGIAANIDFPLP ASFIWDMFVRVLPEIPKESAFN KQSMSWKLMTLLPQLLEREDF TLLRHYLTDDSDKRKLFQLSSK AADLFDHVSGASVSSKVEQLR AQLNERILVLDGGMGTMIQSY RLNEADFRGERFADWPCDLKG NNDLLVLSKPEVIAAIHNAYFE AGADIIETNTFNSTTIAMADYQ MESLSAEINFAAAKLARACADE WTARTPEKPRY\VAGVLGPTNR TASISPDVNDPAFRNITFDGLVA AYRESTKALVAGIVLMPAIPAL WEAEPGGCA
18367	48735	A	18474	606	846	
18368	48736	A	18475	3042	3933	GPHPPAPGGPA\CHYDVHQPYL RQRTEDRRTRHYLAQSFAQYSL RQWAFHFLLDNITPDIQQIVIAH TRRTGGFTITASEAAIEMLLCFK RDFVALQHLFNQIDAPARAVQF IAQKLIGWACCEAARKNQLPH NTTKRSLLMSILYEERLDGALP DVDRTSVLMALREHVPGLEILP TDEEIIPYQCDGLSAYRTRPLLV VLPKQMEQVTAILAVCHRLRV PVMVFPGLRLSREAFLTTAEFG TQELRRPAQLRLQVYRLLSTAG RHHPAQNSPIRVLEVDIDLLGG TQELWGWKETH
18369	48737	A	18476	869	1639	ICSRCKSTRTSPTRCRKAIKVIL VCFVIRELLVVAPELTIIGLPEG NWITVSKGMLAKSPVDSNSTQ LKEAEEERLKAAQYGLQLVES QNELQNQLDKCRNEMMTMTE MQLRNKKRRRELGNLIKRFRSG AESLPDAVVLTTEEGGIFWCNG LAQQILGLRWPEDNGQNILNLL RYP/EVYAISENA*FFSPAQSGA QHRAASGNSRHALYPQTVADG GA*CHANASTGRGAA*LFCQRE P*VTYAIDRVTGLPGDDE

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18370	48738	A	18477	388	2356	
18371	48739	A	18478	137	318	GGQLSSWAMDFCHL/PAFWNS MTWHLQRLWGACGYFWHAQ WERLLTTFEGNEWILIFIGGIL
18372	48740	A	18479	923	1149	
18373	48741	A	18480	1	373	
18374	48742	A	18481	168	360	
18375	48743	A	18482	1	147	
18376	48744	A	18483	161	440	
18377	48745	A	18484	277	2172	
18378	48746	A	18485	164	406	LFRREGSYDRYLLMDDYCRRK DDSYFDRYRDSFDGRGPPGPES QSRAKGKVAETVYSYY**NTL QKREETNNQYPHLKKG
18379	48747	A	18486	405	999	
18380	48748	A	18487	64	288	
18381	48749	A	18488	159	550	CAVCHISFQDTPVLVSSNVTMQ FGSKPLFENISVKFGGGNRYGL\ IGANGSGKSTFMKILGGDLEPT LGNGSLDPNERIGKLRQ\DQFAF EEFTVLDTVIMGHKELWEVKQ ERDRIYALPEMSEEDGYKVAD
18382	48750	A	18489	3	481	
18383	48751	A	18490	2	233	
18384	48752	A	18491	2	3026	SVPTIIFFFLPVLRFWRPGIQQA KKCHLFATGTQSRRNTLRQRT AKGIPQQRMTAKREEISIGILHV TPQQRRECRGDNRFTARFRRTP WRLLGHCVSAAVTGVLPAVAG SPLAYSDTDEFYPVAGGTMSQ HLPLVAAQPGIWMAEKLSELPS AWSVAHYVELTGEVDSPLLAR AVVAGLAQADTLRMRFTEDNG EVWQWVDDALTFELPEIIDLRT NIDPHGTAQALMQADLPQDLR VDSGEPLVFHQTTLGFI
18385	48753	A	18492	2714	3079	RLIGLRMVREFVGLIRRASVAS GSWHCCRMRRKRLIRPKPSILQ SMLWSPSTRRMFFTLVPIFSIEE LPFTFRSLMMVTLSPSASRLPLA SLTISSSLSCAGSASFHS*AHSG QMYMPLSS
18386	48754	A	18493	1	888	
18387	48755	A	18494	1778	2025	
18388	48756	A	18495	1	1425	
18389	48757	A	18496	3	96	FVGRIRRLRRIRRY*FTPLTD*LS CAHQVP
18390	48758	A	18497	420	955	

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18391	48759	A	18498	533	1006	RPSIFACVSP*RINHSRIMPQTN AKNAKPNPAQVMRGVISRRRR AMLFSNSAITRTPTTSFTMAITS ASSSPPAVKVSICPHGINTPTNIC NTTSCFRLIPHFMTPKPLPLYSE SGPSCSSCSASARSNGSLPISIKV ANAQAQSASTSGMLWLSGQ
18392	48760	A	18499	3	418	EWHYLSADRRQCAFQGVSRKT ATVCHHPVDYYAGSLYRLYFT DRLRARLAGHAAES/GTPASHA VFQLVLE*L*SPLFSPVSTSGGR TANSTVLIMKSCMSGAVERQPT NWQAILMFLIFVVFTLGITYWA SNAYVLAG
18393	48761	C	18500	63	500	
18394	48762	A	18501	1	1107	
18395	48763	A	18502	1	153	
18396	48764	A	18503	88	510	
18397	48765	A	18504	204	654	
18398	48766	A	18505	241	771	
18399	48767	A	18506	1655	1909	
18400	48768	A	18507	2	48	
18401	48769	A	18508	1	585	
18402	48770	A	18509	1	723	LQPPGRRWAAPAV\SGLSRQV\ RCFSTSVVRPFA\KLVGPS\VQV SVIEGRYATAL\YYAASRQNKL EQVEKG\LLRVAQILEGTPKWA ASVLESPMLKAFPLKVKKPKM TITAKVGGSLPLTYQTLINFALL ENGSD*GNYPRESFSGLFLTMD GVFHSRERVP\CTV\TSGIFL*EG RPQFSEFKNCSSRGFLRSRAKFL KLGAK\TDPSI\LGGMIVRIGE\K YVDMSVKTK\IQKLG\RAMREI
18403	48771	A	18510	400	894	
18404	48772	A	18511	1	1023	
18405	48773	A	18512	73	424	RPGMWSTRSPNSTAWPLSLEPD PGMASACTTMHTTTIAEPDPG MSGWPDGRMETSSPTIMDIVVI *CAIAAEAIVLVSLLFVMLRYM YRHMGTYHTNEAKGTGVADS ADACPAGDPA
18406	48774	A	18513	141	563	RPGMWSTRSPNSTAWPLSLEPD PGMASASTTMHTTT\IA\EPDPG VS\GLP\DGRMETPTPHP*LTMV VIAGV\IACLWPFVLSLPSSFVM VALTLLTGHKGARTTPNEAKG\ TEFAES\ADAALQG\DPAL\QDA GDSSRK\EYFI

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18407	48775	A	18514	182	935	QAFELHCPCRPKFSTLPSPAWPP RHTDLRKRGRRTAQ*YAGNES HPPSLPRYLRRSRH/SRMQAPSS TCSYSHTSLQCSPAPQNH/AQHP *PALEELACG/SPSVSSPYLVLSS CQEQPHHCCPPSTPRPSW/CPSS GDAICYSPGQ/CPRSRGPLP\EDS SDSPPAEQVLPPSSGSHNTLYLR CKRFSAFILNCEPPSK\C*KPGHR CRS*AGILTLLPPG/ERGP/GDGP CSTGRQSASKTPPPPSHPHTGHS LWSEEK
18408	48776	A	18515	48	676	KARLTWQQTREESLCRETPPYK TIRSRETYSLPREQHGKDLPP*F NYLPPSPSHNTICPG*QDQGRFT Q\PLYLRCKRFSAFILNCEPPSK\ C*KPGHRCRS*AGILTLLPPGGE AQHFKVKHPSIPL/REGGEVGIK PKKTSPGTELLMQP/CHQPSPRT CQPAPRKSNRP/LGCLSPLMKHS TLGYLLWLQKAIWLKGFGTSG W*M*GRFHL
18409	48777	A	18516	86	92	TANAALHQPSPRTCQPAPRKSN RPQAA*ALNC
18410	48778	B	18517	1	2031	
18411	48779	A	18518	98	367	DLFLYLSWQHCHPYSHCHPNQ KPGRFLMKLSS\ETVTIELKNGT TRSHGT\IHQVWDVQ\MNTH\L KAVKMTLKNREPVQL\ETLSIR GNNIR\YFILPD/SVYPLDTLLVD VDPKVKSKKREAVAGRGRRRG RG/TRDVARGR*RGNNIR
18412	48780	A	18519	1	310	
18413	48781	A	18520	37	136	RRRPSSSWALPPSRGPSST*AER GAQHQQPVPA
18414	48782	A	18521	3	305	FFTLCLQWGLFSCESPICSGVGR YWA*VCLCFLQIEAIELPMDPK LNKRRGFVFITFKEEEPVKKVL EKKFHTVSGSKVRCSQLCLASC AAGELALRGMG
18415	48783	B	18522	249	367	
18416	48784	A	18523	1	1008	
18417	48785	B	18524	17	835	

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18418	48786	A	18525	2	1188	SLIKLNSPPPRGGGTARYGAWL LVGGFPCGGGQGGGDTVGAAP WADWGEASAAASFDVLAEAC ARLSSLRVGDEAGSRGVIWRAR SPPRLGLALSEAG\EE\QPMETT GASENGHEAVPE\ASR\GRGCW TPLRRGLEARPRRPRAGIRTAPR D/QRINASKNEEDAGKMFVGGL S\WDTSKKDLKDYFTKFGEV\V DCTIKMDPNT\GRSRGFGFILFK DASSV*K\VLDQKEHRLDGRVI DP\KKAMA\MKKAPVKKIFVGG LNPESPTEEKIRESFGEF\GEIEAI ELPMDPKLNKRRGFVFITFKEE EPVKKVLEKKFHTVSG\SKCEIK VAQPKEVYQQQQYGSGGRGN RNRGNRGQ/GGGGGGG*GQGS TNYG\KTQ\RRGGHQ\NNYKPIL EAGRQERPT
18419	48787	A	18526	3	784	
18420	48788	A	18527	3	1990	PAMNGLSLSELCCLFCCPPCPG RIAAKLAFLPPEATYSLVPEPEP GPGGAGAAPLGTLRASSGAPG RWKLHLTERADFQYSQRE\RST IEVFPTKSARGNRVSCMYVRCV PGARYT\VLFSHGNAVDLGQMS SFYIGLGSRLHCNIFTYDSSGYG ASSGRPSERNLYADIDATWQAL RTR*GRPLVGRVRARWRPRLTL LRRRQVRHQPGQHPSCTGRSIG HGAHRGTWPRATSVPRWCCTR RSTSGMRVAFPDTQERPTASTP FPYIRERCPRLTSPRAHHPTGTK DEVIDFLEAGWRSTRRCHQGG GAAVGGGGPGHNDIELYSQYL ERLASLSFSQELPSQRA
18421	48789	A	18528	82	406	

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18422	48790	A	18529	2	1474	ARASGSGSSSGQGKMGQS\QRG GHGSGGGKKDDKDKKKKYEPP VPTRVGKKKKKTKGPDAASK\L PLVTPHTQCRLKLLKLERIKDY LLME\EEFIRNQEQMKPLEEKQ EEE\RSKVDDLKGGPRLSVGNL GKRFI\DDNHA\IVSTP\VGSEHY\ VSIL\SFVDKDLLEPGCSVLLNH KVHAVIGVLMGDTDPLVTV\M KVEKAPQETYADIGG\LDNQI\Q EIKESVELPLTHPEYYEEMGIKP PKGV\ILLVPPG\TGKTFLPKAV ANQT\SATFLRGGGSELIQKNLG DGPKT/LSRELFR\VSEELAPSLR FIDRILPPLGTKRY\DSNSGGE\R EFQRTM\LELLN\QL\DGFDS\RG D\VKVIMPTNR\IETLDPALIRPR PAFDRKYEFP/LCPDEK\TKKRIF QISHKS/RMTLADVGTPWTTLI MA\KDDLSGA*PSKAI\CT\EAGL MAL/RENRRMKVPN\EDFKKS\ KENVLYKKQEGTPEGVVSLMN PWLVIRKMVGRFLNP
18423	48791	A	18530	2	274	WQDLICRMAASVKEQSTKPIPL PQSTPG/ESHSLSTSGKSEVRDL FVAERQFAKEQHTDGTLKEVG EDYQIAIPDSHLPVSEERWALD ALRN
18424	48792	A	18531	3	844	

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18425	48793	A	18532	261	2814	VRFRNLIRIYCNIKICAVSHCPP KVFKLNSLFFLHRFDSVAFGES QSEDEQFENDLETDPPNWQQL VSREVLLGLKPCEIKRQEVINEL FYTERAHVRTLKVLDQVFYQR VSREGILSPSELRKIFSNLEDILQ LHIGLNEQMKAVRKRNETSVID QIGEDLLTWFSGPGEEKLKHAA ATFCSNQPFALEMIKSRQKKDS RFQTFVQDAESNPLCRRLQLKD IIPTQMQRLTKYPLLLDNIAKYT EWPTEREKVKKAADHCRQILN FVNQAVKEAENKQRL/EEDYQ RRLDTSSL\KLSEYPNVE\RLRN MDLTKRKMIHEGPLVWKVNR DKTIDLYTLLLEDILVLLQKQD DRLVLRCHSKILASTADSKHTF SPVIKLSTVLVRQVATDNKALF VISMSDNGAQIYELVAQTVSEK TVWQDLICRMAASVKEQSTKPI PLPQSTPGEGDNDEEDPSKLKE EQHGISVTGLQSPDRDLGLEST LISSKPQSHSLSTSGKSEVRDLF VAERQFAKEQHTDGTLKEVGE DYQIAIPDSHLPVSKE\RRALDA LRNLGLLKQLLVHQLGLTEKSA LENWQHFPRYRTAFQGPQTDS VIQNSENIKAYHSGEGHMPFRT GTGDIATCYSPRTSTESFAPRDS VGLAPQDSQASNILVMDHMIM TPEMPTMEPEGGLDDSGEHFFD AREAHSDENPSEGDGAVNKEE
18426	48794	A	18533	90	383	ILQLHSSGPCLLWL*LSFRSLST TAV\CQCCRPAADFHPSGSSRVS AVLLIQ/HRRPLPLPIGLKACYFS ALSLQTSLTCLGLVVLLDFPKE AASLDKV
18427	48795	A	18534	1	456	
18428	48796	A	18535	830	1092	

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18429	48797	A	18536	391	1824	GSGADASGFISDAGLIFKKASSK GPKRLEKFSDERAAYFRCYHKL FLLFSSLCYGTYHVVVLPTLKP REDEDWISLCLRHCLMQKDTH SMLGECGERREGKKQKTGALG SSLSLEDAKHLLPFIPALPFSWN ALPQDLCNVFKLLWDYRIRVD PSPIAGTLIRRDTDPQGESHVKT GRHWSDTIKSQRCQGLRQPPDR PIPILLMVKGQHVWPSQLDKAQ IQEVTELNNVKNVARLPKSTKK HAIGIYFNDDTSKTFACESDLEA DEWCKVLQMECVGTRINDISL G\EPDLL\ATGVE\REQSE\RFNV YLMTSP*LRMLHG\ECALQV\T Y\EYICLWGRPRTPQEFKLISW\P LSALRRY\GRGTPWFNYQAGR M\CQTGEGLFIFQTRDGEAIYQK VHS\AALAIAEQHERLLQSVKN SMLQMKMSERAASLSTMVPLP RSAYWQHITRQHSTGQLYRLQ DVSSPLKLHRTETFPSLQDS
18430	48798	C	18537	22	620	
18431	48799	A	18538	48	413	EDSKSKTISHPWRDCGDYCHH QGLERCRGGDSHHTPVQLS*LA CAED\NKSWRMT\GIIVSLTKC* LQMQLLYQMWFHCLSKLTHLL GISTLQLCVTILFREILITFPLHKI SHWSITLMTLR
18432	48800	A	18539	23	124	QWVIISLTKW*LQLQLLYQMW FHCLSKLTRLLP
18433	48801	A	18540	1	1860	
18434	48802	A	18541	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
18435	48803	A	18542	1	1521	
18436	48804	B	18543	1	2265	
18437	48805	B	18544	1	1716	
18438	48806	A	18545	1	1704	
18439	48807	A	18546	1	3618	
18440	48808	A	18547	1	3087	

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18441	48809	A	18548	277	350	SPVEKELKLWKNRHKLLSC*W LTC
18442	48810	A	18549	197	422	IVNKVVLPQGGPASPSLKGFWV YKLAQVWKLIEGP*FPIFIIQISL LSI*PRSFLFV*IK*ECSRLPISFTS SGR
18443	48811	A	18550	1	3171	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLKELEKQEQRHSKPSRRQE ITKMRAELKEIETQ
18444	48812	A	18551	209	2432	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKILNKILANQIQQHIKKLIHH DQVGFIPGMQGWLEVLARA/IR QEKEIKGIQLGKEEVKLSLFAD DMIVYLENPTVSAQNLLKLISN FSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWIGRINIVK MAILPKVIYTFNAIPIKLPMTFFT ELEKTTLKFIWKQKRSHIAKSIL SQKNKAGDITLPDFKLHYKATV TKTAWYWYQNRDIDQWNTTE PSEIMLHIYNHLIFDKPDKNKQ WGNDSLFNKWCWENWLAICR KLKLDPFLTSYTKINSRWIKDL NVRPKTIKTLEENLGNTIQDIG MGKDFMSKTPKAVATKAKIDK WDVIKLKSFCTAKETTIRVNRQ PTEWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAAKRHMKKCSSS
18445	48813	A	18552	1	3255	

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18446	48814	A	18553	1	3139	
18447	48815	A	18554	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
18448	48816	A	18555	1	3345	
18449	48817	B	18556	1	3127	
18450	48818	A	18557	1	3325	
18451	48819	A	18558	1	3145	
18452	48820	A	18559	1	548	
18453	48821	A	18560	1	3229	
18454	48822	A	18561	1	3352	
18455	48823	A	18562	1	1965	MGDFNTPLSTSDRSTRQKVNK DTQEMNSALHQADLIDIYRTRH PKSTEYTFLSAPHHTYSKTDHIL GSKALLSKCKRTEMITNYLSDH SAIKLELRIKKLTQNCSTTWKL NNLLLNDYWVHNEMKAERKM FFETIENKDTTYQNLWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEKTHSKTIRRQ EITKIRAELKEIETQKTLQKINES RSWFFERINKIDRTLARLIKKKR EKNQIDRIKNDKGDITTDPTQIQ TTIREYYKHLYANKPENLEEMD KFLDTYTLPRLNQEEVESLNRPI SGSEIVAIINSLPIKKSPGPDGFT AEFYQSYKKELVPLLLKLFQSIE KEGILPNSFYEASIILLPKRGRDT TKKENFRPISLMNIDAKILNKIL AKRIQQHIKKLIHHDQVGFIPG MQ\GIKYLGIQLTRDMKDLLKE NYKQLLNEIKEDTNKWKNIPCS WVGRINIVKMAILP/KELEKTTL KFIWNQKRACIAKSILSQKKKA GGITLPDFKLYYKATVTKTARL YTKHGTSICCGSFGELLPMQKA KRELAHHMAKAGARVKGQLG HVTQHQLGSIEWFNKYSLSTYY TVDTKPQFSHPTKDNKTGLTCR NRTTVGVDLQAKGNLVVKHLS SLQHCYEFICHI

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18456	48824	A	18563	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
18457	48825	A	18564	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
18458	48826	A	18565	1	3095	
18459	48827	A	18566	2	2678	

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18460	48828	A	18567	1	2478	MKAEIKMLFETKENKDTTYQN LWDALKAVCRGKFIALNAHKR KQERSKIDTLTSQLKELEKQEQ TLSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDAIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGAEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLKLFQSIEKEGILPNSFYE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIISIDAEK AFDKIQQPFMLKTLKKL\EIKYL GIQLTKDVKDFFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIV KMAILP/KELEKTTLKFIWNQK RACIAKAILSQKNKAGGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTETSEITPHIYNYPIFD KPEKNKQWGKDSLFNKWCWE NWLALCRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLGI TIRDIGMGKDFMSKTSTAMAT KAKIDKWDLIKLKSFCTAKETT IRVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRTPTRPIQ
18461	48829	B	18568	1	3403	
18462	48830	A	18569	2	2976	APRFIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVHKDT QELNSALHQADLIDIYRTLHPK STEYTCFSAPHHTYSKIDHIVGS KALLSKCKRSEIITNCLSDHSAI KLELRIKKLTQNRSTTWKLNNL LLNDYWVHNEMKAEIRMFFET NENKDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKTL\QKINE\SR SWFF\ERINK
18463	48831	A	18570	472	829	AIASESASPKAWQLPCGAAQQF AALPGLGNYKFPLTLITGYGSN KSPP*GYLVFQTYSSLPLLRLPP GHFGFLLPLSQ\RLRRELQCWL G*LTQTIKMKSVYHSTTEVRKS MHGIQEIH

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18464	48832	B	18571	1	2293	
18465	48833	A	18572	1	3810	
18466	48834	B	18573	1	4107	
18467	48835	B	18574	87	3161	
18468	48836	A	18575	1	3192	
18469	48837	A	18576	1	1983	
18470	48838	A	18577	1	3156	
18471	48839	B	18578	1	3471	
18472	48840	B	18579	1	2337	
18473	48841	A	18580	1	3852	
18474	48842	A	18581	1	3057	
18475	48843	A	18582	1202	2004	SGIYMIGFEQVLKAQPPLSSPNG PMNKVATVVGMEVMHGLSNM DFHSRRLTWLRPLPGFTGPG/Y QGVKVEVAPLTITPSDPLAKFL LLISATSTSLEVTVPEGEMLPPR DTTKIATFGTQTGFLALQLADG LLWDLVIIPGKGKPSRDLVESPS PYSTYEGIDGWPDEPAPTATKP PVMPAPALPPDTRSGSKAPTVP TPYPQMEHHQVQLASNNSNTE ALGHLSPQSSWVQTPGQNSGP AIPNHLGKDMISPPQMAPAGVK WESQKY
18476	48844	A	18583	1	2832	
18477	48845	A	18584	1	3702	MQKKHDKIRNSFMIKTLKKLRT EGIYLNTIKATYKKPITNIILNGE NQKAFALRSGTRFWILALCQM SRLRKLTNYLSDHSAIKLELRIK NPTQSRPTTWKLNNLLLNDYW VHNEMKAEIKMFFETNENKDT TYQNLWDAFKAVCRGKLIALN AHKRKQERSKIDTLTSQLKELE KQEQTHSKASRRQEITKIRAEL KETETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTI KNDKGDITTDPT
18478	48846	A	18585	1	3139	
18479	48847	A	18586	2	2918	
18480	48848	B	18587	1	3242	
18481	48849	A	18588	1	3640	
18482	48850	A	18589	371	522	
18483	48851	B	18590	1	3918	
18484	48852	A	18591	1	3057	

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18485	48853	A	18592	1	3233	MGKKQSRKTANSKKQSTSPPP KEHSSSPATEQSWTENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITTITNTEKCLK ELMELKAKAQELREECRSLRSR CNQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLTGVPESDGENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSSRRATPRHIIVRF TKVEMKEKMLRAARÉKDRSTR QKVNKNTQELNSA
18486	48854	A	18593	965	4165	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID
18487	48855	A	18594	1	5093	MEGEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDTF
18488	48856	A	18595	1	131	
18489	48857	A	18596	5382	9269	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKK\AGVAILVS DKTDFKPTKIKRDKEGHCIKVK GSIQQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLSTLDRSTRQKVNTDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHIVGSKALLS KCKRTEIITNHLSDHSAIKLELRI KNLTQS
18490	48858	A	18597	1	312	

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18491	48859	A	18598	142	876	RKKGILPPKESLKELEEEAEEEQ RILQQSVVKTYEDMTLEELEDH EDEFNEEDECAIEMCRQQRLAE WKATKLKNKFGEVLEISGKDY VQEVTKA/ERRALWVI\LHLYK QGIPLCAL\VNQHLSWTLPGSFP DVKFIKAISTTCIPNYTDRNLP\T ILVYPGRRYQGLSLLVLWCLAG MNPDQEMSWEWKLSESGAIMT DLEENPKKPIEDVLLVLSAALW SS*RGDSDSEGDLRATASITCRT
18492	48860	A	18599	1	2310	
18493	48861	A	18600	3	1124	LYNRRRRRRCSHCRHRCRRLSS GLRKEEVISLGASLGRVFVPCSP PTVSAARGPTGAPGGPNSKPLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNLVEILP AIFSSFLNLQHVNLWFLAAAM KAVTEQGHELSNEERNLLSVA YKNVVGARRSSWRVISSIEQKT ERNEKKQQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKCRLSNYFRYLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFLTILIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTLC DI*P*QNSACVINFILFLNILRDN LTVSTTSTGFIVSFLFTYLIIHCY LQEGICTIKCSYSFKLLNLL
18494	48862	A	18601	340	1323	AARPQKRHNNHSSLLTGSHIH WKRGRVQNIIADVLQFCLYLLT VLFVPCSPPTGMTMDKSELVQ KAKLAEQAERYDDMACSSERH VTEQG\HE\LSNEEKKSCSLVAY K\NV\VGARRFLPGRVISSI*A*K QRRNEKKAADGQKSTREKIEG RTCRTFCN*CFWELLGQISLFPN ATQPRKVKVFYFEK*KGDYF\R YLF*KWQS*RQQTQPTCVGTSP ARAYPGSNLKI*LRKKMQP\TH PNSVLVLAPKFPQSFYYEI\LNSP \EKGLVSLGKNGHFD*SNLLNL DTLEWKSLIKDSTSDSWQLLR\ DN\LTLWDIRKTRGDEGDAGEG
18495	48863	A	18602	33	89	
18496	48864	B	18603	167	232	

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18497	48865	A	18604	14	600	MAELAPASPSDIKASVSNGDTT LLCSRRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSR AW/PDPHQLFDDTSSAQSRGYG AQRAPGGLSYPAASPTPHAAFL ADPVSNMAMAYGSSLAAQGK ELVDKNVSGRGWWEWGDARG HRASDLSSASPD\HRFIPITKLKY YFAVDTMYVGRKLGLLFFPYL
18498	48866	B	18605	1	1230	
18499	48867	B	18606	41	931	
18500	48868	A	18607	3	166	PRPFPKSRLPPGIIGGEYD\QRPN PILP\GRGGPNDRFPF\RPSRGRP TDGRLSFM
18501	48869	A	18608	212	1881	CLRVLLLKRTWPVEVPETGARP /TGGILRSH\LRQSLLCT\WGYSS NTRFTITLNYKDPLTGDEETLAS YGIVSGDLICLILQDDIPAPNIPS STDSEHS\SLQNNEQPSLATSSN QTSMQDEQPSDSFQGQAAQSG VWNDDS\MLG\PSQNFEAESIQD NAHM\AEGTGFYPSRTPCSW*L NPVEGQVP\HSLETLYQLADCS\ DANDALIVL\IH\LLMLESGYIPQ GT\EAKALSMPEKW\KLSGVYK LQYMHPLCEG\SSVT\LTCVPLG \NLIVVNATLKINNEVRKC*KGC SLLPESF\ICKEKLGENVANIYK DLQKLSRLFKDQLAHPLLAFTR QAL\NLPDVFGLVVLPLELKLRI FRLLDVRSVLSLS\AVCRDLFTA SNDPLLWRVFYICVNFRDNTV\ RVQ\DTDWERTVQGRRAHTKE KESPKGRVLWMLLAIRQTH\TIP FYSQPLWHPRGHFPKLPAFPPGI YSGGWNMDQR\PTFPYVGRTQ SSSLNSWVLGETPKPSFLPLRPR FDPVWPHFPGP*PPSLPRARAGP NDQISPFRPQQGSGQLIGRLSIH
18502	48870	A	18609	1	1065	
18503	48871	A	18610	1	1513	
18504	48872	A	18611	1	2247	
18505	48873	A	18612	3	421	
18506	48874	A	18613	1	103	
18507	48875	A	18614	3	435	
18508	48876	A	18615	268	501	QLECIPGTWELWKEEQERAMA GGGLKKIISATEKKLARMLLAP SASWCCSGP*VFHGST*WGKPG PVSVSLLQGVLGK

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18509	48877	A	18616	3	296	EAMEAVILTCDPATPAASYQW WMNGQSLPMTHRLQLSKTNRT LFIFGVTKYIAGPYECEIRNPS*V PAASDPVTLESPPLLFNGLATTE TLRKRGNP
18510	48878	A	18617	3	1464	GAVRTWGRGFQTEKCQASLLN FWNPPTTAQVTIEAEPTKVSKG KDVLLLVHNLPQNLAGYIWYK GQMKDLYHYITSYVVDGQIIIY GPAYSGRETVYSNASLLIQNVT REDAGSYTLHIVKRGDGTRGET GHFTFTLY\LIPWTLLYL*RSLA QVSHYETPGKTAPPCGSTA**L N*PPDLTLFSPVLFLLKYPVPGQ AFQYPKGLKTIGSSITHL*DVLG KGSCRENIPRAAK*D*N*EDSST ACSK*GPQVETPKPSISSSNLYP REDMEAVSLTCDPETPDASYL WWMNGQSLPMTHSLQLSKNK RTLFLFGVTKYTAGPYECEIRN PVSASRSDPVTLNLLPKLPKPYI TINNLNPRENKDVLAFTCEPKS EN\YTYIWW\LNGQSLPGSVPR VKRPI\ENRVLIFTPCSRGIETG\P Y\QCEI\RDRYGGHPQLPSHPGM SSITTKHSGLYACSVRNSATGM ESSKSMTVKVSAPSGTGHLPGL
18511	48879	A	18618	79	1516	
18512	48880	B	18619	96	1730	
18513	48881	A	18620	9854	11033	ESLCFPKTEQEASQSLSP*IIIHLS CDTCTSYWLSRTHVG*QVGDA NSE*RMPVEESKVPHRTIFCYPH S\KLPMPYITINNLNPREKKDVL AFTCEPKSRNYTYIWWLNGQS LPVSPRVKRPIENRILILPSVTRN ETGPYQCEIRDRYGGIRSNPVTL NVLCEYPLFLCGPGHQLNSKRP EARPLSLSPVQV*TTLLLDIRPG HDSLPWEILGRHSLNQEYKGRG ALVMGH*GPTACNERNRGIPQ AWA**T*MGFGCHLRLCLGSEG HCVPLRDQEHPLPLDDITCGFIL FPPDGPDLPRIYPSFTYYRSGEN LDLSCFADSNPPAEYSWTINGK FQLSGQKLFIPQITTNHSGLYAC SVRNSATGKEISKSMIVKVSGK WIPASLAIGF

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18514	48882	A	18621	3	1350	GRTAQLTAVLRKLLDPRLISTE ENTQAAETMGPLSAPPCTHLIT WKGVLLTASLLNFWNPPTTAQ VTIEAQPPKVSEGKDVLLLVHN LPQNLAGYIWYKGQMTYVYH YITSYVVDGQRIIYGPAYSGRER VYSNASLLIQNVTQEDAGSYTL HIIKRRDGTGGVTGHFTFTLHL ETPKPSISSSNLNPREAMEAVIL TCDPATPAASYQWWMNGQSLP MTHRLQLSKTNRTLFIFGVTKY IAGPYECEIRNPVSASRSDPVTL NLLPKLSKPYITINNLNPRENKD VLTFTCEPKSENYTYIWWLNG QSLPVSPR\VKRPIENRILILPNV TRNETGPYQCEIRDRYGGIRSD PVTLNVLYGPDLPSIYPSFTYYR SGENLYLSCFAESNPRAQYSWT INGKFQLSGQKLSIPQITTKHSG LYACSVRNSATGKESSKSITVK
18515	48883	A	18622	273	2271	CGSWLMTQFSMDKRQGRSRSV TITNTAVTSLEWVPFHAFAIPRS TLVSQQGATSHTDNTQEMDSP GQEPGFAKEVEVEPGFQPLPQM TLLVPAMCLLLHGACSAKGFC AAPHFLLASPMGKGQVPLNPFS FTLSEELDLPQSLKRNPKGCIAR RAKPILAAERHKRLILHTSTKEN TLLDNRVIECLTMEAVAKFNIM KEREGPSHQPALSPPKARWHIL WQKLMFTASLLTFWEP\PTTAR VTTEAMPFNATEEEEEEFFLLA HNLPQNLTRATIW\YK\GQMRH LYHYITSYVVDGEIIIYG\PAYSG RETAYSNASLLIQNV\TRED\AG SYTLHIIK\RGDGTGGVTGRFTF TLYLETPKPSISSSNFNPREATE AVILTCDPETPDASYLWW\MNG Q\SLPMTHSLQLSKANRTLYLF G\VTNYTAGPY\ECEIRNPVSAS RSDPVTLN\LLP\KLPKPYITINN LKPR\EE*GCLRPFTCEPKE*GTT PYIWWVKRFRSLPVSPGVKRPH LKNRI\LIPTPVFTRKWKQGPYS MWNYGDRYGG\IRSLPSSPWNV LLWVQDLPRILPFHFTYYRSGR KSSYLSCSGGTLNPP\AQYSWD N*WKSFQLTRGQKLFYSGHITT KHSGLYVC\SVRNSATGRESSK SMTVEVSDWDITLNSTSTSNSIF
18516	48884	A	18623	1	1131	

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18517	48885	A	18624	1	603	MDIADPFSGFPMGMGGFTNMN FGRSRPAQEPTRKKQDPPVTHD LRVSLEEIYSGCTKKMYQED\KI SHKRLNPDGKSIRNEDKILTIEV KKGISLPEALCG/TTVNVPTLDG RTIPVVFKDAIRPGMRRKVRGE GLPLPKTPEKRGDLIIELEVIFPE RIPQTSRTILEQILSSYLSYLSSP GLTRDLSRAQGFLDLSTSCGP
18518	48886	A	18625	3	1228	WSAAEPVDGDSGSAGRRRGPW PKTTYHPWAVARGASEKEIKR AYRRQALRSHPDKNKEPGAEE KFKEIAEAYEVLRDPRKREIFD HYREEALKGSGPSGG\SGGGAN ATSFSYTFHGEPLAMFAEFFGG RNPFDTFF\GQ\RNGEEGMDIDD PFSGFPMG/LWGGFTNVNF\GRS RSAQEPARKK\QDSP\VTHDLRV SLEGDLTAAVPRRCTKKMKISH KRL/NTPDGKSIRNGDKILTIRSE RRGWKEGTQITFP\KEGDQTSN NI\PADIVFVLKDKPHNIFKRDG S\DVIYPARI\SLREA/LCVGCTV NCPHSGTGRT\IPVVFKECYQGL GMRRKSSWENGLPLPQNTREN VGDLII*GFEVIFP\ERIPQ\TSRT VLEAGSFQYSYLEVPQGLTRGP FPELKDFWDLFLPVVGP
18519	48887	A	18626	321	1121	GDAVPSAPRRPSRRTPGCGSRG ALQPGPPPRA\PPPEP/PPRGAAA AAPPAGPAAPAARQPPRRPPAQ PRSCPRRVRPTPAWSPPGRRGP RRSRRRPPGGPGPAAPLRLSRA HSPPAPPGSPYRPHGAGTSVAP WTRPPAARGTEADPGRCPVSAP GTAPGQMRGRGSATQRLHRGH STAPGAGGRCGRRPGGSGRPG AGAGPRRSTAAPPRCRRRSPTG PRSPRGPRSARPARGSVGGPRG TPGKQPGPRRA*TSGPEPRCCG HARG
18520	48888	A	18628	191	653	KLEIQRLLRMTTECIRHTKQKK FGSPGLQPPLPGNAKSRADSTA LPALPAQQKETKQQEPGESS*E PGGSSPSRMERAEAAPAQS/PA GGTGTGQGWGAPHLGPALARR VTGPPQHGSPGPRTRPTPYPAR C/PSRPIFVPAIVWSRLRAPPGLP
18521	48889	A	18629	141	319	

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18522	48890	A	18630	178	722	PLGNVSCSHRSFQTARVDYSLI YVLAWGQKKEVWELRNWQTH ALMKLKNKLREPRTSVNKD/SP KSLLYSCSYSYFDEPVELRSSSF SSWDDSSDSEYETHLLHLKLV* PNLAVFNCRPTARRKPDYEPVE NTDEAQNSFCKTAHNLWSLTFP FPCLL*YETRARLESWSLSCLR YEHISSG
18523	48891	A	18631	2	367	
18524	48892	A	18632	1	381	QRYSSRRATPRHIIVRFTKVERK ETMLRAAREKGRVTHKGKPIR LTVDLLAETLQARREWGPIFNI LNEKNFQPRISYPAKLSFISEGEI \NPQMLR/DFVTTRPTLRDLLKE ALNMERNNRYLPGRPL
18525	48893	B	18633	1	846	
18526	48894	A	18634	3	1170	VGSMTGEASGNLQSQRKAKRK EARLTCLEPVEEPGSGTHPPMC YLAPPMWKCQKPETGIKEGDR DHNSLPAREENQTENESDELTE AGFRRWVITNSSRLKEHVVTQC KEAKNFEKSLKELLTRITSLEDN INYLMEPRNTAREHREAYSSIN SQIDQAEEKIPEIEDQHNEIKRE DKIREKRMKRNKQSLQEIWDY VKRPNLSLAGVPESDEENGIKL KNTLQDIIQENFPNLAKQANIQI QEI\QRTPQRYSLRRATPRHIIVR FTKVEMKEK\MLRAAREKGR\V THKGKPIRLT\ADLSAETLQAR/ RTEWGPIFNILKEKNF\QPRISYP AK\LSFISEGEIKYFTDKQMLRD F\VTTR\PALKRAPGKEGT*TLE RDN\RYQPLQKHAKL

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18527	48895	A	18635	73	1504	QDLRLFYLKDTMFSKLAHLQR FAVLSRGVHSSVASATSVATKK TVQGPPTSDDIFEREYKYGAHN YHPLPVAL\ERGKGILLMGM*E GRKYF\DFL\SSYSALSNQG\HC HPKIVKCSGRVKWDKIDL*HLE AFYNNGTLVNMREYYY*TFST YHKVLP\MNTGVEAGETA\CKL A\RKWGL/YTVKGIQKYK\AKIV FAAGNFWGRTLSAISSSTDPTS YDGFGPFYARDFDIIPY**SCPH MEQCSFKDPKCGLAFHG*EPIQ G\EAGV\VVPDPG\YLMGSAESS GTRDQVLFICLMEIQTGLARTW *DGLAVDYENVRPDIVLLGKAL SGGLYPVSAVLCDDDIMLTIKP GEHGSTYGGNPLGCRVAIAAL\ EV\LEEENLAENADKLGIILRNE LMKLTLP/SMLVTARKKEKGIY LNAHLAIKGNQKIWDA/WGKV CLRLQDNGLLPKPTSVATLSRF APP\LVIKEDELRESIEIINKTILS
18528	48896	A	18636	2	348	
18529	48897	A	18637	588	801	RTAYFCQYHTASVYSERAMPP GCPEPSQA*ELQETGHRQVALR RSGRPPKCAERPGAADTGAHCT STDGRL
18530	48898	A	18638	175	510	NSESPGPLWWLSCDNPAKDRIY STEADGLGLPDQSFVVHRAQL* CVAG*LGTHSRFQEWAV*D*SD LLKAQLHFKVGRCVWEAGGGL EWVLGGRCRCRVPQPLETLIQ WGPW
18531	48899	A	18640	1	1431	
18532	48900	A	18641	202	994	RWQGQRLLLDSNIRLWVVLPIR YSFTFFRRALIRHYV\SILLAERQ RSFTQGNKYLDSSSPNFEGRV/R FRGKLGNYIPKQSFFG/RRKFLF FPNPEDGIFSKKLKREVVPPSPM TDPTMLTDMMKGNVT\NVLPM ILIGGWINMTFSGFVTTKVP\FPL \TLRF*A*WLQQGNRSYSPFRCI PG*/WFCIPGYFPQCILGFRSI/YT LWISGGKDNGRWNQSRMM/DR SRMTGASHGPWPADSGRRFPN KRWEAL\ELTDHQWALDAAGE DAA
18533	48901	A	18642	97	224	LPTKSTWVAGKK*KKRSNIKD YSTPLTSYRSIRSHAFKIVAS

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18534	48902	A	18643	117	457	IWGDVEKGK\KVFYL*RCSQCH TV*/ERGGKHKTGPKSP*VSFGR RTGQAPWDTLYTAANK\NKGII WG\EDTLM\EYLENPKKVHPLD TKMIFVRHLRKREERADLIALS SKKLLN
18535	48903	A	18644	411	1054	VTGAQRLVTCRMGKQNSK\LA P\EVMED\LVKSTEFNEHELKQ WYKGFLKDCP\SGRLNLEEFQQ LYVK\FFPYGRRLPSFAQHAFPN LSTRMGDGTI\DFREFICAL\SITS RG\SFEQKL\NW\AFNMYGPGW VMGKITRVEML\EIHRGLSYQN G*GTVIMMKMNEDGLTP\EQRV GQDFSARWVRNKDDQIYTGID FKGSCQRADPFIV*LL\QCDIHK
18536	48904	A	18645	3	475	GAEGARGGGSSYSEMAETVAD TRRLITKPQNLNDAYGPPSNFL EIDTNLPIFKLKESTVRRRYSDF EWLRSELERESKVVVPPLPGKA FLRQLPFRGDDGIFDDNFIEGKK TRGWEQFINK/VSLGHPL\AQNE PLFFHMFLQDEIIDKSYTPSKIR
18537	48905	A	18646	1	695	LRARSLRDRCARAPCPHGGQQ RRRRRLNAEGAEGARGGGSSY SEMAETVADTRRLITKPQNLND AYGPPSNF\LEIDVSNPQTVGVG RGRFTTYEIRVKTNLPCFQS*KN LIVRR\RYSDFEWLAKWNLERE SK\VVVPPLPG\KAFLRQLPF\RG DDGNILMDNFI*/EERKIRGWSS FLNKVA\GHPL\AQN\ERC\LHM VFYQDEIIDKKLLLPSKNKAMP WKFGPRKGAKNVDY
18538	48906	C	18647	3	474	

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18539	48907	A	18648	156	1254	RPLHTLEVLRRMTKRLVTKAA ASAARAQPAEPRDRKYDKHLS YLATWGRSAGRAGSPRGARGR ELARAPVSLPAGVPGRGSAAG HSSEARTGPNGKMGGSSREPGT EKVPCPRGLSPTREVGHQVHGT LGAGPNELHPSGPAGARCRPGR REAKLGDAARSEAQSSAHKFHI DSLSLPWNPTAMEMLMPKKNR \IAIYE\LLFK\EGVMVPKK\DVPI PKHPELAEQKCAPTFHVMK\A MQ\SLKSPRPT*KEQFAW\RHFY WYLT\NEGIQ\YLRDYL\HLPPEI VPAHPYGRSPSRRLARPRPKKV WKGEATLRDFTRGEADSFLCH S/DSYRRSAVPP\GA\DKKAEAG GLGQKPNFQF\RGGFVRGRGQ\P
18540	48908	B	18649	1	1053	
18541	48909	A	18650	1	529	MGRYMEREPLQGNHRRSGLSG ERCSHMGGVLIERRELQTETRK EGVVEWCWLEKEVLATITKPV RGDKNGGTQVVKHRKMPRYY PTEDVPQKLLSHG\KKPFSQHM RKL/FLYRRHARNLSLPPQPELII SDVK/IPRHPADA*LEEQQLSEP E/HSEGTSY*RIPEKVLSYPAIRP
18542	48910	B	18651	258	363	
18543	48911	A	18652	197	398	ARMSQEKDFHKVMSALKARTG HLHFFCGGMSSVKVGQGFSLLL *FFSYFRPSGCILPL*ELPEARCP
18544	48912	A	18653	215	932	GTQSCNQKVLNSANNLQELGIG PKFQMRLKPQLAPMQPNRGTS LGRSIPCPPVLCSMRKIHLRPQV LRPTSPRNISPILNRVSEVSDHA GTPALVLHP*RQVPLFWGRGK YPNPFSLCLYPFSAFLGGKKHP TPSPSP*VASPLF*RSKYPNLVSL CPSPLFPRPDLLSLWPNPLF\RTP TSYISVPQSLISMPRPLISAPQPLI STTQPLSRFSGRSLLQVPEIWPP GQGMPAARDSS
18545	48913	A	18654	1	378	
18546	48914	A	18655	14	380	
18547	48915	C	18656	228	260	
18548	48916	C	18657	99	335	
18549	48917	A	18658	55	474	RQVPLFWGRGKYPNPFSLCLYP FSAFLGGKKHPTPSPSP*VASPL F*RSKYPNLVSLCPSPLFPRPDL LSLWPNPLF\RTPTSYISVPQSLI SMPRPLISAPQPLISTTQPLSRFS GRSLLQVPEIWPPGQGMPAAR

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18550	48918	A	18659	1	187	AELATGNVKVEASGTPEEKAG SVLG*ACFAGP*ERCCWQNN*D GIISIQSYCLCNLGCFIQT
18551	48919	C	18660	1	357	
18552	48920	A	18661	3	148	
18553	48921	A	18662	1	312	
18554	48922	A	18663	149	457	
18555	48923	B	18664	1	675	
18556	48924	C	18665	110	928	
18557	48925	A	18666	495	817	LTSPSRCTIIEKSCSSLPPL*DKP QPHLQHTRTSKRLNCSSQVFLQ NLLPEELATSSRNLATGPRNAC SPGFLLSHIPSVWDPTGNRTVQ LTWQPLPEPLELWPKAL
18558	48926	A	18667	228	3021	VFDRTQNVQGRIMEAPEYLDL DEIDFSDDISYSVTSLKTIPELCR RCDTQNE\DRSVSSSSWNCGIST LITNTQKPTGIADVYSKFRPEKR VLPLKHQPETLENNESDDQKN QIVGEYQKGGESDLGPQPQELG PGDGVGGPPGKSSEPSTSLGEL EHYDLDMDEILDVPYIKSSQQL ASFTKVTSEKRILGLCTTINGLS GKACSTGSSESSSSNMAPFCVL SPVKSPHLRKASAVIHDQHKLS TEETEISPPL
18559	48927	A	18668	1440	1764	ERSTYNLRSSDQP/RPRNILTNF KS/VDKGDTFYPWTHNSGASH GLGR\RLPWC*ELATSARNLTP RPRTAGSPGFLLSHVPSVWDPT ANRTVQLTWQPLPEPLELWPK
18560	48928	A	18669	1	3255	MLTLTGAGGESWIIRPGNLLEQ LGAEETLGRRQEPGDEVTAHFL LQGVINMGPVPYPGAHSSNMP GSVSPILGHSVKLFEEYYPVGD PLMGSGRPHTPRKKIWSDLNA HSDLYLALDWTPLPEQSEPGPG LAAWKPFQAEEYTCKCAEGNE NTPFDLRKGTLPCPRNLERARQ AYMHIEEKFPFELTEQHICEFQS MCYVLVRVLGACSQSTWLILEP DGVSGPSKGASEAIGQCQSSAA KPRRSGKESVREPWA

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18561	48929	A	18670	1	1442	CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGDSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKKNGEKRTRL QKRKKGMPPHPA/S*GPKHSCH HSPCQCCPSSAK/SASELQGSWT PFGGLLTRTRMKFGAKTRDLD QGTSLGRSLPCPPTLCSMRKIHL RPQVLRPTSPRNISPISNPRQRR QVLSMDPKLRHRSRTGK/DSLP LVFNHCRDTSLIIHPCFKGVRPR RDACLGPSPLAASPAFLEKGQD LINLAFKVYNNRKKLQFLASTV RQTAATSPAHKNFQMPEPQRP GVPPEPPPTGACYMCRKIWPLG QANARSPGFLLSRVPSVRDPTG NRTVQLTWQPLPEALELWPKA
18562	48930	A	18671	140	327	
18563	48931	A	18672	95	115	IIRHLCND*TPREGCLPSP*PAW SDTFETWVNNQASLQ
18564	48932	A	18673	218	674	MPISRPTARFKRIKVYYHSPAT AWPSKAYKLPLQFPHFTCPKTR QGLQVTSGSAPYQPNCFVYPPR VAKTKYSPILNTSLHNPLLCSGS QTCFLY/SFLCTFHPSLSSLSLGL TLTPIRLSKLRGLYCHKASQTA PITSIKPKFLPHLLPISA
18565	48933	A	18674	1	268	
18566	48934	A	18675	1	458	
18567	48935	A	18676	3	461	LLLTQSLFGGLFTRTRMKFGAV TRIGGPPLGNQSPSSCSLLHEKD PPTTSGPQTDQPKKHLTNFKSA ARPTFLGQGQVPLNPFSFTLS/E QVLLS*AARTPQSLISTPQPLISV PQSLISVPQPLLYFSGGQEPPPPP LLCVSSLFSRLASFTM
18568	48936	C	18677	156	329	
18569	48937	A	18678	449	667	
18570	48938	A	18679	79	311	

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18571	48939	A	18680	1	693	MAPTNCKGSRKCGRPHEQMPH PYLPLLTLFSDSARLHPGEINSR VPHTKPVWWSLHTDAYEIWYH DSDWGDLPWEINPLSSCSLLHE KDPPTTSGPQTNQPKEHLMNFK SGPHWKSDCPTRQPLPGPLELW PKA/HLTDSFPDLLSLAAED*CC LIALEAPWTITDAELWITLTVED SQLYEDTLAGRSVLIKNLTP*TL Q/PLDGLDPT*SSIVPQLPSACRI LPTGFTVPE
18572	48940	A	18681	328	865	
18573	48941	A	18682	451	1238	TALLLTQSLFGGLFTQTRMKFG AVTRIGGPPLGDQSPVLLFFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPIS/ ASHSML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRFTG* FRICALSTKLFCLSTPWCQTHIL SYPQYLPPQSIILFWISNVLSLLF LCTLHPSLSSLSLGLTLTPFRLS KLPGLYCRKASQTAPITSVKPK FLPYLLPISA
18574	48942	C	18683	870	1037	
18575	48943	A	18684	933	4323	AASHLCGTPLEIGLSNSPGSHSQ SPWNSGPRLSDCFPDLLG*VAE D*HCPIASEASWTVT\ELWVTLT VEVAATALILLEALKITSYAPLT LYSSHNFQNLFSSSHLT/PYTFC PQ/GPFSYTHSLLSLPQSPLLLA QTSIRPPTLFLIPHLTPMTVSL*S/ ILTFIPFPHISFFPVPHPDHTWFID GSSTRPNRHTPAKAGYAIVSST FIIEATALPPSTTSQQAKLIALTQ ALTLAKGLLVNIYTDSKYAFHI
18576	48944	A	18685	849	1944	WQVPLFSGRGKYPNPFSPCLYP FSAFPGKRQELATSARNLSDHQ AKECLQPRIPPKPCPIFAGPHWK SDCSTSPGQPLPEPLELWPKA/H LTDSFPDLLGLAA\ED*HCPIAS EAPETITDAELPVTLTVEGKSIP CLIDTGATHSTLPSFQGPVSLAP ITVVGIDGQASKPLKTPPLWCQ LGQHSFMHSFLVIPTCPLPLLGR NILTKLSASLTIPGVQLHLIAAL LPNPKPPLCPLTSPQYHPLPQDL

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18577	48945	A	18686	2	377	KGATIVYALDTLFIMEMKHEFE EAKSWVEENLDFNVNAEISVFE VNIRFVGGLLSAYYLSGEEIFRK KAVELGVKLLPAFHTPSGIPWA LLNMKSGIGR\NWAWASGGSSI LAEF\GTLHLEFMHL
18578	48946	A	18687	215	1135	PITLRRHLFFSGIGRNWPWASG GSSILAEFGTLHGMKIVF*/HFH GNILFSI\KVMNIRTVLNKLEKH YLN*KLNHSKIHFPLFPDHVSV GGLGDSFYEYLLKAWLSINLRR DYKMLKNKCFSQAIETHLIRKS SSGLTYIAEWKGGLLEHKMGH LTCFAGGMFALGADAAPEGMA QHYPVSTVQENNPYSFIPCPLV MKLGPEAFRFDGGVEAIATRQ NEKYYILRPEVMETYMYMFRL SGSDFFSSFLLLPPQASSCFQTLF DLFKVPDSLCSILEFRRHSSRQP YSTDQPFIYLVGKRILFCPLT
18579	48947	C	18688	304	400	
18580	48948	A	18689	16	450	
18581	48949	A	18690	1	777	GHSMDMRVPAQLLGLLLLWLP GARCVIWMTQSPGTLSLSPGER ATLSCRASQRVNSNYLAWYQQ KPGKTPKLLIYGASNLETGVPS RFSGSGSGTDFIFTISSLQSEDIA MYYCQQYNNWPHPS\TFGQGT KLE\IKRT\VAAPSVVHLPGPSD EQLKIWELPSACVPA*NNF\YPQ SRPKVQWEGGITPLQ\SG*LPQE SVHRGRTRQGTAPYSPQQAPW TVRQSRITEETQSLTACEV\TPS GALRFRPVHKGAFNRGESF
18582	48950	A	18691	3	688	HASADAWAANAEEHRHDRPR GTLR\EYKV\VGRCLPTPK\CHT PPLLPACEIFAPNHVVAKS/RAF WYFVSQLK\KMKKVFQGKIGL LVGQVF*ESSPLR/V*KNFRGSW LAAMDSRERAPTNMLPGNNRG P*PPAGGCSTQLLTRDNGVAPG TGAPKPHFHFRFIERLEGRFAG QQSCRRP/ALVQSSFH\DSKIKFP ACPNGVL\RRQHKPRF\TTKRPN TFFLGAGPSSGVCPK
18583	48951	A	18692	1	784	

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18584	48952	A	18693	1	4713	MQGPYLLLWLPDSLEEGKEGL YLGNCIHTCLVTVPEDAFFPHF LTQHSGTHLPPSSDIPSHFMNNS TGRLAQRILGTSTEAFLSPEVM VFVHARNATVRTAMSLIERAK NCGHIPFFFPTQGHDYVLAEKQ VQRSRNKQVRELFPDGFSIHHA GMLRQDRNLVENLFSNGHIKV LVCTATLAWGVNLPAHAVIIKG TQIYAAKRGSFVDLGILDVMQI FGRAGRPQFDKFGEGIIITTHDK LSHYLTLLTQRNPI
18585	48953	A	18694	313	489	SSCFKLHFQQLFKNCNTQMRN QIGFLRF*NNLVMLLSSSSVTNQ LELQKKIILLTCKMQ
18586	48954	A	18695	1	851	ACGWALAQRPARRAMVAGID AGRS\LGVLSVVCLLHCFGFISC FSQQIYGVVYGNVTFHVPSNVP LKEVLWKKQKDKVAELENSEF\ RAFSSFKNRVYLDTVSR*PSLST T*TSSR*KMKYEMESAKIVTD\T MKFLPYVP*VSFQSPTLT\CALT NGSIEVQCMIPEHYNSHRGLIM YSW\DCP\MEQCKRNSTSIYFK MENDLPQK\IQ\CSLSNP\LFNTT SSIILTTCIPSSGHSRHRYALIPIP LAVIPTCIVLYMEWVF*KCARN PDRTQLQLIGNRRMKTTA
18587	48955	C	18696	35	181	
18588	48956	A	18697	75	344	PQVLRPTSPRNISPILNRVSDHA GTPALVLHP*RQVPLFWGRGK YPNPLYLCAPIPYFRT/HNLISLR PNPLCPHPDLVSLCPDPFPAFLE
18589	48957	A	18698	1	268	
18590	48958	A	18699	39	376	QYISELQFLASTVRQTPATSPAH KNFQTPEPQQPGIPPEPPPPGAC YKCWKSGHQAKECLQPGIPRK PRPISGSHSQSPLELWPKA/HLT DSFPDLLGLAAED*HCPIASEAL
18591	48959	A	18700	2	295	CQTTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHP*RQVPLF WGRGNHISGTQELPNT*TAV/V QAF/LPEPPPTG/CLLHVPEIWPL GQGMPAGQDSS
18592	48960	A	18701	81	402	VKFGPEIWCRDSDQGRGGVGT SLGRSIPCPPALCSVRKIYLRPL VLRPTSPRNISPILNRDPTVQLT WQPLPEPLELWPKA/HLTDSFP DLLGLAAEDRCCPIASEAP

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18593	48961	A	18702	165	439	PPRQAKMQNLAAPGSHSQSPW/TLRPKAL*LTPSQIFSA*RLKTDTARSPRKPPSFQGPVSLASITVVGIDGQASKPLKTPQLWCQLRQYSFK
18594	48962	A	18703	284	511	IILVVKWANGLRCLTSRHSFTHQSLPS/PLCPVQLVPN\SRLSPQSQPQASLSLSNLPFLQTHLTSPFLPRLLLARPK
18595	48963	C	18704	414	557	
18596	48964	A	18705	1	1284	MNFEGTETLHCNGHCKVIAMTLGNQEVNQRNFSTGTTGPMEGMWLLSSNSHHSLKYAGALAILSAFQYQERGSQAGHRDSWPETKETHFICGPKTPALVTDWEGSLPLVFNHCRDASLIIHPRFSGVRPRRDACLGPSPLAATPQTITDTELWVTLTVEVWDIST/LFPGN*SHA/TLPSH*NLITLTPLNANI/AIPQHALKGLKPVITRLLQHGLLKPINSPYNSPILPVQKLDKSYRLVQNLRLINKIVSPIHPVVPNPPAFTSQITQAVSQALGIQWNLHIPYHPQSSGKVERTNGLLKVHLTKLSLQLKKDWTVLLPLALLRIRACPRDATGYSRFELLYGRTFLLGPNLIPDTSPLGDYLPVLQQARQAANLLLPTPDPQPHEDTLAGRSVLVKNLTPQTLQPRWTGPHFIIYSTPTAVCLQDPPH
18597	48965	B	18706	1	933	
18598	48966	A	18707	3	435	TKETGFIHGPKTPAPVTDWEGSLPLVFNHCRDTSLIIHPCFKGVRPRRDACLGPSPLAASPAFLEKGQDLINLAFKVYNNRKKLQFLASTVRQTAATSPAHKNFQMPEPQRPGVPPEPPPTG/CLLHVPEIWPLGQGMPAARDSS
18599	48967	A	18708	2	111	
18600	48968	B	18709	1	595	
18601	48969	C	18710	1	1344	
18602	48970	A	18711	227	385	VPILPQPLLLHPAIFLSPPLLTPGPAYSFVP*LALPHLPSNLLLKRWLEPKA
18603	48971	C	18712	148	258	
18604	48972	A	18713	215	693	
18605	48973	C	18714	1	816	
18606	48974	B	18715	1	513	
18607	48975	B	18716	1	1452	
18608	48976	A	18717	1137	1303	

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18609	48977	A	18718	2	2107	IDMIFTPGPPSTPKHKKSQKGSA FTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFVKVERQVQDMG KKLDFLVDMHMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTIICNYSETGPPEPPYSF HQVTIDKVSPYGFFAHDPVNLP RGGPSSGKVQATPPSSATTYVE RPTVLPILTLLDSRVSCHSQADL QGPYSDRISPRQRRSITRDSDTP LSLMSVNHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDTDTDPFTPSGSMPLSST GDGISDSTVPLFLSSEILQKQVG QSITSMLGFLSRGPSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFSLLSVTSYS SFAFHKFSVAVYNISNLKTVDP AKFPTRYCYCLNNRTNDLSDFT ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFICVMTGKSGR NLSDFWEIEEKYPIINYTFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIGGPPLGNQSPSSCSL LHEKDPPTTSGPQTDQPKKHLT NFKSAARPTFLGQGQVPLNPFS FTLS/EQVLLS*AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPLLCVSSLFSRLASFTM GAFTHGTQTPSPTKATAPRYPQ TGDLSAEWPFTAGEEPVLVPRP
18610	48978	A	18719	828	1063	RHSQAAED*HCPIALE/VPQTIID AELRVTLTVEGYSLPPGCLRGL MLSVSGFSRSTVQAVSGSTVLG SGGQWFSCASV

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18611	48979	A	18720	183	1140	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ETKEMHFIRGPKTPVPVTDWEG SLLLVFNHCRDGLSDHSATFQG CQT/MAGMPALVLHP*RQVPLF WGRSKLLLARLS*VPILPQPLLL HPIILLSPPLLTPGPAYSFVP*LS MSIHQVVLRPDEQGPGQEQQPP LYVMEPGEINSFIAHTKPVWWS LHTDAHEIWCHDSDRGTSLGRS IPCPPALCSVRNIRLRPQVLRPTS PRNISPILNQERQRRCILFVDPK LRCQSRTGKAAFSWCLIIAGTA SLIIQPHFKGVRPCRDACLGPSP LAASPAFLGKEQAAPCQAELGP NSSSASAPPPYNPFITSPPHTRSG LQFRSVTSPPPPAQQFTLKKVA GAKDIVKASLAPALAQGVPGTP QATASEGASLKSWECLCGVNL ATAQSARVKEACQEACQSLPRF QRMYEKAWVPKQKTTAEVELS QRASTRVVLRGNVGLESPSRVF SIALSSGAVGGVHCPSDHRMIE PAAFNLSMKNPQRQSCLRA
18612	48980	A	18721	372	906	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQTDQPKEHLTNFKSE KKETRFIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWSFTLSSKSHFSGG RGKSLLQVPEIWPPGQGMPAA QDSS*AV\PICAGPRWKSDCPTH LAATPKAPGTLAQGSLTPSQIFL
18613	48981	A	18722	983	1980	KFGLVQLTLGKPLPEPLELRPK A/HLTDSFPDLLGLAAED*HCPI ASEAA*TITDTELRVTLTVEVW DIST/LFPGN*SHA/TLPSH*NLIT LTPLNANI/AIPQHALKGLKPVIT RLLQHGLLKPINSPYNSPILPVQ KLDKSYRLVQNLRLINKIVSPIH PVVPNPPAFTSQITQAVSQALGI QWNLHIPYHPQSSGKVERTNGL LKVHLTKLSLQLKKDWTVLLP LALLRIRACPRDATGYSRFELL YGRTFLLGPNLIPDTSPLGDYLP VLQQARQAANLLLPTPDPQPHE DTLAGRSVLVKNLTPQTLQPR WTGPHFIIYSTPTAVCLQDPPH
18614	48982	B	18723	1	271	

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18615	48983	A	18724	803	1158	CSWHDRFPDWKAGNLLSLAA* D*HCPIASEAP*TITDAELQVTL TVEGSGDLPWEINPPSSYTLLCE KDPPTTSGPQTNQPKKHSHQFQ IRDKGDTFYPWTHNSGASHGL GRQPSLGV
18616	48984	A	18725	1855	2506	GASPSVWDPTENRTVQLHLGS HSQSPWNTGQRSRDLTSFPDLL GLAA\ED*HCPITSEAPLTITDAR AMG*LSTVEGKPVPFLINTEAT HATLPSFQGPVSLASIT\VVGID G\QAF*TSLKLPNSWCQH*TIRR FKHSFLVIP\TCQVPLLG\EDTLT KLSASLTIPGLQLYLIATLLPNP KPPLCPPLVYPHLNPQV*DISTP SLGDRSCTPYHLIKT
18617	48985	A	18726	2	979	TSTMAVGKNKRLTKG\GKKGA KKKVVDPFPR\KDWY*RRKHPL MFH\IRNIEKDVGSPRTPRDPKL QSDGLKGSVCLKVSPAELPE*L KFAFRKFK\LITEDVSGVKTCPD LTSHGAWDLYP*QNCCSMVQK MGRPMIEA\HVECSRLTD\GYLL \RLFCVGFYLKNRNISDHGRPSY AQPPNRVR\QIR\KKMMEIHDPQ RLQTNVP*KEVVNKLIPASIGK\ DI\EKACQ\SIYPL\QNVF\VKKV KMLK\KPKF\ELGKLMELHGEG SSSGKATGDETGAKVERADGY GPPVQESVGKFRLPIVGNRSGH CVKKEKQSSRRRDFGVSVHPRI
18618	48986	A	18727	1	615	ASTAAPRMLLLFQPRYRTLQPQ RLLMPKKNR\IAIYE\LLFK\EGV MVPKK\DVPIPKHPELA\DRNVP NLHVMKAMQVSQSPRG\YVK\E QFA/WKKISYWCLTN*GYQGVS ISSRDYL\HLPP\EIVPA/TPLRRS RPED/SGRPSA*KGLEG*SDLAR LHKNGEAGQRLPYRR\SAVPP\G \ADKKAEAGGLGQKPEF\QF\RG GFVRGRGQ\PPQ
18619	48987	A	18728	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL\GILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH

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18620	48988	A	18729	323	1973	PCMWIGFAAVRKGLKDSSSASC GCTRRVRGTWWQGLSRVCVA RNEEVRLWGLCWLGSSPPAGW NNVFYMLISADVLACLEPRAN KEAANELAGAVDLGWMANVR RNPRDMVTSTHLGTHFHLRKTP PRGEKTCELASQQPLIEATTKT KSVAVSHILTYTPPTLNGVAAV SSRVHFSFWPPTLQTGLEQGSM SFTICFTTSTNYQSLHSIQPHSHS VQFISSTAKVYAVLRGLGSRTS VSFSTSFWSGWGSGGLAAGMP GIDNARLAADDFRVKYKTELV MCLSVESNVRGLHKVTDDTNV TRLQLETEMEALKEELLFMKK NQEKEVKGLQALIASSELTMEV NAPKSQDLSNIMADLPAQYDEL A\RKN*EELDKYWSQED/IEEHT TVVTNTSLLEVWSC*DARLTEL RRTSPGLWRFDLDSM\RNLK\AS LENSL\REVEAPYAL\QMEQL\N GILLHLESQLGQTPRTEAQRQA Q\EYEALL\NIKVKL\EAEI\ATLP GRLLGRMAKDFNL\GDS\LDER NSFQNL\QKTNTPPGNVDGKVV S\ETN\DTKVLRH
18621	48989	A	18730	1	897	MGHHRRQSLSPVLSLYSPDSMS FTTRSTFFTNYQSLGSVQAPSY GARAVSSAASVYAGAGGSGSRI SVSRSTSFRGGMGPGGLAAGM AGGLAGMGGIQNKKTMQSLN DRLASYLDRVRSLETENRRLES KIREHLENKGPQVKDWSHYCK TIEDLRAQIFANTVDNACIVLHI DNARLAADDFRVKYETQLAMR QSVENDIHGLRKLETEIEALREE LLFMKNHEEEVKGLQAQIASFR LTVEVDAPKSQDLAKIMADIRA QYDDLAGKNREELDKYWPQQF EENTTVVT\QSAEVGAA
18622	48990	A	18731	3	423	SLSPVLSLSPDSMSFTTRSTFST NYRSLGSVQAPSYGARPVSSAA SVYAGAGGLATGIAGGLAGMG GIQNEKETMQSLNDRLASYLDR VRSLETENRRLESKIREHLEKK GPQVRDWSHYFKIIEDLRAQIF ANTV\DNAR

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18623	48991	A	18732	663	2089	AFTTRSTFSTNYRSLG\SVQAPS YGAGPGRAARPASYAGAGGSG SRISVSRSTSFRG\GMGSGGLGQ RELAGG\LAG\MGGIQ\NEKETM A/QALNDRLGLFTWDRVRSLG DRRTRKLGRAKFREHFGRKKG PQ\VR\DWSHYFKI\EDL\RAQIF RKYLLDNAPHPFLQDLTIAPSLL LD*F*EFKY*GQSLAMRQFLWR NDIPLGSAKV\IDDTQYHTDLQ AWRQRFEAPQRRELALSMKKE PRRRKLKGLSSPRLPSSWG*PVE VRLPPNFQDLRQRSLADIPGPN MNELGSKKNPRRKLRQSTWSQ QI*GRAPQLVTTTSLLEVGSLLK TTL/TQKLRRTSPGPWKIRPWTS MKKS*KAQLGRNSP*REVGRPP YGPYKMEASFKRGSLLHP*SQS W/QTRPGAEGTAPQAPRSYEGP C*NIKRSKLEA*DRPPYPPALLE D\GEDF*SLVDPLDSKQLHAKPI QKTTTPPG*VGLGKVVS
18624	48992	A	18733	53	1100	NFRVEAGVRGVQQKETCAFKV LESI\GKF\GLALAVAGGVVNSA LYNVDAG\HRAVIFDRFRGVQ\ DIVV\GKGTHF\LIP\WVQETQLS FD\CRSRPRN\VPSQSTG*AKDL QNVQHHTAASLFRACRQPSFPR IFTSIGEDYGWSVCLPS\ITTEV\L KVSVGSLWMLGELITKRE\LVS RQV\SDDL\TERAATFGLILDDV SLTHLTFGK\DFT*AVEAKQVA QQEAEKGQICWLEKAEQQKK\ AAIISAEGDSKAAELIANSLATA GDGLIELRKL/E*AAEDIAYQLS RSRNITYLPTG\QSVLLQ\LPQLR GPPLPCTSRGLDLGPQPRLILNN SLSFLLPTPEINCEIFMIGLK
18625	48993	C	18734	222	458	

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18626	48994	A	18735	2104	2758	QFCPSRQKGCLQKTFRHFVAGH GGDFLFRSPTHAFPFCVPLFPLP P/VTIVRPCPPFS*VLSSSPRNSQ NTIPRSPFLSPGTLSRSPAGSRDP GNPAPGSNTRLGPTAPVSRLAP VDIGFRSTDCWSLQPQVPVNPG SRPAPTNPRSRSTPVDPGSNTRL GPTAPVSRLAPV\V*ALGPLTAG PYSPR/CPVNPGSRPAPTNPRSR STPVDPGSNTRLGPTAPVSRLA PVDIGFRSTDCWSLQPQVPVNP GSRPAPTNPRSRSTPVDPGTRTT PEGL
18627	48995	A	18736	2	280	AMGFIVAPSLGCF/VGSRFVHG EGLRWYAGLQKPSWHPPHWV LGPVWGTLYSAMGYGSYLVW KELGGFTGVSRASEVAPPEPPP GSSVLCFLHA
18628	48996	A	18737	331	972	TAAAAAMAPPWVPAMGFTLAP SLGCFVGSRFVHGEGLRWYAG LQKPSWHPPHWVLGPVWGTLY SAMG*VGVHWPGDKPGPLQGE AWPRTEDTGQLALNWAWPPIF FGARQMGGALVNLLLVS\GAA GHTTLGGRGAS\QWLAARLLYP \YLGLAWPSTTTTQTTCVWR\D\ NHGWHGGRRLARVSARPTMG LQLHQAGAITLVMWWPSRFHD HWAC
18629	48997	A	18738	1	603	
18630	48998	A	18739	1	1782	
18631	48999	A	18740	237	876	CESFCWHHFFWDIFNLFVTAPF LVHVDYQGFESVAKKYDVMN DMMSLGIHRVWEGFSCSGKMH PLPGD\QLLDVAGGTGDIAFRFL NYVQSQHQRKQKRQLRAQQN LSWEEIAKEYQNEEDSLGGSRV VVCDINKEMLKVGKQKALAQG YRAAHKSGVILDCLWFPPILHPI AQQICQLYLQNTSGIWPSLPYL CYHLLVQATIPSYLDCCNSL

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18632	49000	A	18741	112	995	VLGSLSQEKRAAETHFGFETVS EEEKGGKVYQVFESVAKKYDV MNDMMSLGIHRVWKDLLLWK MHPLPGTQLLDVAGGTGDIAFR FLNYVSVPASEKTEEAVKGPTK FILGKNLPKSTRMKKIPWAG/TR VVVCDINKEMLKVGKQKALA\ KDTRAGLAWLL*DAEELPFDD DKFDIYTIAFGIRNVTHIDQALQ GSSFGCLKPG\GRFLCLGFSQVE QSP\LSRLYDLYS\SRVIPVLGEV IAGDWKSYQYLVE\SIRRFPSQE \KFKD\MIEDAGFPQ/V*LTKV*H QGIVAIHSGFKL
18633	49001	A	18742	117	403	
18634	49002	C	18743	62	370	
18635	49003	A	18744	179	527	IQEPPVI**GLHMVHNFNTIFVSS YFKFESTFAISFLKVFNT/CFFSI* IKSLDEQCVVGKISKHWTGILR EAFTDADNFGIQFPLDLDVKMK AVMKVGICGKNLVKQGNFTMT HSN
18636	49004	A	18745	3	1242	AAPQAGLSPVAIAAAIQLHLHS TQCSSPNTCCLPRRTRATIYYSR WSYHPLGSVP*SP*PFQEAS/AL TLPPACSFYGPLT*FQPKP*GSFP LSQ*MEYTIGLYT*TFHCPGTSR RQIPSSYLNCKDAFLPLL/SNPP QCRPFTGVGLVDVLTGFETNN KYEIKNSFGQRVYFAAEDTDCC TRNCCGPSRPFTLRIIDNMGQE VITLERPLRCSSCCCPCCLQEIKS LDEQCVVGKISKYWTGILREAF TDADNFGIQFPLDLDVKMKAV MIGACFLIDRNCSPAMEQSWM ENYFDEMTEIGFRRSVITNFSEL KEHVLTHCKEANKNLDKMLDE WLTRKNSVEKTLNELMEVKTI NEKLTIGKISKYWSGFVNDVFT NADNFGIHVPADLDVTVKAAM IGACFLFAFRLGSELHN
18637	49005	B	18746	277	2415	
18638	49006	A	18747	102	196	

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18639	49007	A	18748	897	1656	SNAGLRHVCRTSCQSGRARSCH VGLHTPWVS*VPWHPWGIRWR GDPQKSQRSRKCCVPGGAP/QK GGDPEPQPSLSVSWNWLSGSCA GFRAVLPRKPQRKVWLFASSA GTAATEPPR**LAWKADSGGDP WQQPQQSARPHA*TWTWRGD GAPPGRVA/QGRGTAGGASAG VSSGRSRGSPQTGFQALQSCLE ASRRPPVVACNPHPAGALPAAQ AGNRATLMTGSCLQMPIMYEE AQLRLEELCTKARLNCQWFL
18640	49008	A	18749	756	884	CLQRLLPPGFRRQPSKYRRNRG KSGKG*RPSPVATWQPDYNI
18641	49009	A	18750	1826	2772	RRVLEAMGPSRAAKVLSVCVR SRIGPLICSQRHPATSKTKPQGR PPGEQGTPRDNPRRNNRPARSA TPRGA/PQGAPPRPGEEPNAPQT IDKGPPSPPSRGHTRRLARSGNQ PPERHTPAAGGKTRYVRQSVL HRARGGEPVRMPRLPRIAEA/P APDRVECF*VVQSPAREMHSCQ ADSMCPVW*GRIWRSAGSC*SR SEKILVWIPQSGLQAHACPSEA HKMPGNPRDGGAGICKSSPGG KGERRKVEGGSTTRAGTSRDS VSKRHANTMGEQAQGEKHPRG TV*KTKRRGPKGQTRGTKAPEE ETSREPPCTGPI
18642	49010	A	18751	196	322	
18643	49011	C	18752	189	650	
18644	49012	A	18753	1	53	
18645	49013	A	18754	31	449	
18646	49014	A	18755	1	389	GMPTSTIASCSQDGRVFIWTCD DASSNTWSPKLLHKFNDVVWH VSWSITANILAVSGGDNKVTEG QQNEQ*QDRWGLAPHPPAPGL PLPGPTNQTTGKSPQLQQDYFP RRSYRCSHRLIICLNVIGNAL
18647	49015	A	18756	1	1041	
18648	49016	B	18757	15	782	

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18649	49017	A	18758	1	1425	EVKKINNAHTIGCNAVSWAPA VVPGSLIDHPSGQKPNYIKRFAS GGCDNLIKLWKEEEDGQWKEE QKLEAHSDWVRDVAWAPSIG/ LWPPSTIASCSQDGRVF\IWTL** CPQAITVVPLNCLHKFNDVVLG MLNWGPSQPTSLAVSGGDNKN GTNTVCPTGWLQDSNTLVHLV TYKMPRSLGLGFLWCQLLSPR KYREGTSPVSLWVGEVWFINP DWWGSIRVYHPSPSGSYRTHKP PLNNLSCDTSIIRELLKGKKFLL FVSVYPVPSTVLGRKKVSVINT VDTSHEDMIHDAQMDYYGTRL ATCSSDRSVKIFDVRNGGQILIA DLRGWPRASRYQQGHQDLFIL RSDLPSQVFIRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSVPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
18650	49018	B	18759	323	1583	
18651	49019	A	18760	3	419	PSASSSPARIPAATRQGRRSPRIP PAPSNEAPRLPADREFLEQQPPR FPKPTIQASGADRAVDCGILKL QKS\PARLARPRWPRRPSKRFW SAAGSVEEQPKPPRRRAKSPEQ SPQLSVLPLVTITPQASGASFEK MKN
18652	49020	A	18761	2	385	WGRGGGRGLLYGRRHFVRRRR RGGRSPGESPALTVT*GAV\PSA AFRESAQPGPRSSEAHISTSPKR TDGGRDS*PGLPRSSLTPSLPRP ASFSTSPGRVSAPHRLPRHS/AG PGLSGSS*PQPYSDPT
18653	49021	A	18762	242	422	

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18654	49022	A	18763	2	992	AREKKQKTRRQNKNIPRQINKT QRICC*QSCLTMTQDFFWPLCQ GHSRGAPCLLVPPGLSLTCAPA QPAARPGVSQLTCAIACTHIQW FPSSCPPSEKNGDTLTV\KTPSA SSSPARIPAATRQGRRSPRIPPAP SNEASPAPGRPRVPGAA\PPRFP KPTIQASGADRAVDCGILKLQK S\PARLARPRWPRRPSKRFWSA AGSVEEQPKPPKAP/PAKSPEQS PQLSVLPLATITPQAYGASFEK MKNLKTRRGGRSRWHFPFNVIP QAPSLKWGFQTSDASSAEVFH VDRSLASHKMGPGRRPRSPLW APPFCEAAAARRQEPGVCIMVE
18655	49023	A	18764	292	348	
18656	49024	A	18765	2	466	LITVVKLLDTMVDTFLQKLVA AGSYQRFTDCYKCFYQLQPAM TQRIYDKFIAQLQTSIREEISDIK EEGNLEAVLNALDKIVEEGKVR KEPA/WQRDTLRRHVQKQEAE NQQLADAVLAGRRQVEELQLQ VQAQQQAWQALHREQRELVA VLREPE
18657	49025	A	18766	2	511	FNMAEASSANLGSGCEEKRHE GSSSESVPPGTTISRVKLLDTMV DTFLQKLVAAGS/YSTPSLGRK CWS\RLPSGGQSVKQAFSWAAC RLPQGRKEEISDIKEEGNLEAVL NALDKIVEEGKVRKEP\AWRPS GIPEKDLHSVMAPYFLQQRDTL RCHVQKQEAENQQLADA
18658	49026	A	18767	224	748	NRPSVGRRAGYHRGGSYQRFT DCYKCFYQLQPA\MTQRIYD\K FIAQ\LQTSIREEILFDNQKQEGE PRKLSWNALG*KFVGTKGKVR KEPAWRPSGIP\EKDLHSVMAP YFLQQRDTLRRH\VQKQEAENQ QLADAVLAGRK\QVEELQLQV QAQQQAWQALHREQRELVAV LREPE
18659	49027	A	18768	1	421	

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18660	49028	A	18769	666	1445	AGITTIEAAKRTIQVLHLQAND AQERA\ERSQREFREERRAREPG LRLK*SFLNRRIQ\LVEEEL\DRA QERLGHLPCKKL*RS*KKLADE SERRY*RLFEN\RALKRLKEKIG TSREIPTQKKLKHICRKEAD\RK YEEV\ARKLGDHLKEDLEPTE\E RA\ELAESRC*EIDEQIRLIDQNL QCLSAAEDKYSQKEDKW\EEE MKI\LTNKLREAET\RAEFAERS VAKLKKTIDDLEDKLKCTKEEH LCTQRMLDQTLLDLNEM
18661	49029	A	18770	2	158	SAAPGAVPPPEADSTSAGMSRR PCSCALRPPRCSCSASPSAVTAA GRPRPSDSCKEESSTLSVKMKC DFNCNHVHSGLKLVKPDDIGRL \VSYNP\AYLEGSCKDCIKDYER LSCIGSPIVSPRIVQLETESKRLH NKENQHVQQTLNSTNEIEALET SRLYEDSGYSSFSLQSGLSEHEE GSLLEENFGDSLQSCLLQIQSPD QYPNKNLLPVLHFEKVVCSTLK KNAKRNPKVDREM\LKEIIARG NFRLQNIIGRKMGLECVDILSEL FRRGLRHVLATILAQLSDMDLI NVSKVSTTW\KKILEDDKGAFQ LYSKAIQRVTENNNKFSP\HAST REYVMFRTPLASVQKSAAQTSL KKDAQTKLSNQGDQKGSTYSR HNEFSEVAKTLKKNESLKACIR CNSPAKYDCYLQRATCKREGC GFDYCTKCLCNYHTTKDCSDG KLLKASCK\IGPLPGTKKSKKNL *RLHVGWHEPAPLQLRPTATPL LLQRQPQRSDSRRAPSTLG

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18662	49030	A	18771	4	1276	RKAASSYVSRMALPIIVKWGG QEYSVTTLSEDDTVLDLKQFLK TLTGVLPERQKLLGLKVKGKP AENDVKLGALKLKPNTKIMMM GTREESLEDVLGPPPDNDDVVN DFDIEDE/R*FEVENREENLLKIS RRVKEYKVEILNPPREGKKLLV LDVDYTLFDHRSCAETGVELM RPYLHEFLTSAYEDYDIVIWSA TNMKWIEAKMKVKPLGVIWG KFSEFYSKKNTIMFDDIGRNFL MNPQNGLKIRPFMKAHLNRDK DKELLKLTQYLKEIAKLDDFLD LNHKYWERPRVRCHIFHGKED RYDPCPMGACSCKTVCTTNLA LPALPLGSMKNGQPCRNVIGQK GYALTVINSGPQQGLFVRILLG LFIRDFFPAGCGARPFWNEGLM AYFQRRTLVGVMLVLSSSKSFK
18663	49031	C	18772	113	257	
18664	49032	A	18773	143	330	HHGPVPFPRGLIS*HSLHCPCPT PGGKNVFFFCEYFLKLAGIETT NCSADKRGKKVCCLIPR
18665	49033	A	18774	3	432	
18666	49034	C	18775	112	192	
18667	49035	A	18776	3	1015	SSRPVRPRPAARLSAMSSTQFN KGPSYGL\SAQ\VKNRLL\SKYD PQKE\AELRTW\IEGLTGLSIGPD FQKG\LKDG\TIL\CTLMNKLQP G\SVPKINRSMQN\WHQLENLS NFIK\AMVSYGMNP\VDLFEAN DLF\ESGNMT\QVQVSLLALGG KRPKTKGAAEGGLDIGVKYSE KQERNFDDATMKAGQCVIG\L QMGT\NKCASQSGMTAYGTRR HLYDPKNHILPPMDHSTISLQM GT\NKCASQVG\MTA\PGTRRHI YEYQAGNPTSCDNFSM\SLQ\M GYTQGAQTQSGQVF\GPGRPDI *TPSTCPQGTI\ADGAPSGTGDC PDPGEVPEYPPYYQEEAGY
18668	49036	A	18777	2	110	
18669	49037	A	18778	74	289	

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18670	49038	A	18779	138	2039	GAAMAAAGRLPSSWALFSPLL AGVALLGVGPVPARALHNVTA ELFGAEAWGTLAAFGDLNSDK QTDLFV/LAGKK*LNRLFGRPE CTRILNPK*RYLSRITVH**QV*S LGAYDGDSQMDVLLTYLPKNY AK\MN*ELLSSGDKIKH*ILTI*P YSIGL/LQDEPLIMDFNGDLIPDI FGITNESNQPQILLGGD/CYHGI QH*PLQVKCEFHI/PHAFIDLTE DFTADLFGATLNGTTSTFQFEI WENLDGNFSVSTILEKPQNMM VVGQSAFADFDGDGHMGSFTC QGCGR*K/CAKRVPSYLVRSGM KQWVPVLQDFSNKGTLWGFVP FVDEQQPTEIPIPITLHIGDYNM DGYPDALVILKNTSGSNQQAFL LENVPCNNASCEEARRMFKVY WGADRPKSN/SKGAMVATFFDI YEDGILDIVVLSKGYTKNDFAI HTLKNNFEADAYFVKVIVLSGL S\SNDCPRKITPFGVNQPGTLYH VYNCRCKWVSEKWIRWPNSAQ SAHLALQLPYNVLGFRVGSANF LDHL\SLGIPRPSWRKIFYGKQE WTAIIPNSQLI\VIPYPHNVPPKL GVPNCILYTKLILFWLTAIALIR CLCFQSLAINWHFTLGREKKAG WIEEKRTRKAHRFPFWMAMW
18671	49039	A	18780	1	966	
18672	49040	A	18781	1	1035	RPPFPVPGVQKCPLPTRGGLHIG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSPVASGREM VVLSVPAEVT\VILLDI\EGTTT\P IAFVKG/DILFPYIERKMLK\EYL QTHW\EEEEFQ\QDVSLFEGNK A\EEDAHLDG\AVPIPGKHLGIG V\DD\LQQMI\QAVVDNVCWQM SLDRKTTALK\QLQGH\MWRAA FTAGRMK\AEFFADVVPA\VR\K WREAG\MKVYIYSSGSVEAQKL LFGHSTEGDILELV\DGHF\DTKI GHKRRRVKVTRK\IADSIGCST\ NKHFVFWTDVTSRRASAGLRE AGCCTLAVV\VRPG\NAGINR*L RKTYYSLITSFQWNYYLPSST

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18673	49041	A	18782	1	528	DNELLDYEDDEVETAAGGSMS/ EAPAKKDVKGSYFSIHSSGFRD FLLKPELLRAIVDCGFEH\PSEV\ QHECIPQAILGMDFLCQAKSGM GKTAVFVLATLQQLEPVTGQV SVLVMCHTRELAFQTR*KTRPF WNVTVCPSGEDTRVGVKETLL PPPLTAPTPWLPSFASPPLLNPH
18674	49042	A	18783	207	309	
18675	49043	A	18784	85	348	PPHSALLPFPTPFLPPSQLEIFVD DETKLTLHGLQQYYVKLKDNE KNRKLFDLLDVLEFNQVS*TSS RGMSIGALQL*QKPGY*VHFY
18676	49044	A	18785	1	930	CCCRHTRSPCLVMAENDVDNE LLDYEDDEVETAAGGDGAEAP AKKDVKGSYV\SIHSSGFRDFLL KPELLRAIVDCGFEHPSEVQHE CIPQAILGM\DVLCQAKSGSGER QAVF\VLATLQHLEPV\TGQGV CAG*CCHTRELAFQISKEYERFS KYMPNVKVAVFF\GGLSIKKDE EVLKKNCPAYPSVGTPGRILA\L ARNKSLNLKHIKHFILDECDKM L\EQLDM\RRDVQE/IFFRMTPH EKQVM\MFSATLSKEIRPVCRK FMQDVNTLLPSLPPLPARCLLPF LALFLRLPCHSSAKKAACAQLG
18677	49045	A	18786	96	1618	LFTPCFHLFCENPSRSPFPSSPAG PVMAENDVDNE\LLDYER*MR WETAAGGDGAEAPAK\KDVKG SYVS/LSHSSGFRDFL\LKPELLR AI\VD\CGFEHPSEVQHECIPQAI LG\M\DVLCQGKSG\MGKTAVF VLATLQQLEPVTGQVSVLVMC HTRELAFQISKE\YERFSKYMPN VKVAVFF\GGLSIKKDEEVLK/R RNCPHI\VVG\TPGRILS/LWVRN KSLNLKHIKHFILDECDKMLEQ LDMRRDVQEIFRMTPHEKQV\ MMFQCYLGAKEIRPVCRKF\M QDPMEIFR/VDDETKLTLHGLQ Q\YY\VKLKDN\EKN\RKLFDLL DVLEFN\QVVIFVKSVQ\RCIAL APAY*WEQNFPA\IA\HRGDAP RKERLS\R*SSSFKDFPTNEILIG YPTLFGRRHGTSEAGETIAF*FM NMP*GILKTLPCHR\VGPEQGRF GHPRGL\AITFVSDEE*LPRSCD DVQGSALRVKFSELPDEIGHLP PTLEQDTGRRLAHFGNVDRLFL
18678	49046	A	18787	1	363	

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18679	49047	A	18788	78	714	GTTEGKRQEAVGYLCVLPLTTL PLVTRLPPQVADTMLPPMALPS VSWMLLSCLILLCQVQG\EETQ KELPSPRISCPKGSKAYGSPCYA LFLSPKSWN\DADLAC\QKRPSE KLVSVLSGAEGSFASLLA\RSIS NSYSYIWIGL\HDPKKG\SEPDG DG*EWSSTDVMNYFAWEKNPS TILNPGHCGSLSRSTGFLKWKD YNCDAK\LPYVCKFKD
18680	49048	A	18789	52	186	QSEVHHGIISYTTGQGENLSEPI WKSWQRSQDL*QENHPEIYSLT
18681	49049	A	18790	666	2732	KQLIKMCYFILLLLILSSHIGKD KAIDKNGILVQYWQE*KLVEPF *KAIWPPCMETLNVDTPFPQPV CLGIYPNE*KLSK/CFKP*APKV YFHGCL*Y*NHWEPTETIPPVK GWIK*ILF
18682	49050	A	18791	112	340	
18683	49051	A	18792	3	323	LSSLASMSFTTCSAFTNYWSPG SVQVPSYGTQPVSHAASVYAG LGGSGSRISVSH\SPMAGGLAG MGGIQNEKETMQSLRDRLASY LDRVRGLETENWKLESKIQEH
18684	49052	A	18793	1	994	APSYRA/RLVRSVASVYAGPGS SGSRISMSRSTSFQGGLGSRSM AA/GMAGGLAGMGGIQNEKET MQSLNDRLASYLDRVRSLEMG NWKLESKIWEHLEKKGPQVRD WGHYFKTIEEDLTQIFTSTVDN TCIILQIDNAHLAADDFRVKYE TEPATCQSVENDIHGLHKVIDD TSVTQLQLETEIEAL\KEALLFL\ KKNHEEES/WRHTVQALEIDLD WMKNLEASLENSLK/EGVEAC YTLQMEQLNGILLHLESELAQT WAEGQGQAQEYQALPNIKVKL EAEIATYRRLLEDGEDFNFGDA LDSSNSTQTIQKTPTC/RTVDGK VVSETNDTKVL
18685	49053	A	18794	3	377	
18686	49054	B	18795	54	136	
18687	49055	A	18796	149	419	

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18688	49056	A	18797	83	1402	AEKAGGKKGEAPSYRA/RLVRS VASVYAGPGSSGSRISMSRSTSF QGGLGSRSMAA/GMAGGLAG MGGIQNEKETMQSLNDRLASY LDRVRSLEMGNWKLESKIWEH LEKKGPQVRDWGHYFKTIEED LTQIFTSTVDNTCIILQIDNAHL AADDFRVKYETEPATCQSVEN DIHGLHKVIDDTSVTQLQLETEI EAL\KEALLFL\KKNHGEEIKGL SRRQIASSGVDPWRVDAPKSSG PSPKIMGRHPGPKYDEL\ARKR TREE\LAKYSSQ\QIEEST/TQLV TNTSLL/GGLELAETNLHRS*TY KSRSLEDSTLDSIEKS*KAQAW KKQPLKGSWKAPLRPLPDWSK LQTGILACTFESRAGNKTRARG TSAPGPQEL*GPLLKHQKVKAG GLRSPTLPARLLEDAEAL*SLV DPLDSKQLPCNTIQKTTTPPG*V
18689	49057	C	18798	140	283	
18690	49058	A	18799	2	783	VVQFARREKPSSSKVSQRHPCT EAVREVLHG\NQRKSPQRSWET VELQISLKNYDPQEGQSAFSGT RQALSPLPRP\KFSCVCPGGTQQ H\CDEA\KARGISPPHGTFEGA* KNLNKE*KNWSKKAGPRKY*L RFFGPQKSLDQSKIPPNPSGPGF K*RAGK\FPFPWFTHN\ENMGG PKLDEGEVPPIQVFQMKERCLC L\AVAV\GHV\KMTD\DELVYNI HLGCQLSWVSLLKEKNW\QNV\ RALYIKSTHGQSPKRLIFKAHFE
18691	49059	C	18800	239	555	

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18692	49060	A	18801	401	3014	TRASSTMSKSFQQSSLSRDSQG HGRDLSAAGIGLLAAATQSLSM PASLGRMNQGTARLASLMNLG MSSLLNQQGAHSALSSASTSSH NSQSIFNIGSRGPLPLSSQHRGD ADQASNMLASFGLSARDSDELS RYPSDTITPENLRPILLQLKRRR TEEGPTLSYGRDGRSATREPPY RVPRDDWEEKRHFRRDSFDDR GPSLNPVLDYDHGSRSQESGYY DRMDYEDDRLRDGERCRDDSF FGETSHNYHKFDSEYERMGRG PGPLQERSLFEKKRGAPPSSNIE DFHGLLPKGYPHLCSICDLPVH SNKEWSQHNGASHSRRCQLLL EIYPEWNPDNDTGHTMGDPFM LQQSTNPAPGILGPPPPSFHLGG PAVGPRGNLGAGNGNLQGPRH MQKGRVETSR\VV\HIMGFSTE GKTLRYQLLQLVEPFGVHFKFI *FLNKNLLRAFIEMATTE\DCFK AAV\DYYTTTPA\LVF\GKPVRV HLSQKYKRIKKPEGKPDQKFDQ KQELGRVIHLSNLPHSGYSDSA VLKLAEPYGKIKNYILMRMKS QAFIEMETREDAMAMVD\HCL KKALWFQGRCVKVDLSEKYK KLVLRIPNRGIDLLKKDKSRKR SYSPDGKESPSDKKSKTDGSQE AERST\EGKEQEEKSGEDGEKD TKDDQTEQEPNMLLESEDELLV DEEEAAALL\ESGQFSGETSTDL
18693	49061	A	18802	3	1013	NCRAAWRAKLEGCLSLRRNAC QCFLIWTQTPDREQSYSLDQLP REVLNQEEKSISIWDIYLHLEM GNGLSDQTSILSNLPSFQSFHIVI \LGLDCAWKRQLSYTRLQFQLN L*NT\VPYPKGFNTEKI*/RVTLG NSKTV\TFHF\WDVGGQEKLRP LWKSYTRCTDGIVFVVDSVDV ERMEEAKTELHKITRISANRGV PVLIVAN\KQDLRNSLSLS\EIEK LLAMGELSSSTPWHLQPTCAIIG DGLKEGLEKL\HDMI\IKRRKML RPTRKRKDEYQFPNIICVGVGF LWSDFDKNRRVSTAGVCLSAPP WMLLKLCFVEQFRCPTRVALW KMSKCSAS
18694	49062	A	18803	3	1103	
18695	49063	B	18804	34	734	
18696	49064	A	18805	1	1741	

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18697	49065	A	18806	6460	6635	RTSTERSHLKTRYQRTSCSSNR*LNSSSSKTSFRCSLTTSLFWRHTIFNMLLINRRLL
18698	49066	A	18807	5567	5853	IGILEA*LLRNLPNDSIKALVDA*YKSLLSAVERCSFMVLFGEPMNKPPLAILRIQSGVNRPPVISIMALIGPLVTPSASTYSGVTNADLSSATK
18699	49067	A	18808	664	992	SCADIHGYHRGNSSNNDSNLIPKQTNRDCLNNGHQNHSCNG/D*PQPQR**QLTLQNLMQHQ*KQQYPLPQHQQQE*RTR
18700	49068	A	18809	3	1698	
18701	49069	B	18810	227	883	
18702	49070	A	18811	180	373	PDTLRSILPMLLEQLFCRTFGLLSP**RDTSLHLGHKTEQHT*LVMGSWFYLLASQQPRCCYAC
18703	49071	A	18812	495	701	
18704	49072	A	18813	138	418	AYRLLLCLVYSEGFYMHLEFQNRLYHQLVF*GRLWHFW\KSIKRFSIY*FFWYRW*YICKLNKGRLQDVIGVINT*CHFLS*GLH*TIPGIHRL
18705	49073	C	18814	62	175	
18706	49074	A	18815	644	828	
18707	49075	A	18816	1	1107	
18708	49076	B	18817	84	342	
18709	49077	A	18818	3	1399	
18710	49078	B	18819	1	1377	
18711	49079	A	18820	1	546	
18712	49080	A	18821	855	1099	VTLYSEYQHPSVREYGLYLTSHRIEPLECVHRTL*PVLLSMQPSVLEYYEQQGYEAEY*LQEECHHQRTSSL*DLLKQLLQ
18713	49081	A	18822	1	1680	
18714	49082	A	18823	1	3951	
18715	49083	A	18824	2	6446	
18716	49084	A	18825	2497	21785	SSPYPFTKQSSTNNFVFDGNELFNSRDRLSQRLFYILQSSVHLINRQ/LEGYVQHHLNLAEI*HHGLGKDAYIAAMYNNDDGATFQMEIGGIHTNAALAAGDKLQCIWRYLDVNGNAPAAENEFEVVSYEGFGTSNFSVKCKGMLPGKFIGCDAFYGKYLQTDGPIKQVDSVKWFTNLTVSGSGRKQLGQRKYPQVVMGMGMTSGFDDGYNLTPERQVKMAYGLGYRDWWTTYIGMSHYWKGLTAFQDKETGELI
18717	49085	A	18826	31	479	

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18718	49086	A	18827	255	1002	SQFSLSQVLVDSAEEGSLAAAA ELAAQKREQRLRKFRELHLMR NEARKLHHQEVVEEDKRLKLP ANWEAKKARLEWELKEEEKK KECAARGEDYEKVKLLEISAED AERWERKKKRKNPDLGF\SDY AAAQLRQYHPV*PKQIKP\DME TY\ERLREKHG\EEFFPTSNSLLH G\THVAFHRGKFDRVVLRSGKN QFEKRD/KF*ARRRPYNDDADI D\YINERNAQFNKKAERFY\GK YTAEIKQNLERGTAV
18719	49087	C	18828	91	225	
18720	49088	A	18829	3	212	
18721	49089	A	18830	88	239	
18722	49090	A	18831	865	1898	QQQQQQQHRRYPRRRSPRAWC SHPRSPLLFLPSLAPWPDQLTEE QIAEFKEAFSLFDKDG\DGTITT KEL\GTVM\RSLGQEPNKKLEL\ QDMINESGMLMG\NGTHLTFPR IF*LMMARKMKDTDSEEGN/LR EAFRV\FAKDGNGYISAAELR\H VMTNLGEKTTRF/KKVDEMIRE A\DIDGDGQVNYEEFVQMMTG KMEDLTFQLPFSPPLEESNWNL LLTFLQKKEKKKKVHLFHSCFL YSKTECQKYLLVHTHQNLHVL VGGPCPLKDQATHQFYNINTCT NLNDNGLLKRSILLMINTLFGL ASFFHACSFDDWSTSQGLWYL KLENGKNQISKPIPNGVLVHFV
18723	49091	A	18832	1	330	WVVLKNCVGVGLLIAT*MWFI SNKYLVQRQSRDYDVEWGYAF DVHLNAFYPLLVILHFIQLFFIN PLPFLKNTVILLYPFAPLILLYGL SLALGWNFTHTLCSFYKYRVK
18724	49092	A	18833	1	534	VPSNSVNSLVQGNGVLNSRDA ARH/TAGAKRYKYLRRLFRFRQ MDFEFAAWQMLYLFTSPQRVY RNFHYRKQTKDQWARDDPAFL VLLSIWLCVSTIGFGFVLDMGF FETIKLLLWVVLIDCVGVGLLIA TLM/WHCHFWKKQVILLYPFAP LILLYGLSLALGWNFTHTLCSF YKYRVK
18725	49093	C	18834	295	570	

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18726	49094	A	18835	418	1567	SFTLKNCVLQRVSSILPSNTAEV DFPSWTTQSDWQQTRAQVLLQ ARARAALRLVLIILRHDGASPP MRTRLSPTATLATGSGASEAPV SGDRKPAATTSGGPRRKMLPST SVNSLVQGNGVLNSRDAARHT AGAKRYKYLR\RLFRFRQMDFE FAAWQ\MLYLL\TSP*RVYRNF H\YRKQTKDQWAR\DDPAFLGF PFKYSGFCVSTIGFG\FVLDMG\ FFETIKLLLWVGLID\CVGVGLL \IATL\MW\FISNKYLVKRQS\RD YDVEWGYAF\DVHLNAFYPLL VILHFIQLFFINHVNLTDTF\IGY LVGNTL\WL\VAVGYYILR*LSL GYSVGLLFFSSIAHF*KNT\VILL YPFA/PL*FLPPTGFPLALGWNF THTLCSFYKYRVK
18727	49095	A	18836	1	888	MPGLLLLRGSQNLKQQAEILCG LGLALVISAVKPLSKKFMLPNP TSMKPESDGIYSINLKRTWEKL LLAGHAIVVIENSADVSVISSRN TGQKAMLKFAAATGATPIAGH FTPGTF/TNQIQAAYWEPRLLV VSDPRADHQSLTEASCVNPPAI ALCNTDSPLCH/VDIAITCNNKG APSVGQMW*MLAWEVLHMRG TISCN/SPWEVMSNLYFYRDPEE TEKEEQAAAEKAVTKKEFQGK WTVSAPEFTVTQPEVADWSEG MQICNLGKAQQGQLSSDAEDD FWSLESLDGYSHTVTFR
18728	49096	A	18837	74	848	REIFINVRSLLMACFVKEEDVL KFLAARNP/HVGGTNLDFQME QYIYIRKSDGIYIIRLKRTWEKL LLAARAIVAIENPADVSVISSRN TGQRAVLKFAAATGATPIAGRF TPGTFTNQIQAAFRE\PRLLVVT\ DPRADHQPLTEASYVNLPTIAL CNTDSPLRYVDIAIPCNNKGAH SVGLMWWMLAREVLRMRGTI SREHPWEVMPDLYFYRDPEEIE KEEQAAAEKAVTKEEFQGEWT APAPEFTATQPEVADWSEG
18729	49097	A	18838	72	528	DEACGVCCYSPGASPMPP*GRT RKEGRTAGKVRPKERPKTPVN\ KSGGQGPKRKNWSKRQKFRDK L\NN\LVLFDKA\TYDKLCKEVP N\YKLITPSLWSPERL\KIRGSLA KGKPFQEAP*VKGLI/RNLVSKH RAPSNFTPGNYQGWEDAPSLL

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18730	49098	B	18839	6	125	
18731	49099	B	18840	249	291	
18732	49100	A	18841	128	669	RPGHAQTLGSPSLALGMAGQF RSYVWDPLLILSQIVLMQTVYY GSLGLWLA\VVDGLLRISPSLD QMFDAEILGFS/TPFQGRLSMM SFILNALTCALGFAVISSGEEKQ CLDFTVTVHFFHLLGLLGSNSS PFSPSGG*TLVGLGPKPVVALH SLAVIGEYLCMRTELKEIPLNSA
18733	49101	A	18842	1	818	MAELTVMRFHTEPQGSEGLRLP RISGSKPKQMHVTWLEPLENGI CNGNTGNAQLLIPPGVIFHKYP SHYVTAMLKSLKWPPLQTELTS SSGQALWGLVGGGSPHRQAST EKLFSEKVPKTAENFPCSELSCF HGENGFGL*GVPCFHRLFPRVY AVRGGDFHTAINGT\GGKSHPM GKKFEG*ETSSLKHTG\PGDLVP WQNAGP\NTNGSPVFLTSCTAQ ELSGLDGKPCGVLAKVKE\GM NIVEAMER\FGSR\NGKTSKKITI A\DCGTTPNKV
18734	49102	A	18843	4	454	
18735	49103	A	18844	1	978	MRWACDFTKLLSSTWTLIQYPE NAMIIARWALLADCPEKTKAL RTTEDGIVDAANFEQFLQERIK VNGKVGNLGGGVVTIEKSKSKI TVTSKG\PFNSM*I*GSASSFVEK KRLLEF*KLLSSTWTLIQYPENA MIIARWALLADCPEKTKALRTT EDGIVDAANFEQFLQERIKVNG KVGNLGGGVVTIEKSKSKITVT SKGHFQFYVNLRISFLICGKEKA VGILEEIVLNLLIIFSSIDILTVKG TCSGCERGFFLEIYDEVEDSSYD NHLKDDDPKREGPGAEQALST PPCCPLEKRPINDQTLIISWSGST NVIEEAGRHSVVQEGWGALGV LRTTLPSLPQITGGAGFVGSHLT DKLMMDGHEVTVVDNFFTGR KRNVEHWIGHENFELINHDVVE PLYIEGRAENQLSHTVPGPVDL SDRIVNGYFLSL

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18736	49104	A	18845	167	1440	RDIWLSASAAAMVPVRKLV/AE GGQKTKQVLRFTLGCTHPIEDG IIDAANFEQFLQERIKVNGKVG NLGGGVVTIEKSKSKITVTSKG\ PFNSM*I*GSASSFVEKKRLLEF *KAENLSSKNWNKTRMPTFTTL TQVAPNPITGYTSKGKKISTLKR YLAFCLRCCHGAREKACGEGG QKTKQVLRFTLGCTHPIEDGIID AANFEQFLQERIKVNGKVGNL GGGVVTIEKSKSKITVTSKGHF QFYVNLRISFLICGKEKAVGILE EIVLNLLIIFSSIDILTVKGTCSSC ERGFFLEICDEVEDSSYDNHLK DEDPKREECRKRDAYAPLKDQ GNAEKRRHNVRKSWPLLSAKL LKIRTNLTGTEEAELHANHIQQ VPIKCLSYKLTERKNGTQKHLH YALILHVKCDRRETSKFTKFYG THPLTALFVPRAWDGPPSALPE SELAVFLVAYEGNTLLHLFLSG AEQRGNSSLKERAGRARFSHQR KLNEQTIPPDNLTKSSVDLQSSF SAVHPNSQPTVWVDMPAHPLS QYLVPARKTVLPIWYGNSCPD VIFGSLSDSKLSEGKEFALPLKF
18737	49105	C	18846	713	831	
18738	49106	A	18847	2	303	
18739	49107	A	18848	97	233	RTVTCYHRNSRACHPQQITSCP *HRALPCLPLWSPKCPSRWPWF G
18740	49108	A	18849	229	359	MKWVYCSVTGMGKGQHRMP\ SKG*GWVQRYNRDGIPSPRVLE LF

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18741	49109	A	18850	1	1185	MSTIDDPRLQGRRMCLMLRGT PEQKALVIGGEACMWGEYVDN TNLVPRLWLCPPSTQDLANEGI REMTILHRHIPDRGKGVMRSCS FRTPRPFTLACGPEKSLMDPQS QSNSEGASSSLVVKLADTDRER ALRRMQQMAGHLGAFHPAPLP LGACGAYTTAILQHQAALLAA AQGPGLGPVAAVAAQMQHVA AFSLVAAPLLPAAAANSPPGSG PGTLPGLPAPIGVNGFGPLTPQT NGQP\APTRSTITGSPLI/SGWSQ SRPILRIMKYAEQRIPTLNEYCV VCDEQHVFQNGSMLKIQPDTII QVWREDIPVNYMKELELVTKA GFRALLSAPWYLNRISYGPDW KDFYIVEPLSFEGTPEQKALVIG GEACMWGEYVDNTNLVPRLW AHRIQL
18742	49110	A	18851	231	416	
18743	49111	B	18852	184	594	

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18744	49112	A	18853	247	2296	PVYLSIFMSCVGENGGSHIENW HSILRNGLVNASYTKLQDIKGQ FWNDDDSEGDNESEEFLYGVQ GSCAADLYRHPQLDADIEAVK EIYSENSVSIREYGTIDDVDIAL HIN\ISFL\DEEVSTAW\KVLRTE P\IVLRLRFF\LSQYLDGPDPS\IE VFQPSNKEGFGLGLQLKKILGM FTSQQWKHL\SNDFLKTQQEKR HSWFK\ASG\TIKKFRAG\LQHSF SPIPKS\PSFPYS*Q\DSMAGKGK LGV\PELRVGRLMNRSISCTMK NPKVEVFGYPPSPQAGLLCPQH VGLPPPARTSPLVSGHCKNIPTL EYGFLVQIMKYAEQ\RIPTLNEY CVVCDEQHVFQNGSMLKPAVC TRELCVFSFYTLG\VMSGAAEE VATGAEVVDLLVAMCRAALES PRKSIIFEPYPSVVDPTDPKTLAF NP\KKKNYE\RLQKAL\DSVMSI\ REMTQGS\YLEIKKQMDKVWIP L\AHPLLQWIISSN\RSHIVKLPL SRQLKFMHTSHQFLLLSSPPAK EARFRTAKKLYGSTFAFHGSHI E\NW\HSIL/RGNGLVQWHSYTK LQLHGAAYGKGIYLSPISSISFG YSGMGKGQHRMPSKDELVQR YNRMNTIPQTRSIQS\RFLQSRN LNCI\ALC\EVITSKDLQK\HGEH LGCCPVFRPMSCTRFLPL*YED G\QVGDAQHYIPHGPQRVHERE
18745	49113	C	18854	122	486	
18746	49114	A	18855	1	535	KNAAGNFISPT/ERLSPNAWKTI TDIVLNGTAFVTFLSITTIYAET GSGFVVPSASAKAGVEAMSKS LAAEWGKYGMRFNVIQPGPIK TKGAFSRLDPTGTFEKEMIGRIP CGRLGTVEELANLAAFLCSDY ASWINGAVIKFDGGEEVLISGEF NDLRKVTKEQWDTIEELIRKTK
18747	49115	A	18856	3	356	
18748	49116	A	18857	1	1581	

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18749	49117	A	18858	2	1242	RRLGPSPRPIPRRPRQRFQPREL CSFCPAPCGPTACGGFRPEFWRI NMKLPAKVFFTLGSRLPCGLAP RRFFSYGTKILYQNTEALQSKFF SPLQKAMLPPNSFQGKVAFITG GGTGLGK\GMTTLLSSLGAQCV IASRK\MDVLKATAEQISFSNW EIKVHAIQCDVRDPDMVQNTV SELIKVAGHPNIVINNAAGNFIS PTERLSP*CWKNQ/ITNIV*NGT AFVTLEMGKHLIKAQKGAAFL\ SITT\IYA\ETGSGFCRYPSASAQ SRVWEAHGASLLQLEWG*NM GLRIPIVDSNQGPIKTK\GALYPS GPPTGTFGEKKMIGQKFPCGSP WGLVEELRKSLPAF\LCSDYA\S W\INGAVIKFD\GGEEVLI\SGDF\ NDLRKVT\KEQWDTIEELIRKT KRFLRPLWPSSWLQKRE
18750	49118	A	18859	8	432	NSKLPPVVTSQQMRFMY/DPQT DQHMKI\FPEQLPLDEFLQKTDP KDPANYILHAVLVHSGDNHGG HYVVYLNPKGDGKWCKFDDD VVSRCTKEEAIEHNYGGHDDD LSVRHCTNAYMLVYIRESKLSE VLQAVTDHDIPQQL
18751	49119	A	18860	1	211	
18752	49120	A	18861	1	242	
18753	49121	A	18862	3	733	LVHSRDNHGRHYVVYLNPKGD GKWCKFDDDVVS/QLVERL*EE KRINAQKVDR\RQEVHLYMQA QVASEDQFCGHQGNDMYDEE KVKYTVFKVLKNSSLAEFVQN LSQIMEFPQDQIQLWPMQARSN GTKRPAMLDNEADGNKAMIEV SDNENSWTIFLETVDLELAASG VTLPKFDKAHDVMFFLKMYDP KMRSLNYCGHIYTPISCEIRDLL PVMCNRAGFIQDTSLILYEEVK LNLTERIQD
18754	49122	A	18863	261	659	KHLFYLFIT*EITLYPDKHGCVR DLLEECKKAVELGEKASGKLR LLEIVSYKIIGVHQEDELLECLS PATSRTFRIEEIPLDLLEECKKA VELGEKASGKLRLLEIVSYKIIG VHQEDELLECLSPATSRTFR
18755	49123	A	18864	107	407	CVFFADTSWRSEATFQFTVERF SRLSESVLSPPCFVRNLPWKIM VMPRFYPDRPHQK\SVGFFLQR NAESDSTEDSLNDATTNPHIVA FHYWKPNLNSLV

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18756	49124	A	18865	2	3698	YVRVSLPPPPPAAGRPGAAVAD DAREEEEEAAPPPPPPPPPRLAA ARPPGSQPRPPAAGEAQAAAD MNHQQQQQQQKAGEQQLSEPE DMEMEAGDTDDPPRITQNPVIN GNVALSDGHNTAEEDMEDDTS WRSEATFQFTVERFSRLSESVLS PPCFVRNLPWKIMVMPRFYPDR PHQK\SVGFFLQ\CNAESDSTSW SCHAQAVLKIINYRDDEKSFSR RISHLFFHKENDWGFSNFMAW SEVTDPEKGFIDDD
18757	49125	A	18866	16	450	
18758	49126	A	18867	3	26	QSGHSMDMRVPAQLLGLLLLR LRGARCDIQMTQSPSSLSASVG DRVTITCRASLDISRWLAWFQL KPG\EVPKLLIYAASTLQSGVPS RFSGSGSGTDFTLTISSLQSEDIA MYYCQQYNNW/SSAPYTFGP\G TKVEIKTKLWAA\PSVLHLPGPS DEAVENLGTAFCLCALLEKTSN PQSRPKSTSGRVD\NALPNGGK LPQGECSQKQD*TAWT
18759	49127	A	18868	3	694	
18760	49128	A	18869	47	1712	FPTKMAAVGRVGSFGSSPPGLS STYTGGPLGNEIASGNGGAAAG DDEDGQNLWSCILSEVSTRSR\S KLPAG*NVLLLGEDGAGKTSLI RKIQGIEEYKKGRGLEYLYL\N VHE*MTGNDQTRCN\VWILDG DLYHKGLLKFSLDAVSLKDTL VMLVVDMSKPWTALDSLQKW ASVVREHVDKLKIPPEEMKQM EQKLIREF\QEYVERGEDFPASP QRRNTASQEDKDDSVVLPLGA DTLTHNLGIPVLVVCTKCDAIS VLEKEHDYRDEHFDFFQSHIRK FCLRYGAALIYTSVKENKNIDL VYKYIVQKLYGFPYKIPAVVVE KDAVFIPAGW\DNDKKIG\ILH\E NFQTFKRQEDNFWKDIITKPPV RKFVHEKEIMAEDD\QVFLMKV \QSLLSKSKPP/TTEAGRPVDA\S PKESQGGSPPNTKIESVSS*CCQ ACHPIPCWGQKKIDPNMESWE LTSGRAFLGKFSFNSFV*VKRL GSPRRPLVVSGG*PCRVGLGGG \SSG\LPP\STKKVQAYKPV\LDV\ HAELDRI\TR*PV\TVS\PTTPTS\P

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18761	49129	A	18870	3	885	LVCLVRELLGPRRFFLKVFFLPT FPG\VPAPVLTATLPFFHPEGRL YQVE\YAFKA\I*PGGPLPSLAV RGK\DWAVIV\TQKKST*PNYL DSS\TVTSLFPR*LKNIW\CVMT GMTS*PADSQV\QRAR\YEA\AN WKIQSMGYEIPVD\MLCKKNCP IFLQVYHTEMLKMKASLRC\CM IFNWVIDEEQGPSRYIRC\DPA\G YYCGV*KPTASGS*TKLRSTGF LEKKKCKKKFD\WTF*TRQWET AI\TLPCLTVPIQLDFKTFQEIEV GVVTVENPKF\RILT\EAEIDAQL VAPSKRRD
18762	49130	A	18871	1	471	
18763	49131	A	18872	1	1524	
18764	49132	A	18873	2	719	RPQRAGPVRRAGVMALLDLAL EGMAVFGFVLFLVLWLMHFM AIIYTRLHLNKKATDKQPYSKL PGVSLLKPLKGVDPNLINNLET FFELDYPKPLFFSVAPMKRIEKT QM**P*CSTY*YEVLLCVQDHD DPAIDVCKKLLGKYPNVDARLF IGGKKVGINPKINNLMPGYEVA KYDLIWICDSGIRGTMEMPMSL EQSYDPNVRDPIYRNNGDADG QHLVLHDFYQQGSGPKCSLINA
18765	49133	A	18874	200	370	
18766	49134	B	18875	323	448	
18767	49135	A	18876	2	421	FVGPGPGDPPPSETHKLVVVGG GGVGKSALTIQFIQ/ILDTAGQE EFGAMREQYMRAGHGFLLVFA INDRQSFNEVGKLFTQILRVKD RDDFPVVLVGNKADLESQRQV PRSEASAFGASHHVAYFEASAK LRLNVDEAFE
18768	49136	A	18877	2	236	
18769	49137	A	18878	1	763	MTPHSALRARGKGGGTGGGSE GSSSGGDMSSGAASGTGRGRPR GGGPGPGDPPPSETHKLVVVGG GGVGKSALTIQFIQSYFVSDYD PTIEDSYTKICSVDGIPARLDILD PAG\QEEFGAMREQYMRAG/HT GFLLVFAINDRQEFSTRWGKLF HADFCGFKDRD\DFP\VVLVGN KAD\LESQRQVPRSEASAFGAS\ HHVAYF\EPSAKMRF\NVDEGF* RSWCGVVREIPRNKELPPSPPK CPPGRMGGGCPCVLL

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18770	49138	A	18879	2	403	RFLARRTNSTFNQVVLKRLFMS RTNRPPLSLSRMIRKMKLPGRE NKTAVVVGTITDDVRVQEVPK LKVCALRVTSRARSRILRAGGK ILTF/DEVYRHFGKAPGTPHSHT KPYVRSKGRKFERARGRRASR GYKN
18771	49139	A	18880	1	1006	PKLR*PEPSRNQVLLTRFQIAVH F/LLSRLLQFFPRPARSRAFLSRK PKPGPGKKPMALIVEFIGELPTG VHARPPSHVETLCNTFSSQIEW HNLRTDRKGNAKSALALIGTDT LAGDNCQLLISGADEQEAHQRL SQWLRDEFPHCDAPLAEVKSD ELEPLPVSLTNLNPQIIRARTVY SGRAGGIQTPISSLDLNALGNLP AAKGVDAEQSALENGLTLVLK NIEFRLLDSDGATSAILEAHRSL AGDTSLREHLLPVGQCANAASS TNHPFVTKKRQQCFVFRQRLA NGRNDSGWQITHAFWFRFHQH SRIMKYLYGFTARLKEHQPKLR
18772	49140	A	18881	1	716	VCCEFCRAERRHHGEWTIRHN K\DRKGSGARDPKEPGFLL*RC CVKLYRFSGPEEPNSNIQPRLW LKRLFMS\RT\NRPPSVPFSRDES GKMKASLARGKQDRPVVVGG PLT*LMLRVSGRVPKTERYVAL RRGPSPGPQAAFLQGQGGKIPS LFDQAWPLGLPLKGLLALVPGS SGSLGKGAREGGTRQFSAKAP KETPQKPHQNPYVR\SKGRKFE RARGPTGPARGYKKLTLGSYSL
18773	49141	A	18882	3	168	
18774	49142	A	18883	23	2669	
18775	49143	A	18884	279	396	
18776	49144	C	18885	960	1250	
18777	49145	A	18886	52	925	EVLEPRLGVFSNGCFQGLSSVM ALGLKCFRMVHPTFRNYLAASI RPVSEVTLKTVHERQHGHRQY MAYSAVPVRHFATKKAKAKG KGQSQTRVNINAALVEDIINLEE VNEEMKSVIEALQG*FQ*GLSI* GPHQDPIDKIAVVTA*REALL*T RFSQISMKSPQLNFG*IWASFPE CTAAAIKAIRESGMNLNPEV\EG TLIRVPHSPK*PESTEKCWVKL GQTEHQQGPKTLLREGFRTQLN EQAGRNPKD/NSLQEDTIRLTEK QISQMADDTVAELYRHLAVKT KELLG

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18778	49146	A	18887	2	389	DSGSHCHAPPTTARRAFPIPFGS KSNMATLKDQLIYNLLKEEHTP QNKITAVRVGADGMACAITIL M/KDYNVTANSKLVIITGGARQ QQGESRLNLVQRNVNIFKFIIPN VAKYSPNCKLLIRSNPVDI
18779	49147	B	18888	217	423	
18780	49148	A	18889	27	1217	ARRPTRPPDLIATRPRRPARRCI SRFPFGSKSNYWQPLKDQLIYN LLKEEQTP\QNKITVVGVGAVG MACAISILMKDLADE\LALVDVI EDKLKG\EMMDLQHGKPFSFR NTKVLSSGKRL*M*LANSKAGS FITGWGHRQQEGKKAVLILVQ AVNVNIFKFIIP\NVVKYSP\NCK LLIVSNPVDILTYVAWK\ISGFP KNRVIG\SGCNL\DSA\RFR\YLM G\ERLGSSPH*ACHGWGPWGEH GRFPVLPVMGVGLNVAGVSLE DFWHPDFRTDKD*E\QWKE\VH K\QVVE\SAYEVIKLK\GYTSLG LIGLSCKPD\LAE\SIMEESFRRV HPS/SSHHGLKGLYGNKRMNVS LSVPCILGQNGIS\DLVKG\TLTS EGRGPVGSKSADNNSWGSTKK
18781	49149	A	18890	1	264	
18782	49150	A	18891	3	736	
18783	49151	A	18892	81	1065	GKGPVAAFIDQSNIFLTDPKIFL GQWREEPKMPLLLLGETEPLKL ERDCRSPVDPWAAASPDLALA CLCHCQDLSSGAFPNRGVLGG VLFPTVEMVIKVFVATSSGSIAI RKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMRENVS*REKP Q\NGIPLPSQI\FNEE\QYCG\DFD SFFSAKKENIIYSF\LGWAPLPDS KGSEKAEEG\GETEAQKEGSED VGNLPEAQEKNEEEGETATEET \EEIAMEGAEGEAEEEEETAEGE EEPGEDEDFLGLFMLHFFHFSQ KMEAMKQHSNVLSTNQTETEY FGLKPAHPRVTEDIMLPDLIR
18784	49152	A	18893	19	445	

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18785	49153	A	18894	1	622	QAAWILKARALTEMVYIDEIDV DQEGIAEMMLDENAIAQVPRP GTSLKLPGTNQTGGPSQAVRP\ TSHSEKPITGFLRPSTQSGRPGT MEQAIRTPRTAYTARPITSSSGR FVRLGTASMLTSPDGPFIN*SRL NLTKYSQKPKMAKALPEYIFHH ENDVKTALELAALSTEHSQYK DWWWKVQIEKRYYRLGMYRE AEKQLISAMKQ
18786	49154	A	18895	1	1651	MKAEICKSRTVKDWHNHQKLG EGNKTDSPPQPSEGTNTANTLIL DFWPLEMIACCWETFPQRLTAE LFMNPTHRWHGYKNQSVGAL RAPLGQGPSRRGLPGRVGRRQL FTPRPPLSWSAGPSLAAPAAMS SEMEPLLLAWSYFRRRKFQLCA DLCTQMLEKSPYDQEPDPELPV HQAAWILKARALTEMVYIDEID VDQEGIAEMMLDENAIA/PSSTP ITQAGRPITGFLRPSTQSGRPGT MEQAIRTPRTAYTARPITSSSGR FVRLG\RLGMYREAEKQFKSAL KQQEMVDTFLYLAKVYVSLDQ PVTALNLFKQGLDKFPGEVTLL CGIARIYEEMNNMSSAAEYYKE VLKQDNTHVEAIACIGSNHFYS DQPEIALRFYRRLLQMGIYNGQ LFNNLGLCCFYAQQYDMTLTS FERALSLAENEEEAADVWYNL GHVAVGIGDTNLAHQCLRLAV VNSNNHAEAYNNLAVLGDAEG /RHVEQARALLQTASSISTPYV* TAFLILQQSLIRFGDLQRSYVAA QKSEAAFPDHVDTQHLIKQLRQ HFAML
18787	49155	A	18896	2	295	
18788	49156	A	18897	1	4470	MLGLGLLRLRQGSHAVTRCRP LPVRREGRRDGSPWRSVVCRY CRCSRQTGASVTTVSLPSSSSSP GLDPRGPRQASVKKPAEANPV LRPLVRHGTPYRDSEEGKREGL SRLRAVCRRAGPRGRGSFSPRD ARASPRLHFLVAAVTTGAASRR QRGARVRQPSPSSSRRAKRLRE CERRSLHAPPAMDASYDGTEV TVVMEEIEEAYCYTSPGPPKKK KKYKIHGEKTKKPRSAYLLYY YDIYLKVQQELPHLPQS

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18789	49157	A	18898	89	810	QRRSGCVLRMTEWETAA\PAG GQRTPDIKALWGSGAPDDVAR SMNISLQ\DYIAS*RRKLCPSYLP \HSCQGGYAAKNLSRKAQ\CPI\ VER\LTNSPMMMHRPQQPARK LMTVRIVQA/HAFEIITPCSQAE NPL\QVLGEPPSINSG\PREDSHT HLGAAGTVRRQAVDV\SPLRRV EPGPFWVACCTRRLVKGLAFPG TFKTIG*VAWAD\ELI\NACQGA PSNSYCL*EEGRVAFLEHVAKS NR
18790	49158	A	18899	1	365	DTHFK/DSHHRTSTAHLL\SLSQ GPSPPNLPLGVPIS\GMGLGPRG EGRANPIPTVLKRDQEGLGYRS APQPRVTHFPAWDTRAVAGRE RPPRVATLSWREERRREEKDRA WERDLRTYMNLEF
18791	49159	A	18900	203	427	
18792	49160	A	18901	95	482	ALQSPKLWGYFSGRKVFLNYFF SSQQVSEAVVATGSPRAWLTC LILPLPGIIFSVLPKAMSRPLLITF TPATDPSDLWKDGQQQPQPEK PESTL\DGLAAKLFYEALIGDES SAPDSQRSQTEPARERKR
18793	49161	A	18902	348	1660	GVTHLFLFGKRKLRNGIAGRIK GPGWIFFSYCRSLRLWLLTGSP LSLALPCLILPLPGIIFLKFSQKAI VPGPLLITFTPATDPSDLWK\DG QQQPQ\PEKPESTL\DGAAARAF YE\ALI\GDESSAPDSQRSQT*T WPEERKRKKRGLLKAPAAEAL AEG\ASGRPVQGRSLEADDPMT YRILTSAQEGD\LP*LM\RLLEPH EAGGAGGNINARDAFWWTPL MCAARAGQGAAVSYLLGPG\A AWVGVCELSGRDAAQ\LAEEA GFPEVARMVRESHGETRSPENR SPTPSLQYCENCDTHFQD\SNHR \TSTVHLLSLSQGPQPPQLPLGV PISTPRF*ILLLGGVGSPGMGLG PRGEGRANPHPQLILK*GPRKG LG\YKISTPSPEVTHFPSFGIPRA VAGRERPP\RVA\TLNWKE/ERR RREEKDRAWERDLRTYMNLEF
18794	49162	C	18903	135	299	

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18795	49163	A	18904	3	2074	ERSRPVALRAAVPRMNPSTPSY PTASLYVGDLHPDVTEAMLYE KFSPAGPILSIRICRDLITSGSSN YAYVNFQHTKDAEHALDTMNF DVIKGKPVRIMWSQRDPSLRKS GVGNIFVKNLDKSINNKALYDT VSAFGNTLSCKVVCDENGSKG YGFVHFETH\EA\AERAIEKMNG ML\LNDRKVFVGRFKSRKEREA ELGARAKEFT\NVYIKNFGEDM D\DGRLK\DLFGKF\GPALKCEK LMTDESGKSKGFGFVS\FERHE DAQKAVDEMNGKELNGKQIY VGRAQKKV\ERQTELKRKFEQ MKQDRITRYQGVNL\YVKNLD DG\IDDE\RLRKEFSPFGTIQLVP KVMDGGLVAAKGLGFVCFSSP E\EATKAVTEMNF\RIVATEPL\Y VALA\QRKEERQAHLTNQYYG RGM\ASVTEAVPNPV\IQPLPGQ APPFRFTFMGRFSHRFRNRA\AY YP\PSQIAQTKTKFLRWTGQGA RT\HPF\QNMPGCYPAQLAPRPP I*GTM\RPASSQ\VPR\VMPTQR\ VANTSNTDKWVPRSCSLQAAA AYVL\RPAPFPQYKYAAGVRNS \QQHL\NAQPQVTMQQPCCSMV PRVQGTLWTCLPMVGHLPPPSR SKSQMLGWNGLFPSYSKPMHP YSLLVKSLG\MLLEIDNSEL\LH ML\ESP\ESLPF*RVDEAVAGTTS PPQAKRGLAQKAG*QVPTGVP
18796	49164	A	18905	1	988	MAEDGEEAEFHFAALYISGQW PRLRADTDLQRLGSSAMAPSRK FFVGGN\WKMNGR\KRRLGELI GTLNAAKVPADTEVVCAPPTA YIDF\ARQK\LDPKIAVAAQNCY KI\TN\GAFTGEISPG\MIKDCGQ PWVVLGHSERRHVF\GESDELI\ GQKVA\HALAEGL\GVIRLHLG RS*DERGSLGIT\EKVVFE\QTKV IRR*T*KDWKQ/VVVLGLMSPV WGLWLLARLATPQQA\QEVHR RSSRGWL\KSNVS\DAVASEPPV TIYG\GSV\TGATLQRSLAKPSP DVDGLPLWGGASLQARNSWDI IQCHNNEPPSHLSLPLRCQAQG LKQTQKPK

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18797	49165	A	18906	46	468	TGPTHASAAILVPRSLHKMPGE ATETVPATEQELPQPQAETGSG TESDS/GKSPASDTYIVFGEAKIE DLSQQAQLAAAEKFKVQGEAV SNIQENTQTPTVQEESEEEEVDE TGVEVKDIELVMSQANVSRAK AVRALKNNS
18798	49166	A	18907	1	360	
18799	49167	A	18908	52	513	QLGPHGHRQGPGGPAVPHPRG LVPLPPALLPSGPRRGRTQAPR HSGPAL*GHPASDTYIVFGEAKI EDLSQQAQLAAAEKFKVQGEA VSNIQD\NTQTPTVQEESEEEEV DETGVEVKDIELVMSQANVSR AKAVRALKNNSNDIVNAIMEL
18800	49168	A	18909	1	422	RSLCQTGLRQ/VTG/VTKVTIGN LENLFVI/TKPDVYKSPASDTYI VFGEAKIEDLSQQAQLAAAEKF KVQGEAVSNIQENTQTPTVQEE SEEEEVDETGVEVKDIELVMSQ ANVSRAKAVRALKNNSNDIVN AIMVSVQAFVP
18801	49169	B	18910	427	529	
18802	49170	A	18911	122	252	
18803	49171	A	18912	44	189	SKLDYKSSKRHRKPVSFNFITSF QIWD*FLFFF*LKCQLQPRVFSQ PN
18804	49172	A	18913	2	609	PFLPEAHLGNQKCQNCNSTSGI CRVSVKVCPGPWVHAKLCAPT LMSRDVTLPDAPVKKPCGEGG AKKKKQVLKFTL\DCTHP\VED G\IMDAAQF*ASFCKERIKV\NG KAGNL\GGGVVDPSKGARGKIT VT\SEVPFSKRVF*KYL/TPKKY LKKNNLR*PGLPRSLPNQPKEK LPNFRYFQINQGRRKEGGRRGF KFPLSGKILL
18805	49173	A	18914	107	524	AGTHLPPFLPVAVRQPMALR\Y P\IAVGLKQGPTKVTQEP*ASPR HHVRRGRL\TKHTKFVRDMIRE VCGFSP\YE\RRAMELLKVSKD K\RALKFIKK\RVGTHIRAKRKR EELEQQYWPAIEEKLACQERLE PLPLPSPLK
18806	49174	A	18915	39	465	

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18807	49175	A	18916	439	1586	TWGPPARRLPSGSHVPSA/ASSR LPSHPREEPQLPQPAPVTITATM SSEAETQQPPAAPP\GAPALSAA DTKPGTTGSGAGSGGPGGLTSA APAGG\DKKVIATKVLGT\VKW FNVRNGYGFINRNDT\KEDVFV HQTAIKKNNPQKYLRSVGDGE TVEF\DVVEGEKGAE\AANVTG\ PGGVPVQG\SKYAADRNHYRR YPRRRGPPRHYPQ\NYQNS\ESG EKNRGIGRVLPEGQAQQRRPY\ RRRRFPPYYMRRPYG\RRPQY\S NPPVQGEVMEGADNQGA\GEQ GRPVRQNMYRGYRPRF\RRGP\ PRQKTA*ERAAMEEDK\ENQGV WDPRFGSPPQ\RRYRRNF\NYR\ RRRPQKTPKP\QDGQKRPKAAG SHPA*EFVPLPEAE\QGGAE
18808	49176	A	18917	1	651	MTAFNSGKVDIVAINDPFIDLN YMVYMFLYDSTHGKFHGTVK AENGTLVINGNPIT\IFQDQDPS KIKWAP/LAKVIHDNFGIIEGFM TTVHTITATQTINGPSG\NCHVM AAGLSRTSSLSLLA/LAKPVGK VIPELNGKLTGMAFHVPTANVS VADLTCRLEKPA/KYDDIKK\NT HSSTFDAGAAIVLKDHSVKLIS WYDNEFGYSNRVVHLMAHNA
18809	49177	A	18918	2	5264	

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18810	49178	A	18919	3	1466	PRSAPRAASWLEDPREVRSVCL SAPPVRQSAAIFFCVASRATSLR TPMGKVKVGVNGFGRIGHLVT RAAFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFHGT\VK AENGKLVINGNPITIFQE\RDPSK IKWG\DAGAEY\VVE\STGVFNQ PWRKAGAHLQGG\AKRVI\ISAP SG*MPPMFVMG\VNHEEV*QTA FKIISN\ASCTNQLA*QPLAKG*F HDNFG*SWEGLMTTVPWPSLG NPRKTVD\GPSRG\NCGPWMGR GGFSRNIFLCLYWALPRAVGKG HP*A*TGKLTG\MAFPVSPTAN VVSGWTLTCRFRKNLPKY\DDI KEGW*KQAFGGAPSKGIPGLQL SHQVV\SSDFNSDT\HSFHPFDA GA\GIA\LNDHFVKL\ISWYDNE FGYSNRVVDLIGPHGLQGSKTP WTTEPQARSKKGKERPSLLGSP CHTQTPTTLNLPSSQLPCRPLEE GRGLWEPHLVMYPSNKVSLCS TKKKKKKKKP
18811	49179	A	18920	3	364	STVINIHSETSVPDHV/VLVPVQ HPLLE\RCCLGFIAFAYSVKSRD RKMVGDVTGAQ/ALCLHRQVP EHLGPDSGHPHDHWIHPVTGIR LCDSLPYYVTDNTGKTGLLVA AHSLQPLHSTVQCW
18812	49180	A	18921	41	696	PDRRWSSLGHHESHCPNHSSLL STVASPPNYEDAQGR*SR/EVA VLGAPHNP\APPTSTV\IHIRQSR PPWPDHVVWSRVQHPLQ*TPA C\LGFIAFAYSVKSRGQGRWLG DV\TGAQGLMPPPAKVPETIWG PDFWGILNDHF\VHRHPQWLIFP G\HGIDQGRHHWRPGALPI/VTC IPRLLPT\SIPRPAPRSPKSCISPYI LTRFSTMAFNKSARVSGKKKK

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18813	49181	A	18922	127	1016	SNLILRNLFCPHLALASSAFDKC QEEETVEKTELLAERRGLTENH PGNPITAGHHEPHCANLLSCQQ RPRLPNYEMLKEEQEVAMLGA PQKPCLPECPPVIHYPQARPPWP DHVRLGPCFNNPLQ*TTCCPGL SLGISAYFRGSFRGTGKMV\GD VEPGPQGLMPPTAQVAP*TSGA PDFLGSLHEPILAHQSSPPKCW VVPGPAIDQE\ASLRP\GA\LPVT C\IPRTL\SSIPSPLPPEARELLPFD LYSTYSTFHSSPCPHSRVLHQPF ILTRFSTMAFNKVYMFLVKKK KKKKKKV
18814	49182	A	18923	115	652	VSESTDLVSIGRLVTRA\AFNSG KVDIVAINDPFIDLNYMVYMF\ QYDSTHGKFHGTVKAENGKLV INGNPITIFQE\RDPSKIKWGDA G\AE\YVVES/TLGVFTTMEK\A GGSFCRGGAKRVIHLLPPLA*C PPCFVMGVN\HEKDDN\TLKIIS N\ASCTTN\CLAPLASTGAAKGC GQGHPEA
18815	49183	A	18924	91	399	
18816	49184	A	18925	26	304	
18817	49185	A	18926	18	203	
18818	49186	A	18927	23	355	
18819	49187	A	18928	1	211	RLLRVRGPPSPRPPGTPAGRQA RHTAPVPARASPSTPPRKLKER APALASPERGSHSAAEG*RAPQ VPPK
18820	49188	A	18929	2	800	
18821	49189	A	18930	1098	1560	VSCPFTVIIFCYNFCRGGFSTTA VMARAKSMFLMLKGKAGPDF GIRFTASSGWFT*FEDRYALHN VNMNAESVGADVKAAE\DFGS LIMEEIYLPTQFFNMEEPSLFWK QMPERTFVICPKGFFPDHCNKE RPWHFCKRKSLTDTRVATPCG
18822	49190	A	18931	33	211	
18823	49191	A	18932	110	624	CILSKMLRSPQELARLPGGQRQ LTRW*QRWPLWTIALVLVLWR VKSGP*S*RVPSPSP/PVEPWVT LNMAGAPHGNPAFPPGGPPHP VPQPGYPGCQPLGPYPPPYPPPA PGIPPVNPLAPGMVGPAVIVDK KMQKKMKKAHKKMHKHQKH HKYHKHDKHSSSSSSSSSSDSD

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18824	49192	A	18933	2	664	CEPLRISGRPTRPGERSKPRRRL ER*WGWRTHLNMWNPNAGQP GPNPYPPNIGCPGGSNPAHPPPI NPPFPPGPCPPPPGA\PHGNPAFP T\GGPPHPVPQP\GYPG\CQPLGP YPPPYPPPAPG\IPPVNPLAPG\M VGTKQLISRQEDCRRKLKKAS* KRCHKA/HQKHHK\YHKHGKH FLLFPPPSFQAVISGLEYRALDP SLKSHQFCSPIKLQMPCCTGGM
18825	49193	A	18934	3	409	QTQVVIDAG/ALAVFPSLLTNPK TNIQKEATWTMSNITASR/QDQI QQVVNHGLVPFLVSDLS/KDFE TQKEAVWA/GGTVEQIVYLVH CGIIEPLMNLLPAKDTKIILVILD AISNIFQAAEKLGETEKLSIMIEE CGGV
18826	49194	A	18935	133	400	VLGPHGLGDHLGQFHSCQSRA EPPIAGEDIHAGLDEPDCLTKDF LRI*LQLSTQLHAGQEEEDQNV VPETTSEGYTFQVQDGAPGTFN
18827	49195	A	18936	218	863	
18828	49196	A	18937	106	1879	TQSALQPLIPPASPSPWKAQARF GAFSLCLITMSTNENANTPACP VVHRFKNKGKDSTEMR\RRRIE VNVEL\RKAKKDDQMLKRERL *AHFLDDATSPLQEN\RNNQG/T LLNWSVDDIVK\GINSS\NVENQ LQATQAAR\KLLSREKQPPIDNII RAGLIPKFVSFLGRT\DCSP\IQF ESAWALTNIASG\TSGQTKAVV DGGAIPAFIFSGWASSHAHISEQ AVWALGNIAGDGSVFRDLVIK YGAVDP\LLALLASS**CQSLAC GYLR\NLT\WTLSNLC\RNKNPA PP\IDAVEQILPT\LVRLLHHDDP GSVRQDT\CWGYFPTLLDGSK WNGIGHGWV/VKQGVVPQLVK LLGASE\LPIVTPA\LKSP*GNNW HLGTDEQTQVVD/IDAGALAV\ FPSLLTNPKTNIQK\EATWTMSN ITAGRQ\DQIQQV/V*NHGLVPF PLSVFLSKADFKTQKEA\VWAV TNYTSGGTS*TELVYLV\HCG\II EPLMNLFYCKRLPRIILLILDAN FKISFQPAENLV\DLEKPSINLE\ ECGGLRPKLKALPKPMKMESV YKASVKA*FEKYFPCRGKEGRI KTVVP\ETT\SEGYTFPSSRMGPP

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18829	49197	A	18938	2	251	KVTNVKDGTTH\QTSLELFMYL NEVAGKHGVGRIDIVENRFIGM KSR/GMNVQGDYEPTDATGFIN INSLRLKEYHRFQSKVTVK
18830	49198	A	18939	1	888	
18831	49199	A	18940	1	1155	MSSKGSMVLAYSGGLNTSCILV WLKEQGYDVTAYLANTGQKE DFEEARKKALKLGAKKVFIEDV SREFVEEFIWAAIQSSALYEDH YLLGTSLTRPCIAHKKVETVQR VGAKYEGPWRAPWRMPEFYN WFKGRSDLMEYAKQHGIPILVT PKNLWSIDKNLMHISYKAGILE NPKNQVPPGLYTKIQDPAKAPN TPDILKIQFKKGVPVRVTSVKD GTTHQTSLELFMYLNEVAGKH GVG/YIAIVENIFTRQRP\SPECEF VRPCIAKSQEPAEGKVQVPVLK GQVYILGWESPLSLYNEELMSV NVQGDYEPIDDTGFININSLRLK EYHCLQSLLEFAGCRLQTLFAW VSPAGAAEQQRLLPVPSSGNFIP EGHLPDASWSSPV
18832	49200	A	18941	1	993	MSSKGSVVLAYSGGLDTSCILV WLKEQGYDVIAYLGQAVKGN QLLPVSLVKRKTTPGAQYANR LSPRVGRFINAAGTTGFPTGKR AGNDQVRFELSCYSLAPQIKEM GSLKVRNE/LQEVSTVPMPAST QLPADTQCKLAE/LSAPVKK*T LGLSKT*QTQVMSSQSADSMPR AWYRN*LFTNPTVRRLGNSPVT GSSLPRLPG/RGIYETPAGTILYH AHLDIEAFTMDREVRKIKQGLG LKFAELVYTGAECKLLVASVPE PWRGRGGVEEGGRDIKEVQEH GSDSAESSTHPPASRPGEGCLA CIFCGKWRHLNTPLSCERYPRH SRDHRPH
18833	49201	B	18942	324	1035	

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18834	49202	A	18943	29	1516	KQIPDAGNSRLQSQTLLSSKGS VVLAY\SGGLDTSCILVWLKEQ GYDVIAYLANIGQKEDFEEARK KALKLGAKKVFIEDVSREFVE\E FIW\PAIQVQAHLY\EDRYLPGH LSLPGPCI\ARKQVGNSPSGRGA KYVVPTGATGKG\NEQV\RFEL S\CYSL\APQIKVIAP\WR\MPEFY NR\FKGRNDL\MEYGKATLGFPI PVTPKNP\WSMDENLMHI\SYE AGILENPKNQAPPGLYTK\TQGP SQKPPTPLDILGDSSFKKGVPVE GGPTFKDG\TTHQTFL\ELF\MY LNEVAG\KHGRRAVFDIV\ENRF \IGN*SPRGILRRTP\AGHHSFYH AHLDIRGLSPWDRGSCGKIKQG PGAWKFAEL\VYTGFPAQAPE\ CEFCPPTGIAKVPRKPSGKGKV QVVRSFKGPQVYI/LSGREIPHC LLLTMRELVKHGTCKGDYWRP IDGHRGSSKHQIPFKAEGNYHR LPRAKVTCQIDPVYNEELGPPQ FSGSPQVTGANCCDNL
18835	49203	A	18944	1	560	GRARTPANMALRVVRSVRALL CSLRALWAPAVPCLPRPWQLG AGAIWTLLTGPVLLWVCKFTE KHEWITTENGIGTVGINNFANE ALGDVVYCSLSEVGTKI*TKPS WSLVLLE\SVKAASEL\FSPLSG EVPDFNEALAE\NPG\LVTKSRY EDG\WLIKM\TLSNPFRT*MHL MSEEAYEKYIK\SIEE
18836	49204	A	18945	3	108	
18837	49205	A	18946	1	845	MAIPGIPYERRLLIMADPRDKA LQDYRKKLLEHKEIDGRLKELR EQLKELTKQYEKSENDLKALQS VGQIVGEVLKQLTEEKFIVKAT NG\PRYVVGCRRQVIELPLTNPE LFQRVGIIPPKGCLLYGPPGTGK TLLARAVASQLDCNFLKVVSSS IVDKYIGESARLIREMFNYARD HQPCIIFMDEIDAIDIDLPNEQA RLDILKIHAGPITKHGEIDYEAI VKLSDGFNGADLRNVCTEAGM FAIRADHDFVVQEDFMKAVRK VADSKKLESKLDYKPV

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18838	49206	A	18947	3	1181	LLIMADPRDKALQDYRKKLLE HKEIDGRIKELREQLKELTKQY EKSENDLKALQSV\GQI\VGEVL KQLT\EEKFIVKATNGPRYVVG C\RRQL*QKVSLKPG\TRVAL\D MTTLTI\MEDILPR\EVDPLVYN MS\HEDPG\DVSYSEIGGLS\EQI RGI*GEVIGLPLYKPQSYFQRVG IIPPK\GCLLYG\PPGTGKNT/LLA RAVASQLDCNFLKVVSSSIVDK YIGESARLIREMFNYARDHQPCI IFM\DEIDAIGG\RRFSEGTSADR EIQRTLMELLNQMDGFDTLHR VKMIMATNRPDTLGP\ALLRPG RLDRKIHIDLPNEQARLDIL\KIH AGPITK\HGEIDFESNC*SFRMG FNGADL\RNVCT*SQACSPIRAD P*FC*YREDF\MKA\VRKVA
18839	49207	A	18948	1	220	VNMRDRFGQIMIENLRRRQCEL AGVETCKSLES\RIESLEFLDEM */LLEQLM/RHYCLCWATKGGN ELGLKEITY
18840	49208	A	18949	1	645	
18841	49209	A	18950	10	1226	AAPAEPGRALPSSVAFSLWLAP SPAARRPRFHVPGGAQLPGTVH ARWPARQR\ESSI\TSCCSTSSCD ADDEGVRGTCEDASLCKRFAV SIG\YW\HDPYIQDL\VRLSKQR\ KAPEINRGYFARVHGCSVQLIK\ AFLR\KTECHCSNCSNLGGQGM GSPPFW\RLKDEDLSSQVNIFEV DFPMIVT\RKLHSIKWLAFPLSS PILELHSEDTLQMASDCIC\DGH ILDSKRYAVIGADLRDLSELEE KLKKCNMNTQL\PTP*IAECVL VYMTPE\QSANLLKWAA\NSFE RAMFI\YYQQVNMGDLFGQIMI ENLRGRPV/CDLAGVET\CKSLE SQKERLLS\NGWENKHRPVRT* LEFVPPGLPSKLK*SRIESLEI\LD ENWELLEQLIP\HYCL\CWATQR RK*SLGLKEITY
18842	49210	A	18951	3	502	TEANTLN*RGLQNME/ARLAE/ RKFM/NPFNMPNLYQKLESD/P RTRTLLSDPTYRELIEQLRNKPS DLGTKLQDPRIMTTLSVLLGVD LGSMDEEEEIATPPPPLPSSSMS LSPAPSCCLGCSPIVGFFFIWGS GHVMGRGGGSSSLRSQLSHVV YSASPSPIKQASWAWL
18843	49211	B	18952	1	1071	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18844	49212	B	18953	67	1026	
18845	49213	A	18954	2	1910	PVASSMFQKAARAVGNAERTD SIQRCSGPRCAMEQVNELKEKG IKALSVGNIDDALQ\CYSEAI*/R LDPHNHVLYSNR\SAAYAKKG DYQKAYEDGCKTVDLK\P\DW GKGYSRKAAALEFLYRFEEAK RTYEEGLKHEANNP\QLKEGLQ N\MEARLAK\RKFMNPFNMPNL YQKLESDPRTRTLLSDPTYRELI EQLRNKPSDLGTKLQDPRIMTT LSDLLGVDLGSMDEEEEIATPA PPPPAKKETKPEPMEEDLPENK KQALKEKELGNDAYKKKDFDT ALKHYDKAKELDPTNMTYITN QAAV\WFEKGDYNKCRELCEK AIEVGRES\REDYRQIAKAY\ARI GNSYFKEEKYKDS\IHF\YNKSL AEHRTPDVLKKCQQAEKILKEQ ERLAYINPDLALEEKNKGNECF\ QKGDYPQ\AMKHYTEAI\KRNP KDAKL\YSIRAACYTKLLEFQL ALKDWEEWYQLEPTFIKGYTR KA\AALEA\MKDYTKAMDVYQ KALDLDFSCKEAADGYQRCIM AQYNRHDSPEDVKRR\AMADP EVQQFMS\DPA\MRFILKQMQK DP\QALSE/HL*RNPLLPREIQKL MDVGSDCKFGDDLFIPAFLCPS CGKRSWDRGEQAARSGRESST ERKGEQGERRPSSPYIYT
18846	49214	A	18955	2	293	
18847	49215	B	18956	53	182	
18848	49216	A	18957	2	403	
18849	49217	A	18958	3	1646	
18850	49218	A	18959	3	408	
18851	49219	A	18960	1	2458	

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18852	49220	A	18961	88	1511	LWPLGMASNSSSCPTPGGGHL NGYPVPPYAFFFPPMLGGLSPP GALTTLQHQLPVSGYSTPSPATI ETQSSSSEEIVPSPPSPPPLPRIYK PCFVCQDKSSGYHYGVSACEG CKGFFRRSIQKNMVYTCHRDK NCIINKVTRNRCQYCRLQKCFE VGMSKESVRNDRNKKKKEVPK PECSESYTLTPEVGELIEKVRKA HQ\ETFPALCQLGKYTT\NNS\SE QRV\SLDIDLWDKFSELSTKCII KNGEGRQGRLPGFTTLTI\ADQI TLLK\AACL\DILILRICTRYTPE AGTP*PSWDGLTLNR\TQMHNA G\FGPL\TDLVFAF\ANQLLPL\E MDD/ARETGLLSAICLICGDRQ DLEQPDRVDMLQEPLLEALKV YVRKRRPSRPHMFPKMLMKIT DLRSISAKGAERVITLKMEIPGS MPPLIQEMLENSEGLDTLSGQP GGGGRDGGGLAPPPG\SCSPSLS PSSNRSSPATHSP

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18853	49221	A	18962	143	2159	LTHSSTWLGRSCNHDRRQMGS KVMSYVVAGRGTCAQETPIYT TIRYLEDKEQYGGSLGVDSVLA RLFSGASVLFISGPPFSSYLSGVP PGHPMEDSM\DM\DMSPL\RPQ NYLFGCELK\ADKDYHFKVD\N DENE\HQLSLR\TVNLGGLVAK G*VAHLLKAEAIEFTEASPNLK VTTWAT\LKM\SVPAQRVFPLG GLLKITPTRWVLKGLKVWVQG PVHISGTAL**LWEGRCQSPEDE E\EEDVNRVLFMKPKGRGLKH MFGDLVCSWKLAAIETQSSSSE EIVPSPPSPPPLPRIYKPCFVCQD KSSGYHYGVSACEGCKGFFRRS IQKNMVYTCHRDKNCIINKVTR NRCQYCRLQKCFEVGMSKESV RNDRNKKKKEVPKPECSESYTL TPEVGELIEKVRKAHQETFPAL CQLGKYTTNNSSEQRVSLDIDL WDKFSELSTKCIIKTVEFAKQLP GFTTLTIADQITLLKAACLDILIL RICTRYTPEQDTMTFSDGLTLN RTQMHNAGFGPLTDLVFAFAN QLLPLEMDDAETGLLSAICLICG DRQDLEQPDRVDMLQEPLLEA LKVYVRKRRPSRPHMFPKMLM KITDLRSISAKGAERVITLKMEI PGSMPPLIQEMLENSEGLDTLS GQPGGGGRDGGGLAPPPGSCSP SLSPSSNRSSPATHSP
18854	49222	A	18963	748	1075	ILPTSLFFLFCFVFFVCF*DRVLL LSPG\WSAVARSWLYCNLSLRG FKGFSCLSLLSNWDYRCTPLRS ANFVFL/CRDRVSPCWPTSVSNS *PQ\VIHPPWPPKVLGITRV
18855	49223	A	18964	3	674	GRRRLLRDAEGPEETVRLWPA ARAAMDAAEVEFLAEKELVTII PNFSLDKIYLIGGDLGPFNPG\LP VEVPLWL/ARLNLKQRQK\CRL LPPEWMDVEKLEKMRDHE\RK EETF\TPMPKPFTTWELT\KLL\L NHA\SDNIPKGRTEFRDPGSRVF WGHSY*AKFRVFG\DSF\VRQQ EAHAKLD*LGPWMGDQQPAVT FLTQA\LNPHVTNSRTNPPSPLE STSVLRTS

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18856	49224	A	18965	261	876	VAQKIDMPEYQGEPDEISIQKC QEAVRQVQGPVLVEDTCLSFN ALGGLPGPYIKV/WFLEKLKP\E GLHQLLA\GF\EDKSA\YALCTF CTQAPGDPS\QPV\RLVSGGRDL RGRIRWHPEGCQ\DFGWD\PC\F QPDG\YEQTYAEMP*GGRRNA V\SH\RFRAPCWEPAREYFWQV WPSLTSASWKEGPSRPGDLGK GLAPKPSPHRGRAPP
18857	49225	A	18966	2	181	TAEKMAVLAPLIALVYSVPRLS RWLAQPYYLLSALLSAAFLLVR KFPPLCHGLPTQREDGNPCDFD WREVEILMFLSAILMMKNRRSS TK*AHPTRRR
18858	49226	A	18967	5331	5454	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18859	49227	A	18968	5186	5308	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18860	49228	A	18969	4570	4691	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18861	49229	A	18970	5666	5788	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18862	49230	A	18971	5630	5752	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18863	49231	A	18972	224	456	
18864	49232	A	18973	5543	5665	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18865	49233	A	18974	4602	4725	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18866	49234	A	18975	3	313	
18867	49235	A	18976	5480	5602	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18868	49236	A	18977	269	394	
18869	49237	A	18978	5322	5445	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18870	49238	A	18979	164	434	
18871	49239	A	18980	5364	5487	ETEA*RINDLL*LLEFFCNI*QN* P*IRPTVIRSSLKYNT
18872	49240	B	18981	18	1904	
18873	49241	A	18982	1296	1973	RILPGGQQNSSWNFSEDTVISIL NTINEVIAENLEAAKKLRETQGI EKLVLINKSGNRSEKEVRAAAL VLQTIWGYKELRKPLEKEGWK KSDFQVNLNNASRSQSSHSYDD STLPLI*PGPKNQIRNLIGKKFR* AIWDQTQNH*IT/DYSTPNERGD HNRTLDRSGDLGDMEPLKGTT PLMQDEGQESLEEELDVLVLD DEGGQVSYPSMVCPSVTPKIVL EEGGS

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18874	49242	A	18983	5844	5967	ETEA*RINDLL*LLEFFCNI*QN*P*IRPTVIRSSLKYNT
18875	49243	A	18984	5781	5904	ETEA*RINDLL*LLEFFCNI*QN*P*IRPTVIRSSLKYNT
18876	49244	B	18985	1	1477	
18877	49245	A	18986	152	1539	
18878	49246	A	18987	5571	5694	ETEA*RINDLL*LLEFFCNI*QN*P*IRPTVIRSSLKYNT
18879	49247	A	18988	4551	4674	ETEA*RINDLL*LLEFFCNI*QN*P*IRPTVIRSSLKYNT
18880	49248	A	18989	2	1043	GVRLRYSPIAVVMVGEAGRDLRRRRAVAVTAEKMAVLAPLI/SLSVYSVPR\LSRWLAQPYYLLSA\LLSAAF\LLVRKLPPLCHGLPTQ\REDGNP\CDFDWRE\VEILMFLSAIVMMKN\RRSITVEQHIGNIFMFK/SKVANTILFF\RLDIRMGLLYITLCIVFLMTCKPP/LSPYMGPEYIKYFN\DKPFDEELERDNRVNW/ILLEFFGNWSNDWQSFAPIYADLSLKYNCTGLNFGKVDVGRYTDVSTRYKVSTSPLTK\QLPTL\ILFQGGQGGQCGRPQI*QGKGR/ALFSWDLL*GT*KEGQENVIREFNLNELYQRAKKLSKAGDNIP\EEQPVASTPTTVSDG\ENKKD
18881	49249	A	18990	1	1105	MESTGEDAVNIVEMVTEDLVYRLVVLKSLQVWLSPGDFMGSEGTECMLIGPWVAMGRPSESTLSSHSGPRSPHGTGSPAPRLQAVHVLKCPKSRGVQGGWGLASQCLPEHRHTQLSCDSTQAWPQLCSAQSLRHNRSGQGAGAVTSEPAGAGGLPRPPRTQGCLGAES/PAGQLHSQQRGGPEEGRLLSDVDHPDLSSSQQRGPEGP/QVAGGWCVSAAWSSTHLAGPQQRWDQEEARQWEQIPLSLLMMGDPPGYSRAPGDPGPQPQPRQLQLCLGSSHPTNS*GAELPPVPGSAECAALTVLPSLHLPQWWQVGRPGPT*VDPRVGLPGQQAPEQRVYSLTHPEQLPVLQVPLLIYRYSSTYNGV
18882	49250	C	18991	105	393	
18883	49251	A	18992	38	230	LYWQKRKGKLLNNLTQGIVADPVR*KKFHFKCPSNCPKIHNTESAYAVSFMKYSAHVLGSLYEM
18884	49252	A	18993	487	747	
18885	49253	C	18994	179	649	
18886	49254	A	18995	3	3187	
18887	49255	A	18996	274	423	

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18888	49256	A	18997	1333	2243	RCWRPRTLGFASPPTRPCSPTH APGCEMTPRDWHRVLSFASPLR IEEIFQGYDKTFGLKNKKGAKQ QKFIKAVTHQVKFGQ/SKSTSGS TE*SWKRKLKKDDKKKELQEL NELFKPVVAAQKI/RVKGADPK SVV\CAFFKQGQCTKGDKCKFS HDLTLGEKM\EKRSVYIDARDE ELEKETKSSLIQADTMDNWDE KKLEEVVNKKHGEAEKKKPKT QIVCKHFLEAIENNKYGWFWV CPGGGDICMYRHALPPGFVLK KDKKKEEKEDEISLEDLIERERS ALGPNVTKITLESFLAWKKRKR
18889	49257	A	18998	1	322	
18890	49258	A	18999	1	822	MGKAKEEVFLADELVHAKTNR NKECDYSVTANSKIVVVTAGV RQQEGESRLNLVQRNVNVFKFI IPQIVKYSPDCIIIVVSNPVDILT YVTWKLSGLPKHRVIGSGCNL DSARFRYLMAEKLGIHPSSCHG WILGEHGDSSDHPGRPRPHPVPI KPPETLPGRDTSSWTSRGAHWR RNTQAAGRREHIDRHQQAIDR WNNVGFGRGGQRRARLLSDLT PTGKPSSYSVSLLAPPSAESYFH SIKPCIHSPS*CMQRPIEIKN/RD YSVTANSKIVVVTAGVRQQEG ESRLNLVQRNVNVFKFIIPQIVK YSPDCIIIVVSNPVDILTYVTWK LSGLPKHRVIGSGCNLDSARFR YLMAEKLGIHPSSCHGWILGEH GDSSDHPGRPRPHPVPIKPPETL PGRDTSSWTSRGAHWRRNTQA AGRREHIDRHQQAIDRWNNVG FGRGGQRRARLLSDLTPTGKPS SYSVSLLAPPSAESYFHSIKPCIH SPSPREIQFFGYTKARNPRVQK

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18891	49259	A	19000	1	1337	MEKPKRLRWLWGPAPSSLLAE PAPEETHAADFVFSARLLQRSP EPSLSWGGRALAEEQKAEGSSC GSAERLVAFAAKTRPYLSLCK MATLKEKLIAPVAEEEATVPNN KITVVGVGQVGMACAISILGKS RAMEHTTAGAPYTPRQQTCQC NMMSLADELALVDVLEDKLKG EMMDLQHGSLFLQTPKIVADK DYSVTANSKIVVVTAGVRQQE GESRLNLVQRNVNVFKFIIPQIV KYSPDCIIIVVSNPRDI\LTYGTW KLSGLPKHRVIGSGCNLDSARF RYLMAEKLGIHPSSCHGWILGE HGDSSVAVWSGVNVAGVSLQE LNPEMGTDNDSENWKEVHKM VVESAYEVIKLKGYTNWAIGLS VADLIESMLKNLSRIHPVSTMV KGMYGIENEVFLSLPCILNARG LTSVINQKLKDDEVAQLKKSA DTLWDIQKDLKDL
18892	49260	C	19001	462	728	
18893	49261	A	19002	1	1033	MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTFPRWTVWEEPP PPGLVGVKACARWWGKGEPD RKAPAPPPPPGTEKVDQTSE\E RGTLIQRPPAPALPGWVRKTGR P/PPPA/TGRLQQVPLLGASTQPE /PPGRGV/PPGVSPGLGEDVE/N DGMSLSYLAE*PQATSQRAP*G ENTVALSGRLGRNSSSYTCRPA GERNFHPRGGPSSTAALHLRK MPGTPQCEGRRAVPRALPET*M LQGPGTTR*T/PPGPLAFSPPSSP TGPQKVKSLGNSSARTILPPKW
18894	49262	A	19003	2	212	
18895	49263	A	19004	1	425	PTRPAAVAEDGGLKKCKISSYC RSQPPARLISGEEHFSSKKCLA WFYEYAGPDEVVGPEGMEKFC EDIGVEPEN\CDCTEKLQNKFDF LRSQLNDISSFKNIYRYAFDFAR DKDQRSLDIDTAKSMLALLLGR TWPLFSVFY

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18896	49264	A	19005	229	1028	GASKRTGTPFPGFPAHPAREGR KMPVKKKRKSPGVAAAVAED GGLKKCKISSYCRSQPPARLISG EEHFSSKKCLAWFYEYAGPDE VVGPEGMEKFCEDIGVEPENII MLVLAWKLEAESMGFFTKEEW VKG\MTSLQCNLHRKGYKPNF DFFAAHS*IDISSFKNIYRYAFDF ARDKDQR\SLDNDTAKS\MLAL LLGEGHGPLFS\VFYQVPGGQS KYRVMNKD\QWYNVSEFSRTV\ HADLSNYDEDG\AWPVLLDEF VEWQKVRQTS
18897	49265	A	19006	3	373	
18898	49266	A	19007	3	418	GRAGSRKWLLLTGSLASTSPSL LSGQGPWAPLQRAMKPPGGES SNLF\GFPEEATPSSRPNRMSSNI FGPTEEPQNILKRTNPPGV*GSG IFDESTPVQTRQHLNPPG\GKTS DIFGSPVTATSRLAHPNKPKDH VFLM
18899	49267	A	19008	1	684	
18900	49268	A	19009	3	81	
18901	49269	A	19010	1	465	
18902	49270	A	19011	120	344	
18903	49271	A	19012	3	1334	SPQLISSASRPAVRNSRHDATRP VVFQIMSGGSADYNSREHGGPE GMDP\DGVIESNWNEIVDNF/D VTMNLKESLL\RGI\YAYGFEKP SPIQQKA\IIPCIKGY*CGLLKLQ SGTGKTATF/SLISILQPVGRLSF KETQSTSYWAPTREL\AQQIQK VILALGDYMGATCHACIG\GTN VRNEMQKLQAEAPHIV\VGTPG RVFDMLNRRYLSPKW\IKMFVL DEADEMLSRGFKD\QIYEIFQKL NTSIQVVFASATMPTDVLEVTK KFMRDPIRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITQAVIFLNTRRKVDWLTEKM HARDFTVSALHGDMDQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINYDLPTNRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFY\NTTVEEMPMN
18904	49272	A	19013	75	540	

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18905	49273	A	19014	774	1529	RWGERILLTWRKRQLQVPPSAL EAGGSSGLEDVLPLLQQADELH RGDEQGKREGFQLLL/TQQAW CMEAGRTFLWRLARAYSDMCE LTEEVSEKKSYALDGKEEAEAA LEKGDEE/SLTCHLWYAGALW SAG*AMRASRRRIQELALTFKE HCGQKPFALQP\KTPMAHFLLG RWCYQVSHLSWLEKKTATALL ESPLSATVEDALQSFLKCYREL GKNSEARWWMKLALELPDVT KEDLAIQKDLEELEVILRD
18906	49274	A	19015	97	452	GTERRTGKLPALLTPNLVQLRR LLFPGIQTI*VPAQGRGHLLQRP AAA/RPRTRSAPPAAAAAPPQV EARPP*LQPTRQEEAAELQTAR AGLWELWAGPQSPRDLNSLESI RITCSPTP
18907	49275	A	19016	1299	1800	FWGGRSGTVGYGADMGKFKN NTTNNQS*K*YRNTSRNPDHKD *FLKGMDPKFPKNMHFA*KHN EKGLEKMQDNNMRAEAIKA/L PKPMEVQPRVPKSASRKLD/LA YTAHPKAGKHARAHIATGLRL CWPKAKAKDQTKAQASASAA APASVLAPAQASKGAQAPMKA LE
18908	49276	A	19017	410	1323	RQEGTLIGVFIPAAAAAAAAVAA AAAAAAAAVAAAAAAAAAAV AAAAAAAAAAVAAAVAAAAA AV/GTSFSKPHKLMKEHKEKPS KDSREHKSAFKEPSRDHNKSSK ESSKKPKENKPLKEEKIVPKMA FKEPKPMSKEPKPDSNLLTITSG QDKKAPSKRPPISDSEELSAKK RKKSSSEALFKSFSSAPPLILTCS ADKKQIKDKSHVKMGKVKIES ETSEKKKSTLPPFDDIVDPNDSD VEENISSKSDSVPGQSPVTNIFF TSSSTPTILKSYQLDNSDQQGA QEASDKQIEGYFSGEVPAYRQG ELILVASRQ

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18909	49277	A	19018	91	890	GAERLPEGPGKRMVFRRFVEV GRVAY\VSFGPHARK/MWVAIV DVF*SEQGLLVE*PCTQVR\RQA \MPFRCMQLN*FHPSRFPNSAQP ESMFRQAWQK\ADI\NTKWGSP HDGAKKIEAQRKGKPKDDQIF D\RFKVMEGQKKMREQE*SKE* S*RSFKRAALLEKLSPKKKHLG T*GYCCLLLLAAAAAAAAAA AACCLLACCLKVPSKKRSPAAS KKAPAQKVPAQK\ATG\QKAAP APKAQKGQKAPAQKAPAPKAS GQESISGNHKK
18910	49278	A	19019	280	1249	SLNEGIMYAQP\VTNTKEVK\W QKV\LYERQPFSLDKLWWDRRF LGRSSGKNIHAPENTQY\WGCG *FESSV\VIQQLCSVCVFVVIR\W YMDEGLLAPHWLVGTGLASSL IGYVLFDLIDGGEGRKKSG\QTR WADL*ELP*SFITFTYG\FSPVLK TLTEFCSALTPIYAMSVFMLLR HLIFFDYG\ANAAIV\SST\LLVN MAIFAS\VCWASRLP\RS\LHAFI MVA\FAIQIFCPGGPML\QKKLK \ACTP\RS\YVGVTL\LFAFSAVG\ GLLSISAVGA\VLLA\LLLMSISC LC\PFYLHFACSLFKENI/HMGP WDEA\EI\KEDLSPGSLS
18911	49279	A	19020	1	310	
18912	49280	A	19021	2	411	
18913	49281	A	19022	374	1275	VLTRLIRKRERRKAQSQRERCR CVLAKDFLAGGVTAAISKMAV APTE/RVKLLLQVQSASKQITAD KQYTGVVDCMVRIPKE/QGVLS LWH\GIQFWHKFAGSLASGGAP GATSLCFVYPL\DFARTRLAAD VGKAGAEREFRGLG*PAGLRIY KSDGK/LRGLYQGF\NVSVQGIII YRAAYFGIYD\TAKG\MLPDP\Q NTHIVISWMIAQTVTAVARVDF PIPFDT\VRRRNE*MQSRAPKEL TIHVHQARFDCWAEGLLRDEG G\KAFFKG\AWVPMFLRGHGVG AFCALSLYGWKSKEGTHKLIS
18914	49282	A	19023	461	705	TERKKKGILPGNGNGFMSLRRT IRVWRNTPNYLGTNAVSP\RQD *IGKKGVCQRKQAGPCPPSNIQ GILEWRKHRISETKP
18915	49283	A	19024	2	408	

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18916	49284	A	19025	1	885	MTQHAGKRDSELPVIVQDTET VPSVMDGKEYQAGRFARGLRL QCFRRRRRRRRTRRRRKEEEE EEEEEEEEEEEEVEEEGMKKEE EGRRRKKKKKKKAEEEEEKKK KEEEEKKRRRREEPPRPRNDDD ARRRRKEEEEGRRRSM/LGKRD SELPVIVQDTETVPSVMDGKEY QAGRFARGLRLQCFRRRRRRR RTRRRRRKEEEEEEEEEEEEEE EVEEEGMKKEEEGRRRKKKKK KKAEEEEEKKKKEEEEKKRRR REEPPRPRNDDDARRRRKEEEE GRRRSMKKEEEEEEEEEEEEE EEEEEEEEEKKKRRIGPASKMM GGFEELRRGLNVGPTMAIFFLQ SAALAPAILYFCPSLKSNISKCN FQFLMFCQLLGRVTIPFLVSQRS RIEVGRHSLSTLNAETAHELYL GRTEPDECGKTAGLGTGLDLK
18917	49285	A	19026	1	378	
18918	49286	A	19027	36	3415	ESAANAQVLAAPSPCSPFAFTL SKVNMSLKNEPRVNTSALQKIA ADMSNIIENLDTRELHFEGEEV DYDVSPSDPKIQEVYIPFSAIYN TQGFKEPNIQTYLSGCPIKAQVL EVERFTSTTRVPSINLYTIELTH GEFKWQVKRKFKHFQEFHREL LKYKAFIRIPIPTRRHTFRRQNV REEPREMPSLPRSSENMIREEQF LGRRKQLEDYLTKILKMPMYR NYHATTEFLDISQLSFIHDLGPK GIEGMIMKR
18919	49287	B	19028	37	147	
18920	49288	B	19029	10	264	

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18921	49289	A	19030	3	1255	HASGGRAANMAADRGAVQQQ SQDMMEVDRRVESEESGDEEG KKHSSGIVADLSEQSLKDGEEP G\EEDPEEEHELPVDMETINL\D RDAEDF\DLNHYRIGKIEGFEVL EES*RLSCLRQNLI\KCL\ENLGR ELPESFRELDLYDNQIKKIENLE ALTELEILDISFNLLRNIEGVDK LTRLKKLFLVNNKISKIENL\SN LHQL\RMLGAGDLNRIRGQFSK YPTTL\TNL\ESWFLGKKTKITN FQNPGCASPNLTVLSMQSNRLT KIEGLQN\LVNLRELYFSHNGIE VIEGLENN\NKLT\MLDIASNRIK KI*KISAHLTEL\QEFWDGTTIPL KSWSDLDELEGEPGALEDSVP WGGNPLARRTPKYRRK\VMLA\ LPSVRQDRCPRSVRFLKSFLGSL MWSLSSEELPSHGVFNPPCCS
18922	49290	A	19031	138	564	YREVMVSES*ETPAGARGRPYY FSAPGTAP\PAINVHPPPPSLSAT PHPPQPQPPPPHQHNAKARVAT IRTKRTSNCRIRSRKVRKSPPEK WVGFNRRPKASCPSPPGAARV DVGGETERREQAAAPGEMGK WARPGEEYFHS
18923	49291	A	19032	1404	1586	ENESRFSDRNQASAGLGYLSDS L*QWIVGNGHATDLWQNCSTS SSGNVHHCFSSSPNGSG
18924	49292	A	19033	187	701	AELAARMLLLLLSIIVLHVAAL VLLFVSTIVSQWIVGNGHATDL WQNCSTSSSGN\VHHCFSSSPNE W\LQSCSRGTMDPVDSSFSILSL FLFFCQLFTLTKGG\RFYITGIFQ ILAGLCV\MSAAAIYTVRHPEW\ NLNSGY\S*RFA*I\LAWVAFPL\ ALLSGVIYVILRKRE
18925	49293	A	19034	1	493	
18926	49294	A	19035	105	307	
18927	49295	A	19036	32	302	
18928	49296	B	19037	119	641	
18929	49297	A	19038	496	653	
18930	49298	C	19039	568	747	
18931	49299	A	19040	522	656	ESSQSHGKNFYMGKRIKLSLY WNVWRMLNSKSETTNCPLIRH RLSKRVGAPFLPAVLVLTKITIY QT*KFQIRNHKLPSNKTSAI

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18932	49300	A	19041	111	277	RHVVAVVLGDVGRSPRMQYH ALSLAMHGFSVTLLGFCNSKPH DELLQNNRIQIVGLTELQSLAV GPRVFQYGVKVVLQAMYLLW KLMWREPGAYIFLQNPPGLPSI AVCWFVGCLCGSKLVIDWHNY GYSIMGLVHGPNHPLVLLAKW YEKFFGRLSHLNLCVTNAMRE DLADNWHIRAVTVYDKPASFF KETPLD\RTHRLFTKLTNMHSPF RARSEPEDPVTERSAFTERDAG SGLVTRLRERPALLVSST\SWTE DEDFSILLAALESRV*TTDS/SIG HNLPSLVCVITGKGPPREYYSR LIHQKHFQHIQVCTPWLEAEDY PR/ILGSVDLGVCLHTSCSGLDL PMKVVDMFGCCLPVCAVNFK WQEQNPNLSGDSFTDPPLRRKQ CRASCPQ*GPAPGLHELVKHEE NGLVFEDSEELAAQLQVLFSNF PDPAGKLNQFRKNLRESQQLR WD*SWGSATPNPMMSSCRTTE
18933	49301	B	19042	110	2294	
18934	49302	B	19043	81	1538	
18935	49303	A	19044	21	1158	AVVAALPTSSSSRHSLTQKPGS RRLRIESLLPPSSCEIFLIFSYIFR LCEKPYHQTRSASNVTNKTDPR SMNS\RVFIGNLNTLV\VKKSDV EAIFSK\YGKI\VGCSVHKGLCLS VQVMLMRRNAPGLL*QGE\DG RMI/ALGQVLDINLAAEPK\VN\ REKSSVKRSAAEMYG/SQ*QNT LLRPLYFSSSFDLDYDFQRDYY DRMYSYPARVPPPPIARAVVP SKRQRVSGNTS\RSGPRGFNSKE WNSGVSSKFWKR*KGDDLQ\AI KEELT\QINQK\VDSLLENLEKIE KATGANKQLEMK\ND\KSEEEQ SSSSREGKMRTNVKDGV*GGV PDDSAEGGGPTWMNDDNVKS GGMTSWELI\KDDEKEAEE\GE DD\RD\SANGGG
18936	49304	B	19045	93	303	
18937	49305	A	19046	1	246	
18938	49306	B	19047	123	487	

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18939	49307	A	19048	584	1664	SGLFLFLFFYSEIFLIFSYIFRLCE KPYHQTRSASNVTNKTDPRSM NS\RVFIGNLNTLV\VKKSDVEA IFSK\YGKIVG\CSCFIKGFAFPFK *C**EEMPRACCSGRRVGRIDLL GQVLDI*PGLAEPK\VNPREKPG VETILPAGDVRGQ*QNTLLRPL YFSSSFDLDYDFQRDYYDRMY SYPARVPPPPPIARAVVPSKRQR VSGNTSRRGK\SGFNSKEWNSG VSSKFWKR*KGDDLQ\AIKEEL T\QINQK\VDSLLENLEKIEKAT GANKQLEMK\NDK\SEEEQSSSS REGKMRTNVKDGV*GGVPDDS AEEGGPTWMNDDNVKSGGMT SWELI\KDD\EKEAEE\GEDDKR QGPMARNDS
18940	49308	A	19049	158	1001	KRLGSSAISMSKYKLIMLR\HGE GAWNKENRFCSWVDQ\KLNSE GMEEARNCGKQLKALNFEFDL VFTSVLNRAIPTARL\IL\EELGQ EWVPVESSWRLNERH\YGAL\I GLNREQ\MA\LNHGE\EQVRL\W RRSYNVTP\PPIEE\SHPY\YQEIY NRPGGIKVCDVPL\DQLPRSES\ LKDVL\ERFLPYW\NERIAPEV\L RG\KTILISAHGK*AVGALLKHL GRYPSGLKTSINIYSFLLGVPILL \ELD\ENLRAVGPH\QFLGDQEAI QAAIKKVEDQGKVKQAKK
18941	49309	A	19050	1	521	SASWVGVAMASRVLSAYVSRL PARFAP*PRVRMLAVARH\LST ALCSEGTQTRLGTLQPALVLA\ QVPW*ELHMLCRQYSDMP/PRL TLEGIQ\DRVRLA*LKTLSDKVD PREAFQ*ILHFMKDLGLDSLDP KWKII\MALED\EFGFEIP\DI\DA EKLM\TPPRKLVDLHCQDKKD
18942	49310	A	19051	1	516	IRALTMIWRRALLAGTRLVWS RSGSAGWLDRAAG\LR\DCG\TA ASGMESNTSSSLENLATAPVNQ I\QETISDNCVVIFSKTSCSYCTM AKK\LFHDM\NVN\YKVVELDL LEYGN\QFQDASLQK*LVERTV PRIFVNGTFIGGATDTHRLHKE GKLLPLVHQCYLKK\SKRKEFQ
18943	49311	A	19052	825	1080	KRKIHQNFHKLSLKKAIEKDYS ESGSSVNQYKRIRPTDNVVIKQ Y\WPGAVAHTCNSSTSVGQGR WIT*GQEFETSLANVVKPHLY
18944	49312	A	19053	80	429	

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18945	49313	A	19054	3	752	FKNAVGNLAMEGGGGIPLETL KEESQSRHVLPASFEVNSLQKS NWGFLLTGLVGGTLVAVYAVA TPF\VTPALRKVCLPFVPATTK\ QIENVVKMLRCRRRDPLWDIGS GGRDGIVHRRLRRKGFTAVGF MEFKPMG*FWVFPRY\RAWRE GVHGSAKFYISDLWKVTFSQYS NVVIFGVPQMMLQLEKKLERE LEDDARVIACRFPFPHWTPDHV TGKGIDTVWAYDASTFRGREK RPCTSMHFQLPIQA
18946	49314	A	19055	157	829	TWGKGDPKKPRGKMSSYAFFV QTCRGG\HKKKHPDASVNFSEF\ SKKCSERWKTMSA*R/EKGKFE DMAKA\DKARY\EREMKTYIPP QRGRQKRKFKDSQLHPRRPPSG LLSSSCSEYRPKIK\GEHP\GL\SI GDVAKKLGRDVGINTAAD\DK QP\YEKK\AAKLKEKYEKDIA\A YRA\KGKPDAAKKG\VVKAEKS KKKKEEEEDEEDEEDEEEEEDE EDEEDEEEDDG
18947	49315	A	19056	85	267	GHLSHAWCGTYKPWPSPKEQS RAWKKDGLLFPPPP/PLFPTGLK VRGRESF*SVELIRPQG
18948	49316	A	19057	1	1158	
18949	49317	A	19058	452	517	
18950	49318	A	19059	93	1069	YEGVTTSRLPELPRGCLVLQEQ ELVQMSGMEATVTIPIWQNKP HGC/SLRSVVRRIGTNLPLKPCA RASFETLPNISDLCLKRCAPSSL PWL\AWLGFLAE*KGSQKARV\ RSDTRPLRHTWKPSPLIVMQRN ASVPNLRGSEERLLALKKPA/L ASPKAALLSCRTS*ATLRTKICK DSGKLMQLRLH*RQISYLQEVQ MSLLPLPCFGSSFHSTTSFCH**/ PSPRRQRWRSLSFHQSPCFVLP ALNVANQNTKLPAVRLKRMTA SLCPRPAALQDMMGILKGLFTG MKQSQDLNRSLLKEEDPAVLIS EVLRRKFALKEEDISRKGN

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18951	49319	A	19060	162	1410	GQASCPPPALGQQTPASSYTVQ IQTYAPSSPHPRQGPGQGSSDPR GLRGAIPRGRQGQGV*QQGPRC RPPSSPVLPHIPQLSCCGHDGRD PEEGLGILELTLLHHAHPWSPN SW*KDS\PSPHGEFPAHSEPHSR DQTSPMATTKHEVQPLPQASLS QPSLGIGCLVDWLRQLRTTQGS /PQDAAQDSTWERP*DAS/GKP WLL*PGVPTPGPPCQAKERKPP FMGNCPL*SRVPWPSRLPEEL/P AMPLAPPVAGEAAGPASSHQSL SPSQDPTPLPGADRREKERGGE EGSSWPQTPRLTTHTTSPPPEKQ QQIESPPIRLSSFKTGFHLASSGH SYAIKPNSKTKAEKVGQVRVPR SHTIREQRQGKRPGEHHRRTER DAKPQGEEDHQATVVSQKLGT DRRLIKKQRTSVLSATAES
18952	49320	A	19061	1	340	GSVGSGTTLNQLGFWSSPGTSP LEPPCPWLDSHIFPVPFWKDVA FGEGVCLPPGAPQPRRICPRRG QQPEFQQEEPETIPERTPADPGV LPPAFPGICLPRRLRAPPDPGPA A*AVPPVADA*GSVGSGTTLNQ LGFWSSPGTSPLEPPCPWLDSHI FPVPFWKDVAFGEGVCLPPGAP QPRRICPRRGQQPEFQQEEPETI PERTPADPGVLPPAFPGICLPRR LRAPPDPGPAA
18953	49321	A	19062	3	396	IPLASLHLALPGHQRGPPPGRLP SCSSQGTVPPPRAGPYQAGCPG TAPAPAAPASAPWSAPQASATG GTAHAAGPGSGGARSLPPARA HPPARCWQGRPLRSLLL*PSSVP ETGGPEKARLVKALSPNTAP
18954	49322	A	19063	563	1269	LEESTGRITHFKATLHCTMSNN LAWGGTKWLQESRVFFHIRRLP SDASAGPGCVYRVVPDGGSQG RPQGAPP*AAQA/GTPRGRPP\P GAPSALLPPPPSGTSVGPGGLQ QRRPPTGQEDSPTEPGFWKPRL WRSHLATSLATRCTMQGEPAR AHPPGGRGPAASEERHQRGPPP GGCFAALRYCATPRPDLSGRCP GTAPAPAAPASAPWTRLRHQPL AAQLMQPGQVWWGPAASW

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18955	49323	A	19064	1	1158	MELKAKARELREECRSLRSRCD QLEERVSVMENEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLHLIGVPESDGENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSSRRATPRHIIVRITK VEMKEKMLRAAREKGRVPHK GKPIRLTADLSSETLQARREWG PIFNILKRIFSFPQRGGTGGRRM VKLTAELIEQAAQYTSAVRDRE LDLRGYKIPVIENLGATLDQFD AIDFSDNEIRKLDGFPLLRRLKT LLVN/NNRIC/RVLDFQKVK/LK ERQEAEKMFKGKRGAQLAKDI ARRSKTFNPGAGLPTDKKKGG PSPGDVEAIKNAIANASTLAEV ERLKGLLQSGQIPGRERRLGPT DDGEEEMEEDTVTNGS
18956	49324	A	19065	2	431	RKLDGFPLLRRLKTLLVNNNRI CRIGEGLDQALPCLTELILTNNS LVELGDLDPLASLKSLTYLSILR NPVTNKKHYRLYVIYKVPQVR VLDFQKVKLKF\NPGAGLPTDK KKGGPSPGDVEAIKNAIANAST LAEVERLKGLL
18957	49325	A	19066	92	303	NCFLVFSPARSTVGEFASMSSE ECI*MHVVFLFPLTLCVVSLYER QEAEKMFKGKRGAQLAKDIAR RSKT
18958	49326	A	19067	208	293	LLLLWWFPLGPTDDGEEEMEE\ DTVTNGS
18959	49327	A	19068	22	904	ARNPWSTHASGWREATGFPQR GGTAGCTMGKLTAE\LIEQAAQ YTNAVRDRELDLRGYKIPVIEN LGATLDQFDAIDFSDNEIRKLD GFPLLRRLKTLLVDTTRI\CGIGE GLDQA\LPCLTELILTNNSLVEL GDLDPLASLKSVAY\LTYLRNP VTHKKHYRLYAIYKAPHVRVL DFQNVKLK\ERQKAEKMSKGK RGAQLAKDIA\RRS\KTF*FPGA GLPN*PKRKGGP/SLPGDVEAIQ ECP*QNAFNSGLKVERLKGVCC KSG\QIP\GRERRSG\PTDDGEEE M\EEDTSHQTGS
18960	49328	A	19069	1	395	AINYNEKIYELRVMETKP\DKA VSIIECDMNVDFDAP/LGYKEPE RQVQHEESTEGEADHSGYAGE/ LGFRAFSGSGNRLDGKKKGVE PSPSPIKPGDIKRGIPNYEFKLG\ EAGGRFVAFSGEGQSLRKKGR

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18961	49329	A	19070	1	1108	
18962	49330	A	19071	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESPSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
18963	49331	A	19072	2	1112	RLGAAAAAAAAGRAVGGVSSL HCPERSGVCQVVSIMFSFNMFD HPIPRVFQNRFSTQY\RCFSLS\M LAGPNDR/SSIGEKEGKIIMPPLG PGTKLSRL*HYRIPMLFK\LTNK NSGPHGRHCGVAGSLWA**GA SAYLPHWDDGRTYSLGRKAA WVQGGRSVNLSSGPLISNFQPQ SP\DFL\DITNP\KAVFEN\ALRNF ALS*PPGDVI\AINYNEKILRNCV VMETQTPTRPVSHH*SVNH*TV EL*LLPPGATKEPRKDQVQP*G VRTEGESRPHSG\YAWKSLGFP RFSRGSG\NR\LDGKKKGVEPSP\ SPIKP\GDIKRGIP\NYEFKLGKIT F/VSRNSRPLVKKVEEDEAGG\R FVAFSGEGQSLRKKGRKP
18964	49332	A	19073	1	415	SGGGRNRSATGSWVGTMAGIT TIEAVKRKIQVLQQQADDAEER AERLQREVEGERRARE\RGMK VIENRALKDEEKMELQEIQLKE AKHIAEEADRKYEEVARKLVII EGDLERTEEPSLSWQESKCS\EL EEELKNVT
18965	49333	A	19074	1	421	
18966	49334	A	19075	3	388	
18967	49335	A	19076	1	1332	
18968	49336	A	19077	49	483	
18969	49337	A	19078	227	1030	AVSWVGTMAGITTIEAVKRKIQ VLQQQADDAEERA\ERSQREFR EERRARE\QA\EAEVASLN\RRIQ \LVEEEL\DRAQERLGHCPCKKL *RS*KKLADESERRY*RLFEN\R ALKRLKEKIGTSREIPTSKKPKH HCRKEAD\RKYEEV\ARKLGDH LKEDLERTE\ERA\ELAESRC*EI DEQIRLIDQNLQCLSAAEDKYS QKEDKW\EEEMKILTDNLKEAE THAELAERSVAKLEKTIDDLED KLKCTKEEHLCTQRMLDQTLL DLNEM
18970	49338	A	19079	50	864	
18971	49339	A	19080	1	1014	

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18972	49340	A	19081	1	1650	MGFHHVGQAALELLTSGFSQT QELQKFLFLLFLLVYVTTIVGN LLIMVTVTFDCRLHTPMYFLLR NLALIDLCYSTVTSPKMLVDFL HETKTISYQGCMAQIFFFHLLG GGTVFFLSVMAYDRYIAISQPL RYVTIMNTQLCVGLVVAAWV GGFVHSIVQLALILPLPFCGPNIL DNFYCDVPQVLRLACTDTSLLE FLMISNSGLLVIIWFLLLLISYTV ILVMLRSHSGKARRKAASTCTT HIIVVSMIFIPCIYIYTWPFTPFL MDKAVSISYTVMTPMLNPMIY TLRNQDMKAAMRRLGKCLKG PAVAVGPGPGPGDAEAAAEER RVKVSSLPYSVDALVSDKKPPK EASPVPAKSASSGATLRLLLLP GHGAREAHSPGPLIKPFETASV KWENS\QDGAAWMQEPC*\YSP PPRHK\HKTNPKPRTAFTTSQLL ALEGKLLQKQYLSIAEGADFSS SPNLTETQVKILFQNRRAKTKR LQESELEKLKMAAKPMLPSSFS LPFPISSPLQAASIYAASYPFHRP VLPIPPVGLYATPVGYGMYHLS
18973	49341	B	19082	62	440	
18974	49342	A	19083	1	902	METEALMPGLGVAVAGAQVTL GFLALETQLPFTGHKRILRLFFS SPRDPPHVPSKGLKRKWGARR GRTFALREAEPQRLPSLSRAFG TLARPYARLVRPGNPVVPFPLA GSAEAARAAATCERQARTCPM PGVTVKDVNQQEFVRALAAFL KKS*V\GKLKVPEWVDT\VKLA KHKELAP\YDENWFY\TRAAST AQAPCTIRGGAG\VGSMTKIYG GRQRN\GVMP\SHFS\RGSKS\VA RRVPPKPWRG*KMVEKGTKNC GPQNLTPSRDKRDFGTEFAGQV AAANKEALEQIHCFGLIKLAHS
18975	49343	A	19084	1	673	AGPDAEASERVPEGPEAPGAGP SRPLEPRPRASGRPGHGRCLGV TVK\DV\NQQEVRHELWAAFLS KSLR/LRVS*TVPEWL\DTVQAG QAQKSLLPYDE\NWFYHAELAS TA\RH\LYHPGSALGVGSMTKIY GGTSDETASMPKPLSARGFQEI WARRV\LQSPGRGLKMGGKRD QELRAAKLDTFKGQKRFWDRI RRNRLAVAYKEALEQTMAGV NKLPQFVKKKK

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18976	49344	A	19085	1	427	HPVRFFVHRGPH/VDFSLEVVS QWYELVVFTASMEIYGSAVAD KLDNSRSILKRRYYRQHCTLEL GSYIKDLSVVHSDLSSIVILDNS PGAYRSHPDNAIPIKSWFSDPSD TALLNLLPMLDALRFTADVRSV LSRNLHQHRL
18977	49345	A	19086	2	832	WNSAELGRGGPGAGGAGVIGM MRTQCLLGLRTFVAFAAKLWS FFIYLLRRQIRTVIQYQTVRYDI LPLSPVSRNRLAQVKRKILVLD LDETLIHSHHDGVLRPTVRPGT PPDFILKVVIDKHPVRFFVHKRP HVDFFL\EV\VSQWYELVVF\TA SM\EIYG\SAVGRLNWDNSRSIL *GGRY\YRQHCTLELG\SYIKDP LLWFHSDLS\GIVIL\DNSPGAYR SHPGYGGR\DNAIPIKSWVSVTP ANTAILNLLPMLDALRFTADVR SVLSRNLHQHRLW
18978	49346	C	19087	69	206	
18979	49347	A	19088	312	438	
18980	49348	A	19089	635	826	QWISLWKCYKPEESGGQYLIFL KKSIFNDEFHVKPN*AS*GKEK* TPLQTSNC*GILSPPGLP
18981	49349	C	19090	1	390	
18982	49350	A	19091	336	551	ARPLGSLASAPFPAPM*NVYPT GP*\YNADCPNVTAPVCASNGH TFQNECFFCVEQREFHYRIKFE KYGKCD
18983	49351	A	19092	76	309	KGRFVIALTFTT*HSNLEKSCSK ICKIK\NKSLVCKHQLAKSIQSPS **WNGMNN*FTTLFICCHNTEK TFIHCGKRP
18984	49352	A	19093	181	447	NKYQTDNIKLSDNDLTIGHQTG NTTAHC/RYIMLFRSFQQMAITT ILS*YRKNIYPLWKETLKRMWQ RHREKVGSFEKVNDIKILFHHW
18985	49353	B	19094	1	639	
18986	49354	A	19095	1	160	NLHSQMLWNQRIR*LTSV*LEL LCKNPNRVATRDQLLCLSGHL GMGRILELGG
18987	49355	A	19096	2	456	YKNTITDYYEHLYAHKLENLEE MNKRRASTICTETIPKKLRRRD SSLTHSMRARRLSVDVKPQDRS RGPSECTIFRAGVPEGTRGALW LPHFQTESDPGSKPAITLLVIHP DELQIYVRTKTC/T/RMFIAALFI IAKT*KQPRYPSCLITST

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18988	49356	A	19097	138	1193	LCFFGQHAPIYCSLRHSLLSYTR PASLICCLPGSHRYLEFVLLLLK HHRLHEDLNHCPIGSRSGRDVR SQTTQEQHVIAMPFPLRKLEPL HSGLYSHSCCSRYLAGWLALA TGGAARSPPAISILQPQEPSVTPS DTQRACGRSTEAFESKEQKASV RVETTVSFSCSIKVDGGLLEPKR ADTGWHGHHCRPASITPAGWV PARYLLYVFFSRQCVLSMVCGP QYTRGEIPGAVLKEECLPSLLT GRFDLSGRARRLSVDVKPQDRS RGPSECTIFRAGVPEGTRGVLW LPHFQTESDPGSKPAITLLVIHP DELQIYVRTKTC/T/RMFIAALFI IAKT*KQPRYPSANTLLL
18989	49357	A	19098	3	247	
18990	49358	A	19099	1	1048	MQLKPMEINPEVSARCTATRRA RGRGRGSRVADRFGFAFFFAFA FQMLNKVLS\RLGVAGQWRFV DV\LGLEEESLGSVPAPA\CALP ACLFPLTAQ\HENF\RKKQIEE\L KGQEVSPKVYFMKQTIGNSCG TIGLIHAVAQ*SKTNLGFE\DGS VL\KQF\LSETKKNVPLKDRAKC F\EKN\EAIQAA\HECRGTRKGQ CRVDDK\VNFHFYSG*PTVDGP PSMNLDG\RMPFPRGPMAPS\Q GDTLLEGRFPRSCRRISPRREQR RSPASSARGFSCKGSLNALWGG TWLISPLSPQHENILPPHASLKC FSTCETQAVLLFCQTRPSPQPHP RHLSTSRVHSCPLGHCGVSFRW
18991	49359	A	19100	57	450	VGDCLTSRGMSWVQATLLAR/ ALCRAWGGT/CRGALTGTSISQ VPRLAP\RGLHCSA/ASVSSEQS LVPSPPEPRQR/PPGGERDKASF LQTVQKFADTSVVDSGHIDFIY LALRKMREYGVERDLAVYNQL LNIFP
18992	49360	B	19101	307	390	

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18993	49361	A	19102	431	1267	SGTRTTSTAARTSRTWRS*TPLL ACTPRPCGSAKLATATSRTCIRP *SPSATQTLTVTKVPLPKDSTG AADPPQPHIV/GAQGMYVSTPG IQSPDQQAALARHNPARPVFVE GPFSLWLRNKCVYYHILRADLL PPEEREVEETPEEWNLYYPMQL DLEYVRSGWDNYEFDINEGKE QHVTI/LCSSGEC*ILRRRQNV*R LLDW/LAGKALTSPTCAPKITC VPLALPTPYCSGQNLNSSCSMT SVSDHLSPVPTLLSTISKAHGTP PPNTKVVTKVTVRQ
18994	49362	B	19103	49	691	
18995	49363	A	19104	89	95	VGDCLTSRGMSWVQATLLARG LCRAWGGTCGAAL/SQEPPSLR SLASLPRGLHCSAAAHSSEQSL VPSPPEPRQRAHQGSWCPLR/VP VLGQGAGLGERGQGRAFL/LD GCRNLRTTSVRKRGPH/VDLFY LALRKMRE\YGVERG/DLAVYN QLLNIFPKEVFRPRNIIQRIFVHY PRQQECGIAVLEQMENHGVMP NKETEFLLIQIFGRKSYPMLKLV RLKLWFPRFMNVNPFPVPRDLP QDPVELAMFGLRHMEPDLSAR VTIYQVPLPKDSTGASKIPPKPH IVGI/QRSPDQARPPLARHNPS\R PVF\VEGPFSLWLRNKVCV/YY HILR\ADLLPPEERVRA*SKACV GAGEWAGTTLRVHGRGWRRE TERALASDPACTPHLG\EEVEET PEEWNLYYPMQLDLEYVRSGW DNYEFDINEVEEGPVFAMCMA GAHDQ\ATMAKWIQG\LQETNP TL\AQIPRGLSAFAGSTRKLQTS SAGLEEPP/HCPRTTKEEDDNLQ RQSRAQS*SPCAGIRAQQQDRA GLESAAGRVSR

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18996	49364	A	19105	1	1199	EFGALRRTRLGSSFPRRRDSSA MESYDVIANQPVVIDNGSGVIK AGFAGDQIPKYCFPNYVGRPKH VRVMAGALEGDIFIGPKAEEHR GLLSIRYPMEHGIVKDWNDME RIWQYVYSKDQLQTFSEEHPVL LTEAPLNPRKNRERAAEVFFET FNVPALFISMQAVLSLYATGRT TGVVLDSGDGVTHAVPIYEGFA MPHSIMRIDIAGRDVSRFLRLYL RKEGYDFHSSSEFEIVKAIKERA CYL\SINPQKDETLETEKAQYYL PDG\STIETGPSRFRAPELLFRPD LIGEESEGIHEVLVFAIQKSDMD LRRTLFSNIVLSGGSTLFKGFGD RLLC*VKKLAPKDGRIRISAPQ ERLYSTWIGGSILASLDTFKKM WVSKKEYEEDGARSIHRKTF
18997	49365	A	19106	1	3288	MPSGGDQSPPPPPPPPAAAASD EEEEDDGEAEDAAPPAESPTPQI QQRFDELCSRLNMDEAARAEA WDSYRSMSESYTL/EGSGLWLP RGLFGHPGHCTGLLLLLRSGCV RSQPSDRACR*EK\CHSSHLIEFF NKMKKWEDMANLPPHFRERTE RLERNFTVSAVIFKKYEPIFQDI FKYPQEEQPRQQRGRKQRRQP CTVSEIFHFCWVLFIYAKGNFP MISDDLVNSYHLLLCALDLVY GNALQCSNRKELV
18998	49366	A	19107	56	3552	GPAAQGCAMPSGGDQSPPPPPP PPAAAASDEEEEDDGEAEDAAP \PAESPTPQIQQRFDELCSRLNM DEAARAEAWDSYRSMSESYTL EGNDLHWLACALYVACRKSVP TVSKGTVEGNYVSLTRILKCSE QSLIEFFNKMKKWEDMANLPP HFRERTERLERNFTVSAVIFKK YEPIFQDIFKYPQEEQPRQQRGR KQRRQPCTVS*NFSIFCWVLFIC AKGNFPH*LSDDLVNSYHLLLG ALDLVYGNALQCS

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18999	49367	A	19108	1	1193	GRRRRFWWRKRIGGGGGGMA MPAEAPWMASSFNGFLSLPPG WLLLPPPSDRNPPLQPSSRPPLC VRMWMNAFTPLISLFFWASLV SSGARRLHPIQPQPCREQAPMP APGAARSAVAASMSDCTVAGP CTGSHTPCHSTSDSQSP/CGGVG SSLVV*AERSCAQCRMSPRKGH \CCCCCCCCCCCC/SCCCYCHYC CCYCCCCCCCCCCCCCCCCC CCCCCCCCCCYCCCRCYCCC CCCYCCCCCCCRCCCCCCRC CC*HYCCCCCCCF/GCCCCRYC CCCRYRRCYCFCCCCCCCYCY CCC*RTAHAWPSMNKSQCVLP/ CICKVPLGRLAVTTGCPGFG*G GCWEDCMFPAKGPSIRLEQWFS TTAILLPSGPGDFWQYLGTLLV VTTREEVLLESGG
19000	49368	A	19109	1	762	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADRVPKASQKIFVALS\TGEKG FWL*GVPCFHRLFP\GFYVSRGG DFHTAINGTG\GKSILWGENLK DENFI\LKHTG\PGI\LSMANAGP\ NTNGSPVFLTSCTA\KT\EWLDG K\HVVFG\KVKEGMNIVEAMER SLGPRMGKT\SNKFTIADCGQL RIKFDLVFYL
19001	49369	A	19110	95	240	LHSEITVCL*GSEHHFFENGTYI PHRSCHDPLEARAEDFL
19002	49370	A	19111	1	1644	
19003	49371	A	19112	237	632	AIGFPSYSSMQLVNIFGLLNLFSI ISSSFRHQG*HS*ELP\YPLEPGA EDFLR*GP\LAGHGHTGSQPFFC RVSEA/CGSHLVNSSRAALKRW AGV*RKIWPRGSPETPRNLKDL SVLEYENTPDTSGKKALED

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19004	49372	A	19113	274	2704	GISVLHGCGYRFQPRGMAAPGP FSEKPVPGCDAGDLQTPALSSW TQTFIISHEQGIKFLNQRWSCWS KERNHGHCRVRGHVTAAQCDL FGNGLKHNLDLHIHDRNDASK NVKKSTNYGKMSFYTYCECTP TGEKLWDHNQHRKIIGYKPASS QDQKIYSGEKSYECAEFGKSFT WKSQFKVHLKVPTGEKLYVCI ECGRAFVQKPEFITHQKTHMRE KPYKCNECGKSFFQVSSLFRHH RIHTGEKLYECSECGKGFPYNS DLSIHEKIHTGERHHECTDCGK AFTQKSTLKIHQKIHTGERSYIC IECGQAFIQKTQLIAHRRIHSGE KPYECNNCGKSFISKSQLQVHQ RVHTRVKPYICTEYGKVFSNNS NLITHEKIQSREKSSICTECGKA FTYRSELIIHQRIHTGEKPYECS DCGRAFTQKSALTVHQRIHTGE KSYICMKCGLAFIRKAHLITHQI IHTGEKPYKCGHCGKLFTSKSQ LHVHKRIHTG\EKPYMCNKCGK AFTNRSNLITHQKTHTG\EKI\FI CSKCGKAFTQRSDLITHQRIHT GEKPYECNTCGKAFTQKSNLNI HQKIHTGERQYECHECGKAFN QKSILIVHQKIHTGEKPYVCTEC GRAFIRKSNFITHQRIHTGEKPY ECSDCGKSFTSKSQMT\EH*A\V HSG*KPYV\CAECGKAFSGRSN LSKHQKTHTGEKPYICSECGKT
19005	49373	A	19114	3	180	
19006	49374	A	19115	95	433	PVLRTHPGPQSLPRVPGVPCGG LLEPLSRAEVSPRLGLRRDLLG GMAPSGSST\VF\LLALTIIASTW ALTPTHYLTKHDVERLKASLDR PFTNLESAFYSIVGLSSLGAQVP
19007	49375	A	19116	196	706	ISISNETKDLLLAAVSEDSSVTQI YHAVAALSGFGLPLASQEALSA LTARLSKEETVLATVQALQTAS HLSQQADLRSIVEEIEDLVARL\ DELGGVYLQF\EEGL\ETTALFV\ AATYKL\MDHVGTEPSIKEDQV IQLMN\AIFSKKNFE\SLSEAFSV\ ASAAAVLSHNRYH

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19008	49376	A	19117	275	2192	MVVSPQGSSTVFLLALTIIASTW ALTPTHYLTKHDVERLKASLDR PFTKRLCFSWFTTCVTT*H*LFP TV*KACTYIRSKSLPCLPQIAKT CSKTLCLPILS*ISISNETKDLLL AAVSEDSSVTQIYHAVAALSGF GQVREGVSG*NKTCHSLGFYSL PSRTVDSGSCISFLLLLDIQHISV LLWQDLVARLDELGGVYLQFE EGLETSTAVALPPSQQRKRNSCI SHFFQDQVIQLMNAIFSKKNFE SLSEAFSVASAAAVLSHNRHPR NKILCSCSLCCNK*FFIYFQLQV TNVLSQPLTQATV\KLLFVISMT F/RT*VLAKPIVILNRDVFELNF MNVKFYICM*IPEHPPIDLATVF SIFL*LRVKISTDIFSACSQRYTD PL*RLTLYASFRVTYPAKAKGT FIADRDSMLGPGRILKLSDERL YYSSI*TFVRLHNQKTGQEVVF VAEPDNKNVYKFELDTSERKIE FDSANIIY*VSPTSLPLCFYRLSL FF*ADVVINPGIHGCPYWEGHIL KSSWCVFRQHLFREPEKSWHG LCCFPFKF*CLFNLFLPIIQWILT FLNRRASLCFI*LDVMTPLLAA MLGLMYVYWTQLNMFQTLKS LAILG\SVTFLA\GN\RMLA\QQA
19009	49377	A	19118	3	413	PRKEAPSTFLSQ/NLFTPKQEIQ\ HLF\REPEKR\PPTVV\SNTFTALI LSP\LLLLFALWIRIGA\NVSNFT FGLPST\IFHWG\HAAMLG/LSM YVY*TQAQPCSQTLEVPWPILG QCDRFLAGQSGMLAQRTAVQE NQHN
19010	49378	A	19119	2	535	GRVDPKAKKEAPAPP*SLKPKA *AFKGPRKAVLK\GV\HSPQKA GRSRTSTPPFRAGRKTTADSRR PAPKIILRKSRVPGGNKLD\HYA \IIKFPADH*SASAVKKIEDN\NT L\VFIVD/VLKANKH\QIKQGCE RSLYDI\DVGQGQHPWIRPD\GE KKAYCSTWLLDYDGFGMFAN QNWGSI

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19011	49379	A	19120	159	801	GAAGRRRLPEGEGEDEASAWR RLARCLMPKKNRIAIYE\LLFKE G\VMVAKKDVHMP\KHPE\LAE VKNVPQPFMVMKGHAGLSSPR G\YVKGTSFA\WRHFLTGTLTQ* GVSQYSPWITLHLAPGRFVPCP PLRPVARPRRMGRP\RPKKVLG GVEATWRGFHKRGEV\DRGYL TRRSACCQLGA\DKKSRGWGL GSSNPNFQFRG\GF\GCGRGQ\PP
19012	49380	A	19121	334	989	EPPAETLPVAARDPTGLSPTYLS SHKHEKFQQVRHFPVLLGYPIA SSGASPEVRQRRTTFFRFRPGES LCGDMKLLTHNLLSSHVPAGG SLPFSGGMVGRGPVLA*TP/LAL QATEGR\ICPVEINPQLRGRVMI P*KWKWS\AF\LEAGPDKLAV*I PGARKGPG*GDMRENEEFS*GP WHHLACWEVGSD*EGTL\QVP GNLGRYFSPFKPRGSPNMLAE
19013	49381	C	19122	61	177	
19014	49382	A	19123	4	191	
19015	49383	A	19124	1902	2187	
19016	49384	A	19125	55	340	GELVLKALSAFIRAFRCPAEGS DPVGRAADP\SPPAPRGISQGGS ACGSPFLPGPITESLPLPPGLGSG SELPSLYLVSGIYGGVRRGPPA RLEA
19017	49385	A	19126	1228	2447	TSQGSSPPAHIGRWSSNHKKGL GSSFSQSCCKAEALVKNAWPPT QA*VSICCFEQDLGRGQQKGKS GGKWQKTAESREAVTECPACY RAARCRAAGDRGLRAEGAAAG HTASPSAYRVRGERGHRDMHS ASARLSHPGETNLMLGLAEPSV TSH*SHPFRQS*LP*QAGP**EM/ PLPPSARDSSDLCSG\SPSHDLLP LPNTVIFWGPSSPQDWQPLPLSP FCVSQAAGSPCSPLLQGLEPGGI STSCPPGPAPYIDFGAVSGAGQS AAQRGAHFPAAMAERPSAGTS GSSGISGAIAATVVSWVAEGEQ AVKCLAEGSTRQTGQPSRRAPS RGCPAPGAPPGRAAPPQAPPAA PAAGGGRGPPAAPRAPAPRPQP QGAPRPVSPCRGTGAAPPPTLV WGLSSEAEG

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19018	49386	A	19127	164	563	CEAALKGDSGGSPWPDEKPKE GVKTENNDHINLKVDGAEMVT VV\QFKIK\RHT\PL**T*LKAYL* TDRGLSMRQIRFRI*PGNPIN*K QTHLHQLGNGRIEDYNLMCFQ QARPGGVYLKKGTCFFYSKNS VSF
19019	49387	B	19128	166	426	
19020	49388	C	19129	76	285	
19021	49389	A	19130	3	179	
19022	49390	A	19131	93	172	
19023	49391	A	19132	1	2742	
19024	49392	A	19133	1287	2571	ILRQWLLASPEEKTGRPALASG SAETLSWLRAQGREPRGPA*SA VGAEHRTRTAPGSDPRCGILPS GRSPPSP/PARLFLASVPATI*AM TPSPTRLPAWPPPCRG/PDASPE VVRKGGKAGQPRGSPQPWRSG AEEIVEVGLLPLTPRALLFPQVP TALPAVYHFLAACEGICPHSCA APSMIELWDFLIQQHQPEKAVA CTTTHIPGLRISALNKHRAWGG TDDDVAASEMPLGAAGAEPW D/VE*LLPAALKIPTGHTATTSW GAGP*SPQGSCKG\SGVGSGAT ADLLAPTAGVGTSRTACGGGT QFMSEGAPGVMNNGSPDWSST QFMSEGAPGVMNNGSPDWSSN LSQPQPMHLLYLTTWFLERPM CCPDTTALTQTLPVPSFSYPVCT SHIRQNPHLHFLRAPSPHYTTA CSFEPQRFLEQQQDLL
19025	49393	A	19134	31	202	ILITYIIKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQFL
19026	49394	A	19135	410	867	LLTLSRTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRVWTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISFRVFAA GQGLLGGYSNPRYSFSF

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19027	49395	A	19136	111	743	VITILTPMLADRTRRIERPPKKK GTTSLGQRKWLLTQDWPSVYP VA\HPFKPSAVP\LPV\RMGYPV KKGRAHGDRRGNLELLKISQFF WILTSCSNLKSTCEALKDF\CTG VGQPHWDSGRKKMLKKHFSN WKFGQHLDLCFHQGPSGSGNP RARVVVLKSKAFLV*I*HDHAK KTLITLVGERYCKTPDVLTIKQ NRWPLRSQITIMPVYL
19028	49396	A	19137	305	2291	YLDAEKMGQKASQQLALKDSK EVPVVCEVVSEAIVHAAQKLKE YLGFEYPPSKLCPAANTLNEIFL IHFITFCQEKGVDEWLTTTKMT KHQAFLFGADWIWTFWGSNKQ IKLQLAVQTLQMSSPPPVESKP CDLSNPESRVEESSWKKSRFDK LEEFCNLIGEDCLGLFIIFGMPG KPKDIRGVVLDSVKSQMVRSH LPGGKAVAQFVLETEDCVFIKE LLRNCLSKKDGLREGGASPGSL RLAAPGPPLTLNAACPLRLAVL AAMAAAALPAWLSLQSRARTL RAFSTAVYSATPVPTPSLRVDD LHLTEIVGMLDSVLTPEDSSGK YRFISGEVLCRITGCFTGVRVEA KDLFGGCCSNPNEVMVTWIKVI VEKEVWLYLRYILKALPPRTEK MAVDQDWPSVYPVAAPFKPSA VPLPVRMGYPVK*GVPMAKEG NLELLKIPNFLHLTPVAIKKHCE ALKDFCTEWPAALDSDEKCEK HFPIEIDSTDYVSSGPSVRNPRA RVVVLRVKLSSLNLDDHAKKK LIKLVGERYCKTTDVLTIKTDR CPLRRQNYDYAVYLLTVLYHE SWE\TEEWGKK*D*SRHGKSIY GENSSSERKYPGERFSR*KLLR KNMGN*LKKSS/CGTKEIEEYK KSVVSLKNEEENENSISQYKES
19029	49397	A	19138	3	233	
19030	49398	A	19139	1	256	
19031	49399	C	19140	5	114	
19032	49400	A	19141	8	444	TTDKEQ*EL*LLLDTE*GSYTKE CHTDSLSRY*TSSTSAEDRDDSL LRRSGSYRDL*E*IPYSCRLDKD DSTDCIKLYEQILAE\NDKLKAQ LHDTNMELTDLKLQLEKATQR QERFADRSLLEMEKRERTALQR RISEMEERLQM
19033	49401	A	19142	1	287	

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19034	49402	A	19143	211	346	
19035	49403	A	19144	175	3381	EDPAAGEGMKMADAKHKRNE QLKRWIGSETDLEPPVVKRQKT KVKFDDGAVFLAACSSGDTDE VLKLLHRGADINYANVDG/LSH ALHQACIDDNVDMAKLLVDNG ANINQPVNDGWIPLHAAPSCGY LDIAEFLNGQGAHVGAVNSEG DTPLDIAEEEAMEELLQNEVNR QGVDIEAARKEEERIMLRDARQ WLNSGHINDVRHAKSGGTALH VAAAKGYTEVLKLLIQAG\YDV NIKDYDGWTPLHA\AAH\W
19036	49404	A	19145	1	2406	
19037	49405	A	19146	1154	1365	
19038	49406	A	19147	1	293	MGVSVLDFSHSDKCEVASRFAS GMPEPTNIVLPKLEVADTLGGC TTIPESDLEERSVEQDSTELFTN HRHLTAETPR/PW*RLDGLHKQ VSPLQGVSE
19039	49407	A	19148	3	1290	VSQATDVEVGTDLVPSVTVKV TLQNRVILQKAKLSVYVQPPLE LTCDQFTFEFMNRNPDGIPRVIQ CKFRLPLKLICLPGQPSKTASHK ITIDTNKSPVSLLSLFPGFASQSD DDQVNVMGFHFLGGARITVLA SKTSQRYRIQSEQFEDLWLITNE LILRLQEYFEKQGVKDFACSFS GSIPLQEYFELIDHHFELRINGE KLEELLSERAVQFRAIQRRLLA RFKDKTPAPLQHLDTLLDGTYK QVIALADAVEENQGNLFQSFTR LKSATHLVILLIALWQKLSADQ VAILEAAFLPLQEDTQELGWEE TVDAAISHLLKTCLSKSSKEQA LNLNSQLNIPKDTSQLKKHITLL CDRLSKGGRLCLSTDAAAPQT MVMPGGCTTIP\ESDL*ERSVEQ DSTELFTNHRHLTVETPRPEVSP
19040	49408	A	19149	48	642	WNSALREPRLNGADMAKSKN HTTNNQ\SRKWP\RNGIKKP\RSP KIRILLKGVAPPSFL\RNM\RFAQ ESPNKKGP*RRLQANKLPRAMS ATLPRAIKA\LVKPQGGLSPKIP\ KGVSSRKLDSTCLTFAQPQALG SVARCP*LPRGPRL\CPPKAKAK AKAKPRPKPRPRAKDQNQGPG LQPQASVPAQ\APKRTQAP\TKA SE

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19041	49409	A	19150	1953	2447	WTPQYMDTEYKNGPWMMEK KVWLDP/NETNEIPNANFRQQIR KLIKDGLILRHRKPVTVHSRAQ CWKSTLARRKGRHLGIESKKID RHMYHSLYLKLKGNVFKHKRI LTEHSHKLKADKARKKPLADQ AEARGSKTKEARKLREEHLQT KKEEIIKTLSQEEKAKK
19042	49410	A	19151	1	693	MAVMEKLYWVNREESYASLR VHLPICNATTMSMLSLQKRLAS SVLRCGKKKVWLDPKETSEIAN ANSHQWIRKLIKDGLIIHKPVTV HS/*ARYR/KNTLACQKGRHMG I*KATANARMPEKIMWMR/RM RILCQLLRRYCDSKKIDHHMYH RRYHESKKVDRHMYHSLYLKV KGNVFKNKRILMEHIHNLKAD KACKKLLADQAETRRSKIKEAR KHREEHLQAKKEEIIKTLV
19043	49411	A	19152	34	280	EVIHAAIGEKKGSY/NA**PWVE EQLTRQPLIHHQPASLHSVY/RC RYHSLYLKVKGNVFKNKRILM EHIHKLKADKARKKLLA
19044	49412	A	19153	2	625	HEAMSMLRLQKRLASSVLRCG KKKVWLDPNETNEIANANSRQ QIRKLIKDGLIIRKP\VTVHSRLR CRKNT\LAR*KGRHMGIGKRK VPANA\RMP\EKVT\WMRENEG FCRRLASEDTRES\KKIDRPHVV TALYL\EVKGNVFKNKRIL\ME HIHKLKA\DKARKKL\LAD\QAE ARRSKTKEATKRREERLP/ARPR KREII*TLSKEEETKK
19045	49413	C	19154	154	291	
19046	49414	A	19155	3	253	
19047	49415	A	19156	2	474	FKDKQNKPTGFALGSIEGRVAI HYINPPNP*V*LCQLADFTGLFL TKEDLHEPLSFSAKDNFTFKCH RSNGTNTSAPQDIYAVNGIAFH PVHGTLATVGSDGRFSFWDKD ARTKLKTSEQLDQPISACCFNH NGNIF/AYASSYDWSKGHEFYN PQKKK

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19048	49416	A	19157	97	1728	IRGFFRGSQGSFYRRLKEASGS WDFCPRSWPSSLRARSGSQTPE TLLLPAGVFRRSETPMFKMSLF GTTSRFGTSGTIMFGSAT\TDNH NPIEGY*K*HSFSLMDSIG\CSCL FSPPTLPGNFLIAGSW\ANDVRC W\EVQDSGQTIPKAQQMHTGP VL\DVCWE/SDGGSKVFT\ASCG \KTAKMW\DLRQ*PRRLQIAQH\ DAPV\KTIHWIKAPNYSCVMTG SWDKTLKFWDTRSSNPMMVL QLP\ERCYCADVIYPMAVVATA \ERGLIVLIQL/ERIQPSEFRRIESP L\KHQH\RCVAIF\KDKQNKPTG F\ALESIQGRVAIHYINPPNPA\K DTFTFK\CHRSNGTNTSAPQ\DI YAVNGI\AF\HPVHGHPCNCGD LDGRFSF\WDI\DARTKLKNFRE QLDQP/LSSAC\CFNH\NGKHILP YAS\SYDWVKGDH\EFYNP\QK KKFTFFPA*MQAEELKAPGNKE VVAGRTLGSAQSLFLLHSGLIS VRIWAPNLVGVVSPWTMEFQP PGENDVIVQQLESPRRPAGDLP VFSIPTGLVAEVFSGKPKGGLK
19049	49417	A	19158	1	1254	
19050	49418	A	19159	1	921	
19051	49419	A	19160	1	1386	
19052	49420	A	19161	49	731	

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19053	49421	A	19162	61	1533	PLKAKMGKEKTHI\NIVVIGHV DSGKSTTTGHLIYKCGGIDKRTI EKFEKEAAEMGKDSFK\FAWV LDKLKAERERGITIDISLWKFET SKYYVTIIDAPGHRDFIKNMITG \TSQADCAVL\IVAAGVGEFEAG IS\KNGQ\TREHALLAYTLG\VE QLIVGVNKM\DSTEPPYSQKRY EEMWLREVSTF\IKKIWLQPPTQ *HFVPISWFGIGDNM\LEPSA\N MPWFKGW\KVTRKDGNASGTT LLEALDCILPPTRPTDKPLR\LPL QGVH\KLGGIGTVSSAPMET\GF SNPGMVVTFAP/SSTVTTESKIL SKMHP*SFEVKLLPGDQCGPSM SKNVFCQGMFRRGKRLLGDQQ KMTPPNGKAAGLHWSRVIIL\N HPRPK*GAGPMPLYLDC\HTGS HLHAKFAELKEK\IDRR\SGKKL EDGLKFLKSGDAAIVDIVPG\RP MCVESFSDYP\PLGRFAVRDMR QTVAVGV/ISKAVDKKGCWEL GKVTKVWPRKAPEG
19054	49422	A	19163	1	514	EFGTRAKKEAPAPP*SLKPKRK AFKGPRKAV\LKGV\HSHQKEE DPARSPTFPGGPKTLR\LRRQP\K YPRKSRVPGETRLDHLCLSI\NF PLTH*VLPMKKIEDNNTLVFIV DVKANKH\QIKQAVKKL\YDI\D VAKVNT/LWIRPDGEK\KAYVR L\APDLPIAFGMFANKIWGFI
19055	49423	A	19164	433	1015	GLISNLDMASRGAS*\PTGPDTG NKICQFKLSTSGESPAVCKSSLV LRFVKGQF\HEFQESTIGAAFLT QTV\CLDDTTEKFEIW\DTAGQE RYHSLAPMYYRGAQA\AIVVY DITNEESFARAKNWVKELQRQ ASPNIVIALSGNKADLANKRAV DFQ\EAQSYADDNSLLFMETSA NTSMNVNEIFMAIGKINISF
19056	49424	B	19165	1	2511	
19057	49425	A	19166	2	360	

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19058	49426	A	19167	125	211	FRPGSPRQPRAQPISAPDCTRA MVGRRAL\IVL\AHSERTSFNYA MKEAAAAA\LKKKGWEVVE\S DLYAMNF\NPIIS\RKDIT\GKLE GPLRTFQYPGRSLFLAYK\EGHL EP/EIICGLNKKKLEAADLV\IFQ FPLAVGLEVPAIL\KGWFEPSVH KESFA*HFTAGHVMDKGPFPG VKKAVAFPFTTGG\SGS\MYSC QG\HG\DMNVIL WP\IQSG\ILPF LGLPKSLDPQLT\YSIWPPLPAR RPEFSILE\GWKK\RLE\NIWDET\ PLYFAP\SSLFDLNFQAGF\LMK KEVQDEEENKKF\GLSVG\H\HL GKSIPTD\NQIQS*KRECTVHYT RDSHKVAAGAAQLTESLVPAR VAPATTSPANQRPGLHQSHGR
19059	49427	A	19168	2	331	WVDSQQK\RYVPVKGDHVIGIV TAKSGDIFKVDVGGSEPASLSY LSFEGATKRNRPNVQVGDLIYG QFVVANKDMEPEMVCIDSCGR ANGMGVIGQDGLLFKVTLGLIR
19060	49428	A	19169	145	350	QEFHLSSEPSIRLGRSLYHIHHL FASKKVLD*QWLDQSL*VCSW EHMRRSQ*GIFSRLANRGFQNG DC

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19061	49429	A	19170	1	1863	MAVAIRLSADTQWEDSPGKSIL ELHMSCTKIPERCEADKKESTS SWCTRKIRFRMDLEKECKVLLS GGGGSRMGSQKGDGVGRWSSP RVGLPSSQTLLRPPPTDFHIAPL SKARQHLLVSVSVLFCFSAPLD VQPLKVLDECQNQRACHLLVN SRVFGPDLCPGSSKYLLVSFKC QPKQMFTQQGPGPVLSIGETQV STSSVTRSSSPVGPDIHCEFHTN MCKIPDELKNKTVCEDQELKL HCHESKFLNIYSATYGRRTQER DICSSKAERLPPFVFTRYYCFLY APVSSIANPVKGCFHLGKKQDC LSYSALQVLSRRCYGKQRCKII VNNHHFGSPCLPGVKKYLTVT YACATLSSMGPILAEVPPEAKK VTLSTSLDSSSGRMEDGRLDTG HTEVPVTSGLFIRVLNKKQNFS LQIRCSFGRGPGKLRHCWAGA. AIALGTEYILVKGDQVTGIVTA KSGDIFRVDVGGSEPVSL\SYLS FEGATKRNRPNVQVGDLIYGQF VVANKDMEPEMVCIDSCGRAN GMG\VIGQDGLLFKVTLGLN*E SLLASQICE/ISIQEVGKL\LPLEI VFGMNGRIWG*GQKTHPSQTLI LA\NIL\EACEHMT\SDQRKTDLP
19062	49430	B	19171	29	82	
19063	49431	A	19172	1	427	

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19064	49432	A	19173	1	1548	MTMAAAAVVARGAGARAATA AALRGGCGTAARGRPCAGPAR PLCTAPGTAPDMKRYLWERYR EAKRSTEGTKKYTTSLNARHY YTHFTEENEDEINSSSSYASQKK TFEINPRHPLIRDMLRRIKEDED DKTVLDLAVVLFETATLRSGYL LPDTKAYGDRIERMLRLSLNID PDAKVEEEPEEEPEETAEDTTE DTEPDEDEEMDVGTDEEEETG KESDDPMAYIHFTAEGEVTFKS ILFVPTSAPRGLFDEYGSKKSDY IKLYVRRVFITDDFHDMMPKYL NFVKGVVIRKKLVRKTLDMIK KIADDKYNDTFWKEFGTNIKLG VIEDHSNRTRLAKLSRFQSSHH PTDITSLDQYVERMKEKQDKIY FMAGSSRKEAESSPFVERLLKK GYEVIYLTEPVDEYCIQALPEFD GKRFQNVAKEGVKFDESEKTK ESREAVEKEFEPLLNW\MKDKA LKDKI*K/ALWVSSAALTESPVL LLVAQPVRDWS\GQHWERIMK AQAYQTGKDISTN\YYA
19065	49433	A	19174	37	266	WADRAAGGVRILTQGCVGGG GSCDRRGLETSPARTPVRALWV LG\LCCVLLTFGSV/READDEVD VDGT\VEEDLG*KYEKDQVTDD EVVQREEEAI\QLDGLNASQIRE L\REKSENFPF\QAEVNRMIETLF IQFHCIKNKEIFLERLISNSSC\AL DRLSLISLT\DENALSGNEELTV K\IKCDKEKNLLHVQHTGVGM T\REELVKN\LGTIA\KSGTKRVF *TKRPEA\QEDGPSQPS*IDWPS LGVRF
19066	49434	A	19175	233	664	RAPEQSSGVSAAEQERVPNAG WPCSVAPTCPSPRSAEPARCT* GKEEGG/CEDSDRADSGSPFQE PRYPSSGPFPIPQASFPCPCLLVL GIRGHSTILQYRGQEHHVLFTG RCLLVDPTLLVLVVSKKSPNAA RDQPARYPRGPL

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19067	49435	A	19176	1	672	MAEAGPKPQRTLMWAWESVL SQRKPREAGRLSEGCVKATGTP GFGWQARPDQKEHRLDGRVID PKDRHGLVKDTEPRLNEQSLCG GLNPEATEEKIREYLASLGRRR PVKKVLEKKFHTVSGS/KCGPQ VPPSWSETYRTRA*SGDQLGTP AAPNPRWPME*EQEIEAQRRSA HSGARAPWPPWPPRPDGPPGNP GPKFMVSLSCWNISSLRAGLLY AGCGCSP
19068	49436	A	19177	3	684	RHASARKKYNPPSWFHRGLPPP EDQEDEMSVSEELE\PITLTPSSA LKPSDRMTMSSLGERACCRDY QRLGLGTLSSSLSRAKSEPFRIS PVNRMYAICRSYPGLLIVPQSV QDNALQRVSRCYRQNRFPVVC WRSGRSKAVLLRSGGLHGKGV VGLFKAQNAPSPGQSQADSSSL EQEKYLQAVVSSMPRYADASG RNTLSGFSSAHMGSHGKWGSV RTSGRSSGLG
19069	49437	A	19178	1	341	
19070	49438	A	19179	1	3710	MVSGARAAAAAAAAAAAAER TRGVPGHPDSTGRLPAHQQLQ RGLLFRQLGITNVLSLVCATLM EHEVLFLSRSYQQLTDACRSLL ALLFPLRYSFTYVPILPAQLLEA LSTPTPFIIGVNAAFQAETQELL DVIVADLDGETVTIPECVHIPPL LEPLQSQTHSVLRMVLDPELEL VDLAFPPPM/HDKELRLFHQLL QGYLWCLHV\VCIHPEPVIRFH KAAFLGQCGLVEDNFLMNVLE GMAFALFVLECGVP
19071	49439	A	19180	1	303	
19072	49440	A	19181	14	942	TKLTGSRG*LA*NPCM/HNNCE SCVDLLFVRGAGNCPECGTPLR KSNFRVQLFEDPTVDKEVEIRK KVLKIYNKREEDFPSLREYNDF LEEVEEIVFNLTNNVDLDNTKK KMEIYQKENKDVIQKNKLKLT REQEELEEALEVERQENEQRRL FIQKEEQLQQILKRKNKQAFLD ELESSDLPVALLLAQHKDRSTQ LEMQLEKPKPVKPVTFSTGIKM SVGITLCPAEEHTFNDERSFNLS SSWSKFNKPPSTLPFKVLDEER LVELKVPNTLITKLVPFAISPCS EAIQDHPAILLAYKKTPFWRLQ
19073	49441	B	19182	49	456	

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19074	49442	B	19183	53	333	
19075	49443	A	19184	2	208	VYPELQITNVVEANQPVTIQNW CKRGRKQCKTIPHL*FPYRCLG EPAGRGAGVDWGPGLEGRKRG CSC
19076	49444	B	19185	51	300	
19077	49445	B	19186	148	3568	
19078	49446	A	19187	1	3411	
19079	49447	A	19188	2	2416	NSRGAACAGPRETAAVAARAE QGRGGSHSHSSALGAPRRVAM LPGLALLLLAAWTARALEVPT DGNAGLLAEPQIAMFCGRLNM HMNVQNGKWDSDPSGTKTCID TKEGILQYCQEVYPELQITNVV EANQPVTIQNWCKRGRKQCKT HPHFVIP\YRCLVGEFVSDALLV PDKCKFLHQERMDVCETHLHW HTVAKETCSEKSTNLHDYGML LPCGIDKFRGVEFVCCPLAEES DNVDSADAEE\DDSDVWW\AG ADTDYADGSEDKVVEVAEEEE VAEVEEEEAD*LTRTDEDG\DE VEEEA\EEPYQEATERTT\SIATT TTTTTESVEEVVREVCSEQAET GAVPSNDLPLVL*CD*REVCPIL LRRMWRQPEQL*HRRVLHGRV WQRI\PTTAASTPDA\VDKYLET PGDENEHAHFQKAKERLEAKH RERMSQV\MREWEEAE\RQAK NLPKADKKAVIQHFQ\EKVESL *QEAANE\RQQLVETHMARVE AMLNDRRRLALENYITALQAV PPRPRHVFNMLKKYVRAEQKD RQHTLKHFEHVRMVDPKKAAQ IRSQVMTHLRVIYERMNQSLSL LYNVPAVAEEIQDEVDELLQKE QNYSDDVLANMISEPRISYGND ALMPSLTETKTTVELLPVNGEF SLDDLQPWHSFGADSVPANTE NEVE\PVDARPAADRGLTTRPG

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19080	49448	A	19189	1	2355	MKSIFTSEISSVLIFVNPEPGRVV SFLGSGRREHAEERARGPRETA AVAARAEQGRGGSHSHSSALG APRRVAMLPGLALLLLAAWTV WAL\EVPTDGNAGLLAEPQIAM FCGRLNMHMNVQNVKWDSDP S\GTKTCIDTKEGILQYCQEVYP ELQITNVVEANQPVTIQNWCKR GRK\QCKTHPHFVIPYRCLVGEF VSDALL\VPDKCKFLHQERMGC FAETHLHWHT\AAKETLQ*RRS TNLHDYGMLLPCGIDKLRGVEF VCCPLAEESDNVDSADAEEDDS DVWWGGADTDYADGSEDKVV EVAEEEEVAEVEEEEADDDED DEDGDEVEEEAKEPYEEATERT TSIATTTTTTTESVEEVVRVPTT AASTPDAVDKYLETPGDENEH AHFQKAKERLEAKHRERMSQV MREWEEAERQAKN\LPKADKK AVF\QHFP\EKVESLEQEAANER QQLVETHMARVEAMLNDPRRL ALE\NYI\TALQAV\PPRPRHVF\ NMLKKYVRARTEGLVSTSL*HF EHVR\MVDPKKAAQIRSQVM\T HLRVIYERMNQSLS\LLYNVPA VAEEIQDEVDELLQKDANYS** RLWPTMISEPRI\SYG\NDAL\MP SLTETKTTRGSSVPVNEE\FSLD\ DLEPVHFFWWLTSVPANTENE VE\PVDARPAADRGLTTR\PGSG LTNIKTEEISE\VKMDAEFRHDS
19081	49449	A	19190	103	463	PLLYAMSTGKRWLSFGSMIPPV AICASNKRIPWPFSMSSLFMAW NKEMMFPVSGSLYPVTARSAD RSFSLNSMPTRPLL*ASSTGNLK LLTGSTIKPVAAWASSNSRAVP GRTKPIFMAS
19082	49450	A	19191	1	182	
19083	49451	A	19192	3	437	MVHAEISDEGFFLSAPIALTQA WLNIPKT\RRTFCK\KCGKHQPH K\VTQYKKGKDS\LYAQGKRRY DRKQSGYGGQN*KPIFRKKAKT TKKIVLKALSALSPTCRSKSKC WLFKR\CKHF*TGEEIRKRKGQ VDPVLKCHLLFMEGH
19084	49452	C	19193	341	421	

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19085	49453	A	19194	15	1066	VLACTVEASVIGGQKREMNMG SIVREGFMEEAGPRIGFNLSFFI QSTVTGSSSVGSTQLQPLSLPPA TAGQEPRGTGPLGSHNSCPAPE PVSYGRLNDPPATTHPGSFTRF HSKPLTSSCWDSEMEGCVSNL MVCNLASFLNVSTNPCAFFPW YFYYLLLL*AGWSPLHIAASAG RDEIVKALLGKGGVLNVYTNT DRFLHCFLLSSPSFQIAVMLLEG GANPDAKDHYEATAMHRAAA KGNLLARNPNHYIELVVINWSL VVPDFRHLACDEERVEEAKLL VSQGASIYIENKEEKTPLQV\AK GGLGF*YSREWVGRFKQLGFIL YFVLLCLLSPVSYKLMYLCTRH
19086	49454	A	19195	1597	1923	
19087	49455	A	19196	551	747	
19088	49456	A	19197	1059	1296	
19089	49457	B	19198	1	1281	
19090	49458	A	19199	3	565	LPGRLLLLNFRQRRQIDRPSMN DTRNLSRT\RKFHAPTRPTSEEN KWVIDVLSPAGRPTVP*DQKFR EK\LA\KMYQAPHPDV\ILVFGF\ RT\HFGGGKTTGFG\MIYDSPWI MQRKNEP\KHRLAR\HGLYEKK KDLKKATEKERQEPELKKVQG GLAKGPLLGAGQKEEMKCLAV ELEIGSQPKELKVLQ
19091	49459	A	19200	2	476	

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19092	49460	A	19201	1	2448	MRGSILKECGSKERASQVDLEY SRGNTASFAMCFHDRARIMKG SQRSRKLTGGEGREEGERVENK DFLDLHGQIQVRLVVKTASLLS RVTYIAEVEGRETDAGWRNEL QVGRLDSGPDILVVSISTDHTLV DTHLEAVGGHSHEFPYFKNHL ACHVESELQRDRNGHRDAGWR NMRHGITDKEMQDSQGSSDNH VLGSLRSWSARAAPALPGLPEE AFVEMSTEGGFGGTSRSDAQQS LKSFWLRPRFFITELTLRAWIHT EDNNCRTYVAMAITKFDQLDF LIDIVLRDELKPPKCQEEVLQSV TPAEPVQYYFTLAQQPTA\VQV QGQQQGQTTASSMTTMQPGQII IAQLQQGQTTPVTTQVGEGQQ VQIVQAQPQGQAQ*AQSGTGW TVQGQIQTLATSAQPITQTEVQ QRQQ*FSQFTDGQQLYQIQQVS IPAGQ\DLAQ\PMFIQSANQPSD GQAPRSHEVIAAAPAARRERER ELAGRGPFCPPPAGNVRALKSR RCLPGERRERARKKKPEGGAA ASERGETDSHPGASGQGPRDSG RVPLGMWSRRGLGVSRAPLHL LLGVSTSFPLPLTPLIPTTAVVN PLKPLKNRIKAPHRRMPLVPGG SQNLGTVRARISTRQSHAEPST DNERVLSMTQDIHSIFLNLKNIT WICTLQSCGFLLSNLCKDIVHK AGSGEARTRWSPRAQAGTHED
19093	49461	C	19202	124	369	
19094	49462	B	19203	739	870	
19095	49463	C	19204	787	969	
19096	49464	A	19205	101	331	
19097	49465	A	19206	137	415	
19098	49466	A	19207	86	221	
19099	49467	A	19208	1	1347	
19100	49468	A	19209	120	899	FGARGNLKKAYSTRSKMAELN THVNVKEKIYAVRSVVPNKSN NEIVLVLQQFDFNVDKAVQAF VDGSAIQVLKEWNMTGKKKN NKRKRSKSKQHQGNK\DAKDK VERPD\ACPLQPQPPQIQNGPM NGCEKDSSSTDSANEKPALIPRE KKISILEEPSKALRGVTGPNIEK SAKDLQRCTVSLTRYRVMIKEE VDSSVKKITAAFAELHNCIIDKE ASLMAEMDKGIEEAMEILTAR Q\RKAEALKRLTDL\AS\QMAE

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19101	49469	A	19210	211	2150	ADTKPERGVSSAVFASGSEGRR LGCVLLSSSETRLLSGTLLWIPR AYSTRSKMAELNTHVNVKEKI YAARSVVPNKSNNEIVLVLQQF DFNVDKAVQAFVDGSAIQVLK EWNMTGNKKNYKRIRSKSKQH QGNKDAKDKVERPEAGPLQPQ PPQIQNGPMNGCEKDSSSTDSA N\EKPALIPREKKISILEEPSKAL RG\VTEGNRLLQQKLSLGG\NP KPIHGTTERSDGLQWSAEQPCN PSKPKAKTSPVKSNTPAAHLEI KPDEL\AKKRGPNIEKSS/VKDL QRL/CTVFF*LEYRVMN*RERK WDSSGERRSKLPFAE\LHNCIIE QKEV\SLMGRKWD*SLKEGRP WEILDWLVRKKSKKKLKRLTD LGQSRMAEMQLGPKLR\AEIKH FVSEAVNYDE\ELGKSCPGFSC DIEQ\LK\AQIIALPGKITHPK\NN YFLKELPCSSLL\PLLNAARSKP LGKTEVTFSRKSSTHNKPSEGK AANPKMVSSLPSTADPSHQT\M PANKQNGSSNQRRRFNPQ\YHN \NRLN\GPAKSQGSGNEAEPLGK G\NSRHGTQEGQPH/NRFGFRPK NKGRCQKIQEASLGIEGPPRAP AHFLKRPRAKGSHAADTFGRA RAFSGVS/GSVRGSQCNLFPT\RI EVSTDAAVLSVPGCDRWVA
19102	49470	A	19211	93	180	
19103	49471	A	19212	3	39	
19104	49472	B	19213	1	888	
19105	49473	A	19214	863	1509	GCAGPCLVNQMFTSSILCKSHC HSLVSINQGHNAPWKAAG\PLP LKAGYC\QSFSPCDSLKYG\SWD EKDLTVPQPDTRKASVLRWISQ RGKPLAVDMEEG\HCL\CLPPG N*NVLGCKTPIVHLFNSELGRK AALWREARHVG\SNAALLFFTP LRCLGGEKHKSGLHAHPGIVP\S LELNYDIDSFAHVFVFVVAVEL PLIITLLPYCIPLCCNNEK
19106	49474	C	19215	289	510	
19107	49475	B	19216	534	1686	
19108	49476	B	19217	1	1062	
19109	49477	B	19218	1	1878	
19110	49478	B	19219	1	747	
19111	49479	B	19220	230	786	
19112	49480	B	19221	67	6011	
19113	49481	B	19222	1	3455	

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19114	49482	B	19223	1	4763	
19115	49483	B	19224	65	4534	
19116	49484	B	19225	512	4782	
19117	49485	B	19226	345	2194	
19118	49486	B	19227	267	7391	
19119	49487	A	19228	578	739	
19120	49488	A	19229	419	1410	KQRQARERHLPRIPQLSAVVTIE TL*RK*RNFAELKIS/RLRKKFA HKMLQKARRKLIYEKVKHCHK EYRQMYRTEIQMATMARKAG NFFVHPKPKLAFVIRISAISGVSP KWKNKQLCPLNHVFGLGMGD LRAFGLADGTGPSGGEITGMRD LRGPLSVRAPSAGVAEIPRHLIV FEDVVNGKFLQTSRCEISGSKN KVWQTLLKNKRERQRLPTGFG RLADQRAYGEAKNNCGQVGL VETLWERHLLRIGVYIATSSLA VPTLSSNYNGLAHDQSCSDTVQ RSTGAPEAWDRGYCVGRGAQG IPIFFLDRPLTSLFDEARGSSSAS
19121	49489	A	19230	3	307	AGTMEGVEEKKKEVPAVPETL KKKRRNFAELKIKRLRKKFAQ KMLRKARRKLIYEKAKHYHKE YRQMYRTEIRMARMARKAGN FYVPAEPK\LAFVIRIRGI
19122	49490	A	19231	3	160	GRVLL*DKTSRGTIRQQQLLFT NICCSAASA/G*YPGKQGLEWT SSRLQQTCS
19123	49491	A	19232	303	570	GLCIRHVLVPSAAGLLEFAGGP LQTLFAWVSAAEAAEQQIWVN SKCC/CPDRSSGSFVSEEYLAV* GVGLTLSSASLMLGAVDWSCS HSA
19124	49492	A	19233	1	176	MQYVQQKPKLKFQVHICAYRK TVLQPPLLIPRQT/WVWSGPPA NSNRPAAGGADC*KEN

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19125	49493	A	19234	1	1977	MFAVLQAPLVIPRQT/WVWSGP PANSNRPAAEGPDC*KEN*RQT GSGVDLQQTPTDLQLRVLIVRR KTNEQKGHPHQNPICTSPSSKT KVDTTTNMGEKQSRKTENSKN QSASPPPNLKKKREKNQIDAIK NDKGDITTDPTEIQTTIREYYKH LYSNKLENLEEMGKFLDTYNLP GLNQEEVESLNRPITGSEIEVIIN SLPTKKSPGPDGFTAEFYQRTK DKNHMIISIDEEKAFDKIQQPFM LKTLNKLGIDGTYLKIIRAIYDK PTANIILNGQKLEAFPLKAGTR QGCPLSPLLFNIVLEVLAREIRQ EKEIKGIQVGKEEVKLYLFADD MIVYLENPIISAQNLLKLISNFSK VSGYKINVQKSQAFLYTSNRQT ESQIMSELPVTIASKRIKYLGIQL TRGVKNLFKENYKPLLNKIKED TNKWKNIPCSWIGRINIMKMAI VPKVIYRFNAIPIKLPMTFFTEL EKTTLKCIWNQKRAHIVKSILS QKNKAGGIMLPDFKLYYKATV TKTAWYWYQNRHIDQWNRTE PSEIMPHIYSYLIFDKPDKTRNG ERIPYLIRWCWCWQNWLAICR KLKLDPFLTSYTKINSRWIKDL NVRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRQ PTEWENISAIYSSDKGLISRIY
19126	49494	A	19235	206	456	
19127	49495	A	19236	2	385	NLCCSAASAGDTQANRVWSGT PTNSSRPEVSSGAMDGEGWGL PVDPLTPGHQDALPWQRCYHP CSSSSVPPRQACASPASCSSSAA W/TSASTGPWHSGCGSSCGSCC CWGSPSASVGVGAGAIRSRTV
19128	49496	B	19237	1	642	
19129	49497	A	19238	128	584	
19130	49498	A	19239	4054	4578	QSGPSAAGLLEFAGGPLQTLFA WVSAAEAAEQRILVNSRCCCLI VP\RKFCLRGVASHVRCQSAPY DVFCHGITLAKCWCSALGLPSL QSCEPNALFFINYPVCGI/TAPCC KVEGTMG\VGPKSPQL\SYNVL GSDNNGVLLGSMAIFTILILLIH EHGMFFHLFVSSFISLSSGL

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19131	49499	A	19240	1	948	MVLEKAREEVDPPSMLIPPVTQ CGQLPRSQCPQPTLSRMLTLEV GISLGIIVLMISLWPDTVKEYQS REALSFKKYNKNPGLLKFAGDP LQTLFAWVSPAEAAEQQISALC FLWKLRPRGAPTRCQPLLSYTR CLSAPAGSFVYTMRGKPPIQAS VMADASPPTKIEHPRTTSDCCV ASKNFKPVDLSLLCSMGVGSAE LDHWATWLQSPFQGSERFCLA GVPGTTGV*KETPAASSVSAQM AAQFCA*N/HRTLVV*APKGIL WVCGLRRPWEKRSICAGVHHS SWHSPSWLPLARGGSSSTPCTS WVRRCPTLHL
19132	49500	A	19241	171	1345	YCPKEGTLDFNFAFNMTAVNV ALIRDTKWLTLEVCREFQRGTC SRADADCKFAHPPRVCHVENG RVVACFDSLKSVTAVPFLFMAL GLSREPETVPASMVQTFSLGVG GGAGSV*PDENCKYLHPPPHLK TQLEINGRNNLIQQKTAAAMFA QQMQLMLQNAQMSSLGSFPMT PSIPANPPM/SFESLRYHILGMG LVPAELVPNTPVLIPGKPTSLQL PGSCLGPKLMAFQINWEVLPRN FQRG\NC\SRGEND\CRY\AHPTD ASMIE\ASDNTVTICMGYIKGRR TVGVWGIKAKSSKQRILDTKGS HQGNSFVRGTDYLIPICTNMSK AKGTAFLKWMQKLVYNGSSG QCSPAFFCCAWKEHSEKAGRA SGAKCNRHRHTNPVFLMREGA IS
19133	49501	A	19242	61	544	KFNP\FVTSRPRARIRKRAF\NAP \SHIPKGRLLSFPPLSPKSLRPEG TNRADSHAPIPKRMIESSRLYR GHL*GSAKLAKVVPRFTRKKY VIYIER\VQREKA\NGTTVH\VGI HPSKQVVITKAKTGTKTRKKIP PNRKAQSRQVGKEKG\KYKER T\IEKMQE
19134	49502	A	19243	652	1042	TPLSSCFLSREKATQLLFPAVVA VPMVLSAMGFTAAGIASSSIAA KMMSAAAIANGGGVASGSLVA TLQS/LG*VSWRGLPTVLPTELP RQACPTLSTLCFFPGATGLSGLT KFILGSIGSAIAAVIARFY
19135	49503	A	19244	48	397	

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19136	49504	A	19245	42	296	GCVGVRPSLHPATSTASGSASP TLARAMASVSELACIYSALILH DDEVTVTEDKINA/APAEEKKV EAKKEESEESDDDMGFGLFD
19137	49505	A	19246	172	519	LGPSFLHDDEVTVTEDKIQMPLI KAAGVNVEPFWPG/LCFAKAL GKRSTLGSLILAMLGGPVGPGS QPAGCLQPAG\GSCPPSTCCWF QLEGEEKWEAKERKIPREF*LID MGFGLFD
19138	49506	A	19247	3	175	
19139	49507	A	19248	2	390	GWDWNCVWEPHHWLCQSL/N SVTQAGVQLCNLSSLQPLPLGF KQFSCLSLPSSWDYRNPSLKQQ LFSYAILGFALSEAMGLFCLMV AFLI\SLPCEGAVSTSHSSPASG WPRVFLFLYLPRQPGERGWLR
19140	49508	B	19249	139	13320	
19141	49509	A	19250	28	450	TNDFNLQNPGSCFPSACPAGVG SERLPVLGWFVGNRSFPPPPQST LSVLGKRLGRNGAIAAGVFGA LFIGYCIYFDRKRLK*PQLKDAE AVQKFFLEEI*L\GEEILAKGVD HLTNPSAFFG/QPNHFPLQMDSF GPFLRFQA
19142	49510	A	19251	164	420	
19143	49511	A	19252	1	329	STHTTYWEGCRTTSAGLLRKH EPGEEAF/FYHST\SKKPGIAGLI KVNVQFVRMMKRSIPWAELNP YHQAHKATGGPLKNMVLFTRQ RLSIQPLTQEEFDFVLSLEEKEP
19144	49512	B	19253	39	368	
19145	49513	A	19254	1014	1290	
19146	49514	A	19255	122	680	LARITRIVRTKVPCSVTMSRPRK RLAGTSGSDKGLSGKRTKTENS GEALAKVEDSNPQKTSATKNC LKNLSSHWLMKSEPESRLEKG VDVKFSIEDLTAQAKQTTCWD GVRNYQAS/RNFLRAMKLGEE\ AFFYP*QLAKKPGIAGLMKIVK EAYPDHTQF*EK\NPHYDPSSKE DNPKWSMKSLILF

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19147	49515	A	19256	2	1005	RISTSTLCPKPKKLIAPPGRAGL ASMGLNEEQKEFQKVAFDFAA REMAPNMAEWDQKDRKADGK GGAVTQEVQAQLLVKHGQKL VSRFQLSSFSYVDSVRTTQSKQ EHLQTDKGLSGKRTKTENSGE ALAKVEDSNPQKTSATKNCLK NLSSHWLMKSEPESRLEKGVD VKFSIEDLK\AQPQ\QTTCW\EG VRNY\QARNFLRAMKLGEE\AF FYH\SNCK\EPGIAGLMKIVK\EA \YPDHTQFEKKQPPPL*PPS*QR GTTPKWPHGWMV/QVWFGMM KRFHSPLAE\LKS\HHQAHKA\S GGPL\KNMVLFTR\QRLSI\QPLT \QEEFDFVLS\LEEKEPS
19148	49516	A	19257	3	727	VRLQFLTPTLRAARTMAAPPQL RALLVVVNALLRKRRYHAALA VLKGFRNGAVYGAKIRGPSRR WVMTFLFREWAASREKLWAIL Q\ATYIHSW\NL\ARFVFHLTRV FRCPAVPYITRARTYP\AHAFPG AGLSFGGIL\VFGRKQ*TFNSQI\ NMYLLSTRPCLP*SR\LAVRRK GLHP*NPRWDPFP/VCLTAVVW GLVLWLFEYHRSTLQPSLQSSM TYLYEDSNVWHDISDFLVYNK SRPSN
19149	49517	A	19258	1	849	MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHS\DPEEIE KEEQAAAEKAVTKEEFQGEWT APAPEFTATQPEVADLSEGVQV PSVPIQQFPTDDWSTQPATENW SAAPTAQATEWKMQQQSTILE AESSPHQTPNLPAPWSRTSQPPE

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19150	49518	A	19259	1	1309	GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQMKEEDVL KFLAA\GTHLGGTQFLLSRGHG YFYKGKS/DGLSFIINPKRAREE\ LLLPARQIVPHKTPS\DVSVISSG NTGQVCGTVRA/VCLKFAAAT G\ATP\IAGR\FTPGTFH*PRSKA AF\REPR\LLVVT*PPGADPPALS RSASYVNLPYHLRCGNT\DS\QL RYVDIAIPCNNKG\AHSVGLMW WMLARGSFCAMRGTI\SREHPW \EVMPDLYFYRDPEEIEKEEQA AA*E/RQVTKEEFQGEWTAPAP EF\TATQPEVADWSEGVQGAPL VPYSAIPPTEDWSSQPAMEDWS AAPTAQATEWCSRTSLRQNPSD TELKKEGLYSARSISKTHVSKT ELPNQGTKKCSRTSHRQNPSVT ELKKEGLYLARSIGKTHISKTEL
19151	49519	A	19260	965	2495	AFTTRSTFSTNY\RSLGSVQAPS YGARPRQAARPASYAGAGGSG SRISVSRSTSFRGG\MGSGGLAT GTSPGVMAGMG\GIQNEKETM QS\LNDRL\ASYLGQE*RSLEDR RTRKLGRAKFREHFGRKKGPQ V\RDW\SH\YFKII\EDLEGFRFFR KILVGQCPASVSARFDNAPSLL LD*F*EFKY*GQSWPMCPVLLE NDIPLGSAKVI\DDTNYHTDLQL \ETEIRGSSRRELLFQ*RRNHEE\ EVKGLQAQIASSG\LTVE\VD\AP KSQDLAK\IMADIR\AQYD\ELA RKEPEKEA*TKYWSSADLREST TVGHPHKSA*GWKLAEDDASQ KLRRT\VQSLEDRPWTSMRKSE RPALENSP*GEVEAPLRPLQDW SQLQTGIPACHLWSQELGTRHR AQRGQRPGPQGV*GPLLNHQG SSLEAEICHLTRPPSWKIGEDFN L\GDS\LDERNSMQTIQKTTTPP G*VGLGKVVS*DQLTPKVLKAL SQQEAVVPFWGSRRPIKSFRVQ KKKKEKESF

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19152	49520	A	19261	387	1125	CCRPCATPYALRSPLR*PACPPP RWRPSSMPTSRPPVSPAASPTC GTCMLSP\CPPAEHLLHLPHAQP QDPALLQPCHPAPPLRPRALHA AHHVGWPAPHQPLLPPPVLCPC GGAGRGGG*RCPWRGPSSSSPG PTLIAGQDPGAAQP*TWPQ/PTL TSVSATASPKAP\LPLAAAVPGA PAEGCCPLLRQALPAGQLPPGG RRATSAVPPAVPGD/PPAQPTM PGSMSCWALAPARPCPPGRCW AWRS
19153	49521	A	19262	3	1097	RGNSRLRYSHEDELQLPRLPEL FGNCRQLLEEVEVAT\DPAGFR\ IVQEK\VFKG\LDLLE\RAAEML\ SQSTLFGRECRFWKDLSPTHLIT FWGP\AFQGALTM\KQVNPSKR LRSFCSGAREHFI\NYLT\QCH\C YHVGQSFEL\PKT\MNNSAENH TANSSMAYPSLVAM\ASQRQA KIQRYKQKKELEHRLSAMKSA VESGQADDERVRGYYLLHLQR W\VDISLEEIESIDQEIKILRERDS SREASTSN\SSRQERPPVKPFHS HFGTWLHSQSTFGAGYSKGWP TYGR*VSWYE\QHRKLWSTYP DQGNMPRAAPEGISEKAAQQQ EDQEEKEEEDDEPNNFHRARE W\DDWK\DTHP\RG\YGNRQNM
19154	49522	A	19263	2	262	
19155	49523	A	19264	3	1062	GRTAENPARAVSSPNFYAHRKT EVLFPCLTQPLARGPKKHLK\R VAAPKH\WMLDKLTRVFAPR\P STG\PHKLR\ECLSRIIF\LRNRLK \YAL\TGDEVKKI\CMQR\FIK\ID GQGSELDINLPLLGFMGCPSAF DKTGEENF\RLDLIDTQGVRFC WYIRI*PPWRKAKLQVWCQK* GKILCGPTKRESPSSGLTH*CPA PHPAYPPIPPHPR*NGYPIPD*I*E DLAKINLISIQSSEHW*TLCMGD LEGA*P*GRNWVLITPTERGHP GIFLTVGSR*KDANGQQAFGHF GLFQHFLVIGKGNKTHGISL\PR GKGIRLHHLLEERDKRLA\AKQ SQWGEMGSLGVDIVQIFWYRN
19156	49524	A	19265	62	298	

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19157	49525	A	19266	1	555	MAWQMMQLLLLALVTAAGSA QPRSARARTDLLNVCMNAKHH KTQPSPEDELYGQ/SP/WMCKG SCRKTKSWNI/HRKSKCEVGLA/ WEACSVSAGTGRGPGCGRWV GAPQGP/CPRKCSSG*PTW/VQR SQNMEEMAVVNQSWRKERILN VPLCKEDCERWWEDCRTSYTC KSNWHKGWNWTSAPSAVCDP LL
19158	49526	A	19267	216	974	MDMAWQMMQLLLLALVTAA GSAQPR\SARA\RTDLLNVCMN AKHHKTQPSPEDE\LYGQCSP\ WKK\NACCTAS\TSQELHKDTS RLYNFNW\DHCG*KWNPTCK\R PLYPQDSCL\YECLTPTLGPW\IR QFNQSWRKERFLNV\PLCKEDC ERWWEDCRTSYTCKSNWHKG WNWTS\GINKGRPGAF*STFES YFPTPAALCEGLWSHSFKVSNY SRGSGRCIQMWFDSAQGNPNE EVAKFYAAAMNAGAPSRGIIDS
19159	49527	A	19268	345	2138	QRLTATSSWTTMAKNRRDRNS WGGFSEKTYEWSSEEEEPVKK AGPVQVLIVKDDHSFELDETAL NRILLSEAVRDKEVVAVSVAG AFRKGKSFLMDFMLRYMYNQE SVDWVGDYNEPLTGFSWRGGS ERETTGIQIWSEIFLINKPDGKK VAVLLMDTQGTFDSQSTLRDS ATVFALRHNDPASIQVYNLSQN VQ\EDDLQ\HLQLFT\EYGQDW AMGGKHFLEAIFRSLDYFFVRD W\SFPYEFSYGADGGAKFLEKR LKVSGNQHEELQNVRKHIHSCF TNISCFLLPHPGLK\VATNPNFD GK\LKEIDDEFHQKL*KYLIPWA YFRSRGA*DI*RRSNGGLKI\T\C RGLVEYFKAYIKIYQGEELPHP KSMLQATAEANNLAAVATAK DTYNKKMEEICGGDKPFLAPN DLQTKHLAT*GRNLWKLFRGV KKMGGEEFSRRYLQQLESEIDE LY\TNISSHNDSK\NTFPCSSYPQ PTLFCSHPLITYVIAGVTGFIGL DIIASLCNMIMGLTLITLCTWAY IRYSGEYRELGAVIGPRWLQLC GTREVQMRPWNKLYQCQQAT PTDILYPSKPFPLHPKVGNLTEQ IQKRKKMVMPKF

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19160	49528	A	19269	351	509	VVPLPLPPLDSWTCESWLRSHI LTGESENPDHKRI*PYTSDLPEG PGPWATD
19161	49529	A	19270	781	4324	ESVREKVLCGLIQQTVTSVC/W SGTYIFAVLLVCVVFHSGAQEK NYTIREEIPENVLIGNLLKDLNL SLIPNKSLTTTMQFKLVYKTGD VPLIRIEEDTGEIFTTGARIDREK LCAGIPRDEHCFYEVEVAILPDE IFRLVKIRFLIEDINDNAPLFPAT VINISIPENSAINSKYTLPAAVDP DVGINGVQNYELIKSQNIFGLD VIETPGGDKMPQLIVQKELDRE EKDTYVMKVKVEDGGFPQRSS
19162	49530	A	19271	3	644	FRSLPRRCLPRWQPSSFLGHHG PPFRPPCEAPKIVKKENPRKFIR APSQTGY\AKLSVNW\RKTPEAI DN\RVR\RRF\KGQILMP\NIGYG SNKK\TKHM\LPSGFRKFLV\HN VKEPEIAADVATNLTVPRSLTM FPPRNRKAIRGKGACPIGPFRSS PNPIARVAQLKEN*VRQLMCN KSYCAEIAHNVSSKNRKAIVER AAQLAIRVTNPNARAQ
19163	49531	B	19272	27	161	
19164	49532	A	19273	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19165	49533	A	19274	482	832	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19166	49534	A	19275	121	201	SMYMDEN*RLELITL*FSSMYM DHSLL
19167	49535	B	19276	1	1147	
19168	49536	A	19277	305	442	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
19169	49537	A	19278	133	527	GFLERPRILIKVTLSIKQKSTSIF VGGQFSKFRFLTVLAWKCLSQP CF*A*TPASQHVS*SIRAISSMIS KRSELLVRLWRRPSP*AGLFKS RKVSSICIRFE*ILTSCLGVRIST GKLVARTHGSFADAE
19170	49538	A	19279	531	669	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE

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19171	49539	A	19280	80	428	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
19172	49540	A	19281	10	426	
19173	49541	A	19282	1	900	
19174	49542	A	19283	314	451	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
19175	49543	A	19284	1	1139	MWGIGSRTPIYNKILVYSSPEVS CEKPKYVKSQTSTHTGFESHKR YIFYLRLVGKNLHVSAMGLGK SQERRKKALKSQPQQPADSFPS LPTVEGLTTSGEVAAGFWLSGE ALSSC*LLSASVHLLLACLGMG KCSCSGFWLYF
19176	49544	A	19285	1	864	
19177	49545	A	19286	306	444	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
19178	49546	A	19287	189	1089	HHTAHCQ*CWL*S/DHGINPLRS WVGTG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNGSLLTNWPSVPP TIKEEENSEEELAAATTSKEQEP IGTDLDAVRTPEPLEEFPKREDQ EGSPPETSLPYKWVVEAANLLI PAVGSSLSEALDLIES
19179	49547	A	19288	1	549	
19180	49548	A	19289	80	430	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
19181	49549	A	19290	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19182	49550	A	19291	773	1015	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADASF STDLYHGTLKPASLTMSGVVLL GRMLARSARNWS

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19183	49551	B	19292	1	1488	
19184	49552	A	19293	2	133	YAQTDDNRRNLILNGTPLRRVK VLVFDIEYP**KVYGYNSTLA
19185	49553	B	19294	1	879	
19186	49554	A	19295	80	428	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
19187	49555	B	19296	1	1575	
19188	49556	C	19297	1	2187	
19189	49557	A	19298	473	613	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADADT
19190	49558	A	19299	410	547	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
19191	49559	A	19300	876	1005	
19192	49560	A	19301	167	263	KLIEAIWSS*FITGSSLRHNERLG ASTSSGEY
19193	49561	A	19302	258	396	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
19194	49562	C	19303	1	1641	
19195	49563	A	19304	1221	1327	ALHPRNRHLHKERLGCIPVAC* LYLFGQYDAHCTC
19196	49564	C	19305	1	1353	
19197	49565	B	19306	1	2047	
19198	49566	A	19307	80	429	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF

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19199	49567	A	19308	1	2597	MAMFMLLAAALLSTFLTNDVA LYTVVPLTITLKRLCEIPYNRLII FEGAGSQRWFATDANWQPAK YSYLGTFWSFVCRIYCPNGTAG WRNDADAPAPVLAMQYHTGV QTPEWKPRLVWSCLGLYIVFLT ALEFKQELWGLVIVAAGFALL ARRVVLSVDWTLLLVFMAMFI DVHLLTQLPALQGVLGNVISNV PSTILLLNYVPPSLLLVWAVNV GGFGFLTCRHARIAAPADLKDG LAVHEKRETRSLTEKTGKMLLP KLGVGSRECGGNVKEVGIRAIE EFGPYKINGDKEIMRRMDDLLQ GFDAQHRMKLPAQPTSLATKS ARRVRYPLFCPSIFNGFFEEFIFH RFLAEQALEFFNLLHGGSKFRG RNNLFSGGDSSRKNQRSTRTHC HHPSPKIYSASAKEPWVLATNL PVEIRTPKQLVNIYSKRMQIEET FRDLKSPAYGLGLRHSRTSSSE RFDIMLLIALMLQLTCWLAGV HAQKQGWDKHFQANTVRNRN CKMATLKEKLIAPVAEEEATVP NNKITVVGVGQVGMACAISILG KSRAMEHTTAGAPYTPRQQTC QCNMMSLADELALVDVLEDKL KGEMMDLQHGSLFLQTPKIVA DKDYSVTANSKIVVVTAGVRQ QEGESRLNLVQRNVNVFKFIIP QIVKYSPDCI\IVVSNPRDI\LTY GTWKLSGLPKHRVIGSGCNLDS
19200	49568	A	19309	435	777	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP CRLVDWADIPEQKQLMVLRAS VALHGRSVTLYEKAFPAFRAM FKRSS

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19201	49569	A	19310	69	1270	LCLLRHDCYRGLQSLLLILCKM ATLKEKLIAPVAE\DEA\TVPNN KIT\VVGV\GQVGMA\CAISIPGK VSWPDEL\ALVGCFWEDKLKG GNDGSFQHGELIFFQTP*NCGQ DKGLFL*PANS*RFVSW*LAGS PVQPRRGRIRLQSWVPEKWLM VFQIPLFLKIVQVQSLICIIIGGFN PQLDILTYVT\WETKVGLPKHR V\IGSGCN\LDS\ARFRYLMAEK TWHFIPSSC\HGWNFGGNMGDS SV\AVWNGV\NVAGVSL\QEL\N PENGNLTNDKLKIWKEGA*IW WLKSA\YEVI\KLKGYPQLGAI WI*VLAESYWNPMLKKSYPRI\ HPGCPTNG*RQGMYGHWRME SPSLEPSLCIPQCPRGLNPAVIQP RSLKDDEVASASRKSARIPLWD NPEWTLKRPLT
19202	49570	A	19311	52	406	HVEAAGSR*CAAPAGALLRFLG TPSFEDVSIPEKPKLRFIERAPLV PKVRREPKTLSDIRGPSTEATEF TEGNFAILALGGGYLHWGHFE MMRLTINRSM\DPKNMFAIWR VPAPFQAH
19203	49571	A	19312	1	783	
19204	49572	A	19313	15	397	LLAEWTMGHTPVGGFRGAISL DAAP*EQGTMLVSWLCDLFLV LRILVGKTVSSKNIFIERVNGDG KHENIPMSSPPRSWFPSEKRFTN RRKTSSHLQNLVLGAVSLRQH WRGGVPRNLTRAPAGAAH
19205	49573	B	19314	127	181	
19206	49574	A	19315	242	1067	CAAPCGCPCQIPGALLPASAGV KTLLPVPSFEDVSIPEKPKA*DL LERAPTCAQK*RREP*KFKVTIR GP\SH*KPTEFYRKAIFAILGIGV VGYLHWG\HF*K*WRLTIQPAL WTPRTWFAIWR\VPAPFKPITRK SVGASHGGEAKGAI*HYLTP\V KAGRLV\VEMGGRCEFARSAK VSLTQVALRSCPFASKRL*ACG TPREGCEQDQEERERQQPRTPW TI*AE*PTAQHGWAYGKVPEPH MTLTPQGEILGARFYMPKTCVV SVGDILYIGY
19207	49575	A	19316	1	520	

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19208	49576	A	19317	104	763	SAAADGPDRLRRRPPANLRARP VLAPASATASARRACSPPHPQT MSESK\SCPEYASFFAVMGASA A\MVFSALGAAYGTAK\SGTGI AAMSVMRPEQIMKSIIPVVM\A GIIAMLRPGWVAVLIANSLNDD ISLYKS\FLQLGAGLSVGLSGLA QPAFA\IGFVG\DAGVR\GTAMH AADIFRGA*FLILIF\AEVLRL\Y GLIV\ALILFHKVDLFRAHQPTE
19209	49577	A	19321	36	164	
19210	49578	A	19322	190	743	NDRGKEGSLSTVPSIRNTDSGH LAPRRKPQLLKPSLNTSFPKAR KIHKGEHEVASAGGNPPAPILP KVPP*FNIHRRGPPWPDHVRFG SLF\NTLFL\NW\CCLGVSLAFRL LP*KSRDTGKMGLGDVEPGAQ ALCLPPPKCLNI\WALILG\IL\MT IGFIL\LLVFGSVDSLTILWFQIIQ GKTGGY
19211	49579	A	19323	2	257	
19212	49580	A	19324	1	1227	MGRARKSGLGQRSRPTASRSEA AVQPGVRKARGAGNWRVGLQ TGEAAPSPHRDLRDTPDPRPWL ARTHRMTTTLVSATIFDLSEVL CKGNKMLNYSAPSAGGCLLDR KAVGTPAGGGFPRRHSVTLPSS KFHQNQLLSSLKGEPAPALSSR DSRFRDRSFSEGGERLLPTQKQ PGGGQVNSSRYKT\ELCRPFEE NGACKYGDKCQFAHGIHEL\RR LTLHTKD*TELCRTFHTIGFCPY GPRCHFIHNAEERRALAGARDL SADRPRLQHSFSFAGFPSAAAT AAATGLLDSPTSITPPP\ILSADD LLGSPTLPDGTNNPFAFSSQELA SLFAPSMGLPGGGSPTTFLFRP MSESPHMFDSPPSPQDSLSD\QE GYLSSSSSSHSGSDSPTLDNSRR LPIFSRLSISDD
19213	49581	A	19325	204	456	
19214	49582	A	19326	1	323	IVEYHGPGVDSISCTGMATICN MGAEIGATTSVFPYNHRMKKY LSKTGREDIANLADEFK\DHLVP DPGCHYDQLIEINLSEMV*PDM LPAPRLAHGVTVVVVGGFLK
19215	49583	A	19327	2	131	
19216	49584	C	19328	2	283	
19217	49585	A	19329	1	206	
19218	49586	B	19330	217	435	

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19219	49587	A	19331	1	565	PWE*SPKGIGVSCGPLSGWS/SP KD/VILKVQ/GILRFKGGTVQIV ESTGLG*TPFSCTGMRQFCNMG AEIGATTSV\FPYNHRMKKYLS KTGREDIANLADEFKDHLVPDP GCHYDQLIEINLSELKPHINGPF TPDLAHPVAEVGKVAEKEGWP LDIRVDALACQSLAFGAAWVQ CGCEEHGAWSQMAWA
19220	49588	A	19332	117	2603	GQHCLLPWGVFPFLKKALGV\R Q*\HVASVLCQRAR\VAMSHFE PNEYIHYDLLEKNINIVRKRLNR PL\TLSE\KIVYGHLDDPASQEIE RGKSYLRLRP\DRVAMQDATA Q\MAMLQFISSGLSKVAVP\STI HCDHLK\EPQVGGEKDL\RRAK DINQEVYNFLATAGAKYGVGF WKPGSGIIHQIILENYCVPWLSF *LGPDFHTPNGGG\LGGI\CIGSC GWPNAWEWNGLGIPWE\LKCP\ QVIGVKLTGSLSGWSSPKDVIL KVAGILTVKGGTGAIVEYHGPG VDSISCTGMATICNMGAEIGAT TSVFPYNHRMKKYLSKTGRE\D IANLA\DEFKVHLVP\DPG\CHY EPTELKINLSEL\KPHIQWGPFTP DRGSPCWQEVGKVGREGKGW PL\DIRGGS*LVACTNFKLWKIW GRSAA\VAKQALAHG\LKCKSQ F\TITPGFPRQI\RATFE\RDGYAQ ILRDLGG\IVL\ANACGPCIGQW D\RKDI\KMGEKNTI\VTSYNRN FTGRN\DPNPETHAFVTSPEIVT ALAIAGTLKF\NPETD*PDGAR MGKKFQAWRFPD\AD*VFPKG EF*PRGRDTYQHPPK\DSSG\QH VGT*APRSQRLQLLDPFDKWD GKDLEDLQILIKVKGKCTTDHIS AAGPWLK\FRGHLDNIPN/NHLL IGAINIENGKANSVG\NAVTQEF GPAP*QLAR\YYQETLASRLGW
19221	49589	B	19333	1	1311	

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19222	49590	A	19334	2	1390	PRVRPRVRARPTKMSALGSLSL PSVLWGQLF\AVDSGNDVTDIA DD\GCPKPPEIAHGYV\EHSVRY QCKNYYKLRTEGDGVYTL/NTI EKQWIKLRLFGD\KLP*IVEADD GCPKPPEIAHGYVEHSVRYQCK NYYKLRTEGDGVYTLNNEKQ WINKAVGDKLPECEAVCG\KPK NP\ANPV\QRDPGVGHL\DCQRS FFPWARLKDGFPHH*SSTHQGP RWIQLNQWLA*PRLKNLLSLN H\SENCQQRKDICPYF*HFMWG KKQLVGD*GRLFLQP*LTPRVD IGLI\KLQTEGCSC*LRRVMPICL PSKGLWQK*GRVGLCFLAGGR NAQF*NLLTHLKVCPCCPVA*P KTQCHKAIYERPSNKSPRKRKN TRKKPL*GVQAPILK*NTPFLCL AMS*RYPKERHPAYG/QNAGAS ALCPFHRPLEEDTPGMPTGIL\S FDKS\CAVA\EYGVYV\KVTSIQ\ DWVQKTIA
19223	49591	A	19335	65	665	GVRGFWAGTMASRAGPRAAG TDGSDFQHRERVAMHYQMSVT LKYEIKKLIYVHLVIWAAAWLL R*AVGHPEALV/DMIRWPCPIQ WE/YPVFC*AFLPSLLGPSFPFPR NNIRLTWVL/YHESSMGIFFSIG SIHFIGQHGDVPWLHSSFYRHG KAYRFLFGFSAVSIMYLVLVLA VQVHAW\SLYYSKKLLDSWVH QHTGEEA
19224	49592	A	19336	65	665	GVRGFWAGTMASRAGPRAAG TDGSDFQHRERVAMHYQMSVT LKYEIKKLIYVHLVIWAAAWLL R*AVGHPEALV/DMIRWPCPIQ WE/YPVFC*AFLPSLLGPSFPFPR NNIRLTWVL/YHESSMGIFFSIG SIHFIGQHGDVPWLHSSFYRHG KAYRFLFGFSAVSIMYLVLVLA VQVHAW\SLYYSKKLLDSWVH QHTGEEA

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19225	49593	A	19337	71	1265	RCSKSLRMSTFFSDTAWICLAV PTVLCRTVFCTYKKSSGQLWS WMVCLAGLCAVCLLILSPFWG LILFSESCFLMHTYLSGQELLPV DQKAVLPTGGDCGLDHALSKY LDELGFTVFAGVLNENGPGAEE LRRTCSPRLSVLQMDITKPVQIK D\AYSKVAAMLHDRGLWAAIN NAGVLGFP\TDGELLLMTDYQR CMVVNFFGTVEVTKTFLPLLR* SKGRLVNVTSMGGGAPMERLA SYGSSKAAVTMFSSVMRLELSK WGIKVASIQP/GEGFLTNIAGTS DKW\EKL\EKDILGPPPPLRVQE DYGQDYILAQRNFLLLINSLAS KDFSPVLR\DI\QQAILAKSPFAY YTPGKGAYLWICLAHYLPIGIY DYFAKRHFGQDKPMPRALRMP NYKKKAT
19226	49594	A	19338	1	861	
19227	49595	A	19339	248	930	DVHQLGNMAVIHSHLWEGLQE KFLKGEPKVLGVVQILTALMSL SMGITMMCMASNTYGK*PLFP CISGYTIWGSVMFIISGSLSIAAG I*N\TKGLVRGSLGMNITSSVLA ASGILINTFSLAFY\YSITPYCNY YGQPPN*LSMGTMSHLKGVW MGMVLLLSVLEFCIAVSLSAFG M*SALLVPPGGGCVNSAITFFT WAETASSTTLNEGLRGTQRFNR QMLPEIYA
19228	49596	A	19340	167	1164	RNLRLPSSALAGVAPSHREPRV RTISQTDRRKDA/PDPARRDRVE LAPAYTSPPRCSANVGTSTRRL RALCPARVRAPLRLPPPASSPLG SEEQRRKVPAAARMRPRAGAG RSTLPWLPAT/WPGLPSLPLYL* ICGGNNSY*R*RKGEQFE*RNSS *DYRYLPSSPASPNV\RERQPNE NGPDDKEKDRPERPSPLDTSPL LDPPAVSDIAGKMSDEFSLADA LPEHSPAKTSASYPDHMVLPTD PAAAGPLGPWGSMSSGPWVPG MGGQYPTPNMPYPSPGPYPVPP PPQASGAAPPVPWGTVPLGAW GPPAPYPAPTGSYPTPGLYPTPS NPF

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19229	49597	A	19341	2	716	SDPSPLLDPTAVSDIAGKMSDE FSLADALPEHSPAKTSAVSNTK PGQPPQGWPGSNPWNNPSAPSS VPSGLPPSATPSTVPFGPAPTGM YPSVPPTGPPPGPPAPFPPSGPSC PPPGGPYPAPTVPGPGPTGPYPT PNMPFPELPRPYGAPTDPAAAG PLGPWGSMSSGPWAPGMGGQ YPTPNMPYPSPGPYPAPPPPQAP GAST/ILFHGAPFPPGAWGPPAP YPAPTGSYPTPGTLS*FPPGAW GPPAPYPAPTGSYPTPGTLS
19230	49598	B	19342	54	178	
19231	49599	A	19343	3	249	RHKGSPSPHQTQEPSWLHPVDP ALGPQVELPASLVLCARTPQPL GGR*DWV/PGTPAGPQESRAAP VPASAPPSTPRGRGGRI
19232	49600	A	19344	2	504	WAPVRPEPPRRAPPPAPQRPVP STTQGLRSAGA/PAPGLAGSYP CSPGYVNAPIDSLYLATFMGIR VKRPPNR/PLCEQ*SFYHLGAGE *PGKSRVPIPQFQSP\GDPTVRV V\PRR*SVPPTSCATPRSWCCSD T\PGHPLGSPEQLPQPGPAAELP GGVVPRSTPPCPAL
19233	49601	A	19345	3	335	
19234	49602	A	19346	2	447	CACTPQPLGGRWDWAPWSRG RRSSGRLRLHRNPRRRGKAQA WRAAVPRPAPREGS*GPGRPAA PSAGPPSPRPPGTPAGPQAPRAA PVPA\PRLPPHLPAS*GSGLRPSP AQKGAPTVQ/PVG*RAPQVPPK WEPRQRRRRERARAVRTA
19235	49603	A	19347	108	729	QHAGSPQSPRLLSAPPLPGLPL WWHLRSPSAPPLHCGSPFLGWP RLEPTPSACREVWRERHKWEP G/PACGACGPAGVPGGRG/PWW APHSEHPASPAGPG/PMGNLAP GPVAAEGVLSPPAVPAHRRCAR FLAGP*L/PFPRGRAWDLQPAM PEPPT\PPWAPV/PAEPP*RAPPP APQRPVPS\PPKGAQDWQAAPP AAPVRDPLGEASWAPE

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19236	49604	A	19348	1	816	MWESLTLSRDFLNGFDQNADS GIDNKVQVEVASDEDEELVGN WNKERENPFSGEKLKPAAEICIS YKEPNANHQDNGENVARACQ RPLQHPLPSQAQRPRRKQRFPG PGSGPTWDLVPCIPGAP/RLD*K GPRKPKSWYSEGQRYESPSFGIP LGSDLF\PTNALLLKPYKLPPSR PRDYCGRAAFPRGRVRDLQPA MPEPPT\PPWAPVRPEPPR*APPP AP/PAPSPIDHPRAEECEHTAQD WQAAPPAAPVRDPLGEASWAP ESGGDVESLYV
19237	49605	B	19349	4	669	
19238	49606	B	19350	1	930	
19239	49607	A	19351	170	444	
19240	49608	B	19352	1	1122	
19241	49609	A	19353	1628	3591	KGLRLKLCSFVQLRFSIRNFRLG ILTYWKKEFEIVGWPRLEPTPL ACREVWRERREREPGLRAALA GQLEFRVGVGLAGPSLGAAGQ PCWPRVIRDLAPGPVAAEGVLG PPAVPAHRRCAGFLTEP*LPSRG AGLGTCSPPCLSLPPTPWAPVRP KPPQRAPPPAP/PAPSPIDHPRAE ECERRAHDWQTAPPAALVPDP LGEASWAPESGISDEYITPMFSF YKSIGELKMTQEEYALLTAIVIL SPAWATERHPVFKKRERKKPSN CLEGVIKAAAELAVGLPWNLG KFHTGDGTSAGLQGIAPNSVGP GQPAPEWMWGWERLLTDQDK TQGSAFSCTATFQDAQKQLLQ ARFIHLSGLWEQQDGLWLSNW LSLKGQIGGPALTEPLRLSVNR GTWPPKLRDARRRSAGRADRR APTGRVLPGSPGAGPQTTPPPY DWSLRNRRRPAATDPEAQAAA AAAAVGQGRVGPAQIEPSCRPA GRSDPPAPGPEAEVCWVSRLRE PVRSAFAWLRQSRALIGSWGR QGDVAPAFTCPPNAERGATGV RGGWGCWCGRAQLGRRDPAA TRPALNPERYQSPKSMQGLERP HVRNWGIELETLRDAFRPQPSV WRTARGEAGKRKGRLVECLGS QRKVLEGVLLYAVTRGSFPNLF
19242	49610	B	19354	1	412	

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19243	49611	A	19355	951	1453	FQTQEPSWLHLVDPTPGLQVEL PASPVPCAHIPQPLGGRWDWVP WSRGWCSSGRLGPHRSPWSGW EAQAWQAAGPEPCPMGRQVRP GEKSSAVPVGQPG/SGHSVHPP QPLARVLSPPLPGASRAGRLLR VWGPPSPRPPGTPAGPQARHTA PVPARASPSTPPCKLR
19244	49612	A	19356	111	658	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPQGAPPPAP/PAPSPID HPRAEECERTARDWQAAPPAA LVRDPLGEASWAPESGGEPTPS GPGVAGSGSTHTHALTHACTH AHTRAEPLRLPPPPRPLPPPLSPP /PPAPLLPSKPFSLSTDRISSKSR QQKVPFGPRDPEPRGVRAGSW NRTTH
19245	49613	B	19357	1	552	
19246	49614	A	19358	1299	1813	AHFPRAGTGAACSACWPAGVP GGRGLGGPRTRSSRPCWPRAK GDLAPGPAAAEGVLGPAAVPA HRRCARFLAGP*LPYHGAGLGT CSPPCLSLPPTP/SGSCAPEPPRR APPPAPRHPVPSTTQGPPWETC LLSIYGNAMNDERAWSLEGFW VLKPSDSWMTSLSERTISFF
19247	49615	A	19359	380	905	WIPHWGCRWSCLPVLRRALAF LSPWVVDGTGRRGVGSGAGRG GSGRTGAHGVGGRLRHGGLQV PSPAPREGS*GPARNRAQ\PGGP ALLGDSVHPPQPLAQVLSPP\FP GPAGLAGCSECRGPPSPRPPGTP AGPQAPHAAPVPARASPSTPPL VHLTNDVLRVKVKWAFFFTLH
19248	49616	A	19360	1	1052	MGLAERCPLNHLTLTVSSVKCS FLLAHILSVAGACYGVLRGAPH TFPGITCPGCSQENNPIKKWAE DLNRHLIQEDTQMANKHLKDA PHRYIIRELQVKPTMRYCHAPT GVAHIQSTNTPNAGEDVEHQEL TFIADGSPVTTRGHMDLVQTSL SRTLGVRSTGSWSACAEFSHGY CLAKRLLQLLKHGNGNSNSGG NAECITRHCQKPLTGILSFILAL NKVKNTRPFDRCHSEGSEKEPS FCVTCPRRPEVNQPSPYMPQPG KSSTHLSVVQLRALEVGEPQAF PPVE/PEGPAGLRHPLWL*V*GQ GSGP/SSPPCLSLPPTPWAPVWP EPPRRAPPPAPQRPVP\RPPKG

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19249	49617	A	19361	417	1092	KWCSKRTAFSFSLQGGVEGEA RAGTRAACGACGPAGVAGRRG LGGPPHSGQPASPAGPG/PVRDL APGPVAAEGVLGPPAVP/APPA LCSIS/PPGCSCLPAG/PRLRTCSP PCLSLPPPPWAPVRPKPPR*ATP PAPRRPVPST/NPRAEECGRTAR DWQAAPPAAPVRDPLGEASWA PESGGDVENLYVQLRDCKYTN QHPVSSSGFVNAPISTLYLVNL VGTWRIFMSS
19250	49618	B	19362	817	1596	
19251	49619	A	19363	350	644	
19252	49620	A	19364	60	1362	SRVEPRVRSASQDSRSRDNGPD G\MEPEGVIESNWNEIADS\FDD MNLSESL\LRGIYAYGFEKPSAI QQRAILPCIKGYDVIA\QPQSGT\ GKTATFAISILQ\QIELDLK\ATQ GLGS*APT/RENLAQQIQ\KVVM ALG\DYMG\AS\CHACIRGAPTC VAEVQKL\QMEAPHIIVGYPLG RVF\DMLYR\RYL\SPKYIKMFV LDEA\DEM\LSRGFKGQIYGHIQ KAQAAPPRVVLLSATMPFD\VL EVTKKFMRGPH/IRILVRKEELT L\EGIRQ\FYI\NVEREEW\RLDTL CDLYETPDPSPQASHLPSTTRR\ KVDWPHPRRMHALRFPWESAQ HEDMAQKERR/DVIMKEFRLAS SRV\LITT\DLLA\RGIDV\QQVSL SHQLNY/SFPTTRENY\IHR\IGR GGRFG\RKGVPINMLTE/EKTKR NLEDIETF\YNTSI\EEMPLNVA
19253	49621	A	19365	911	1278	NCGIVISKHLVFTLA*MMCHFL ASLQRKGILKRSASV*AHSH/DP SFHMKIYNAGW\GHRT*HPAGG FAGPPPWGSVWGLAARTRENA PRPALPLPRPAPSGLAHGADGD SNTEKIQSRDNRKG
19254	49622	A	19366	26	743	ETSADMAPSVPAAE\PEYPKGIR AVLLGPPGAGKGTQAPRLAEN FCVCHLATGDMLRAMVASGSE LGKKLKATMDAGKLVSDEMV VELIEKNLETPLCKNGFLLDGFP RTVRHAEMLDDLM\EKRKEKL\ DSVDLNFSIPDSLLIRRITGRLIH PKSGRSYHEEFNPPKEPMKDDI TGEPLIRRSDDNEKALKIRLQA YHTQTTPLIEYYRKRGIHSAIDA SQTPDVVFASILAAFSKATS

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19255	49623	A	19367	40	1002	VASGTRTELQDRRFRDTSGDM FPSVPP*EPEYTKGIRTVLLWPP GAGKGTQ/SGETEV*MACSLGY IASNLQSLHLNDSKAPALSAAIY CPRHPNWAENFCVCHLATGDM WR\AMVASG/SSELGKKLEGNL WDGWGNWVE*WKWVSWSSF GEGILENPLVAKNGFLL\DGFPS GPVKARQK\SPMDLMGEGGKE KLDFC*FEFSIP\DSLL\IRRNHKE GLIPPPKKWAGSYPRREFQPLP KEPP*KMNITGGNPLIRRSR**M KRPLKIRPASPTHTQT\TPLIE\Y YRKRGIHST\DASQTPDVVFASI LAAFSKATCKDLVMFI
19256	49624	A	19368	793	1152	SGRKRRGCGGQSVKQAPALTP GPPAPVFPIPEAPAACAPHHPGQ GNRRKCNFPPVCPT\PKTASSCP/ EPLPPPPSLQR*PCPCHPWHHLE FSFLDEVTFSFNKTFPKRLVSSK MLPLKVGH
19257	49625	A	19369	1	873	
19258	49626	B	19371	1	322	
19259	49627	B	19372	64	2250	
19260	49628	A	19373	20	368	CEARGGSGHGGRAERAGVCGG PAELLPKGSKEEQRDYVFYLAV GNYRLKEYEKALKYVRGLLQT EPQNNQAKELERLIDKAMKKD GLVGM/AIVGGM/ALGVAGLA GLIGLAVSKSKS
19261	49629	A	19374	3	492	
19262	49630	A	19375	62	570	GSRGQWPSEAVLNELVSVEDL LKFEKKFQSEKAAGSVSKSTQF EYAWCL\VRSKYNDD\RKGIVL L\EELL\PKGSK\EE\QRGFTSFYL ARGGGTTRLQGITEKALKLRSA GLLAAQEPQEQPRPKETGNGLI DKA/L*KKDGLRGAWPIVGGM ALGVLAGTCRSSSDFAVFQ

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19263	49631	A	19376	1	944	MACHLQAGSPGNLVVYFQSKP EGLRTREPMMSVPVQVKGPST RKLMMSEDPLTLGNWHELRVS RTAKNGILQVDKQKIVEGMAE LQQVVGKNMDSGVGPVVHGG GLTRTGYLLNPESLQQKAFERR QIQGCDEKLACVGKQTLGTWP LSESPSLTRLYCRRQLTQGSLR MSLNNAGVPGQTAPDQRSGEG VAAPAGPGEEVGREEGEGAAA GKRQCPCQQGSLCVDTSRPRLP KSQAQIPSSSRSSPSSSEQQRGQ LPSVREHVEGGQGEERAPHCD GGGRVLLASGLAWLGTENIMD LASSPKDDWGVAVPSRGCERPS TFTLVLVPSPIVRRRACSGQPISP GGGQETHGADTSHLTNP*ICLL SKAFCCRDSGLSK*PVLVRPPPC \PQALPQSPCSYLLLAVALPFPP LSSAYPPVRFHSLLCEIHEARAS
19264	49632	A	19377	1177	1603	WVSSFSSSSFSSFPPPPPPPPPPP PPSFLPPPPPPP/PPI*DRARRCQQ TSIPLNKLNINKLLLLLLSPRPD DREKFTPQPQSARQREPIKGTA SRRGEGPICPTLSLYFLHVFLCF SCLSSQIHIYILRLSTVLVLIKNS
19265	49633	A	19378	1	896	FPFSLLPPPKMPKGKKAKGKKV APAPAF\VRKQDAQE*WLNPL\F KKRP*DFR\IGQ\DIQPQKRPPPL L*KWPR\YIRLQR\QRAILYK\RL K\VPSAITPVSPRALDPANQLLS LLKL\AHKYRPRDKAQRSKQR\ LLA\RAEKKAA\GKGDRPNQRD PPVLRARS*HPSPTLVEEQEKLS WVVIA\HDVD\SIELGLSFLA\AL CRKNGGSPYCIIKGKGQDLGR\ LVHRKDLAPLVAFTQ\VN\SED KRRFWLKLVGSYQGPNYNDRY RYDEIRRHWGGNVLGPKSVARI AKLEKAKAK\ELATKLG
19266	49634	A	19379	3	491	AKEALDWEEGHQ*DQRL*SRN SQLGICGGLRGFRGDRAASVFS R*AEKESVRQL*ARVPGALGVA ARANKHQRRWREGDSTQTATN TVDRRATRGRPMEWRATRVAD EEDGDRRRGDNRPQARTFRPRT SVRRAAGTNNSEGRRPTNAGT NGGRGVDIYTVN

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19267	49635	A	19380	1	1501	MRRSTPGVLPAAVGGARVRRA VGLSGTGAEAGRAGAMVEKEE AGGGISEEEAAQYDRQIRLWGL EAQKRCHRMKEALSTAPFTDK ETHPKVSLAQVTRSSASVMVY GAFEVIGQRQSSAAKPRRSQSE SLGPEFQGLWEWLPASQHIMRS LKKQDGMGQGYRVSLEWEVG QLIFLEEKVTP\EDPGAQFLIRT\ GSVGRNRA\EAS\LERAQNFNP MV/DMLKVDTEDIEKKPESFFT QFDAVCLTCCSRDVIVKI\DQIC HKNSIKFFT\GDVFGYHGYTFA NLGEHEFVEEKTKVAKVSQGV EDGPDTKRAKLDSSETTMVKN KVF\FCPVKE\ALDGWILDACDE MQMAALKRTTSDYILLQVLLK F/RVTDKGRDPSS\DTYE\EDSEL LLQI\GNDVLDSLGISPDLLPEDF VRYCF\SEMAPVCAVVGGILAQ EIVKALSSAGTLP/PTTNFFFFR WA*KGEWGLWECLGPQVNSG FGQPQRCQLQHAHLYSLFPFFM
19268	49636	A	19381	2	411	PGTSQGVFSPHRLGGAVRSPCP PPQDSRQASAGGAESQ\LKQRG FPGE*GCRSPVSCAWPQNRMG* GPQHREAGAWSGE*KTPIWLK QERCNRPGLLVTAELAAPAPRP DGMAPGCGGIRCTPGRPRRLLH SGPPSP
19269	49637	A	19382	165	309	
19270	49638	A	19383	1	825	LATQPEGAGRVPSIHPQGGPEA ALQDLRTLMGSSRLHSGKESIG HNSSAGSSSQGPHHPRRKTAIL EKGGKQPHRMLPFSPGLGSSPE PANAGSPDTWLCPP/AAARVL* NPVKPRKGRSEPRSGWASQLPG GDSRLPLRPGTSQGVFSP/APAG *AGKLVLGVLSLSLKQRGFPGE *GCRSPVSCAWPQNRMGCRTSP GPSPTSPTAAGE*GSRPRRRKPG RVQGLQRDGPTLTQEDALTAA KRCPLPVTSVPQTPETSTGAAA PGSQPVGAPPSR
19271	49639	A	19384	1	378	

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19272	49640	A	19385	381	1653	QRPRSGTFTMGRKSLYLLIVGIL IAYYIYTPLPDNVEEPWRMMWI NAHLKTIQN\LATFVELLGLHHF MDSFKVVGSF\DEVPPTSDENV TVTETK\FNNILV\RVYVPK\RKS *STKEGGLFYIPCGGWRRGSYS LIVYDLPSSWTVE\RPGSSLVSN HL\RLAT*F\HFPLQLGELYDAL R*FLRKKVLAKYGCEP*GESGIS G\DSAGRGI*LSAV\TQQLL\DDP \DVQDPNFKIQS*IYPALSASWM *VLPSYQGKFKFSYFYSKSLQ\C RFWSEYFTTDRSLE\KAMLSRQ\ HVP\VESSHLFKFINWSS\LLP*E GLLKGH\VYNN\PNYGSS\ELAK KYPG\FLDVRAAPLLADDNKLR GLP\LTYVITCQYDLLRDDGLM YVTRLRNTGVSG*LNN\HVEG\ GFHGAF\SFLGLKISHRLINQYIE
19273	49641	A	19386	3	667	DAWADAWVPVSSEVAYLFGG CHTCGGLPVAHPMMPRGSRSR TSRMAP\PASRAP\QMRAAPRPA QVG\QPPAAAPPSAVG\SSAAAP RQP\GLMAQMATTAAGVAVGS AVGHTLGHAIT\GAFSGRK*LPE PARP*HHFNQEASG/TPPAQHSK QQRHPHLQQPCP\YEIQTVFWE FCPGTRGDIQAL/CEGFNE\VLK Q\CRL\ANGFGPNEEVSTFGRD WKFSSHNLS
19274	49642	A	19387	81	1257	RHQSDQTVPRLSRPHVQSQKSS MAAAAKPNNLSLVVHGPGDLR LENYPIPEPGPNE\VLLRMHSVG ICGSDVH\YWEYLS/RFGNFIVK KPMVLGHEASGTV\EKVGSSVK AP*NQGDRVAIEPGCSPEEN*W NSC\KMG\RYNLSPSIFFCATPPD DGNLCRFYKHNAAFCYKLPDN VTFEEGALIEPLSVGIHACRRGG VTLG\HKVLVCGSWANRGWVT LLVAKAMGAAQVVVTDLSATR LSKAKEIGADLVLQISKESPQEI ARKVEGLLGCKPEVTIECTGAE ASI\Q\AGIYATRSGGTLVLVGL GSEMTTVPLL\HAAIREV\DIKG VFRY\CNTWASGGFSMLCVPKS V\NVK\PLVTHRVSSWRKVLEA FETFKKGLGLKIMLKCDPSDQN
19275	49643	A	19388	2	431	

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19276	49644	A	19389	2	326	ARGSTRLMESRVQHL*CTRKEL TPEVLQEWLDELEEMMLVVH MPRFRIEDGFSLKEQLQDMGLV DLFSPEKSKLPGIVAEGRDDLY VSDAFHKAFLEVNEEGSEAAAS
19277	49645	A	19390	2	368	
19278	49646	A	19391	1	2123	MAQFSIVGMCLGLFNQSPTDGS GVQLFVIMNQVMAANLAETHA ALCPTLSSGTSARFRGKNQFSG GLPQITLSPLAQPCGRLAAMYS NVIGTVTSGKSLPSTSPLVPLLL SGFAPLFLKGLQNWTQTTQEG KSPSAAPASSQPQACPTDHVRE SALGACLSLPGEDGKIQKVYLL SLLLIGFWDCVTCHGSPVDICT AKPRDIPMNPMCIYRSPEKKAT EDEGSEQKIPEATNRRVWELSK ANSRFATTFYQHLADSKNDND NIFLSPLSISTAFAMTKLGACND TLQQLMEVFKFDTISEKTSDQIH FFFAKLNCRLYRKANKSSKLVS ANRLFGDKSLTFNETYQDISEL VYGAKLQPLDFKENAEQSRAAI NKWVSNKTEGRITDVIPSEAINE LTVLVLVNTIYFKVLRMALERP QGLPLALQLTPFFFKWRDRSPE RANGLPKATQGLWKSKFSPEN TRKELFYKADGESCSASMMYQ EGKFRYRRVAEGTQVLELPFKG DDITMVLILPKPEKSLAKVEKE LTPEVLQEWLDELEEMMLVVH MPRFRI\EDGFS\LKEQLQDMGL VDLFSPEKSKLPGIVAEGRDDL YVSDAFHKAFLEVNEEGSEAA ASTAVVIAGRSLNPNRVTFKAN RPFLVFIREVPLNTIIFMGRVAN PCVNLSEALAVLVVNLTTLMK RTHGESLDFMERKRRPAESILL

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19279	49647	A	19392	9	1630	PALCPTLSSGTSARFRGKNQFS GGLPQITLSPLAQPCGRLAAMY SNVIGTVTSGKRKVYLLSLLLD SFGDCVTCHG\SPVDICTAKPRD IPMNPM\CIYRSPEKKATEDEGS EQKIPEATNNRRVW\ELSKANF PLLLTTFLFSTWADSKD*H*LTF FCSPLSIFQGFLLWTKV\GACND TLQQLMEVFKF\DTIS\EKTF*SR SHFFFA\KLN\CRL\YRKANKSSK LVSANRLFGDKSLTFNETYQ\DI SELVYGAKLQAPGTSRENAEQ\ SR\AAINKW\VSNKTEGRIHRCS FPSGRPFNELTVLGGGFNTIYFQ GACWK\SKFSPENTRKELFYKA DG\ESC\SASMDVTREGKFRYSG AWLEGT/QVLVVCPFKGDDIT\ MVLILPKP*EGAWAKVEK\ELT PEVLAKSGWD*FWREMMLVV HMPRF\RI\EDGLQV*REQPAKN MGPLSD\LFSP\RKSPQTPPGIVA EG\RDDPPMSSDAIPIRHFLEVN EEGSEAACKYPLL*LPGRS\LNP NRVTFQGQQAFPWVFIREVPL\ NTIYLHGAELANPCV
19280	49648	A	19393	3	737	
19281	49649	A	19394	1	705	
19282	49650	A	19395	2	757	
19283	49651	A	19396	1	1764	
19284	49652	A	19397	1	710	MAWALLLLTLLTQDTGSWAQS ALTQPASVSGSPGQSITISCTGT NNDVGSYNLVSWYQQHPGKA PKIMIYEVSKRPSGVSNRFSGSK SGNTASLTISGLQAEDEADYYC CSYTSSRPD\VVFGGGTKLTVL GQPKAAPSVTLFPPSSEELQAN KATLVCLISDFYPGAVTVAWK ADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSC QVTHEGSTVEKTVAPAECS
19285	49653	A	19398	1	679	
19286	49654	A	19399	1	743	
19287	49655	A	19400	2	736	
19288	49656	A	19401	2	718	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19289	49657	A	19402	1	711	MAWALLFLTLLTQGTGSWAQS ALTQPASVSGSPGQSITISCTGSS SDVGGYNYVSWYQQHPGKAP KLIHYEGSKRPSRVYDRFSGSM SANTASLTISGLQADDEADYYC CSFAGSSALRIFGSGTRVIVIGQ PKANPTVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKAD GSPVKAG\VETTKPSKQSNNKY AASSYLSLTPEQWKSHKSYSCQ VTHEGSTVEKTVAPTECS
19290	49658	A	19403	3	720	
19291	49659	B	19404	1	711	
19292	49660	A	19405	105	858	RRQDSGQSPAWPAGALLLTLLT HCAVPGSW\AQSVLTQPPSASG TPGQRVTISCSGSSSNIGINDVT WYQQVPGTAPKLLMYSDNHRP SGVPDRFSGSKSG\TSASLGPSV GLQSEDEADYYCGTWGLAA*M VFMSSAGGTTLTVTSQPKAAPS VTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAG \VETTTPSKQSNNKYAASSYLSL TPEQW\KSHRSYSCQVTHEGST VEKTVAPTECS
19293	49661	B	19406	63	756	
19294	49662	A	19407	1	757	MAWTPLLLLFLSHCTGSLSQAV LTQPSSLSASPGTSASLTCTLRS DINVGSPFIYWYQQKPGSPPQF LLRYKSDSDNQQGSGVPSRFSG SKDASANAGILLISGLQAEDEA DYYCSSYVGTNNFGVLFGG\GT \KLTRP*GQPKACPPRVTL/FPHP PSEEASKPNKA\TLVCL\ISDFLP GKP*QLPWKAA*QPPSLAGVET PPHPPTRSNNKYAASSYL\SLTP EQWKSHRSYSC\QVTHEGSTVE KTVAPTECS
19295	49663	A	19408	1	224	YISLPAGVLSLACCTLYGISWQF DPCCKYQVEYDAYKL*RLPLH TLTCSRPTRDNRVFRSPHSVRQ QSLGRCLA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19296	49664	A	19409	235	955	ESTVQVSVFCHRVPARTSSQTA LPVLLGLLGFTVSGPLNLPEPSV IVGNGELVGPQTCLHCGMEIYN G\ENAQ\DQF*VTELGAGP*EGP VTSYIVIE\PTRIGDETARWITVG NCLHKTAVLAGTALLLHPGLR CTLRFIPHHISPAPLGVL\SLACC NL\YGIS\WQ\FEPFACK*QVEVR TPNKLSRLPLHTLTLLPPRVVLV RKDDLH\RKRL\HNPIGTGPPLV YCVK\KIYELYAVMIFK
19297	49665	A	19410	1	764	MRLGIGFACPWKGLADEFDLKI EKQRNQGRLLGFKLQHLVPFTE MEKMGGDRQKHRTAPRQAER RRSGRVSFQPPLQPLDVTLLPG ATREGNCPRASRGRRPSPISHCQ ETQGPEGRSDCTIRGVLSSIPAA RPLRKGSGFPTVCEKRPEQGQQ PALGP/AGPAAVPAPAASRTQW GSRCPCGAGARRGYWRGLLGL CNLISPLDPGSPGSGRWGSAGA LSRPADSCPPWWPRAGA*RRG AAAEAGNSPSRCGASRPAEEQS GAFAGPLPSSPSQ*RAPGAEV
19298	49666	A	19411	209	536	TRSSCVTLVC*LAMVSLRVARP HGVPGTMFGKRKKRVEISAPSN F/EHRVHTGFDQHEQKFTGLPR QWQSLIEE/SARRPKPLVDPACI TSIQPGAPKEVCSPRASGTRSR
19299	49667	A	19412	124	1983	
19300	49668	A	19413	424	1582	PPWAAVHGDRPHRVPGTMFGK RK/KRVEISAPSNFEHRVH/TGF DQHEQKFTGLPRQW/QSLIEES ARRPKPLVDP/ACITSIQPGAPK WGETGSWPPF/RHLPEG*HGPPI PGCQREPQRVSHEQ/FRAALQL VVDPGDPRS/YLDNFIKIGEGST GIVCTPPSGKLVAVKKM/DLRK QQRRELLFNERPWQCP*HP/RR* EAQVPLPVLQALSV/LHAQGVI HRDIKSDSIL/LTHD/GQVSKEVP RRKSLVGTPY/WMAPELISRLP YGPEVSPGWLGCPAVDSVRCH FQLQRWREMGPSLGSHCQNGA LDKEEGQRPSHTGSLQWGSLG VERTLRVNMYECVHACNSFYL VNKLFQKDSTQEASVTMVPDP DKDGKNRASQKRKAHSQGARR

SEQ ID NO:	ID NO: ptide nce	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19301	49669	A	19414	488	707	TCGEGLSWTRPLPTASSLQV\H* SLSAGERPYLCDYPDCGKAFVQ SGQLKTHQRLHTGEKPFVCSEN GVNLVF
19302	49670	A	19415	16	454	GPAGRCPADCSEEKEGPSA/GD SGRPPSCT*PWKGLPVMAILPG EAPVPGPGWPEPDAGG\PLWR WGSPSPCAAALHRP\SGTTPPGR ALSGPGLERAKQRSPRVSPAPR AAPHGHPTHCLPIPAGPRPAKD HPAYGPPASCHHHLAAS
19303	49671	A	19416	166	1191	TAGSLVLAARGT*GPPPRARK* GPAGRCPADCSEEKEGPSAETP GTTPPGRALSGPGLERAKQRSP RVSPAPRAAPHGHPTHCLPIPA GPRPAKDHP\PTHQKPPPRTEGS TGGHCCGPPIFLIPNTSMLTVYP SGPVMPAGFTLSPSDTRPSLLN GQEVLRKMNGAVQYLSLCDYII PTCQCLATTVLCSVSMSLTVFA VSYMVELLLLQNAQVHQLVLQ NWMLKALPPALQDPPHVPPRV PRAARTRLPAV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19304	49672	A	19417	1	2481	MRSGDLKFGKSAAWPSGQKEK LVFRGKIEEGLEYLHKKKPSAN SQDNGKEASKAFHGPLQQPLLS QALGPDREEWFPGQAPWPHCC VHPQDTAGCIPVVPAPAMAQR CTGTAWVTASEVAPSLDCFHIV LSQQVYRIHRPTSSLHPQYGKA TRHTTPAVSMRAAAGAEPCKA TGADWPKTLGAQPSHPCTMDV GQGFKKDDSGAALAPMAALM GWAGIECLWLFHTEGVNCWP WDLGEKNGLLGQPRGPAAVCS LRTLLPASQQPQLLLRPWLKDA QVQLGSLLQRVQAIGLGGFYIV LSQFIDPSKASYPPWVKNSRHS TAAQPMRAAAGAEHCKATGA ELPKALGAQPSCPCVLDVGQGF KKNDFGAVGLNNWPAGFWNV MGTCKSRLCFVLLSGKKSSFRV EVLTQCLDSHTLETYQFYNREV AFEDVLESSQTGLVVQKPQTDR LTKRGRGEATRNLRGLVPSMP RSLLPSTAQPTAWKCQRGPSPY THQDMALIPSPTARCLSPAKEP KQEEVGEKSLLPDPTLPLTDPR LTGSTEQAHAEGLAALMSALR VSHLQGRGGVVTLVDSQLGVI AVSSTQFNKGPSYRLLADVQN RLLPKYDSQKEAELRSWIKGFT GLSIRPDFQKGLKDGIILCTLVN KLQPGSVPKIN\ASV*NWH*LEN LSNFLKAMVSYGM/NPVDLFEA

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19305	49673	A	19418	1	1299	MHQEDLRAWYLDLGLPSHQNE TTDVSVVYERFSLTDATYPKQA KQWDFPFLRVSTAQPTAWKCQ RAPSPYTHQDTALIPSPTARWL SPEKEPKQGEVGEKSLLPDPTLP LTDPRLTGSTEQKKDLAAGPVG SALRRRPPAVSSTQFNKGPSYR LLADVQNRLLPKYDSQKEAEL RSWIKGFTGLSIRPDFQKGLKD GIILCTLVNKLQPGSVPKIN\ASV *NWH*LENLSNFLKAMVSYGM /NPVDLFEANDLFESGNNMQVR VSLLALAGKAKTKGLRSGVDIR DKYSKKQNFDDTTMKASQCVI RLQITNKCASQSGMTAYGTRR HLYDPKNRILPPMDNSTISLQM GTNKYASQVGMTAPGTQRHIY DTNLGIDKCENSSMSLKMGYT QVANHSGQVFGLGRQIYEPKY QPGGPVAHGAPSAGNCPGPGE
19306	49674	A	19419	135	290	HREEESKSSVFLNPRGVQGTGV GDHRMILGRGRAVLSKE*AAG PRGGRHES
19307	49675	A	19420	92	1058	KGQYLNPNRGKGGPEPPFEPPV PPASRSDMAQNLKDLAGRLPA GPRGMGTALK\LLLGAGAVAY GVRESVFNVE\GGHRAI\FFNRI GG\VQQDT\IL\AEGFHF\RIP\WF QYPH/IIYDIRAKTSKKSPPLQGS KDLQM\VNISPAKCWSRPNAQE LS*ACTSRLGLGLTRER/RCLPSI VNEVLK/AVWVAKFNCLTA*FT QRAPGYSLLDSAGSLTERAKGL SSLIL\DDVGQSQKLSFSPRSYT A\AVEAK\QVAQQEAQR\AQFL\ VEKAKQ\EQRQKI\LQGRG*GR GLPKMLGEA\LSKNP\GYIKTSQ RFEPAPEIILQRRIAHIHRNP
19308	49676	A	19421	3	861	LDDSWEPVHPGCGDFICQWSEE SGLWSTAEVWRERRGREPGLC EGARGTARVPGGRGPPHQSGQ PVPPAPGS*GA*\PGPAAVEGVP GPPAVPPASAALEFSRGFSCLPR CHLVVTKIGKQEDDVSIKRKNR PDYWPAPEPVAGCEGSDQEQV KPNATLEKHFLTEGTGPRSPSC LSWPPSGPHAAADPAMVPETPE PDRPQLTKKFCEARVMAVGTS NVLGQTLKPSRTGGTSWSWVF YLLTANRLPFDVKRKGGGPSSI KPRPHYDHRLLQDFKEQVIHHF

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19309	49677	A	19422	808	923	
19310	49678	A	19423	1	339	
19311	49679	A	19424	1	621	
19312	49680	A	19425	3	1836	MAAVEAAAEPVTVVAAVGPK AKDEEEEEEEPLPPCEA/LRWAP VLWRGPAWATAFLEEATAEEP GAAPGSPPDSPDRTLRRLRAER RRLDS/SLLALSSDFAQVQFRLR QVVRGAPAEQQRLLRELEDFA LKG/IPDILGYEGPGDPASDEGD GLPGDRPRLRGEDQSEQEKQER LETQREKQKELILQLKTQLDDL ETFAYQEGSYDSLPQSVVLERQ RVIIDELIKKLDMNLNEDISSLS TEELRQRVDAAVAQIVNPARV KEQLVEQLKTQIRDLEMFINFIQ DEVGSPLQTGGGHCECKAGGK TGNGCSRTGSSRTPPGNSRTKA EDVTKVRKTGLHLMRRALAVL QIFAV\TRLVVPQARSLQPCGRG SRLTETTLPC*R/ELEASVDRVK QLALTAEPHDHVITSANLQDLS L*GKDELTMAVRKELTVAVRD LLAHGLYASSPGMSLGMATIA* LLPAFSSVPEAMHPRELFVKYY HAKNGRAYVESPARKLSQTFA LPVTGGTVVTPKQSLLTAIHMV LTEHDPFKRSADSELKALVCM ALNEHRLVCWMNLICKSGSLIE PHYQPWSYMAHTGFESALNLL SRLSSLKFSLPVDLAVRQLKNIK
19313	49681	A	19426	366	477	
19314	49682	A	19427	3	432	WNSRDAGYEFDICFTSVHLY\AI RTLWTVLDAIDQMWLPVVRT WRLNERHYGGLTGLNKAETAA KHG\EAQVKIWRRSYDVPPPPM EPDHPFYSNISKDRRYADLTED QLPSCESLKDTIARALPFWNEEI VPQIKEGK\RVLIA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19315	49683	A	19428	1	890	MRTRRTPRGEHSLSAFSSCVDK ISRVCKSFGLELENSIQTLWAER EQSICLVAAGHLVSSSGMRNW CHARRHAAYKQVLIRHGEVAW NLENRFGGWYDANLNPAGDEE AKRWEQALPDAGYEFDIC/FKR TIRTLWTVPDAIDQMWLPV\NV SKDRRYADLTEDQLPSCNSLKD TLARALPFWNEEIVPQIKEGKW SDHCLGALVIPVKDGCNLHGD VTTVSSLTPEERALEEPLNRPTN A/P*HQEG*CWESHQKPVPFQT LGCLCEFSRGASRRKQARVVFR ERSNLCRSISGGEGF
19316	49684	A	19429	1	443	RALPFWNEEIIP\QIKEGKRVLIA \AHGNSSGAIVKHLEGLSEEAIM VLNLPTGIPIVYELDKNLKPIKP MQFLGDEETVRKAMEAVAAL VCVLESLPALFHGSEMPLGPVQ VYLSLISESCSSCLTLPHGSSVH LSITVLNPFSISV
19317	49685	A	19430	24	1039	AVLALLRGRRGGLLLRNLLIPV GAASPARRQWPPYKLVLG\RHG ESAWNLENRFSGWYDADLSPA GHEEAKRGGQALRDAGYEFDI CFTSVHLY\AIRTLWTVLEMPL\ SEMWLPVV\RTWRLNERHYWG S*PGLN*KQKLAAKHGLRPRLK I\WRRSY\D\VPPPP\MEPDHPF\Y SNISKDRRYADLTE\DQLPSC\ES LKDTIARALPFWNE\EIVPQIKE GK\RVLIAAHGNSLQGHCSRLL EGLF\EEAIHGSLNLPDLVFPLSI ELDKNFESLSSPMQFLG\DEETV RKAMEAVACPGQGPRSEGRRG RILSPGCTLPCPVFVPSSPSHLA HVTLDHICKTS
19318	49686	A	19431	86	431	VYVSTMSLSCPASELAVRRQR WSSQFQDHPPGPLQPRPV*EML LL*PTLDLQPVVPPAVAILSWKP SALTISSQIVTPGLKTRSFFTRKT FMKIWNHRQKYQKTMLVMFP RYPSL
19319	49687	A	19432	599	900	ATWLFISPTTTTCQLSKTLLVPL NFLEKQYLTFLLFLEFPTFSLFF RHTEDHLMRSGCLKVCSISPLS/ PLPPSSSHVRHLTPSLPFAMIVS FLRAPQKLSR
19320	49688	A	19433	210	341	HFRKIFTVFQLKLVEYNLLSGH STQQSHPGGTVLL*DLVCPVV

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19321	49689	A	19434	239	464	SPKGGPPNPSHGTKFHTRPCEE TTKQALCEEHGCLFHLGAGGLS PKRESAKGDKGGASVHVVCHI S*SPCS*LGP
19322	49690	B	19435	1	838	
19323	49691	C	19436	80	443	
19324	49692	A	19437	1	775	
19325	49693	A	19438	209	469	
19326	49694	A	19439	304	375	NVGE*SERHPCYD*TPREVCPPS P
19327	49695	A	19440	879	1188	
19328	49696	A	19441	615	917	ATWLFISPTTTTCQLSKTLLVPL NFLEKQYLTFLLFLEFPTFSLFF RHTEDHLMRSGCLKVCSISPLS/ PLPPSSSHVRHLTPSLPFAMIVS FLRAPQKLSR
19329	49697	A	19442	674	1554	GQMASSSVSLQQGVPQAADPG WVTAGASLTRAWAAGVQGDG PGTESSISASSRRVLRLGMTRTL LWACVLLWVCILLLGLCPAVG PVS\SVGPVSYCGPVPYCGPYPA VGPCPAVGPVPCCGPYPS/VGP VPCCGPVSCCGPVSCCGAVSCC GPVS\SVGPVSC/VLGLCPAVGP VS\S*CGP*PAVGLCPAVGPVPC CGPYPS/VGPVPCCGPVSCCGPV SCCWACVLLLGLCPAVGPVS\S VGPVPCCGPVPCCGPVSCCGPV S\VVGPVSCCGPVSCCGPVSCC DHSSHSLLLTFTML
19330	49698	A	19443	4688	4824	

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19331	49699	A	19444	1	2274	MLKPLMGGGAHRRAAAGARK WDGTAIIASTSGLEVLWVTTSR SKTVESVGLAKPGQHNDARMN LAIALTAARYGAATANYMEVV SLLKKTDPQTGKVRVSGARCK DVLTGQEFDVRAKCVINATGPF TDSVRKMDDKDAAAICQPSAG VHIVMPGYYSPESMGLLDPATS DGRVIFFLPWQKMTIAGTTDTP TDVTHHPIPSEEDINFILNEVRN YLSCDVEVRRGDVLAAWSGIR PLVTDPKSADTQSISRNHVVDIS ESGLITIAGGKWTTYRSMAEDT INAAVKTHNLKAGPSRTVGLFL QGGKDWSPTLYIRLVQDYGLE SEVAQHLAATYGDKAFEVAKM ASVTGKRWPIVGVRLVSEFPYI EAEVKYGIKEYAC/DCCGYDFT SYSPGLS/EMSRQQRKPYPGLL N*/CGRELNWDDYKKQEQLET ARKFLYYEMGYKSRSEQLTDR SEISLLPSDIDRYKRRCHKFDAD QRGFMTVVEVQRVLESINVQM DENTLHEILNEVDLNKNGQVEL NEFLQLMSAIQKGRVSGSRLAI LMKTAEENLDRRVPIPVDRSCG GLYFCVRNWWVLGLTDFKNE AADPSGVKLQTFTVSVTARKGS VDPKNSGAQLASPSGSRTGAA GGAACQSRALRLHSSALGWSM GLGAVEHGAVLIGEARAAQEP MEGVGGSGMAGCRSQVLPRG
19332	49700	B	19445	439	1542	
19333	49701	A	19446	2	418	CLSLPPTPWAPVRPEPPRR/CAT PCSTAPSPIDHPRAEECERTVQD WRAAPPAAPVRDPLETGKIDQE IHKYNTPGFTGCLSRVQFNQIAP LKAALRQTNASAHVHIQGELV ESNCGASPLTLSPMSSATDPWH LDHLDS
19334	49702	A	19447	111	215	GTCWELE*RKGKPIFWGEIKAS CRNLHKLQGAKC
19335	49703	A	19448	740	959	DLYPHHLSWQSRNAARKRKS* RGQRPIPAIS*GR\SQKQQQNVN TSTPSHCPRLPYECRPLLHGAQS HRPPKG
19336	49704	B	19449	260	508	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19337	49705	A	19450	11	490	RLSTSPPDSGAQLASRSGSHTG AAGGAACQSRTMRSHSSALGW SMGLGAPLQRH*INSSGGSWLV DKESFPVPSALNFSPLGRKSSPC SKVLYMPNPVSHSMIPSGSERS MDTNGSCWYLTCSLSAPGRRD TRIRKVFSQGRLLVLTLMISPSV GHSTA
19338	49706	A	19451	42	263	SGVSPMSFNTFTSAPAFNRSWT TCLCPK*HARCRGVQPKLDLLL PLQLMSAITSFLAMVSNSCLTSS ALPFLA
19339	49707	A	19452	662	1564	GSRICSFQTRSGHPECPQCHWT RQNHSSIQQPHKAAYTKKTTIH PPNRSNSCSSIWCKLQKLYMCG P*GRSFNFSANLHQPQKGHSGE RPF\EKNKGRAILLKSHRVHTQE MPFPCSKVGKGYLVSSGLFQH QAIHNEKPCRSAMYGDMFHTQ QGHFKCIDYGEAFSPKDTPGQH QIIHTGEKPYVCTECEKTCTRSS NLIQHKPKGLLSLLVLSPSTGN ALFSTLSQLTQLLLTFDVRSDA TFFRKGSGRHQLWLALPEDAR ARVTSVSGTRRRDHGGARGVV CLIHGCVPDTRSSPDVW
19340	49708	A	19453	1	1167	MIREQKVKEVYICAGKKKSHM HLWHNGEKYNRLGRKDRKMT HEGWLIKIPHFPGRKYKASGLH WEQMKHMGGRGKVHLEFTEM YVAGRRGEVKDEVLEPMSLTE VYIPTENDREVWRERRLRAPGL CAALEGQLEFRVGVGLAGSAL EAAGQPCWPRAGRARDLQPAM PEPPPASVGSCAARASLRSAAP CSTAPSPIGHPRAEECERTAQD WQAAPPAAPVRDPLGEASWAP ESVMWPPLDSRQSEEVSVSKRH MDATDKIKFPWLKEKRTIEFGE AAGYVCHRRYKDMEPHEKMG EAAKKVHWVQMRSRARDLQP AMPEPPTHSKGSCAARASPT/T HHPLLHDAQSHRPPKGLRSAGT WRGTGRQLHLQPQCGIHWVKP AGLLSLL
19341	49709	B	19454	118	559	

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19342	49710	A	19455	26	813	LSHYLACSLRLPSGSRIRSAWLI PSIMLLNYTSPGLPRHRSKSENR LDDTARRSPGMAGPGCPPLPGG VPDVRAAYGAPTSAQRPRVGW PPGGRWPRGARGARSFLKKPFR GTPTQVRGAWQCPPPPLTV\EK *PWHPCGRFQGRRHEEKGGRE LGHSKSPPPRRSHYPAGEKGEE ERKEREESSCAGLRRGAHEHA QGQSLPGELPAPGDPHPGRCVG GQGRSRMGPCS*SLAQHPPVCT RGQREKQERRATNKPVRGAPK
19343	49711	A	19456	497	756	TWLKSGISFPPALFTIAKTWR*P KCPSMIDWIKKMW/HIYTMEY YAAIEKDEFMYFAGTWMTLDT VILSKLSQEQKTKHRMFSLISGS
19344	49712	A	19457	100	819	EWSSVRRILVEKRALRRPHPQC LCFRMKTILSNQTVDHSQKNV DITLKGTPQ*SCKGPRGT\LR\RD FN\HIKCGTSALLGKEQQRGFR VD\KWWGNRKGNWATRSGLF GSHVQDHDPRGVTTGASGYKD EGPVYASPSPHPTVVIPGRNGSS LLKSRNFLG\EKYIPQGFRMKTR VLLCSVSQSPEKMKLILE\GNDI\ ELVFKFQRALIQQ\ATTVKNKG\ IRKFFGWVSMSLEKGTVQPGLI
19345	49713	C	19458	395	574	
19346	49714	A	19459	1	1476	
19347	49715	A	19460	2	323	
19348	49716	A	19461	539	711	HRPFPQDRKAGECLLHEYEDLV PIRDTLRLFPGGRYLPRAKHVA PSEPDPGWLVLG*FYC*FCHSP ALLSGFCLAVNVYRERSV
19349	49717	A	19462	66	2873	SARTISYDYYQNWGRDGGPRSS GGGYGGGPAGGHGGNRGSGR GGGGGGGGRG/WQGPASRAPE RPRNRHVVREKTGAEEQGSWR GKREL/LVHMDERREEQIVQVL DSGQAENG*RVRTTDF\RFAPE DHGYGTEVSTKNTPCSENKL/G HPGKEVDKSRKKNV/SESGTDH ILTRDSEYLLQENEPDGTLDQK LLEDLQKKKNDLRYIEMQELV NLIDNHQVTVISGETGCGKTT\Q VTQFILDNYIERGKGSA

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19350	49718	A	19463	1	2112	FRKTTRRLRKVKGRTAGCARF RKWLLRQHGLRTLGLICNHTSR MTRCRWSAESDSGDEEEEGPIV LGRRQKALGKNRSADFNPDFV FTEKEGTYDGSWALADVMSPL MKKRAATTLHEKIEKARKRRK TEDKEAKSGKLEKEKEAKEGSE PKEQEDLQENDEEGSEDEASET DYSSADENILTKADTLKVKDRR EEEEERTGSRRIF*RCIS/ATMKT SSFQDMNLSRPLLKAITAMGFK QPTPIQKACIPVGLLGKDICA\C AAPGTGKTPPFALPVLERLIYIP SPGSSL/TRVLVLVPTRELGMQ VHSVTRQLAQFCNITTCLAVGG LDVKSQEAALRAAPDILIATPG RLIDHLHNCPSFHLSSIEVLILDE ADRMLDEYFEEQMKEIIRMCSH HRQTMLFSATMTDEVKDLASV SLKNPVRIFVNSNTDVAPFLRQ EVIRNRPNREGDREAIVAALLT RTFTDHVMLFTQTKKQAHRMH ILLGL\LGVQVGELHGNLSQTQ RLEALRRFKDEQIDILVATDVA ARGLDIEGVKTVINFTMPNTIK HYVHRVGRTARAGRAGRSVSL VGEDERKMLKEIVKAAKAPVK ARILPQDVILKFRDKIEKME\KD VYAVLQLEAEEKEMQQSEAQI NTAKRLLEKGKEAVVQEPERS WFQTKEERKKEKIAKALQEFDL ALRGKKKRKKFMKDAKKKGE
19351	49719	A	19464	354	446	RQHAH*ESSPLPNLTYPGTQILR KAAGTSA
19352	49720	A	19465	42	388	
19353	49721	A	19466	177	497	
19354	49722	A	19467	271	773	TAMSSEEGKLFVGGLNFNTDE QALEDHFSSFGPISEVVVVKDR ETQRSRGFGFITFTNPE\HASSC Q*RSQ*TGEVSWNG\RQIPLLDH AGKSCSGEPRGRWALGPMGVG SQLILEVVGDQG\YGSGRYYDS RPGGYGYGYGRSRDYNGRNQG \GYDRYSGGNYRDNYDN
19355	49723	A	19468	2	414	GRVGPPRRAGGPRASAAGDPA RGGAAPKMSQTAMSETYDFLF KFLVIGNAGTGKSCLLHQFIEK K/WSVTRSYYRGAAGALLVYDI TSRETYNALTNWLTDARMLAS QNIVIILCGNKKDLDADREVTF LEASRFAQEN

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19356	49724	A	19469	397	445	GHRGAHRPRTLRSVVVRRAHR CSYSGIWD/TAGPDRFRSVTRSY H*GRPGALLVYDITARETYNAL TNWLTDARMLASQNIVIILCGN KKDLDADREVTFLEASRFAQE NELMFLETSALTGENVEEAFVQ CARKILNKIESERMGSGIQYGD AALRQLRSPRRAQAPNAQECG
19357	49725	A	19470	2	559	
19358	49726	A	19471	1	483	
19359	49727	A	19472	95	352	RKATKMATIWASGTPKQPCPR ELLAQERRQTRTRYNQ*DQ*QE RRSRQRIMGVGCLHMLRSEKA PQQRSFAHCTPKSSRPSARLT
19360	49728	B	19473	247	1364	
19361	49729	A	19474	422	877	CHTQTQ*QHTP*QPTPIDMAPTS HARMPFHTHFLTQILTLVSRSP DPG/PHGGKVPTRIPIPPAQPWG PSTLPSSSFLGPPRPFPSPPVPGP GGENRKPFTSPP*A*\GFPGPPSG P*AGGEG/PPVVGRGATPSPPTP SPACGPLKCWWHLIKN
19362	49730	A	19475	168	522	LALHPTRPLIPATDDEV\TVTED KINAPH*KQPVVNVEPF\APGLF AKA\LANVNIGSLICNVGAGGP CCQPAGGCTQPGGSCPLHCWL LPA*GRRKWEAKKEGFRGSFD* LTWGFGSF
19363	49731	A	19476	1	328	
19364	49732	A	19477	1	1204	MASRLLLNNGAKMPILGLGTW KGSILRVGFGSSSREPPPYRGQP LMGGPPVRILGPSGRPKRHNAR GRRGKWASQTGGPRAQTGTWS RRQGQVTEA\VKVAIDVGYRHI DCAHVYQNENEVGVAIQEKLR EQVVKREE\LFIVSKLWCTYHE ERGLV\KG\ACQEDTSSDLKL\D LPGPLTLIHWPTGFKPGKEFFPL DESGNVGPSDTHISDTWA\AME KLVDEGLVKAIGISNFNHLQVE MILNKP\GLKYKP\AVNQI\ECHP YLTQEKLIQYCQSKGIVVTAYS PLGLS*TGPWPKP\EDPS\LLEDP RIQGGSQPKHNK\TTA\QVLIRG SPCKRNLVVIP\KSVTPERI\AEN FK\VF\DFELS\SQGYDPP*LSLPT RNWR\VWCPCWSCT\SH\KDYP LPMKEVLKA
19365	49733	C	19478	300	489	

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19366	49734	A	19479	243	471	CDHLQVSRPRIPATVPVEWKRS EMDSKEEEKEKKEKKEKRRRR *RRRGKEEEEERRRRKRRRKK RGRKK*IKKRV
19367	49735	A	19480	1	365	MGLYKDLLDTRYLFYLVPGYG LTQIELEVIAKDSAKPVGTPRV GLKLEMGIYLSGHLDKFIFAMP FKIKDILSLKKEEEK/ERRRRRR RRKEEEDEEEEEEEEEEERRRR RKRRRKKKRKKKID*KKEEEKE EEEGEEGEKKKKMKKKRKKK KKKKGGGGGKGGERRRGRKK
19368	49736	A	19481	96	508	PAGSLVCPNQCSSARLFSSFFCS SAVMSASPAVGKRGWAELTGS FLPKPPLKTLGSGREDR*GQVW WLTPVIPALWEAEVGGSLEGQE FETSLGNMVKPLLYWLGSNGW LWKLGRRLWQLLWLQDDWPT RGSHILVL
19369	49737	A	19482	3	1013	SRPSWGTHWNEYARRLTLAPS WPLP*GHPVSPSLRVSCL/PHYY ESVLEKKGPCDRDYKKFWAGL QGLTIYFYNSNRDFQHVEKLNL GAFEKLTDEIPWGSSRDPGTHF SLILRNQEIKFKVETLECREMW KGFILTVVELRVPTDLTL\LPGH LYMMSEVLAKEEARRALETPS CFLKVSRLEAQLLLE\RYPECGN LLLRPSGDGARQRVGHHAADA QRDA/PWFRHYKVEAGRGPKY VIRCGTAVLLHLPWTTVVNYF VSHTKKALVPFLLDEDYEKVL GYVEADKENGENVWVAPSAPG PGPSPLHKVPPSRCQPASSQDKL PPLPPLRNPGREIT

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19370	49738	A	19483	63	1496	LISAMAC\ARPL\ISVY\SEKGESS GKNVTLP\AVFKAPIRPDIV\NFG SHPNLRKNNRQPVCWQGN*AG HQT\SAE\SWGYWPRAVGSKFP R\VRGGGTHRS\GQGCFLETMC R\GGRNVLHPTKTLGRRWH\RR SSTQPKKRIRPSGSAPGCPQPLP ALGHGLKGHLY*GKFPETSFW* VER*KLKG*QEEPREAVFAPLR KLKRPGNDIQKGSMASSAK*RA GQKAKLRKPVARIPAAGAPCII\ YNEDNGYSFKAF\RKHPWGLL MLNC*GKLEHF*KLAPLVGHV G\RFLHLGLESALREV*DDLY\G T\WR*SHFPLQGVNLPIFSPWHK \MI\NTDS*AESLKSPEIPREPLRA PR\KKIHSQSS*RRNPLEKL*EIM LKA*TPFAKAHAAGTPFFGQAR N\HKLRVDKAAAAAA/ANLQA NSDEKAAVAGKKPVVGKKGK KAAVGVKKQKKPLVGKKAAA TKKPAPEKKPAEKKP\TTEEKKP AA
19371	49739	A	19484	3	730	KRLPKMAEVQVLVL\DGRG\HL LG\RLA\AIVAK\QVLLGRK\VV VV\RCEGIN\ISANF\YRN\RLKY LGFSPPSGMNTNPSRRPLTTSG APSRIF\WRT\VRGMLPPQNPSG GQGRLLDRLQGV*RASPPPYGQ EKSGMVVP\AALKVVR\LKPTR KFCLIWGRL\APEVG\WKYQAV TAPPGGERGKRKAKIHYRKKK QLMRL\RKQAREETWRKKIDK YTEVLKTHGLPGLSPIKTVNSS KKKKKKRAAA
19372	49740	A	19485	1	660	PTRPRTRGRRTRKSTPMKGLGA RYREYKV\VGRCLPTPQNATRG PLLPACEIFAP\N\HVVAKVPAF W*LCILS*KKMKKFFQGKIVYL WGKVF*EGSPLRVERTFGDLGL RLLTPRERAPHNIVTGEY\RGP* PTAGGCSTQLLTRDNGVARHR RPEAHFHFRFMEGWEGDRGP/C KIPPGGLVKASSNDSKIKVSRW PHRV\LAAFRNKARFTT\KRPNT

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19373	49741	A	19486	51	471	EAGRLPGNILLDSIMACGLVAS NLNLKPGECLRVRGEVAPDAK/ S*VLPARCVHGILSDRLVGQWG WSWPRWPHAHPLPPSFVLNLG KDSNNLCLHFNPRFNAHGDAN TIVCNSKDGGAWGTEQREAVF PFQPGSVAEVCI
19374	49742	A	19487	59	527	ETQSWPCGLVA\SN\LNFNTLES CLRFPKPSWLPDA\KSFRC*NLG QRPPTTWCLHFQPSASTAH\GS ARHASLCNSQGTAGHEGGPTQ REAVFPFQ\PGKCCRGVAFTFRT RANLNRSSLPDGITEFQVSPNGF NL\EAINYMAA\DGGLSRSKCV AFD
19375	49743	A	19488	2	440	KQQCRDTGDEVVCSCFVGYQL LSDGVSCEDVNECITGSHSRAF GESCINTVGSFRCQ/RISSCATG YELTEDNSCK\DTLGSFRCRPKL QCKSGFIQDALGNCIDINECLSI SAP\CPIGVT\CINTEGSYKCQKN VP\NCGPLVNHLKE
19376	49744	A	19489	2	2061	
19377	49745	A	19490	2	2120	
19378	49746	B	19491	63	255	

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19379	49747	A	19492	2	1941	PPPMERAAPSRRVPLPLLLLGG LALLAAGVDADVLLEACCADG HRMATHQKDCSLPYATESKEC RMVQEQCCHSQLEELHCATGIS LANEQDRCATPHGDNASL\EAT FVKRCCHCCLLGRAAQAQGQS CEYSLMVGYQCGQVFQACCVK SQ\ETGDLDVGGLQETDKIIEVE EEQ\EDPYLNDRCRGGGPCKQS\ CRDTGDEVVCSCFVGYQLLSD GVSCEDVNECITGSHSCRLG\ES \CINTVG\SF\RCQRNSSCGTGYE LTEDNSCKDI\DECESGIHNCLP DFICQNTLGSFRCRPKLQCKSGF ITRML*GNLLLDIQWSVLSIQLP RCPIGD*HGI\NTEGFYNVPEGT CPNCGPLGYHLQRGRGTRCV\D V\DECAPPCLSPVGKG\HR\CVE LFPGSFPLAECKDGVTIFDGISR DVLFDVQRSCQRLPRGACC\GH K/CTENTLGSYL\CSCSVGF\RLS VDGRSCEDINECSSSPCKPGSVA NV\YGS\YQCY\CR\RG*PASAIV GWEFTCERTFDGVAALPHRGH TFWFLTAGIQTSWGSFPVAACP SSGLTGWAPNGPATCQ\DI\DEL C*LGIHNCFHSTEDLVSNIPGAG FRCLGLSSCPENYRRSAAT*S*G NSCMRAIGAGWEKEKGKLAGS
19380	49748	B	19493	123	237	
19381	49749	A	19494	285	456	VINKRLVCTRLLRRKWSCLQPH RMM*VQAGSRGSQPKYHRHE MGWTGHTDTPPHRL
19382	49750	A	19495	383	693	NFLPAQPCLSAPPS*S/RSLLDNS PLNCKAFHSSSHHLLKLESCSE NSPGPLL\QPGGTCLGACPGCFS FSPGISAGKPLSKAASPPVCTGS GAETSTTPPSPLR
19383	49751	B	19496	28	236	

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19384	49752	A	19497	1	927	PAAPQVAGRLGLGCPLHLHVF AVVSAMLPLLRCVPRVLGSSV AGLRAAAPASPFRQLLQPAPRL CTRPFGLLSVRAGSERRPGLLRP RGPCACGSGCGSLHTDGDKAF VDFLSDEIKEERKIQKHKTLLK\ MSGGWELELNGTEAKLVRKVA GEKIPVPF\NINNSIPP\TFDGEEE TLARARRFEDREPELTSLPKF\V VE\VIKND*WQERPLVLD\VHYP EDEVGQEDEAESDIFSI\REVSFQ S\TGESEWKDTNYTLNPDSFWT GPLYD\HLMGFP*PNRGVDNTF A\DE\LVELSTAPRSPPGVPLPFP
19385	49753	A	19498	3	342	LDTNLPANRVPAGLEKRLCAA AASILGKPADRVNVTVRPGLA MALSGSTEPCAQLSISSIGVVGT ARDNRRH\GAPFFGFSPRELALG QDRILIRFFPLESWQNGKIRTGM TFL
19386	49754	A	19499	3	520	SSARAVSVPLPAMPFLELDTNL PANRSARGGWRKRLCAAAAS\I LGKPA\DRVNVDRYAGGFAIGA *AGST\EPCA\QLS\ISSIRRQWGT AED\NRSHSAHFF*VSSPRELSP GARDRIILFRFFPLESWADWAR *GTVIDFFMIWGTEGFQGHLVN LAASFQKRSSWAEVKGLG
19387	49755	A	19500	7	355	
19388	49756	B	19501	172	479	

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19389	49757	A	19502	1	1656	LEDPDSSSRPRRAGSGHSASFPF PPLEQLWRQVKTLNPKAEVAR AQAALAVNISAARGLQDVLRT NLGPKGTMKMLVSGAGDIKLT K\DGNVL\LHRNCKFQHPTASL\I AKVSNKPQE*YNLVDGTDFLIV LINWESLLKQA\DLY\ISEGLHPR IIT\EGF\EGAKEKALQFLEEVKV SRE\MDRETL\IDVARTSLRTKV HAELADVLTEAVVDSILAIKKQ DEP\IDLFMI/SVIMEMKHKSETD TSLIRGLVLDHGARHPDMKKR W\RDAYILTCNVSLEYEKTEVN SGFF\YKSAEEREKLVKAERKFI EDRVK\KIIELKRKVCGDSDKGF VVINQKGIDPFSLDALSKEGIVA LRRAKRRNMERLTLACGWG/M PLNSFDDLSPDC\LGHAGLVYE YTLGE\EKFTFIEKCN\NPRSVTL LIKGPNKAHTSLRIQRWQ*GDG L*GAV\KNAIDDGCVVPG\AGA VGSGQWAGSPGFKHKPSC*RA RAQLGSPKHLLDAFAHYFPKVL CFRNSGFLTFQGNIKLKFKAE\H SESG\QLVGVDP*TPGEPNWWP ARSKAVWG
19390	49758	A	19503	2	424	EGPVMAPPNPGPATLGGPGPDP DLGRLPLHEVFLHIRVPARPRG APLHRRGLRGRHAVRAVRQRR REPEDGAAGAVDRAGGAGVLG RGDRESEGPLTD*PREPADRAP LLQPERGRFSHPLPTLTCAPSPII FPVAERWG
19391	49759	A	19504	3	174	
19392	49760	A	19505	2	153	LPLHEVFLHIRVPARPRGAPLH RRGLRGRHAVH*PSEPGDPARL LQPERG
19393	49761	A	19506	3	354	EDGRHGAPNPPPATLGGPGPDP DLGGLPLHEVFLHIRVPARPRG APLHRRGLRGRHAVRAVRQRR REPKNGAAGAVDRAGGAGVL GPGDTEYEGPLTD*PSEPGDPA RLLQPERGR

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19394	49762	A	19507	3	1246	GSTHASARMAVMAPRTLPPAT LGGPGPDPDLGGLPLHEGF\LHI RVPARPRGAPLHRRGLRGRHA VRAV\RQRRREPEDGAAGARG* EARKGPE*LGRG\NTESEGPTHR LDPSEPGDPARLLQP\E*GRFFTP FQIMYGC\DVGSDGAFSSAGYP QERLTNGKDYIALNE\DLRSWT AADMAAQITKRKWETPPMRRR SLRAYLDGTCVEW\LRRYLENG KETLQR\TDPP\KTHMTHHPIS*P *RPL*RCW\AL\AFYPCGDHT*P WQRDG\EDQTQGHGSLLETRPA GAG\TFQKWASMVVPSGQEQR\ YT\CHVQQ*RVLPKPLTLKM/W EPSSQAHPSPIRGASFAGPWFSL GSL*ITG\AVGRCW*C*RKEQLR WRRGER*KKEGAYSQGCKASD QCPGASDVSLHSFVKVLRQLAL
19395	49763	A	19508	1	392	
19396	49764	A	19509	1	220	
19397	49765	A	19510	3	500	
19398	49766	B	19511	28	134	
19399	49767	A	19512	1	1662	MAASVVCRAATAGAQVLLRA RRSPALLRTPALRSTATFAQAL QFVPETQVSLL\DNGLRVASEQ SSQPTCTVGVWIDVGSRFET\EK NNG\AGYFLE\HLAFKGTKNRP GSALEERRWRAWGAHLNAYST REHTAYYIKALAKELPKA\VEL LGDIVQNCSLEDFTD*GRNVDV ILRE\MQEN\DAS\MRDVVCNYL HATAFQG\TPLAQALEGPSENV RKLSRADLTEYLSTH*QGPSKW CWAAAGREWEHQQLFRTFAQE GTSVGIP\WTYAEDAVPTLTPCR FTGSEI\RHRDDALPFAHVAIAV EGPGWASPDNVALQVANAI\IG H\YDCT\YGGGVHLSSPLASGA VANKLCQSFQTFSICYAETGLL GAHFVCDRMKIDDMMFVLQG. QWMRLCTSATESD\VDRGKNIL RNALVSHLDGTTPVCEDIGRSL LTYGRRIPLAEWESRIAEVDAS VVREICSKYIYDQCPAVAGYGR SLGLPFHLCSRTAAQLTEQPVK APSSSPQSPGCQGVLAQKTCPSS SLTACQGAFINTLHPSGPIEQLP DYNRIRSGMFWLRF

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19400	49768	A	19513	2	1693	AQSTLARRNRADCSWKMAASV VCRAATAGAQVLLRARR\SPAL LRTPALRSTATFAQALQF\VPET QVS\LLDNG\LRVA\SEQSSQPTC TVG\VWIDVGSRFETEKN/DSGA GYFLEHLAFKGTKNPALAVPW EKEVESMGAHL\NA\YSTREHT AYYI\KALSKDLPKAVGALGDI VQNCSLEDSQIEKERDVILREM QENDASMRDVVFNYLHATAFQ G\TPLAQAVEGPSENVRKLSTA DFTRYL\STHYKAPESVLPQTEG VRTEQLLDL\ARNHRVHIP*TY AEGAL\PTITPCRFTGSEIRHP*D\ ALPFAH\VAI\AVEGPG\WPAPD N\VALQVGNA\IIGHYDCTFGG\ GVHLS\SPLG\SGACGPTKLCQS FQTLS\ICYAEDGLCWVHTLFC DRMK\IDDMMFVLA/QGHWMR L\CTSA\TRSEV\ARGQKNIPQK MPLGISS*DGNYSLCVEDITPAA LLTLWARRNPPGLKWES\RIAG GGFQVVVR*DLAPRYIYGPSCP AVA\GYWPH*SMLPDYNRIP*P ACFWVAFFRAGKPMVKQKGR GGGLWSPPPPQTQHFRLLLTCC
19401	49769	A	19514	46	422	
19402	49770	A	19515	568	1567	GPWAANGVVLAFPPCLGSPPAP HLAPQKAVPPKWGISSLCSFHF HIYQVGGVAFCGRIRFLSSTDF KRRAGGSGSLMSQEEKHELSG KIRSQIMDDHARPYLYTMSNCP CWAGALGPQESKCSRGRLLHR AFPSLV\TLLLAGQATTGLLSCY QQQGAGWDKLDSHRPRNLAA WEEPCGMEAFPKPSQSLVEAKI AQLATPGLLDCKAACPWGAPC PRGP\MQNATKVIGNM\TEDHV DAPGSRNAEPP*KVYPP\LKGSF P/EKNLRHLKNTMETIEWKAFE NW\MHHW\LLF\ELSKQSLWEQ/ QSPLDAPPK/ENSLELEDPSSGL GVTKQDLGPVPM
19403	49771	B	19516	1	1428	

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19404	49772	A	19517	1	2293	MARSEAAAAGPGPGPPGLAAR ERRGGRGCVRGCERASVRVWS VALRRARRAPARPYVARCRRV RRPARVAIGCGGVSSPAGVSGC ARVSPERPPLRLCVWALSRAHG GAVCRAGPGPDSLKRGLTSHPP AFPLHHGSRTLLLGPLSPPPAAL PFLLLLWAGHLVAS/ACPGRCIC QNV/SPTLTMLCAKTGLLFVPP/ SIDRRVVELRLTDNF\RRHFAN MTSLV/QLTLSRNTIGQVAAGA F/VDLRALRALHLDSNRLAGC/ GGDQLRGLGNLRHLI/VGNNQI RRVESAAFD/DLLSTVEDLDLS YNNLEA/LPWEAVGQMVNLNT LT/LDHNLIDHIAEGTFVQLQSW A\RAQAAHPLTVSFGGNPLHCN CE/LLWLRRLTREDDLETCASP N/NLTDRYFWSIPEEESCTRCQR FCG*ASLVAAELTSNSVLIRW/S TQRPVPGIRMYQVQYN/SSVDD SLVYRKYSLSTYMNPTR\MIPST SQTFLVNDLAAGRAYDLCVL\A VYDDGATALPATRVVGCVQFT TAGDPAPCRPLRAHFLGGTMII AIGGVIVASVLVFIVLLMIRYKV YGDGDSRRVKGSRSLPRVSHV CSQTNGAGTGAA/AGPGPAGPG PLRGAARGGVP/WLPPPSPSRPR PWRPR/LASAEPEVVLGRSLGG SATSLCLLPSEETSGEESRAAVG PRRSRSGALEPPTSAPPTLALVP
19405	49773	B	19518	97	255	

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19406	49774	A	19519	1321	1728	EHAHDRDLHHAHYVQATLVR ASLREAVVGSPTDAWLQQRTA RSSASLLLARNRPATSVWLPRA GFIAGTGGRRERRGSEGWEGG GAGGTGAGLSAHSQTSACEGS/ CGGSAGRGRCLLSAATPPLQPP RPAPPTAGLVQPRQVPTAPPRA SAGNEHHQGWSGRL*KSLAAA RVGEAPGKLPRPRDFRKQSNGA LARASLRVSAQPGTCSSSAAAF PPLGPAPLAAPARSCDESGPRQP DGRGGPVPGQQQRGA/ESEPCA AATRRPWVVNRRR/TSRREARTS VACT*CAWCRSRSCACSHSPWS SASSSSAAICSSSPRA*STSS*RT GGRLRRWRRWSWGPTDPPYAP AATAPTPAHFASP/ACAPHYQR LGEANLSESIISLD/CRPFGKKRP VSPSPSESPHAWQSEESAQTLN SAESGKKRAIRAQNFG/RLLLT WNAGRPTVRRPFSTRRWAKLW GQVERAGRGETQRH*SPCDRKS DLLKATQQTHGVSQIRVRVRSP LFSLLPPCPRKGGANKIPLNCKR ARFKKGFVFVCLEIQMFE
19407	49775	A	19520	192	447	
19408	49776	A	19521	1	591	
19409	49777	A	19522	281	421	
19410	49778	A	19523	174	512	
19411	49779	B	19524	67	1166	
19412	49780	A	19525	1	1620	MGAKDGRLLSESSQGLSSCGAS LVPFCVSKSRLLMKTPVRLDKE TVSTVDSGAPTDLAQLPTVLKQ PCCSVMASGQFVNKLQEEVICP ICLDILQKPVTIDCGHNFCLKCI TQIGETSCGFFKCPLCKTSVRK NAIRFNSLLRNLVEKIQALQASE VQSKRKEATCPRHQEMFHYFC EDDGKFLCFVCRESKDHKSHN VSLIEEAAQNYQGQIQEQIQVL QQKEKETVQVKAQGVHRVDV FTDQVEHEKQRILTEFELLHQV LEEEKNFLLSRIYWLGHEGTEA GKHYVASTE/PTVERSQEAH*FP VCLLASYDEISGQGASSQDTKT FDVALSEELHAALTSAHPDLILS QDEIVTLNLASQGGSQKRGNPR RFYRRGFLEVEPLTGFVELHSS GSQCQALIESGSREDLPVCPNK
19413	49781	A	19526	203	359	

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19414	49782	A	19527	135	466	DPAGSSAASMSSAAGLCALTPP /GLLSLGLLLLPLVVAF\ASAEA\ EEDGDLQCLCVKTTLPGSVPGH IHQLGG*FKGRDPHCPTCPT**A TVEGMGRKILLGTWQAPLLQG
19415	49783	A	19528	46	468	TGPTHASAAILVPRSLHKMPGE ATETVPATEQELPQPQAETGSG TESDS/GKSPASDTYIVFGEAKIE DLSQQAQLAAAEKFKVQGEAV SNIQENTQTPTVQEESEEEEVDE TGVEVKDIELVMSQANVSRAK AVRALKNNS
19416	49784	A	19529	337	509	ISQQLLVVLAGINLRSWLPQKL CKYLKQDVLTALDLSVEVPEFC PFVDHLVVALEEEGPAL*GHPA SDTYIVFGEAKIEDLSQQAQLA AAEKFKVQGEAVSNIQENTQTP TVQEESEEEEVDETGVEVKDIE LVMSQANVSRAKAVRALKNNS NDIVNAIMELTM
19417	49785	A	19530	91	1019	GELLALLGHRVPTRPWASGQK GVCGWCPGKSTLQGLRCGPTIR ACRDGSSCSVEGGRGVRLVLG TASQDPEKEMPGEATEPVPA\T EQGVAASPRAETGSGTESD\SD ESVPE\LEEQDSHPGQPHNKAQ AGRQQSEIDEDPVS\KAKQSRN* KEGPGRAMSQTGVFGQVTGVT KEFTI\RKSKNILLCHPPKPDVY QGAPASRYFTIVFGGSPRSEDLS PSKHNLASCLRNSKFQGEAVSN IQENTQ\TPTVQEES\EEEEV\DE T\GVEVKDIE\LVMSQANVS\RA KAVPSPEERTSNDIVNAIMVSV
19418	49786	A	19531	1	261	MWGHFHSHPGTGQARAYTDTS GSPIPLIMHVNRGRHSEIPVLER NLLHFRMDAST*NLGMSSLME AILKNQFRHVSLAVSFAFSGEK
19419	49787	A	19532	277	349	
19420	49788	A	19533	792	1014	

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19421	49789	A	19534	849	1752	GESRGWERRKCVRPLSSYATHL SVCDCHIGNVREGADPAGGAG *L*GARQQQTHTHKPAKATQR GEDREEKKRETKREERLGQQE NERDERGRREKEPRNRGTKRRE AEKGRRR/ESEGKREEKGEEER QERQQKRAREKRRGRGARRRG REKKKTQRPRTQAQRPPLKKIK DYTHHTTQTPTQQHHTHTTKH KQPHTNNTTVFLFFFLLAKEHR RAARKQHEPERGRGGGSKAGA KIKHTSIAAAADRRHDRPTQRD TRRKEGRRAQSGKHGRTAHKT EAGGGIPVHSTSRVQVILLLQPP
19422	49790	A	19535	139	470	
19423	49791	A	19536	2	83	
19424	49792	A	19537	32	434	NRRKGA\GPVFQRAT*KH/RV*R AGLRAVDFA\ERHGYIKGIVKDI IHNPRR/GAPLAKVVFRDPYRFK KRTELFIAAEGIHTGQFVYCGK KAQLNIGNV/LP/VGTMPEGTIV CCLEEPRLCRRKRTSAEGLNKV CVYAT
19425	49793	A	19538	10	443	
19426	49794	A	19539	63	376	
19427	49795	A	19540	170	368	
19428	49796	A	19541	175	427	
19429	49797	A	19542	1727	2262	
19430	49798	A	19543	131	596	
19431	49799	A	19544	695	1337	GFGTQGERRRQCRLRVTQPLG ASSATQKTPALPETPVKAEQSC TLLPSPRTPGHLQPRLLDPSPW AVLIRG\QRKGAGSVVRRATLR HGK/GAVRRLLRRWISPERHGY IKG\IVKDIIHRPRSRRAPPLRQR WFFRDS\YRF*ER\TELF\IAARG AFHTGPSFVYCRQERPSFNIGQ WCSPVGHHCLEGYNSCCLPWK EETLETCGKAGPGAFKGN
19432	49800	A	19545	1	813	
19433	49801	A	19546	227	381	
19434	49802	A	19547	135	740	PQPLPPPTSMARHVFLTGPPGV GKTTLIHKASEVLKSSGVPVDG FYTEEVRQGGRRIGFDVVTVVR HPGGLLSRVGLEPPP/RENVNAE LGSYVVDLTSFWSSWALTRLE GM*ADCQQWAQGQRVCVIDEE LGKMEALSVK\FSFKAVRQTLS YPRDI*SL/VHKSQVPKGKPLAL VEEIRNRKDVKVFNVTQ\ENRN HLLARYS

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19435	49803	C	19548	251	574	
19436	49804	A	19549	2	450	
19437	49805	B	19550	721	3048	
19438	49806	A	19551	3	396	
19439	49807	A	19552	2	450	
19440	49808	A	19553	2	1152	GPPLHCTRAAGIRHEAPLGLAG LCRAADAGLCSAGWGFVKVV KNKAY\FKR\YQVKF*KTPERV KRDYYARKR\LVIQDKNKYNTP KY\RMIV\RVTNRDINLSRLLYA PV*RGDMDSLAQR*LHTELAKI LVVEGLALTNLLPAALFVPGPA CLAPQAFLQ*VLAMDKDLLEG PSWS*LGDEYNV\ESIDGQP\GA FTCYL\DADLARTTTGNKVFG\ APEGAVDGGLSNPHSSKRFLG/ YVYPLHSTQTDSPGFMDSEKQR NFNARSTSGKHIMGQ\NCLQDY IALL*WERKMKDAYKK\QFSQY IK\NSVT\PDMM\EEMYK\KAHA AIRE\NPVLWKRRPKERSLKRR GWNRSQNVPLLRKKDRVA\QR KASFLQSSRSGLLESLTPAIFP
19441	49809	A	19554	3	991	LTSRGVGSCAVMLLLVRAGAR AWLRPTGSQGLS\SLAEEAARA TENPEQVASEGLPEPVLRKVEL PVPTHR\RPVHAWIESLRGFEHE RVCLVDLHPDVFANAPRLDILH QDAMLQKNF*RISYAKTKTRAE VR\GGGGKPLAAERH\WAGPA WQHPLSALARRRCCPWPPGP\T SYYYMLPMKVRALGLKVALTV KLAQDDLHIMDSL*L\PT\GDPQ LP*PELAH\YRRWGDSVLLVDL THEEMPQSIR\EATSRLKTFNLI\ PAVGLNVHSMLKHQTLVLTLP TV\AFL\EDKLLWQDSRLQTPLY PFSL\PYSDFP\RPLPHATQGP\A ATPYHC
19442	49810	A	19555	31	305	
19443	49811	A	19556	213	541	DGGPAAHTPGAARGELSPVGD SGGYFRPSHLRCWILNLCISVPL SSAKDLLHPSSEEE\RRNPMKN RLVQSPNSYFMDVKCPGEETV CCIGESTGPQQLENVVVLAVSY

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19444	49812	A	19557	164	591	DINSRDRSGPRATRIDGSGEGD KMAAQLRRHQGRRGASSPRFA KD\LLHPSPEE\EKRKHKKKRL\ VQSPNS\YFMGV\KCPG\CFKFT TVF*AMAQTVVLCVG/CAAPLF LCQPTGEKARLTEGCSFRRKHA LKATLSQDEWETILQ
19445	49813	A	19558	362	916	GGRCTMARTKADWPANRTGG KAPKEANWLTKSPLRKSAALY LEGSKKPHRYR\PGTVAPP*NLD GYQKST\ELLIRKLPFQ/RRLVRE IAQGLLKQDSRFQ\SAAIGCFAG RQVRAYLVWPFLKDTNLCA\IH AK\RVTIYAKKTFQLSTPAYRG EPCFKDPLMDGETFHSQKKKK KISLLPVIGSSER
19446	49814	A	19559	849	1261	DGHIAGGPCS*GWPRDPAPKSQ PTMSSGSEPEKLPPAPRPQHYCS P\AEVSGPRFAVGIKALNQQAFT ERRLHTSLCPVPAALTVPSPESL PQPQIFPGLAPATHTLYSKAWA GATVSRPGAILGAGLYWGLVR ETAS
19447	49815	A	19560	3	1852	
19448	49816	A	19561	362	1298	QGGRNVRHPSPLLAWGSDLIV KPHWLHWLLDLNHARLSALFA AAGARLPSHIPAPSAGSRRLLLL LLGGCRACLLFFPEMANRGPSY GLSREVQE\KIEQKYDADLENK LVD\WIILQCAEDIEHPPPGRAH FQKWLM\DGRVLC\KL\INRLYP PGTRSPYPRFSESKDGFLGRWE QISQF\LKA\AETYGV\RTTDIFS RRWFLWEGKDMAACAEGP*L ALGSVAVTKDDGCYRGEPSWF HRKAQQNRRGFSEEQLRQGQN VIGLQMGSNKGASPGGP*TGYR ECPRQIHVRTRHPAPWLERTNV STPWSFTKKK

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19449	49817	A	19562	3	2518	AAGEWPQRPRAAVAAAGAAA RQRLPGSRQVAAGAPQPAGGG DPSQR\PPGAEILIKVQVYVSGE LVPLARASVDVFGNRTLLAAG TTDSEGVATLPLSYRLGTWVLV TAARPGFLTNSVPWRVDKLPL YASVSLYLLPERPATLILYEDLV HILLGSPGARSQPLVQFQRRAA RLPVSSTYSQLWASLTPASTQQ EMRAFPCLPGH*G\SSSGNGSW LELMPLTAVSVHLLTGNGTEVP LSGPIHLSLPVPSETRALTVGTSI PAWRFDPKSGLWVRNGTGVIR KEGRQLYWTFVSPQLGYWVA AMASPTAGLVTITSGIQDIGTYH TIFLLTILAALALLVLILLCLLIY YCRRRCLKPRQQHRKLQLSGPS DGNKRDQATSMSQLHLICGGP LEPAPSGDPEAPPPGPLHSAFSS SRDLASSRDDFFRTKPRSASRP\ AAEPSGARGGESAGLKGARSA EGPGGLEPGLEEHRRGPSGAAA FLHEPPSPPPPFDHYLGHKGAA EGKTPDFLLSQSVDQLARPPSL GQAGQLIFCGSIDHLKDNVYRN VMPTLVIPAHYVRLGGEAGAA GVGDEPAPPEGTAPGPARAFPQ PDPQRPQMPGHSGPGGEGGGG GGEGWGAGRAAPVSGSVTIPV LFNESTMAQLNGELQALTEKK LLELGVKPHPRAWFVSLDGRS NSQVRHSYIDLQAGGGARSTD
19450	49818	A	19563	206	1126	LESGSHIYAFSHESLLLHVASAS V*TSFSDFATSVCHSPLHCQLH HALIPHGKGECSS\VSGIVATGF GATGFLGRCVVNHLGRVGSQIP QAIAQVSKEAEVGKFIHVAHLN VNIKSSSRYLRKKAVGEKAVR DTFPEAIIVKLLDIFGREDRFLN YFANMCWFGAIPLVSLGWKAV KQPVYVVDVSKGIVNAVKDPD ANGKTFAFVGPNRYLLFDLVK YIFAVAHSKGWVARDFEISPFE SWTTRDKVERIHITDMTLSHLP SLEDLGIQATPLELKAIEVLRLH HTYCWLSAEIEDVKLAKTVNI

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19451	49819	A	19564	196	553	KLSSEFFLTHSINTAIRNGNLFV NRVTEVTRSGGNELGSFCLLAI KFTLLSFLGTGTRRLLPALRPRR LQQRGSHGLAGRLFTLWILHA GCHARGELLEPDTC*LSLCRAR KPRLSTLK
19452	49820	A	19565	1	505	ATEDPGVAMGRRPARCYRYCK NKPYPKSRFCRGVPDAKIRIFDL GRKKAKVDEFPLCGHMVSDEY EQLSSEALEAARICANKYMVKS CGKDGFHIRVRLHPFHVIRINK MLSCAGAD/RIHISKKWGFTKF NADEFEDMVAEKRLIPDGCGV KYIPSRGPLDKWRALHS
19453	49821	A	19567	6	904	AQLSSLAVPLLVLTPFRSVLVFR SDSLFFVAATEDPGVAMGRRP A\RCYRYCKTKP\YPKSRF\CRG CPLMPRIRIFD\LGRKKGKKWN EFPLLCP/HMVSDEYEQLSSESP GRLPRICPNK\YMVKSCGKDGF/ HISRVRLHP\FHVIRIHKMLSCA GADKAPKQACRGAFWKSPKGN LLARGSQLAQVIMSIR\TK\LQN KEHVI*GPAARPSFKFPGRQK\I HI\SKKWGF\TKFQC*WNLKDM VAEKRVHPHMACGGQSTSPSR GPL\DK\WRALPLHEGLPNVAA HPLNTPPIKFLLPWSKKKKKK
19454	49822	C	19568	346	471	
19455	49823	A	19569	1495	2780	EGLHLFCDLLDGLPGVQVAGG FDSFSSILASFTYWHDFPNSTML LSTFRDINLGMNIIKKSAVCFSR LGSETWEMPANLRPSEGGART RTELSRPQTPSRAHLAWRGRGG LGAVRPRRLSRRRSLS*KP\RSL* AEAPAGAPVRRCRPAAPP/PPRP SRCGPSTPPPPPSPGA\PRRRRPP CSEHNKLSPPPPSSLCLRPAPSPP RPAPRRSPSRRRRRRRHPRPAD RREPLASATRVRPLPPPPPPR*PP SSSCPRRGGRRFLAPWLARPAG APRRAPCSRAARSRRAGASGAR VGDPAGAGRGWRRRAAGRP* APERRPPPPLPAVCEVSGGPLRA SFADSVPGVRRRRPPGLGTPLSS SGV*PRNERGVETTTSWGGGSE GAPGSGEGGNLFPAPQVIVARS GEGTVVPRFPVCQLRDSAVLLC LFD
19456	49824	A	19570	178	256	

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19457	49825	A	19571	622	1726	QGSGRTMMRMLVPASVGLLET GPPGDPSLSHPLSGDVTVLPED Q\STVQKLASDHKDIHSSVSRV GKAIDRNFDSEICGVVSDAVW DAREQQQQILQMAIV\EHLYQQ GMLSVAEELCQESTLNVDLDF KQPFLELNRILEALHEQDLGPA LEWAVSHRQRLLELNSSLEFKL HRLHFIRLLAGGPAKQLEALSY A\RHFQPFARLHQREIQVMMGS LV\YLRLGLEKSPYCHLLDSSH WAEICETFTRDACSLLGLSVESP LSVSFASGCVALPVLMNIKAVI EQRQCTGVWNHKDELPIEIEL\S *SAWYHSVFACPILRQQTSDSN PPIKLICGHVISRDALNKLINGG KLKCRYCPMEQNPADGKTH
19458	49826	B	19573	271	392	
19459	49827	B	19574	58	296	
19460	49828	A	19575	215	861	QLPAESVRTRGPAKAQARAGG PPGPWHCSYKWRAWPSSLSGT GWPDMEGETTAAAPASRENSA DCS\AGELRGPG\KELW\SPIQ\Q VTATSS*MGRDFVLAT*EKVSH VDS*/EQPRSLQR\DPRP\AGPAQ AKQGTPRAQASRESL\SRPTAA V\QLPSGPQHPV\TSGS*KGLAG KTSMGRKGLPWARGWAPWSL EAQNP\RPTRLCDLFITGEDFDD DV
19461	49829	A	19576	65	782	SSSSSAIQRKPRWVLYKYIQEL WRKKQSDVMRFLLRVRCWQ\Y RQL\SALHRAPRPTR\PDK\ARRL GYKAKQGYVIYRIRVRRGG\RK RPSFLKGAT\YGQSPVHSWVFN QLKSFASE/VLSVPFARGRRSLG RH\CGGLLEEFLNFFNWVWVER FPHYQIFLKVIPHLIPFP*KLFRR N\P\DTQLIHQNQVHKHR\EMRG \LTSARPEKSRGLGKGHKFHHTI GG/SLRRATWRRRNTLQ\LHRY R
19462	49830	A	19577	1	179	QEDYLRELLTTMGDR\FTDEEV DELYREAPIDQKGG/MFNYIEFT RILKHGAKDKDGLKEL

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19463	49831	A	19578	144	722	KKGLNHHHVEQNNTRPRPRSG PQRATSN\VFAMFD\QSQIQEFK EAFNMIDPDQDGFHRPGKICND MLASLG\KNPT*WSILDAMMNE \APGPPSNFTPWFPHHGFGEEV* MATRS*KMVIRKCPLTCFE*KK PLGTI\GEDYL\RELLTTHGGIGF TDEEVDELYREAPI**KRGISITS EFTRILK\HGAKDKDD
19464	49832	A	19579	3	429	VACLREHKQRCERATRSLLREL LQVRARVQLQGSELRQLQQEA RPAAQAPEKEAPEFSGLQNQM QALDKRLVEVREALTRLRRRQ VQQEAERRGAEQE/DRPQTGQA DRLAAAGGAGPGGGLRRPAEE PRGQQPEGGPGGGQN
19465	49833	A	19580	1	2454	RFPAGVAPRRAMANVSKKVSW SGRDRDDEEAAPLLRRTARPGG GTPLLNGAGPGAARQSPRSALF RVGH\MSSVKLDDELLEP\DMD PPHPFPKEIPHNEKLLSLKYESL DYDNSENQLFLEEERRINHTAF RTVEIKRWVICALIGILTGLVAC FIDIVVENLAGLKYRVIKGNIDK FTEKGGLSFSLLLWATLNAAFV LVGSVIVAFIEPVAAGSGIPQIK CFLNGVKIPHVVRLKTLVIKVS GVILSVVGGLAVGKEGPMIHSG SVIAAGISQGRSSSLKRDFKIFE YLRRDTEKRDFVSAGAAAGVS AAFGAPVGGVLFSLEEGASFW NQFLTWRIFFASMISTFTLNFVL SIYHGNMWDLSSPGLINFGRFD SEKMAYTIHEIPVFIAMGVVGG VLGAVFNALNYWLTMFRIRYI HRPCLQVIEAVLVAAVTATVAF VLIYSSRDCQPLQGGSMSYPLQ LFCADGEYNSMAAAFFNTPEKS VVSLFHDPPGSYNPLTLGLFTL VYFFLACWTYGLTVSAGVFIPS LLIGAAWGRLFGISLSYLTGAAI WADPGKYALMGAAAQLGGIV RMTLSLTVIMMEATSNVTYGFP IMLVLMTAKIVGDVFIEGLYDM HIQLQSVPFLHWEAPVTSHSLT AREVMSTPVTCLRRREKVGVIV DVLSDTASNHNGFPVVEHADD TQPARLQGLILRSQLIVLLKHK
19466	49834	B	19581	508	4413	

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19467	49835	A	19582	8	331	EVTACWQSSQPSLTLSASSAWA STLAALEEPFSPPLHSESPFLGW PRPELGPSAAPCAPVPPEPPQRV PPPAP*RPVPSTTQGLRSVGAW CRTGRQLHLHPGVGSTG
19468	49836	A	19583	831	1121	
19469	49837	C	19584	1	1524	
19470	49838	A	19585	270	578	RFSKSPPDSGAQLAAPSGSRTG AAGGAACQSRAVRPHSSALGW SMGLGAMEQGAVLVGEAWAT QQPTVGGRLRHGGLQVPSPAPR GGS*GPAKSHSSCWPRC
19471	49839	A	19586	2	298	
19472	49840	B	19587	113	515	
19473	49841	A	19588	1	569	MLPDRLRSPVAHHRCRASGNY HSGRHSPAPAWRVTLTGWLDQ RSSRIHRSLAFKDSYSKGKEERT HIKGMCSELLPSG/EARGLAGFR SEAADLRGECYSS*RQCGPKEL RSPAGFTQWIPHWGYRWSCLS VPRPAPALLSPWVVDGTGRCG AGGGAHRGGSGRSGAHGGGG RLRHGGLQVPSPAPREGS
19474	49842	C	19589	1	1200	
19475	49843	A	19590	511	846	ARHRVLIGVFTIPELDIKVLHVP TRLRSPASFTQWIPHWGCRWSC LPVPRRVPALLSPWVVDGTGG CGAGGGAHRGGWGCTGAHGG GGRLRHGGLQVASPAPREGS*G PARN
19476	49844	A	19591	9	481	QQPLREKPASGDHPAKNANRR WPSPTRYPYVES*NWMPSLHLI QKSIQDGLKT*TLDLKP*KL*KK T*ALPFRT*A*ARTSCLKHQKQ WQQKTKLTNGI*LN*RASA/PA KETKI/SSEQATYKMGENFHNL LF*QRANIQNLQ*TQRDLQEKN KQPHQK
19477	49845	A	19592	1	3339	MSVRKDVEKLEPSDIVCGNVQ CYSCMETNLTVSQKVKHEVTV GPREGATKPNRMKGKEGRSGS LLGEGDFFKDESVMSSQGSSKD GEKRRGKAQRWKWPMQGICR QLGVAKSMEGYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDIESSSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPRC
19478	49846	B	19593	1	631	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19479	49847	A	19594	71	208	PCPKHCSKFPMCPELVGSWSH* LQE*SHGPSRFRLC*KQPQDLQ
19480	49848	A	19595	138	650	AWAQLPSALGSTRVSPPPSARS QPPWRRRHKVCWRLNRCKE/L DEDAVASADFSSMLSEEEKEEL KAELVQLEDEITTLRQVLSAER KAS/ELR*NKNSA*T*/CNELKPE LQQKLA*HAD*HCLQEDT*YAE SRRAKGNCSFQQRWNGHQQEV RRHELLHSPFHKYACYETKVG
19481	49849	A	19596	1	1222	MRADGTAGKDPFATDKQLPEL LIQHCWDGLLAVCGGSTVGVR LPFILHGSWVRPVAASFPPLPDN LHDSAEPAIILLEPTQMRRNQK TNAGTMTKQISSTLPKNHHTSS PAMDPNKEEIHDLLEKEFSRLVI ELIREGPEKGKAQCEEIQKKDT KVKGEIFKEVDSLKKKQLNIQE NLETLLEVLNALESLSNRIEQVE ERNSEREDKVFELTQSNKDKA QRIRKYEPSLQEVWDYVKLPKL RIISFPNEEENSKSLENIFRGRIK EHFHSIARDLDIQIQEEQTTPGK LIVKRSLPRHIVIMRAPTPMDHP RAEECGRRARDWQAAPPAAPV RDPLGEASWAPDSEGRK\WNTS KHQRNKLRTRHL*EL*HSSRGS VASFLKSVRPRTHQFQTQSGYP KLRWRKES
19482	49850	A	19597	381	598	
19483	49851	A	19598	1	1906	
19484	49852	A	19599	493	589	
19485	49853	A	19600	60	261	
19486	49854	A	19601	1423	1831	PRRSANVNLPPPQLATLSPGWP EERKSVGSPTSPPPPRPLRRLSA APG\SGGAWPEPGAWSLD*TAS PAGAPVQRPAGNG/PSALDASH ARALYLQRIPRVTWTPASQPPA PLGPFLPLIPPAASHRQPSSSFFR RHR

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19487	49855	A	19602	1	1535	MEEKTNVQLPPGQTEQHVEIHI MNFCSKNHHRITPEKPKELTDP FKEAACCCKLYEIDKKLYRMA EWIKIHKPSICCLQETHLTHKDS HKLKVSITFKDLAVRFSEEEWR LLEEGQREFYRDVMRENYETL VSVEPGRAVGGGSHADEGQEP AGCG/VSPGPGAAGEGDPRVLV WRSQGRYGQPRER\GRGASLD GERASPEAA/DGKRALPSPRPA QLPSRRPYQPAPPG\PTPTDSSCS SGPTGDGVQGSPLPIRISPGNSP L/PRPHQLSEGNPCAWAPAPRDI PKLLATSP*PGHVQANQSRPGA WEPALGRSDQRACSASGSAELC ERWPQQAP/APPEEPPPASPHPA APTG\PGFWESCGEPGAA\PGKG SAPKPSPLHCLESALRGILP\EGP CASPAWEAPAPAPAPAPARASA A/AEGEDPRPEPELWKPLPQER DRLPSCKPPVPLSPCPGGTPAGS SGGSPGE\APGEQSPGTAAASV Q/VSPAHWPCFS/SPVRYSSGSLP GFSAGEKAQG
19488	49856	C	19603	4	150	
19489	49857	A	19604	148	448	RTRDWSLFLLMFGCVRSFFLLV GLWSCWLRSEAADLRGECYSS *GGASGVVRSSWWVRGLTSFR SETGFTQWIPHWGCRWSCLPVP RCAPALLSPWVVNG
19490	49858	A	19605	136	439	LVHFTEC*LVRLQTLARHSTDW CIYKSLARQKSSPSPHSTQEVQL ASPLTGRQEDCSEPRSAPLHSSL GPTERDSICVAASSVRWTRPGA RFS
19491	49859	A	19606	2	399	SKLQKLKRSLSFKTKSLRSKSA DNFFQRTNSEDMKLQAHMVAE ISPSSSPLPAPGSLTSTPARLVCI QVARLMPFRNTSSRSPLFC/RCL QPHDSGFLFLRPARPRAHREER NNSRRVALRAVTLTTERLQLHS

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19492	49860	A	19607	1	1262	MPLSYAYKNAETLAGRHTSSW MSRGAYQRRNTRAAGRPEECT DRNWHAGRTRRIWLGQLEERC SDVFGVSFFWWVRGLAGSGAK LQTFTVSVTAHRGSKDQKSEQ KQDLLQKAKEQTIHNVKGDPS ELPLLAPAACFYSLICPRPPPHIL LIGPFYRELIGPFYRELIGRQLRP GEKSSTAA/VWPRC*AA/RLPGA G/WTAPSAGPAEPTPTWNSRWP ASATRRPGSRRRLSLHTSPQAE GAGSGLSQPRKGLPQCSGRLKR SSSAARVG\ARQRRRRERASEG/ WPACCHLSVLPCGFGFLEAHSS SPEQTDHEQNCPADIKVMRLA GQPTNARGAANRAQPLHSTSV SHLKAVIFKIQTRQQKNSHFPPL FLEMTTSLATGRLRPSWVDYA RPALSVVSVSRFSLLTSLLELLV ETLGECGLL
19493	49861	C	19608	173	394	
19494	49862	A	19609	1	924	
19495	49863	A	19610	3	689	EVQEELEGPVRGAPHQLHQGP VEHLEAPHQ\HKFGKKVIYFNY LSELHEHLKYDQLVIPPEVLR\T MRSSRACTRAGRRLPPRHHRR GPRCPHSSLASVCNTSKTKIKA NSSPLC*GSQ*RT*ERKACAPRA CSGDPPACRPSARSRGSTT/KGK PVNFDDYGDIHIPAVILKTFLRE LPQPLLTFQAYEQILGITC/GGE QPACHSLPPDLTEPPRAQLRRPP LPHGLPACG
19496	49864	A	19611	1749	2411	APSCLVSEHSAPGPQRELPQPLL TFQAYEQILGITC\GSCP\AQGW GAWSSDAVPQLLARRPPLPHGL PACGEWGRGELGVKPSGLPSH AGPAWGHQVRTVCATAHPQD CISPEGAVEEEIVGG*GC\TEGQ SQRVLQIWP\SQGVSSLSALVPL N\MF\TELLIEYYEKIFSTP\EAPG EHGLAPWEQGSRAAPLQEAVP RTQATGLTKPTLPPSPLMAARR

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19497	49865	A	19612	883	2164	EHRRPMRAQASHEGHRHPMRA QMSHEGYRRPMRVQASHENTG VP*GVQASHEGTGIP*EHRCPM RTQVSHEGTGVP*ECRRPMRTQ \GPMRGTGVP*EHRCPMRGTGV P*EAQASHEGHRRPMRGTGIP* GAQASHEGHRCPMRGTGVP*G HRRP/DENTGVP*GHRRPMRAQ ASH/REHRCP/DEGHRRSP*GHR RPMRAQASHENTGVP*GAQAS HENTGVP*GHRRPMRGTGVP*E \QGVP*GHRRPMRAQVSHEGHR RPMRTQASHEGHRRPMRTQAS HEGTGVP*EHRRPMRGTGVP*E FRRPMRGTGIP*GHRRPMRAQA SHENTGVP*GNR/PYHEGTGVP* ECRRPMRTQASHEGTGVP*EHR CPMRAQASHEGHRHPMSTQAS HEGHRRPMRTQASHEGHRHPM RTQASHEGT\ASHEGHRRPMRT QVSHEGTGVP*EFRRPM/PGHG HPMRTQASHEGHRRPMRVQAS HENTGVP*GHRHPMRGTGIP*G HRCPMRGTGVP*GYRHPMRTQ ASHEGYR/PSHEGTGIP*EHRCP MRTQVSHEGTGVP*ECRRPMR TQVSHEGTGVP*GHRRPMRTQ VSHERHRRPMRTQASHEGTGV P*EHRCPM/MGHRRPMRTQASH EGTGVP*EHRRPMRGTGVP*EH RRPMRAQESHENTGVP*GAQA SHENTGVP*GHRRPMRAQASH
19498	49866	A	19613	1	552	VPQDSLGQALAGQATPEIPLGL QLHTVLVQEIQELIEAQTRAPGP CAEVRALPAPAAEPEPAWEEAP PERALELEGAPAKDQTNEELPEI TA/PYC/EPLALTLELKAWLERE VGGRG\DQHSPSQQLPCCP*SW ARWQTCRQRAGHLAWPPVPRC REASLIH*NHSPAAAGPFILLILV YLCAGGA
19499	49867	A	19614	443	991	VDSRPMLNTRLMRTSGRRWTP RPQVDTRP*VNNKTQ*AIRPQ/C GYSPQVPQDSLGQALAGQATP EIPLGLQLHTVLVQEIQE/RH*G TDTCSWSMCRSKSTASTSRWS Q/RPAWEEAPPER/GTGAGGSSS QGPDQRGAA*NHGGAGEH*KK AGRKSSE\RYACSQRQPPPPGM DAGPQLGIQAVCP
19500	49868	A	19615	16	450	

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19501	49869	A	19616	2	477	PRVRSGHSMDMRVPAQLLGLL LLWLRGANCDIQVTQSPDSLSA SVGDKVTITCRASQGISNGLSW YQQKPGQAPTLLIYAASSLQSG VPSRFSGSGSGTDFTLTISSLQPE DVATYYCLQDYTTPFTVLQAIT KTPQR\RDV*VCTVLATPPGVIN WL
19502	49870	A	19617	2	675	LPLSSSALPTESGSHLPFSGIMA RPSDPLVKPQRSSKREPKKVHP GTQSDR\YVKIKR\NWAENPRG\ IDN\RVR\RRF\KGQDLDAPTLG YG\SNKKTKAHACPSGFREVPG VHNVQGSWEVACLMLQQNLY CCRGSVHNVFLPRNRQSPSWG KELAQLGLSGVHPTPLARAAQL KEN*VRQLMCNKSYCAEIAHN VSSKNRKAIVERAAQLAIRVTN PNAR\RSEENE
19503	49871	A	19618	2	527	VWAANMPSRLRKT\RKLT\GHG AATGHGPHRPSTRKAPPGGPR* MPGGPAIHPPGSNFRQNTHPQA YFGK\VG**KHYPT*KRN\QSFL PPTVNL\DKLWTLVQ*NRHRVK CLPKNKTGAAPHHLMLVRSGY LQSSGERGKLPKASLFFVEGPK FFSRRSLREEGLRGVWGGPVSL
19504	49872	A	19619	45	233	
19505	49873	C	19620	95	154	
19506	49874	A	19621	2	241	
19507	49875	A	19622	63	320	RQWGNRLVTA/WSFFSWLSDC EGPGYGTIAEVGQLWGIMAKD LLRHSLASEELALNQNLTCHDQ FAQSTRSSARACGSIFCSTTQGS
19508	49876	A	19623	2309	2560	RNREARFYMTTPNFTETKR/WF HERVCALERERREREVTKISRLE RDNHRLVGDISQLKKELDQYL QAISDLEDCNGKRLLQILEA

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19509	49877	A	19624	4994	7008	QWQQKPKLTNDNLKFIWNQKR DRIAKTILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRHI DQWNRTEPSETIPHIYNHLNFD KPDKNKKWGKDSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKHLNVRPKTIKILEENLGN TIQDIGMGKDFMTKTPKAIATK P\N*QMGSNILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNMPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMA FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPNFELYY KATVTKTAWYWYQNRYIDQW NRTEPSEITPHIYNYLIFDKPGK NKQWGKDSLFNKWCWENWLA ICRKLQLDPFLTPYTKINSRWIK DLNVRPKTIKTLEEDLGITIQDI GMGKDFMSKTPKAMATKDKID KWDLIKLKSFCTAKETTIRVNR QPTKWEKIFATYSFDKGLISRIY NELQQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKYS SSLAIREMQIKTTMRYHLTPVR MATIKNSGNNRQ

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19510	49878	A	19625	1	764	GSSEKRKFKTGNQKLSMEVEK NQQMRSLSLYQQRVEGSKCAV RRKGGSPKPKAFLAAAEKFLN VPVMRSASHEQLVLTGDPNKT LPGSKSRLSGTDSPRACSTFPIW ATKIVTEMQVQLFAACRVQLIK HPRPSAARTAMEVLESGEQGV LQWDRKLSELSEPGDGEALMY HTACQGHEEQVWEEEALQLGL RSGILLNHWKRQLVGGAGILRS AQLHSPYHHWQMISLVSPSPAV MAVMENDDICMVLCVKVMDE PNHILDAISEHQIPSLEDQWFSE CALWTSKAYENLVERHILGPHC RPTELETLGISEDDIDHNPYLDF PGVAGLGSRRNVKERGWLSEM KKEGDIFMKIQG*AICPTSGPAE GLPPPTPVPHVPDRPCGT*GP/PP SPGSDSS\PACGPTAARPAPRSP APPWRCGPRWAEDVLLTGLCK QQIAEPAFRLQFWWPI

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19511	49879	A	19626	1	1430	MNGTAEGQHPWVHSTFNGEPQ SLSSSVRVKNQGPRDQAELGFQ GNGSTVPAAQARTIARARGSGS GGGDALQGGGAGAGPGATKR TARLLARGLRRAALRPDGRGV LGAGAGSSQRRGGGRRKMETH ISCLFPELLAMIFGYLDVRDKG RAAQVCTAWRDAAYHKSVWR GVEAKLHLRRANPSLFPSLQAR GIRRVQILSLRRSLSYVIQGMAN IESLNLSGCYNLTDNGLGHAFV QEIGSLRALNLSLCKQITDSSLG RIAQYLKGLEVLELGGCSNITN TGLLLIAWGLQRLKSLNLRSCR HLSDVGIGHLAGMTRSAAEGLP GPGAAHATGLPEAHRSFSKAHL PRADGPEAPQPQLLWGNLGRW PPAPVAHGQPAHAQPCAPCDNI SDTGIMHLAMGSLRLSGLDVSF CDKVGDQSLAYIAQGLDGLKS LSLCS/RRGLRRAALRPDGRGV LGAGAGSSQRRGGGRRKMETH ISCLFPELLAMIFGYLDVRDKG RAAQVCTAWRDAAYHKSVWR GVEAKLHLRRANPSLFPSLQAR GIRRVQILSLRRSLSYVIQGMAN IESLNLSGCYNLTDNGLGHAF/R AGDRLPARSQPEPLQADH*QQP GPHSPVPQGP/ARCWSWEVAAT SPTLAFCSSPGVCSASRALTSAA AATFRMW\DRAPGRHDAQRGG G\LPGPGAAHATGLPEAHRSFS
19512	49880	A	19627	293	1520	TTMDGSHSAALKLQQLPPTSSS SAVSEASFSYKENLIGALLAIFG HLVVSIALNLQKYCHIRLAGSK DPRAYFKTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVS VIASAIIGIIFIKEKWKPKDFLRR YVLSFVGCGLAVRG\TYLLVTF APNSHEKMTGENVTRHLVSWP FLLYMLVEIILFCLLLYFYKEKN ANNIVVILLLVALLGSMTVVTV KAVAGMLVLSIQGNLQLDYPIF YVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAIT AGAIFYLDFIGEDVLHICMFAL GCLIAFLGVFLITRNRKKPIPFEP YISMDAMPGMQNMHDKGMTV QPELKASFSYGALENNDNISEIY APATLPVMQEEHGSRSASGVPY RVLEHTKKE

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19513	49881	A	19628	751	2034	VSSSPTSLGCMRQKEYRIPKKL TNMPFLGSQPSLLALRSCHPTG RTCSA/SQVALFCLAAHRVSQIG ALLAIFGHLVVSIALNLQVSFHI RLAGSKDPRAYFKTKTWWLGL FLMLLGELGVFASYAFAPLSLI VPLSAVSVIGKTIIGIIFIKEKWK PKDFLSKFVLSFVGCGLAVVGT YLLVTFAPNSHEKMTGENVTR HLVSWIILFCLLLYFYKEKNAN NIVVILLLVALLGKLTVVTVKA VAGMLVLSIQGNLQLDYPIFYV MFVCMVATAVYQAA*VSQAS QMYDSSLIASVGYILSTTIAITA GKGFYLDFIGEDVLHICMFALG *VLAFLGVFLITRNRKKPIPFEP YISMDAMPGKVNMHDKGMTV QPELKASFSYGALENNDNISEIY APATLPVMQEEHGSRSASGVPY
19514	49882	A	19629	19	933	QSARPSLKRARSQRGRPLPSRA LVFLFLFFFFFFNFLPIHTQPSAH KDMTTNAGPLHPYWPQHL\RL DNFVPN\DRPTWAYTGLGLFSV TGGLRSWTTWAVVQGRAPGL\ PIGDFGRATVPCCWVLQWCGFI HLVIEGLVPFSNYERPCFGDQSL LYSQLW\KEYGQGETARYILGV TNFTV\CM\ETITSFA\WGEPFSL WVVIV\FLLQHPL\RFIL\QLVVS VG\QIYG\DVLYFL*RATPTDFQ HGKPGPTPLLLPGFSFVFHEMP LWLVPAPGSPLCLDA/V*KHPQ LMPQSNAWNAKGPQKPKSKK
19515	49883	C	19630	113	257	
19516	49884	A	19631	143	330	HHGPVPFPRGLIS*HSLHCPCPT PGGKNVFFFCEYFLKLAGIETT NCSADKRGKKVCCLIPR
19517	49885	A	19632	3	432	
19518	49886	C	19633	112	192	
19519	49887	A	19634	1	4410	MARPLALPLTGMSAPGSSLTTIP HTPSHPRSPSTPDTVSHPRSPSTP DTVSHPRSRYTPDTVPPTLPVY TRHRVPPTLPVYTRHRPTHAPG IHQTMCPTHAPGLHQTPCPTHA AGLHQTPSHPRSPSTPDTVSHPR SRSTPDTVPPTLPVYTRHRVPPT LTVYTRHRVPPTLPVYTRHCPT HAPGLHQTMCPTPRSRSLPDTV PPTLPVYTRHRVPPTLPVYTRD RVPPTLPVYTRHRPTHAPRLHQ TPSHPRSR

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19520	49888	A	19635	1	444	
19521	49889	A	19636	3	1017	SSRPVRPRPAARLSAMSSTQFN KGPSYGL\SAQ\VKNRLL\SKYD PQKE\AELRTW\IEGLTGLSIGPD FQKG\LKDG\TIL\CTLMNKLQP G\SVPKINRSMQN\WHQLENLS NFIK\AMVSYGMNP\VDLFEAN DLF\ESGNMT\QVQVSLLALGG KRPKTKGAAEGGLDIGVKYSE KQERNFDDATMKAGQCVIG\L QMGT\NKCASQSGMTAYGTRR HLYDPKNHILPPMDHSTISLQM GT\NKCASQVG\MTA\PGTRRHI YEYQAGNPTSCDNFSM\SLQ\M GYTQGAQTQSGQVF\GPGRPDI *TPSTCPQGTI\ADGAPSGTG\D\ CPDPGEVPEYPPYYQ\EEAGY
19522	49890	A	19637	1	479	MQGLRVSHSTFYTLIPEVTENP HRLDFHWFLSAQLERVASGTIL KKKESPPRPKVLGSARWDLPV/ PPGWCNSTALQ*SPRSDQV*SE RGMEAFFLPMPSESVASVCCRF SPWTSQKPQLSTSRDRKLQGKR *WFSTGVWAS*DHS*ERRCSQC PKTTCW
19523	49891	A	19638	2	501	FVPEERSSETALQRCSLPPGRRA APDPGLQGLRGSLGGSGSELES RKAKLRAAEGLRRKTTEINQRD TADRCTRGHH*SPGESPPKPSAF SL*LSVPRSGKLRFLRSPRREPA AN*SHRLRRHREKKCFHPPFTL NLIASGTSLEGGGVAPTWSTGR SQRALPSTL
19524	49892	A	19639	1	1122	RFLILINHAVFEYQDIFVASFPSI FFNIHCRGEGEREKGFAGKDRT PPPSTLLCGSGHLPPLASRRPPR PRCACCLPGGPLSSSALEAG*Y WRFPKLSG*KRSHTPWVPQPQQ PLPNPSPGKWVWASSEALQ/GT RA*RGIAELTHLLRLPARRGTQ RPA\PGHRAGASPQFRREASSRG PGLRPRPGRTRELGFPKRRVWA TAASWPRGTEPCAAA*RRRRRR RRARGRELSPRSTWSSDTESTF ALSCDPS*PRHQSVPKGRVGSC KGKLANKGFFCPTWQRPIRVAS VDMELLHFVPKRALPGFTIAISF LSSAPPLCPWYSGSNPWLRNPL KPRLAALFQRSAAPRLHFSGAA SLQVGERRQIRDFRVSAGA

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19525	49893	A	19640	14	618	GNENVKSGRKTSLSPFVLSDFT ASSALLASDSSRWMSLQSASEC \PGRAAGSGPGYG*PVSEVTGG PLSAHTHSSL*TSQRGCPPG\PE HHGAGPFP*GPGLKDVSGRGG NGCWGRRKPAHMGGGLGPAT PLQFPPRPSPPPPLGPPQ\PPPPP SPPLGPASSPP/CLPHRPPPPPPPP PSRCVTAPCVTAPGPAPTGAAA RRH
19526	49894	B	19641	42	121	
19527	49895	A	19642	1	153	
19528	49896	A	19643	104	355	
19529	49897	A	19644	459	988	DPRTMNLAISIA\LLLTVLQVSR GQKVTS\LTA\CLVDQSLRLDCR HENTSS\SPSKYEFSLTRETK\KH \VLFGTVGVPEHT\YRSRTNF\TS KYNMEGPLTYSAFH*ARTRGTL QVLQFHQFGALSPPIFLSRNV\T VVQRTNWVKC\EGI\SLLAQNTS WL\LRLLLS\LSLLQ\ATDFMSL
19530	49898	A	19645	1	950	
19531	49899	B	19646	55	1459	
19532	49900	A	19647	1	165	
19533	49901	A	19648	183	700	PNGNQPPRETPQRISRGIQRLGT AVASSGGSRSLPRSASAEPAQG AAARRAAPGPAGRCRAARGAG AGSARRLP*APAHPAPPEQGRR/ SRTARSRAAPQPPPPSQPQSPQL GPRPSQGAPQRRGPSSPGPRAG CRAQ*EALTPRLWRSSRTPSSR GLGPHVRGGIFSPKIPT
19534	49902	B	19649	71	264	
19535	49903	A	19650	3	810	GVSPCWPGWSRTPDFGSNPKCP PIRASPGAELQALSSTVTTPYW GILVTAVFPH*GLRPRQCRQDH PAGRQGPGPGEVPEILGQSGCT DRTWSKAGGRTQAPGPRSRAG RRVSGQEIRAPGPLGCRHGG/V GAPWTPEAASPLTATEPSCPH/L QAPCGYMPLSVSPRRRYRGPA GDQKVKMLKFKAFCLDYWQF LCLQPLHGAYKRDSDLMTWIW GLLPEVTGAAGTTSPNVHTSGR FFRACVFCPVHTLVKKEPHPGQ QEIIMEPSPWSP

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19536	49904	A	19651	258	1378	REILSLDRLPGATPNQALSAEA ACPKGQTSLLCGAMGIQGLAK LIADVAPSAIRENDIKSY\FGRK VAIDASMSIYHFLIAVRQGGDV LQNEEGETTSHLMGMFYRTIR MK\ENGIKPI/YKSGELAKCSEL R\AEAEKQLQQAQAAGAEQVV EKFTKWLVKVTKQHNDKCKH LLSLMGIPYLDAPIEAEASCAAL VKAGKVYPVATEDMDCFTFGS PVLMQHLTASSDYCKSIWSIGP KRAVDLIQKHKSIEEIVQRLDPN KYPLPENRLHKEAYQLFLEPEV LGPESVELKWSEPNEEELVKFV CGEKQFSEERIHSGVKRLRTEK GGGEPRGP/DWTQPGRASPTKR PDHQEDQHTRSRSSEGSH*GWL
19537	49905	A	19652	1040	2322	LPACPPASTPASTMSIMVTQKS YKVST/SRWSSGPQAFGNCSYA RGPGACISSLSFSRVGSSIFRGVL GGSYGGASGMGSITAVTVNQS LLSPLNLEVEPNIQAVCTQEK\T LNNKFASSIDKVQFLEQQNKML ET/ESYINSLKQQLETLGLERLK LEAELGNMPGLVEDFKNKYED EINKRTEMENEFVLIRQYVDEA YMNKVELESCLEGLTEEINLLG QLYEEEIQKLQSQILDTSVVLC MNNSHSLDMDSIIAEVKAQYEE MANHSQAEAESMYQIKYEELQ TLAGKHGDDLRHAKTEI/S/EM NQNGAKQDMA/*QLHEYQELT NIRLALDIKITIYRKLLEGEESQL ESGMQNMNIHMKTTSGYAGGL SSAYEGLTSPSLSYGLGSSFGSG MGSISFSHTSFTRAIVVKKIEIHD GKLVSESSDVLPK

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19538	49906	A	19653	1040	2322	LPACPPASTPASTMSIMVTQKS YKVST/SRWSSGPQAFGNCSYA RGPGACISSLSFSRVGSSIFRGVL GGSYGGASGMGSITAVTVNQS LLSPLNLEVEPNIQAVCTQEK\T LNNKFASSIDKVQFLEQQNKML ET/ESYINSLKQQLETLGLERLK LEAELGNMPGLVEDFKNKYED EINKRTEMENEFVLIRQYVDEA YMNKVELESCLEGLTEEINLLG QLYEEEIQKLQSQILDTSVVLC MNNSHSLDMDSIIAEVKAQYEE MANHSQAEAESMYQIKYEELQ TLAGKHGDDLRHAKTEI/S/EM NQNGAKQDMA/*QLHEYQELT NIRLALDIKITIYRKLLEGEESQL ESGMQNMNIHMKTTSGYAGGL SSAYEGLTSPSLSYGLGSSFGSG MGSISFSHTSFTRAIVVKKIEIHD GKLVSESSDVLPK
19539	49907	A	19654	152	207	
19540	49908	B	19655	75	402	
19541	49909	B	19656	1	2319	
19542	49910	B	19657	1	1341	
19543	49911	A	19658	198	1118	LHAPNSLHHHLPRDLL*LLPLPL QHRVSDPGLHSALRPMEEHRA QS*QPSAPEDAVQA*WGHGGH SPGPDRAGCHHCRGDQERVST HHVLPVCHHPDDAYGGCGAG WNPDL/PGQMRSHWMSPKIRPA NWTRTSWWALPQAPGLSPGAQ SWPSFVPRTTPTTPGTTCPTPSW *SWRSTSRTSSSLNPFTESLKNS LRTSKPFGWSQSAMATPCPLLP PASRVELWPETW\PLGQGHATS SQWKCVPERKL*QGGEAGGEQ LGREPKPSPPSSFLTGQRQEKSP EEYCSLLVPLQYFGSRGTHADL LHG

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19544	49912	A	19659	1	2707	MPGPHPASASCPPRLFTPRRRAF CPLRICAPLAAAAFCPPRFLPHT RRRAFLLLCRRGFLPPPCLGGG LAAAFFPHPPLPFLRPHRRGFLP HRRRGFLLPPRLGFLPAAAFYPP PPRVFARRGFVPPSPPRLFARRA FCHTPPAAAFSPSAAAAFCPTA DTAFCTLAALAFCRRGFLPPRC RGFLPLRHRRSFLPHRRRGFLPT AAFCHRGFLLATAFYPPRLFAP RCHGFLPPCRSDFFAAAAFCPR RRGFLPLSPPLFAPAAVAFCPRH RGFLLPRLFAPVTAAFCHRDFL PPPPRIFVPAATALRAGAADSA ASSTGVLARAALRGPCGLHRV ALPVEAMGEKKEGGGGGDAA ATEGGTGAAASRALQQCGQLQ KLIVIFIGSLCGLCTKCAVSNDL TQQEIQTPEPAKPAKPASQTRQ PSQPSHPASQASQTSQPAKQPA SQASQPAKPAKPPSQPSQPSHR ASQASQATQPERPASQPASEPS QPSLPASQASQDRQPAKPAKPD SHPRQPSQP/YQPSQPASQASQA SQPAKPSRQPSQPRQPSQLASQ ASQSTQPLKPAKSPVQQSQPSQ PASPDSQASQASQATQPAKPAK PPSQAAQPAKPAKPPSQPACQP PSQRAKPAKPARQPSQPSQSSPP ASQPSQACQPSQPGSQASQASQ AAKPGMPAKPARQPSQPSQPAS QARHASQAIQPAKPAG*PSQTS

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19545	49913	A	19660	1223	2286	RQCFKATEQPPAIHHPSSQPSRQ PSSQPPIYPSPICGRKSGIQPKFQ LNG*MVNG*MDE\SRERHEWP CNYQVRPKAGEKQPGAEANRE TRPEGGTP/RGERGRQGPATRR QKSTPEAGPSDLEKQIARQEAP AGTDEIERQQARPH*AP*KIPVE WVNGEWLNGRMPGDPHEWQC NYQPAIQPAIQPANQLSIHNLW TQFRHSTKIPVEWVNGEWLNG RMPGKHHEWQCNYQPAIQPAI QPANQLSIHNLWTQFRHSTKIP VEWVNGEWLNGRMPEDHHEW QCNYQPAIQPAIQPASQLSIHN MWTQFRHSGQIPVEWVNGSRL HGRQQGIFMHGNATSSHSPSIQ PAIQPAIQPANQLSIHNLWTQFR HSTKIPVEWVNGEWLNGRMQR NIMNGNATISHSPSIQPAIQPAIQ PVNHLSIHNLWTQFRHSTKIPV EWVNGEWLNGRMPGKNHEW QCNYQPAIQPAIQPANQLSIHNL WTQFRHSTKIPVEWVNGEWLN GRMPGDHHEWQCNYQIAPML QSNRTAASHSPSIQPAIQAAIQS ATHLSIPNLWTQVRHSTKIPVE WVNGEWLNGRMPGRDMNGH ATIRYGPKPEKNNRAPRQTEKQ GQKGAHQRREGKARAGNEETE KYSRSRAIRPRKTDSASRSSRGH RRNRKAASAATLGPIEDTNQNK LHVRDTGLEVKAISIQGPGTLM
19546	49914	A	19661	39	599	GASPNQGQNRPHARQRAPPQ/G /PPGEPERRAPLPSGHGEPCRHR PPPFPQPP/AGTQKPLLQGPGGG *PAENAPTAALGSPAPPRGCQA APPPRSGAGRPDLPTLAGPRPAP A\PPPSAAPPPPPSGAPSR/PAAG RQRLSGVSSGPSLGWW*VGRG RGLPAFAQIAGHQVGPRRRRTP AGRKPRSPAGPR
19547	49915	A	19662	39	599	GASPNQGQNRPHARQRAPPQ/G /PPGEPERRAPLPSGHGEPCRHR PPPFPQPP/AGTQKPLLQGPGGG *PAENAPTAALGSPAPPRGCQA APPPRSGAGRPDLPTLAGPRPAP A\PPPSAAPPPPPSGAPSR/PAAG RQRLSGVSSGPSLGWW*VGRG RGLPAFAQIAGHQVGPRRRRTP AGRKPRSPAGPR

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19548	49916	A	19663	1	379	YFPHTAIRYPPHLNRQDPLKDL VSLACDPASQQPGPLNGSGQLK MPSHCLSAQMLAPPPPGLPRLA LPPATKAATTSEGGATSPTSP/S PGIWDSKGLLPSPLLHRPRNPR GQHSRPPAHVFGGKLE
19549	49917	A	19664	3	285	
19550	49918	A	19665	2	1556	RLEFPGRRFRSAPAPAGPAPPA APGMYSSPLCLTQDEFHPFIEAL LPHVRAFAYTWFNLQARKRKY FKKHEKRMSKDEERAVKDELL GEKPEVKQKWASRLLAKLRKD IRPECREDFVLSITGKKAPGCVL SNPDQKGKMRRIDCLRQADKV WRLDLVMVILFKGIPLESTDGE RLVKAAQCGHPVLCVQPHHIG VAVKELDLYLAYFVRERDAEQ SGSPRTGMGSDQEDSKPITLVT TDFQESFVTSGVFSVTELIQVSR TPVVTGTGPNFSLGELQGHLAY DLNPASTGLRRTLPSTSSSGSKR HKSGSMEEDVDTSPGGDYYTS PSSPTSSSRNWTEDMEGGISSPV KKTEMDKSPFNSPSPQDSPRLSS FTQHHRPVIAVHSGIARSPHPSS ALHFPTTSILPQTASTYFPHTAIR YPPHLNPQDPLKDLVSLACDPA SQQPGPSWYLG*QRSSSLAPSPS SQESQGAAQPAPGPRFRWKIRV NKNTPADSQPGQKDKTHRRTH SGGKEKTKAE
19551	49919	A	19666	1	477	
19552	49920	A	19667	1	440	WTQDM/EGGISS/PVKKTEMAK SPFNSPSPQDSPRLSSFTQHHRP VIAVHSGIARSPHPSSALHFPTT SILP\QTASTYFPHTAIR\YPPHL NPQDPLK\DLVS\LACDP\SSQQP GP/SYSPPDTSPANR\SFVGLGPR DPAGIYQAQSWYLG

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19553	49921	A	19668	2	1963	CPTGFEHGSPCARRTPTGRVSV TRCRRRAWGSLRVSVCGPRAQ LQAELVQEEQGGGVLCVIVMP LTPGRTPRLPRGRALCNGRGGV WGGGGSPRGLLPAQAPGDPEV CKFRFLDRCFPPYAGPSDLSLR GRAVGPPSASLALLTSRLSGLQ DEFHPFIEALLPHVRAFAYTWF NLQARKRKYFKKHEKRMSKDE ERAVKDELLGEKPEVKQKWAS RLLAKLRKDIRPECREDFVLSIT GKKAPGCVLSNPDQKGKMRRI D\CFRQADKVWRLDLVMVILF KGIPLESTDGERLVKAAQCGHP VL/CALKPQHI\GVAVK/ENLDL YLAYFVRERDA*QSGSPRTGM GSDQEDSKPITLDTTDFQESFVT SGVFSVTELIQVSRTPVVTGTGP NFSLGELHAHLAYDLKPASAGL TRTLSSTFSSGNKRY\KAGSMEE YVDSTPWGDD*T*PSSPTSSSRN WTEDMEGGISSPVKKTEMDKS PFNSPSPQDSPRLSSFTQHHRPVI AVHSGIARSPHPSSALHFPT\TSI LTPDGPSPTFPHTAIRYPPHLNP QDPLKDLVSLACDPA\SQQP\GP LNGSGQLKMPSHCLSAQMLAP PPPG\LPRLALPPATKPATTSEG GATSPTSPSYSPPDTSPANRSFV GLGPRDPAGIYQAQSWYLG
19554	49922	A	19669	332	551	ESWLGRGHQPPP\PGLFHSPKPS SGTAVLPAWRPPSPGPGAGDD ASPSPS*AGPGAGANPGA*QRS ASGEKGS
19555	49923	A	19670	1614	1673	
19556	49924	A	19671	72	227	EEFPMGHTA*WSCEKRATILQI QEW*IQQQLAPCAWQSHRHST RAHESSHG
19557	49925	C	19672	1	604	
19558	49926	A	19673	653	889	VYPQTNWKQNTGTRVFIAALF TM\AKGENK*PSMGEW/IKQM WSIHTMERHAAIKRIEAQVYAT M*MKLKSMLLLERNQT

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19559	49927	A	19674	75	1619	EVSIPAQTMWTADEIAQLCYEH YG\IRLPKKGKPEPSHEWTLLA AVVKIQSPA\DKACDTPDKPVQ VTKEVVSMGTGTKCIGQSK/M* RKNGDIL\NDSHA\EVIA\RRSFQ RYLLHQLQLAATLKEDSIFVPG TQKGVWKLRRD\LINVFFSSHT PCGDASIIPMLEFEDQPCCPVFR NWANNSSVEASSNLEAPGNER KCEDPDSPVTKKMRLEPGTAA REVTNGAAHHQSFGKQKSGPIS PGIHSCDLTVEGLATVTRIAPGS AKVTDVYRTGAKCVPGEAGDS GKPGAAFHQVG\LLRVKPGRG DRTRSMSCSDKMAR\WTVLGC QGALLMHLLEEPIYLSAVVIGK CPYSQEAMQ\RA\LIGRCQKV\S ALPKGFGVQELKILQSDLLFEQ SRSAVQAKRADSPGRLVPCG\A AISWSAVPEQPLDVTANGFPQG TTKKTIGSLQARSQISKVELFRS FQKLLSRIARDKWPHSLRVQKL DTYQEYKEAASSYQEAWSTLR KQVFGSWIRNPPDYHQFK
19560	49928	C	19675	45	140	
19561	49929	A	19676	3	354	AKIKTGYK\REHINLGCDMDFDI VGPSIRGALVLGYEGWLAGYQ MNFETAKSRVTQSNFAVGYKT DEFQLHTNVLLLNLERTCFLTG PTPTPPPLSWLPGTTFSLTWAM TGRYTINSQ
19562	49930	A	19677	1	983	AARSAPLPGSAPCLRVAAPAVA ASEPAATSSEQKMAVPPTYADL GKSARDVFTKGYGFGLIKLDLK TKSENGLEFTSSGSANTETTKV TGSLETKYRWTEYG\LTFTEKW NTDNTLGT\EITV\EDQL\ARGT* SLTF\DSSFSP\NT\GKKNAKIKT GYKREHINLGCDMDFDIAGPSI RGALVLGYEGWLAGYQMNF* DCKIPE*PQSNFWQLANKT\DEF QASR*M*ND\GTEFGGSIYQKV NKK\LETAVNLPWT\AGNSNTR FEIAAKYQ\VDP\DACFSGKVNN SSLIGLGYT\QTLKPGIKLTLSAL \LDGKN\VNA\GGHKL\GLGLEF QA

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19563	49931	A	19678	551	831	CHPSSHVLCAPASLSDHQWPPP ALCPSSRPQ/PCALPWSGTLSSR PQPCPTHPSGIEA*LCLPLVTQL G*LPL\PAPQHLVPPCPSTCPTM LKLF
19564	49932	A	19679	47	980	VCQYCTARMADFGISAGQFVA VVWDKSSPVEALKGLVDKLQA LTGNEGRVSVENIKQLLQCLVP GSTT\LHSA\EILA\EIARILRPGG CLFLKEPVETAVDNNSKVKTAS KL\CSALTLS\GLVEEKELQREP LTPEEVQSVREHLGHESDNLLF VQITGKKPNFEVGSSMQLKLSI TKKSSPSVKPAVDPAAAKLWT LSANDMEDDSMDLIDSDELLDP EDLKKPDPAS\LRA\ASCGEGKK RKACKNCTCGLAEEL\EKEKSR EQMSSQPKSA\CGNCYRGAMPS GCASCPYLGMPAFKPGEKVLLS DSNLHDA
19565	49933	A	19680	29	1270	FPFWPAVFQVCQYCTARMADF GISAGQFVAVVWDKSSPV\EAL KGL\VDKLQAF/TPGNEGRVSV\ ENIKAAVAILPTKNPSFGHYFV Q/CLVPGKAPLWHSA*DFWAG NPPGFLRPGWMFFFLKEPVETA VR*Q*AKWKTASKL\CSAL\TLS GLV/EKLKELQREPLTPEEVQSV REHLGHESDNLLFVQITGKKPN FEVGSSRQLKLSITKKSSPSVKP AVDPAAAKL\WTLSANDMEDD SMCIFCGCSLTHRWPLEHVVQV E/IMMDQPKRRTRVDT\FFTPRT PKFPSRSPASHFSFSIKQKT/TRP VSLIALNTL\QDLIDSDELLDPE DLKKPDPSLLRAASCGEGKKR KACKNCTCGLAEELEKEKSRE QMSSQPKSACGNCYLGDAFRC ASCPYLGMPAFKPG\EKVLLSD
19566	49934	A	19681	3	405	QDFGTRALAAVQIKNGGSWWC PPVSLAAGVGPRPQLGRPYVRV APHGQV\GLSFAMWKTLT\FFR GASPGVGSQAMLKCVA*SPHH WRARRDPEFIAYP\HLR\IRTKP\ FPWG\DGNHTQQYITPH\VNPLS NLATED

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19567	49935	A	19682	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLLKLHDERVLVAF GQRDGIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYP VSIRFGRPRLTSNEKLMLASMF HS\IKFVVLADP\RQAGIDSLLRK IYEIYSDFALKNPFYSLEMP
19568	49936	A	19683	1	2034	
19569	49937	A	19684	202	453	RRLWRGSCPRCGGKARDGMG VRGR/YSEG/RERV*FGGPPRGS TWPLCGRWRRPARPSAPLRWS AMCPNTSDAAGACAAAVRCG
19570	49938	A	19685	269	326	
19571	49939	B	19686	98	562	
19572	49940	A	19687	1	2223	
19573	49941	A	19688	374	1107	IPVSERQGSDWRFFSVYVVNKA GGLIYQLDSYAPTGLRLEKTF\S YPLDLAGSS*HDERVLVAFGQR GRHPEWGHAVL\AINGM\DVNG RYTADG\KEVLEYLG*PLLNYP VSIRF\GRPRL\TSNE\KLMLGLP CFHSLFAIG\SQACLPGTREASR HLKILGRQDTFK\LH\CYQTLT\G IKFVVL\ADPR\QAGI\DSLLRKI YE\IY\SDFALKNP\F\YSLEMPIR CELFDQNLKLALEVAEKAGTF
19574	49942	A	19689	119	288	ALHLNSSDVHQKLLPVQSLKKS *GRHRNNTCNQRVHA/SSTSRE FFTKLNKDNDILKP
19575	49943	A	19690	92	317	KSVGPVNFPLPSGNMNEDN*M H*HPFSSVTQAFRLRVLQSII\QR PL*TFNPGSSSLFSSISGQSNFPL GVAVLRP
19576	49944	A	19691	27	389	NFKTLKNN*IYK*MCSQEIKILS *KLIRFWYEIHAFFPWAHGVVF CVAQEFCLPTVVLLPVPRLLIM KDMVRRLQELRHTEQVQRAYA LNCGEGATVSYEIQIRVLREFGL ADAAAELLQN

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19577	49945	A	19692	313	2255	KTPQVQQPFPRQTGAAGAGAP SGRSGERAAGRAGPSGGSGGG QDSAHAGEAYRVRGILLRKTFQ CLKDYFLTYYTSSKVVPVKVPC RQVLTIDKCSLPRSSHRNARTV SNDFPRKSCSRERCTHCMRPPE GRRPPNGNMNSWKWPSGDESK WRRGEPGAVPEPEPLTGEERAA AAAVGGGWPGVLAPVRTAVL VAAAAEATAAVPAAAAAAGG ASGHCNHPVMQGRNLSHRFLL PLHHSPYQFGTSSYSQQGYGCE SKLYSLDHGHEKPQDKKKRTS GLATLKKKFIKRRKSNRSADHA KQMRELLSGWDVRDVNALVE EYEGTSALKELSLQASLARPEA RTLQKDMADLYEYKYCTDVDL IFQETCFPVHRAILAARCPFFK/I TAFFLTRVWGRDNNGHQYSW Y*YAHVFCFVTLPLYRRVWEW EDSRFQNVDILVQLSEGIWEHQI PLM*DMRGTLLI/DMCYYDVVL SFSSDSELVEAFGGNQNCLDEE LKAHKAVISARSPFFRNLLQRRI RTGEEITDRTLRTPTRIILDESIIP KKYATVILHCMYTDVVDLSVL HCSPSVGSLSEVQALVAGKPN MTRAEEAMELYHIALFLEFNM LAQGSCWECIPPNDEANQEQRS EGSRKWAPTREGSKGRSHASA
19578	49946	B	19693	4	3923	

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19579	49947	A	19694	1	2154	MEYYAAMKTKEIMSFALTWIE LEAIVLCELTHVLSELMQKQKT KYHMLSLGSPVPTFALWNFDV AQDFHHFIENARSSQCRGRPRM TGAGAGAPSGRSGERAAGRAG PSGGSGGGQDSAHAGEAYRVR GILLRKTFQCLKDYFLTYYTSS KVVPVKVPCRQVLTIDKCSLPR SSHRNARTVSNDFPRKSCSRER CTHCMRPPEGRRPPNGNMNSW KWPSGDESKWRRGEPGAVPEP EPLTGEERAAAAAVGGGWPGV LAPVRTAVLVAAAAEATAAVP AAAAAAGGASGHCNHPVMQG RNLSHRFLLPLHHSPYQFGTSS YSQQGYGCESKLYSLDHGHEK PQDKKKRTSGLATLKKKFIKRR KSNRSADHAKQMRELLSGWD VRDVNALVEEYEGTSALKELSL QASLARPEARTLQKDMADLYE YKYCTDVDLIFQETCFPVHRAI LAARCPFFK/ITAFFLTRVWGRD NNGHQYSWY*YAHVFCFVTLP LYRRVW\KEDSRFQNVDILVQL SEEFGTPNSLDVDMRGLFDYM CYYDVVLSFSSDSELVEAFGGN QNCLDEELKAHKAVISARSPFF RNLLQRRIRTGEEITDRTLRTPT RIILDESIIPKKYATVILHCMYTD VVDLSVLHCSPSVGSLSEVQAL VAGKPNMTRAEEAMELYHIAL FLEFNMLAQGSCWECIPPNDEA
19580	49948	A	19695	1	163	
19581	49949	A	19696	1	207	
19582	49950	A	19697	1	579	PTRPGQAGSSSAMAAQRLAKR VL\SKLQSPSRARG/PCAGSPGG LQK/RGHARVTVKYDRPGSLQR RLDVEKWIDGPLEGLYRR\QEA D\MPMRSNIDELLE\LESEE\ERS RKIQGV/LRDS*KSCGKPVEDFI\ QELLAKLQGLHRQ\PGLRQPSPS HDGSLSPLQ\DRARTASPLTLLA LFPGPPERRPALLCVLSCI
19583	49951	A	19698	2	151	PPSPPPLPPPPLPPAPSLPLSLPSF DLPQPPVLDTLGV/LF*LCRKKI SVS
19584	49952	A	19699	2	310	

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19585	49953	A	19700	1	688	LTWMTERVDFTALLPLEPPLPP GTLPQPSPTPPDLEAMASLLKK ELEQMEDFFLDAPLLPPPSPPPL PPPPLPPAPSLPLSLPSFDLPQPP VLDTLDLLAIYCRNEAGQE\EV G\MPPLPPPQQAPSFLLPP\QPSR WGPLTHIPGQPTRGGPAKQKEE RPRNKSAALKVTPSGKRARG*S PWRAKSQGLEGTEFASLKERA\ ESVEREIQ\YVKD\LLIEVYKARS QRTRSC
19586	49954	A	19701	3	902	AAMATPARPGEAEDAAERPLQ DEPAAAAAGPGKGRFLVRICFQ GDEGACPTRDFVVGALILRSIG MDPSDIYAVIQIPGSREFDVSFR SAEKLALFLRVYEEKREQEDC WETFGGAGGEASPA*RRSSSSS GTRRWTWRTL*LGSSATATCW PC\GESDRQVLDLD/LGSTNARS SCARGRAGSGTCQGPSSWGPR G/CYSWYKGQPKTCFKCGSRTH MSGSCTQDRCFRCGEEGHLSPY CRKGIVCNLCGKRGHAFAQCP KAVHNSVAAQLTGVAGHLNTR LPARVNTQASLSLLKCPKLFF
19587	49955	A	19702	1359	1981	QSPFNDTLPGVPVSA*LHSLPPE HHPSKG*GVAKSPPVYPAGILL VCNNCAAYRKLLEAQTPSVRK WALRRQNEPLEVRLQRLERER TA\KKSRRDNETPEEREETDEQ RARRLQRDREAMRLKRANETP EKRQARLIREREAKRLKRRLEK MD\MMLRAQFGQDPSAMAAL AAEMNFFQLPV\NGVEL\DSQLL GKMAFE\EQNSSSLH
19588	49956	A	19703	1	1875	

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19589	49957	A	19704	1	673	MSAKDGTCTLQDCMYKDVQK DWPGYSEGDQQLLKRVLVRAH NTQRQRQNERSDTRPCQRAAP RRFSHGTRRGTLPLASPDRARA PRTGHCRTQRRLDRTGGGFPPL TGAWAMLADWIHEGTPSRGRS DNDEPSAGSVGGLRQHGPGPR APKLTTTKVKALASPVLGQKIA ALCLGLTAQGLNIMDNPGSLAI HVHPDSVLTRKTNPCTHIWGFT QREPPLVANMSAKDGTCTLQD CMYKDVQKDWPGYSEGDQQL LKRVLVRAHNTQRQRQNERSD TRPCQRAAPRRFSHGTRRGTLP LASPDRARAPRTGHCRTQRRLD RTGGGFPPLTGAWAMLADWIH EGTPSRGRSDNDEPSAGSVGGL R/HAWPRTKSPKANNH*SESTG QPGAGPKNCSPVLGAYSPGPQH HGQPGLPGHTCP/SRTQC*PGRP TPAPTSGVSLRGNPLWWPT
19590	49958	A	19705	1088	2273	SPCLLTGGHLPADTSYRRAPAG IWQVPLWDEASQRKE*YQHQQ KKMSTQKPHPKDHNSSPAREQ/ SSMENKFHELTEVGFRKITSLE KNINDLMELKNTARELREAYTS IKSRIDQAKESISEIEDQLNEIKC EDKVREKRMKSNKQNFQEIWD YVKRPNLRLTGVPESDRENGTK LENTLQEIIQENFPNLARQANIQ IQEIQRTAQRQSSSRATPIHIIVR FAKFEIKEKMLRAAREKDISMR QKINKDIQDFNTVLDQVDLIHV YRTVHPKSSEYTFFSAPHHTYC KTGHIIGSKTLLSKCKRMEIITN TLSDYSAIKLELRIKKLTQNHTT TWKVNTLLVNEY

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19591	49959	A	19706	318	873	AYELTPEPSPLPVFPVSADGSTT HPLADKRKASPVPEQHEEHLPA RPVTQRCLTYPFPNITTASEFGP ATGFRARRSGRGSTVCCNPGCY PRARPEPEPRGTPPSVSAPRAAQ EAPARQR\AGPVLADTVP/SPAP RGKRDISPLFGNAHSASPKPSLD LWAPPP*AAGRRGPQQA*DVTE DTQQQQWSAMAVGGTAKWM AALGRFLVTYVEVEGVKLQTF TVTTLTQSFKYSLSKYLQQQPL LSSRTIYPTFYYLSLLRNLRAFK LNAAEAKPMSSPQNLVLFLCFL SLQMAAPPIRLQTKGKQAQCQS STKSTFQRGRSLRGVSPTLSPTS QQPRNLDQQLASEQGEVGEAP LCAVIQGVIPVLGRSRSREEHPP VSALPGLHRKRQRDKEAGPVL ADTVPFRPHAGKGTFLRCLETL TRRAPNPRWTFGLPLRKLQGA VAHSRPEIRTHSVPNRT
19592	49960	A	19707	1	690	DQDMTSSDIPVRLEGSLWLP*IF IGTFKAFDKHMNLILCDCDEFR KIK*GVDCGGRRLEDGNGLSG WAKQ*SLVSMTVEGPPPKDVS QSRKP/CWRRGGPTVSQALC*IL YPSWGSHAPGSCRTCWASPWG WRAIPTGEELGKGYHLLVAKIK DKGEGP*FSNPVPTWPWGSSPT YGPRSTPSR*GAHKETSAN**K MP\SWINDEI*PPMGMPPPGMRP PPPGMRGKCLQW

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19593	49961	A	19708	1	1348	MVFWARPRTLLLCAALGLGAL YTATPAPTVAKRGQGTAQALS SEGASPKPWWLRHGIEPCKQSY WEVRTEQSPGVSERKAAAPVR GLEIKLPSPWDKAPEGGGGCGH SFSRLKCSFMPVLKRAVDLPAQ RSSPANGQTACSSGSLAPVLPD WEIPPSKGRQTPYATGELRLAS DGCPSGTKLPEEGTDSNLCCSA SSAESNNININININKKDAHGKT PSKGPQHQRSKLDKSMKTRKN HHKNAENSKNLNASSPPKDHN SSTAKEQNWTENEFDELTEVGF RRRVIANSSKLKEHVLTQCKEA ENFEKILEELLTRITSLEKNINDL MELKNTAQEHREAYTSINSQID QAEERISEIEDKLNEIKREDKIR GKRIKRNKK\SLQEIWDYVKRA NL*LIAVVPLNKITSPRTSETLST STNMSRSTLSCLLSSFSCPASCT ATSAALF
19594	49962	A	19709	718	1138	GGRAAEGSQPPVAEPRCSRGAR ALPLPDTSWRQPS/APQAAP*D VELPASPSAPFAVLLSKPRLSQN KPKSPFSVASP*HGDKRPQPSRH LI*IPHLSSRAPVHS/PLGWPSNR K/HKHLRPDTAHAPAEGPPLNY VRKQQKQS
19595	49963	A	19710	5	760	RAAACGGAAPGRKRCAPGRKR CGPRRKRSLGPPTLGQRPRQPS QQLRKPRRRRGSPGSLPKSSPLP SSTGKTGWSTRGRSVRPPVTTS RCCPPGHPCSRRAPSCTARAPLP PT*PPTTAPCRASPPAPRPPRRPR PPPGTRSPTSRGRCRWTRSGAG TSRCSWRAGPGTAPAAAGARS RPGAPGVSAAVPCAAACSWMT SAPEVRAASSPGTPSRGSGGRS HPPCSRGLPTTGPATTAPEAPG CWSCRRRS
19596	49964	B	19711	180	300	
19597	49965	A	19712	249	700	RQDPVSGGQSCPASCPSLWAA ARVWLGQ\PAPRAR*CPVCSSC PGPGAPEDTPEAGGCGCSGCRC CLRTQEPPAPLQPPHPPMAQTP REEVGRRGWTPGCPGTDPCLW GLRLLCPLWDPHRSGTRPWAQ VQRDTTETKAQRGLVRCQRGC
19598	49966	C	19713	273	485	

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19599	49967	A	19714	35	779	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGAL PLDTVTFY/KDYGDKLNMELSE KYKLDKESYPVFYLFRDGDFEN PVPYTGAVKVGAIQRWLKGQG V\YLGMPGCLPVYDALAGEFIR ASGVEARQALLKQGQDNLSSV KETQKKWAEQYLKIMGKILDQ GEDFPASEMTRIARLIEKNKRSC KKAVCDFPGFGGGREGRVNLL AVSPLWNIRG
19600	49968	A	19715	2	253	
19601	49969	A	19716	494	1443	LAVPRPAYGPRSPGSLLRIPVPG LHLLNLNVWSRGSAAALHTKG ALPLDTVTFYKVIPKSKFVLVK FDTQYPYGEKQDEFKRFAENSA SS\DDLL\VAEVGISDYGDKLNM \ELS\EKYKL\DKESYPVF\YLFR DGDF\EEPSSHYTGGS*RLGAIQ RWLKGGKGVYLGDGLELVCT V*LTPLAGEF\IR\ASGVEARQAP LEAGAQDNLSKCERRLRKKW\ AEQYLKIMGKILD\QGEDFP\AS EMTTESLGLIEKN\KMSDGKKE EL\QKSLN\ILTALPRRKGAEKR GAVNKAVCDFPRVWWEYGRG ELTLLAVSPLWNIRG
19602	49970	A	19717	286	332	HHHHHPHYHHHHHPHYHHHH HPQYHH\HHPHYDHHRHRQGD HHGQLQYDDDHQPQCHQHDH LRCEHQHYIQ*WLINNLRASRY KPLLNIMLVFAAEMIVLVALGL MVVVVLELTVVVALTMTVVVI VRMMGGDIGDDGGGGSGDDG GGGSGDDGGGVMWQFFDSMS KNDSIIPTTTTTIIPTTTTTTITIRA EQFTILTWKPVVSSQKNTSSFR
19603	49971	C	19718	1	546	
19604	49972	A	19719	1	90	
19605	49973	B	19720	217	951	
19606	49974	B	19721	67	1708	
19607	49975	B	19722	218	3267	

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19608	49976	A	19723	1	634	LGRLSFPRPEQPDPGHRAHPSSP PRPRRPHARGRRGPRRHH/YHD TGANRAPEVRPPCPES/SPVGVA AFEPNGLRGQQPSPRSPGAPKG L*PTPPSASSSPKPREPSALGRPC CRCEESRFLEHRNSNPRVKDSR QARGRHAEFHGRTGVFERRRS RDHLPTHFPASVRWEKLSWCA RKNGLSGLRLCHGSQHFSGYSN RKVGTESLNQVWE
19609	49977	A	19724	3	1090	
19610	49978	A	19725	1	609	
19611	49979	A	19726	23	636	FSYLPPGPSHGTWGLWELQFK MRFGVCRHLMEDSMDMDVSP LR/PQNYLFSCELKADKDDHFK VDNDENEHQLSLRTPTVSLGVF EITPPVLLWLKCGSGPVHISGQ HLVAVEEDAESEDEEEEDVKLL RISGKTKTFMATNGKEYKHYKI SSEKSLDNKYKTRTPGFQAFGF EDLHPWPLGSQAFYLSLRVTPP VFLVLRLLDFD
19612	49980	A	19727	1	830	MEDSMDMDMSPLRPQNYLFGC ELKADKDYHFKVDNDENEHQL SLRTVSLGAGAKDELHIVEAEA MNYEGSPIKVTLATLKMSVQPT VSLGGFEITPPVVLRLKCGSGPV HISGQHLVAVEEDAESEDEEEE DVNRVLFMKP/KRQGPQAYVR GFGVQLEIGSH*DPEQQF*RDSA QPSLATPSTPHLQALLCLSGQV LRLPLWGQRL*GLQGLLPPQHP EEHGVHVSPGQELHHQQGDPE PLPVLPTAEVL*SGHVQGVCEK RPKQEEEGGAQARVL
19613	49981	A	19728	1	684	
19614	49982	A	19729	3	535	DSVLRGCSLEQRSFISVRLLSYL SACRHPMEDSMDMDMSPLRPQ NYLFGCELKADKDYHFKVDND ENEHQLSLRTVSLGAGAKDEL HIVEAEAMNYEGSPIKVTLATL KMSVQPTVSLGGFEITPPVVLR LKCGSGPVHISGQHLVVYRRK HQELQAMQM\DCRALSTS*ASS APRPS
19615	49983	B	19730	1	2268	
19616	49984	A	19731	198	472	AHDIGCPEVSPLVLEVARDEGP AHRPRFSH*SSHCSHWGTSQRA APPPCHPCIQTTW/PGAVTGLG G*PKTRSGPGKDRSSGAASSFP GGRV

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19617	49985	A	19732	92	2049	LTALPPAVSPGGHSSSSSSRTIS GIT*ELQR/LLQAVVPGPWQED VADAEECAGRCGPLMDCRAFH YNVSSHGCQLLPWTQHSPHTR LRHSGRCDLFQEKGEWGYMPT LRNGLEENFCRNPDGDPGGPW CHTTDPAVRFQSCGIKSCRVAA CVWCNGEEYRGAVDRTESGRE CQRWDLQHPHQHPFEPGKFLD QGLDDNYCRNPDGSERPWCYT TDPQIEREFCDLPRCGSEAQPRQ EATSVSCFRGKGEGYRGTANTT TAGVPCQRWDAQIPHQHRFTPE KYACKDLRENFCRNPDGSEAP WCFTLRPGMRVGFCYQIRRCT DDVRPQDCYHGAGEQYRGTVS KTRKGVQCQR/WSLE/TG*DYP ATTSLPLPPRFTFTSEPHAQLEE NFC/RDPDGDSHGPWCYTMDP RTPFDYCALRRCDQVQFEKCG KRVDRLDQRCSKLRVAGGHPG NSPWTVSLRNWQGQHFCGGSL VKEQWILTARQCFSSCHMPLTG YEVWLGTLFQNPQHGEPGLQR VPVAKMLCGPSGSQLVLLKLE RYVDNLGGWTKCEIAGRGETK GTGNDTVLNVALLNVISNQEC NIKHRGHVRESEMCTEGLLAPV GACEGDYGGPLACFTHNCWVL KGIRIPNRVCARSRWPAVFTRV

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19618	49986	A	19733	2	2296	HSAGQRSPSNDFQVLRGTELQH LLHAVVPGPWQEDVADAEECA GRCGPLLLSRAFHYNVSSHGCQ LLPWTQHSPHSRLWHSGRCDLF QEKGEWGYMPTLRNGLEENFC RNPDGDPGGPWCHTTDPAVRF QSCGIKSCRVAACVWCNGEEY RGAVDRTESGRECQRWDLQHP HQHPFEPGKFLDQGLDDNYCR NPDGSERPWCYTTDPQIEREFC DLPRCGSEAQPRQEATSVSCFR GKGEGYRGTANTTTAGVPCQR WDAQIPHQHRFTPEKYAC/KVR WAGGRALGRAAAGETGGG*SR A*GWRLAG*G*VERLLRDLREN FCWNLDGSEAPWCFTLRPGTR VGFCYQIRRCTDDVRPQDCYH GAGEQYRG\TV\SKTRKGVQCQ RWSAETPHKLQ*VPGAPGPAR ALTLGRHALMSGTRAWKWLR LSLPRFRSRSRLGSRLTSEPHAQ LEENFC/RDPDGDSHGPWCYTM DPRTPFDYCALRRCADDQPPSIL DPPPDQVQFEKCGKRVDRLDQ RRSKLRVAGGHPGNSPWTVSL RNR*GTTACLPQRGAEVVSSVV MPLGAGNLSLPPEVLARRWQV *HLSQESVPCPNSPLL*\QGQHF CGGSLVKEQWILTARQCFSS\CE PPLCLGTQSHPTFPFPQAS*QVS LGATD*ESQMT*QSFSPSHMPL TGYEVWLGTLFQNPQHGEPGL

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19619	49987	A	19734	727	3012	PAPTHAHSAGQRSPLNDFQVLR GTELQHLLHAVVPGPWQEDVA DAEECAGRCGPLMDCRAFHYN VSSHGCQLLPWTQHSPHTRLRR SGRCDLFQKKDYVRTCIMNNG VGYRGTMATTVGGLPCQAWS HKFPNDHKYTPTLRNGLEENFC RNPDGDPGGPWCYTTDPAVRF QSCGIKSCREAACVWCNGEEY RGAVDRTESGRECQRWDLQHP HQHPFEPGKFLDQGLDDNYCR NPDGSERPWCYTTDPQIEREFC DLPRCGSEAQPRQEATTVSCFR GKGEGYRGTANTTTAGVPCQR WDAQIPHQHRFTPEKYACKDL RENFCRNPDGSEAPWCFTLRPG MRAAFCYQIRRCTDDVRPQDC YHGAGEQYRGTVSKTRKGVQC QRWSAETPHKPQFTFTSEPHAQ LEENFCRNPDGDSHGPWCYTM DPRTPFDYCALRRCADDQPPSIL DPP\DQVQFEKCGKRVDRLDQR CSKLRVAGGHPGNSPWTVSLR NWQGQHF\CGGSLVKEQWILT\ AR\QCFSS\CHMPL\TGY*GMVG ATFFQNPQHGEPSL\QRVQ*AK MLCGPSGSQL\VLLKLERSVTL N/HRVWALIILP\PEWYVVPPGT\ KCEIAGWGET\KGTG\NDTV\LN VALLNVISN\QECNIKHRGRVRE SEM\CTEG\LLAPVGACESDYG GP\LACFT\HNCWV\LEGIIIPN\R
19620	49988	A	19735	66	234	WCSAWHSWLPHSPSGPAASYP PAACRSAPQWPDP*R*CPRTHR RRSPWRAPWHCP
19621	49989	A	19736	3	500	GRGGGGVRRCARPAPGRPPAA ARRRGDQRGGRLGR\HVPGKTF CCGICGRGFGRRETLKRHERIH TGEKPHQCPVCGKRFRESFHLS KHHVVHTRERPYKCELCGKVF GYPQSLTRHRQVHRLQLPCAL AGAAGLPSTQGTPGACGPGAS GTSAGPTDGLSYACSD

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19622	49990	A	19737	899	2348	GRRRGGGGRCWRGCQSGPERF SCATCGQSFKHSW/DLVTHKYV HLMLLLPPSCEAVAPRGWRRSC SCPECCRVC/ELSSAA/RSATAR CFRRRSPSHAQPAPGPQVPQDW RSPRARIRLPVGPVGMPAFPTSA SGKAWPSLRSVSPHAFWKYHT SPPAMQPSGPLWASVPACAP*K NIPSPTIWQRLAFSGLGLPICWV ENHGPATSSQWLVSGPRSPHLL S/RAEHPFSRPLPRWVATAERQ RRPSGKRTNPFPASPAPPPGA/G PEVSVPPAGALPGEALGPARDL WPCSSWT*AGLPALG/DTGGGE APAP/AAAAEPSEDTLYQCDCG/ TFFASAAALASHLEAHSGPATY GCGHCGALYAALAALEEHRRV SHGEGGGEEAATAAREREPAS GEPPSGSGRGKKIFGCSECEKLF RSPRDLERHVLVHTGEKPFPCL ECGKFFRHECYLKRHRLLHGTE RPFPCHICGKGFITLSNLSRHLK LHRGMD
19623	49991	A	19738	2	358	
19624	49992	A	19739	635	2441	LKAIKRHPFFVTIDWNVSCMPQ SPPPFKPAVGRPEDTFHFDPEFT ARTPTGVCHSGSLYNAHHLFR GFSFVASSLIQEPSQQDLHKVPV HPIVQVTVFACSGFTDGYEIKE DIGVGSYSVCKRCVHKATDTE YAVKVRQAC*VSSLVFPAGTG APGIGEYGSGKLVSILCAQDSP HNLLPQRKVEKPSLSILVGESRS HVDKGQEVDILEMGMEFFFFIE FLVSPLATG*CFPMARSPCMGC SLSVCTAL*GQPLQGNTPTFKY QQVTWPQAKPPTPTAVLSPETA NVTSPQEQTRCLLKDRWLYPV VRNSSTRGPSEEIEILLRYGQHP NIITLKDVSGPRATASLVMELM RGGELLDRILRQRYFSEREASD VLCTITKTMDYLHSQGVGAMP GAAFNILYRDESGSPESIRVCDF GFAKQLRAGNGLLMTPCYTAN FVAPEVSIPRLQTQACDIWSLGI LLYTMLAG*AVTSNRCHDTPEE ILARIGSGKYALSGGNWDSISD AAKVSTCPSVALDPHQRLTAM QVLKHPWVVNREYLSPNQLSR QDVHLVKVPAG\AVRTEWWE WDLNRTPQAPRLEPVLSSNLAQ

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19625	49993	A	19740	144	1143	REAGRGCSAGVGGRPRRRRRK GAASRARLPFSLSIMDPSLLRER ELFKKRALSTPVVEKRSASSE\S SSSS\SKKKKTKVE\HGGSSGSK QNSDHSNGSFNLKA\LSGSSG\Y KFGVLAK\IVNYMKDTGIQRGD THPLTLDEI\LDETQHLDIGLQQ KQWLMTE\ALVNNPKIEVIDGK YAFKPKYNVRDKKALLML\LD QHDQRGLGGILLEDIEEALPNS QK\AVKAL\GDQIPIC*SGPVRR KILF\F\NDKSCQFSVG*RIFRKL WEECQLVDSHGTEEKI\EEYLE ADRVFSSHARESG\PK\KVGPYS RRKGKSPAFTRKKPTFLRTSLT NHLAWNC
19626	49994	A	19741	677	1590	AHPHSPRRTLERQARISGAGRR SSPNAANRGSAPPSRRLASFCT AGSA\GRPA*SSPCSGPWTAVSA PRSPGPRGGGRPPSPGRRRPCCS VFSGGASPSSARVSSPSGSCSAS PPAAPAAWSLRGCGCWPG/VW EVHVNTGGDSV\AAPAAWGSR AACGPNLGCGSHPRAGRRAGH RCGHPWSPRPAPRPSCCGRSPR PGPPGASGCPRPAPRPPTPASRS GRPCSWRRARAAGWPRGWWG SSAGGCRRGSGRREWCPCGTA RGSPAAGVSRWTAPRCRHRRS DASASGTPARFPGAGRKGRTL WQ

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19627	49995	A	19742	754	2179	SKMSRLEAKKPSLCKSEPLTTE RVRTTLSVLKRIVTSCYGPSGR LKQLHNGFGGYVCTTSQSSALL SHLLVTHPILKILTASIQNHVSSF SDCGLFTAILCCNLIENVQRLGL TPTTVIRLNKHLLSLCISYLKSE TCGCRIPVDFSSTQILLCLVRSIL TSKPACMLTRKETEHVSALILR AFLLTIPENAEGHIILGKSLIVPL KGQRVIDSTVLPGILIEMSEVQL MRLLPIKKSTALKVALFCTTLS GDTS*\PGEGTVVVSYGVSLEN AVLDQLLNLGRQLISDHVDLVL CQKVIHPSLKQFLNMHP\IIAIDR IGSDSD/VEPLDLKWTGTQPIGS LGSICPNSYGSVKDVCTAKFGS KHFFHLIPNEATICSLLLCNRND TAWDELKLTCQTALHVLQLTL KEPWALLGGGCTETHLAAYIR HKTHNDPESILKDDECTQTELQ LIAEAFCSALESVVGSLEHDGG
19628	49996	A	19743	1	652	LMPKPGRDTTKKENFRPISLMN INAKILNKILANQIQQHIKKLIN HDQVGFIPGMQGWFNIHKSINV IHHIKRTNDKNHMIISIDAGKAF NKIQQCFMLKTLNKLNIHGVYL KIIRAIYD/KPPANIILNGEKLEA FPLKTGIRQG/CPLLRNIV/LEVL ARAIRQEKEIKGIQSGNEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSGYKISVQ
19629	49997	A	19744	1	834	MGDFNTPLSTLDRSTRQKVNK DIQELNSALYQVDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHIVG SKALLSKCKRTEIITNCLSDHSA IKLELTIKKLTQNRSTTWKLNN LLLNDYWKYKQPSENKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPITRSEIEAITNSLPT/ KKSPGPDGFTAEFYQ\MLEVLA RAIRQEKEIKGIQLVKEEVKLSL FADDMIVYLENPIVSAQNLLKLI GNFSKVSGYKI/NVQKSQAFLY TNNRQTESQIM
19630	49998	B	19745	1	1521	
19631	49999	B	19746	1	1461	

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19632	50000	A	19747	1	2347	MELKTKARELHDECTSLSSRFD QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKMLANQIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQHFMLKTLNKLVLEVLA RAIRQEKEIKGIQLGKEEVKVSL FADDMIVYLENPTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGKDSLFNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLKSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQSL*RRI/W KRLQRTLSIPVLDAV*PPMF*AS
19633	50001	A	19748	1	1818	

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19634	50002	A	19749	1	1725	MELKTKARELREECRSLRSRCD QLEERPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLAKQVN VQIQEIQRTPQRYSLRRATPRHII VRFTKVEMKEKMLRAAREKGR VTLKGKPIRLTADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNRS WFFEKINKIDRPLARVIKKKRE KNQIDAIKNDKEDITTNPTEIQTI IREYYKHLYPNKLENLEEMDTF LDTYTFPRLNQEEVESLNTSITG SEIVAIIS/NSIPTKKSPGPDGSTA EFYQ\MLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKCLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTDLEKTTL NFIWNQKRARITKSILSQKNKA GGITLPDFKLYYTATVTKTAW YWYQN\RWYWYQNRDIDQWN RTEPSEITPHVYNYLIF

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19635	50003	A	19750	1	1719	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNREHGKKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTLTSQLKELEKQEQ THSKAGRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL HINRAKDKNHMIISIDAEKAFD KIQQPFMLKTLNKLVLEVLARA IRQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNIPCSWV\GRINI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP

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19636	50004	A	19751	2	2133	WRRIYQANGK*KNK/QKKAGV VILVSDKTDFKPTKIKRDKEGH YIMVKGSIQQEELTVLNIYAPN TGAPRFMKQVLRDLQRDLDPH TTIMGDFNTPLSTLDRSARQKV NKDIQELNSALHQADLINIYRIL HPKSTEYTFISAPHRTYSKIDHI VGRKALLRKYKRTEIITDCLSD HSAIKLELRIKKLTQNSSTTWK LNNLLLNDYWIHNKTKAEIKM CFETSENKDTTYQNLWDTCKA VCREKFIALNAHKRKQERSKID TLTSQLKE/LEKQEQTHSKASRR KSRRNG*IPGHIHPPKTKPGRI* VPE*TNNRV*N*GNN**LTNQK KFRTRRIHSQILPEHSAGSSGQG NQAGERNKGYSIRKRGSQIVPV CR*HDCIFRKPHHLSPKSP*AVK QLQQSLRIQNQRAKITSSPIHQ* QTNREPNHE*TFIHNCFKENKIP RNPTYKGCEGPIQGELQTTAQQ NKRGHKQMEEHSMLMDRKNQ YHENGHSAQGNL*IQCHPHQAT NDFLHRIGKNYFKVHMEPKKSP HCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMVLVPKQTYRP MEKNRGLRNNTTHLRPSSL*QT *QKQEMGKGFPI**MVLGKLAS HM*KAETGSLPYTLYKN*FKM D*RLKC*T*NHKNLRRKPRQYH SGHRHEQGLYV*NTKSNGNKS QN*QMGSN*TKELLHSKRNYH
19637	50005	A	19752	1	1314	

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19638	50006	A	19753	1	1998	MVKGSIQQEELTILHIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQAALIDIYRTFH PKSTEYTFFSAPHHTYSKIDHIV GSKALLNKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKA\PL ARLIKKKREKNQID/TIKNDKGD ITTDPTEIQTTIREYYKHLYANK LENLEEMDTFLDTYTLPRLNQE EVESLNRPITGSEIVAIINSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEASII LIPKPGRDTTKKENFRPISLMNI DAKILNKILANRIQQHIKKLIHH DQVGFIPGMQGWFNIRKSINVI QHINRAKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLVLEVLAR AIRQEKDIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS KFSKVSGYKIHVLKSQAFLYTN NRQTESQIMRELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLN EIKEDTNKWKNIPCSWIGRINIM RRSSSAPSGCHLCPPSLYLHSPN VELKQASFSVAGFQWKLGITAP TQPRGVGDDFVTSTSPPSLDMF PRLKGAENSPHRSGRD
19639	50007	A	19754	1	3288	
19640	50008	A	19755	1	1293	
19641	50009	A	19756	264	490	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPL\LKEI*EDTSKW KSIPCSWI
19642	50010	A	19757	1	1845	
19643	50011	A	19758	1	3144	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
19644	50012	B	19759	1	1743	

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19645	50013	A	19760	1	1500	MGKKQSRKTENSKNQSASPPPE ECSSSPAMEQSWMENDFHELR EEGFRSNFSELKEDVRTHSKEA KNLEKRLDEWLTGITSVEKSLN DLMELKTMARELCDKCTSFSS KFHQLEERVSVTEDQMNEMKS WFFEKINKIDRLLARLIKKKRE KNQIEAIKNDKGDITTDPTEIQT TIREYYKHLYTNKLENLEEMDT FTGTYTLPRLNQEEIESLNKPIT GSEIEAIINSLPTKKSPGPDGFTA EFYQRYKEELL\FNIRKLINLIQL INRTQDP*PPL/VLSRIGRRVHQ YLENPIVSAQNLLKLKSNFSKV SGYKINVQKSQAFLYIKKRQTE SQIMSELPFTIASKRIKYLGIQLI RDVKDLFKENYKPLLNEIKEGT NKWKNIPCSWIGRINIVKMAILP KVIYRFNAIPIKLPMTFFTELEKI TLKFIWNQERACIAKTILSKKN KAGGIMLPDFKLYYKA\TVIKT AWDWYQNRYLDQWNRTEPSEI TPHIYNHLIF
19646	50014	A	19761	1	3192	
19647	50015	B	19762	180	190	
19648	50016	A	19763	1	3212	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ

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19649	50017	A	19764	1	2607	MTNHCFKRQFQKHEMLLKEDC EPGDSSFILGEQHWENMLCEPK QHPPQQGEGRAAGQAQNPLNT DVSPGAGAKESEEKIYQHLNYT YFKQKCMSCSGFTFSSYAMHW VHQAPGKGLEWVSAIGAGGGT YYADSVKGRFTISRDNAKNSLY LQMNSLRAEDMAVYYCARDTI DAYGDEKPSTIVTRIRVLRKLR DTCHMGEADRTFLSPIAQHPPV CHVETHLGMQVANSSEEDELV WSKWDVDVKFILCCAKYHREQ LQESALDLKSLHCPSASPALFL ATPSQPVLTTGPGSASSQGGAE MGAHFLVQLVQSGAETRESFD PALPEMETQRTDEQCRAVHPGP QKERHGNMSPPLLMKGSSSPVP SGPGEEPSHREPVSFICGRCILLT LLLGDCLWGEGAWTQGDVLQ PSDRASFLAMGVNTTVQQVGD LSGYFPNSVGKACKCREFHTLT PLAHTSSTTHETFPGAQCEVQL VESGGGLVQPGGSLRLSCPDSG FTFSNHYMSWVRQAPGKGLEW ISYISGDSGYTNYADSVKGRFTI SRDNANNSPYLQMNSLRAEDT AVYYCVKHTARGKLEKQEQTY SKASRRQEITKIRAELKETETQK TLQKINESRSWFFEKIYKIDRPL ARLIKKKREKNQIDAIKNGKGD ITTDPTEIQTTLREYYKHLYAN KLENLEGMDKFLDAYTLPRLN
19650	50018	A	19765	1	1251	
19651	50019	A	19766	1099	4113	
19652	50020	A	19767	1	2628	
19653	50021	B	19768	1	2970	
19654	50022	B	19769	1	4142	
19655	50023	A	19770	1	4091	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRSLRSRCDQLEERVSV MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLKNTLQDIIQENF PNLARQAKVQIQEIQRMPQRYS LTRATPRHIIVRFTKVE

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19656	50024	A	19771	156	450	LQVEIYKTVKMHCIWHKQMVS SYFFYQKKNELSNFEEVFLKTA SGMFFSTVGCHPTRCGEFEKNN PDLYLKELLNLAENNKGKVV\A IGECGLDFDRLQ
19657	50025	A	19772	173	1009	LHGGNLQDSKDALHLAQTNG MFFSTVG\IHPTRCG*/YFEKNNP DLYLKGVAKIFA/EKTLKGKLW QLGEC\GLDFD\RLQFCPKDTQL KYFEKQFE\LSEQTKLPMF\LHC RNSHGWNFLDIMKRNRDRCVG GVVHSFDGTKEAAS\SLIDLDLY IGFNG/CASPENLEANLGRFWK SI\PSEKLMIEA\DAP\WCGVKST HA\GSKYIRTAFPS\KKKWESGH CLKDRNEPCHIIQILEIMSAVRD EDPLELANTLYNNTIKVFFSWN IIGICLPLSIMYVKFHSKTS
19658	50026	A	19773	16	1558	QEHLQRASPRLLQLLPPLPPPPP PPAFGGSLSSLGSRMSRQV\VRS SKFRHVFGQPAKADQ\CYEDVR VSQTT\WDSGFWC/SVNP*VLW ALICEASGGGAFLVLPLGKIWT LWDKNAPTGCGSHS/APVLDIA WCPHNDNVIA\SGSED\CTVMV WEIPDGGLMLPLREPVV\TLEG HTKRVG\IVAWHTTAQNVLLSA GCDNVIMVWDVGP\GAAMLDT GPRGA/HPDANYRGDWEP\DGG LICTSCRDKRVRIIEPRKGTVVA EKDRPHEGTRPVRAVFVSEGKI LTTGFSRMSERQVALWDTKHL EESPV/SLRKLHTRNGVPVAFFG P\DTNIVYLRGKG\SGPIRVFE\IT SE\APFLHYL\SMFS\SKESQRG\ MGYM\PKRGRKVNK\CEIAGFY KLHDGR/CVSPMPKPVPRKSDL FQEDLGPTPPRGPDP\ALTA\EE WLGGRDVG\PLFISLKDGYV\PP KSREL\RVNRGLDP\GRRR\AAP EASGTPSSDAVSRLEEEMRKLQ ATVQELQKRLDRLEETVQAKL
19659	50027	A	19774	229	475	

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19660	50028	A	19775	225	965	EWAWRSQLRSEHSRADPTRSSC RSCGAKMSGEENPASKPTPVQ DVQGDGRWMSLHHRFVADSK\ DKSGSKKKNPPPPEVVFIGDSL VQLMHQCEIWRELFSPLHAL\N FGIGGDGTQHVLWRLENGELE HIRP\KIVVVWVG/TPNNHGHTA EQGLLPRGQHPNPLREKNRQV NELGTGGTWLGHPRAHFLDAD PGFVHSDGTISHHDMYDYLHLS RLGYTPVCRALHSLLLRLLAQD QGQGAPLLEPAP
19661	50029	B	19776	691	1077	
19662	50030	A	19777	481	1308	PSVAFL*PSLHRYGHTGTAGPG WPCAAGS*AA/SSSRRGLPSVLQ ASSNSSHRRCNSTPSGSAGQRR VRRAP*MASTTPGGTESGPCKA RNAFRMRSTSAFCRGQ*QRPVP SSSSSRSSSRACA\AGETASGDP RAQRQLRS*DEESSSPSLDFRQA /PWPTAPCVKVSYSSSRMFSGM SPWRSSDNKRNSSFLRKTTGSN FSADLDTPPMPEVCLLPSLGYP LVPPVAEVHMPVPAPILPSAGIR RKIQKAASAKQLPLFQMDDSFS QHRVQGDTKK
19663	50031	C	19778	41	318	
19664	50032	A	19779	970	1193	INNHIRDSCWTCHCSC/QPPPPPP LLPQPPP*LSAPRVIERKE*DRL/ CPGEQTSSPTPSPRTQSAAAAT QLSLPPP
19665	50033	A	19780	1	494	MDGRVMAAGGRQAPGQKKAG TSEAPPSSQEWPEAWYGCLQQ KLRAVYLVQSQPCTGPVLAPG AACPAAAASTPGCAQW/CGPR ACSPTQSSQLCAWFAFSSRCPD FCPNPPRPL*DPPSWPTDPADRC SPELTIRDSCWTCHCSCRRRHR RPCCRSRRPDSPRHG
19666	50034	C	19781	120	392	
19667	50035	A	19782	174	375	

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19668	50036	A	19783	33	1154	QFALCAGWWLCGRGGGRTPAT MSGFSTEERAVPFSLEYRVFLK NEKGQYISPFHDIPIYADKDVFH M\VVEVPRWSNAKMEIATKDP LNPIKQDVKKGKLRYVA\NLFP\ YKGYIW\NYG\AFPQTW\EDPG\ HNDKTLLGCCGLTMDP\IDVC* NWEGKVCARGEIIG\VKVLG\IL AMI\DGGGTDWKVIAINV\DDP GCQPINNDI\NDVKRLK\PGYL* KLPVDWFR\RYKVPDGKPENEF AFNAEFKDK\DFA\IDIIKSTPWT LGKALVT*ENRMGKGISCMNT NFVLRAPFKVCILDAAQSPLWD ALPTHPCGICPCHSTQQTVDKG VPITQKNLMRFPLEYQADIAYIR VPSWMVLEVKVVAFSKAFKFV EPHPNLK
19669	50037	A	19784	1	612	VTQEDDIIEEHKPRTPRPSPPLL APSPACQAFGEGHSPGHPAIST GAGPRPSASFSHPHLSGLHREPP LNWSVCPGLVWSPKPALDETH PFVQQFPHQATLEWGVFHRDV GRRWGRRLGNLQIGSEVARRR RVGGGGLQCRRLGVGASPGAD W**SG*EEACGGRWAA/GADG WGLGRPRELIGCRGWRRSLAA APGPQRPGFVSVSTPRCRPRSG METQTPALRVQQDDLFQS
19670	50038	A	19785	1	951	MEEGISSQIGRRENECQQKKCQ TLIKPSDLVRTHSYHENSMGETI LVIQLPPPGTAFDMWELQFKLI TQTFSHHNQLAQKTRREKRAR QEA\ERREKAERAARLAKEAKS ETSGPQIKELT\DEEAERLQLEID QKKDAENHEA\QLKNG\SLDSP GKQDTEEDEEEDEKDKGKLKP NLGNGEDLPNYRWTQTLSELD LAVPFCVNFRLKGKDMVVDIQ RRHLRVGLKGQPAII\DGELYNE VKVEESSWLIEDGKVVTVHLE KRGPADAHSRALSVLQASRLL GVHCVPGTVPNAEIQVVDFVIY FWQSVIPQASPISE

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19671	50039	A	19786	87	1191	SAELRDVDRSAARLGGEQEEER FDGMLLAMAQ\QHEGGVQELV NTFFSFLRRKTDFFIGGEEGTAE KLITQTF\SHHNQL\AQKT\RREK ESPRRRAE\RREKAERAARLAK EAKSETSGPQIKELTDEKA\ERL QLEIDQKKDAENHEAQLKNGS LDSPGKQDTEEDEEEEDEKDKG KLKPNLGNRADLAQ*RLNPDPC RELDLAVPF\CVNFRLKGKDMV VDIQRGTPR\VGLKGQPSDSLM GELYNEVKVEES\SWLIEDG\KV VTVHLEKI\NKMEWWSRLVS\S DPEINHPRKINPENSKA\SDL\DS *DFASMVEKDDGMTQRTESPM GLPNFQTNRRKQEILK\KFM\DQ HP\EMGFFPKAKFPTNPCFFPP
19672	50040	A	19787	3	403	
19673	50041	A	19788	281	1952	DPVPGCRRLVAMAPTIQTQAQ REDGHRPNSHRTLPERSGVVCR VKYCNSLPDIPFDPKFITYPFDQ NRFVQYKATSLEKQHKHDLLT EPDLG\VTIDLINPDTYRIDPNVL LDPADEKLLEEEIQAPTSSKRSQ QHA\KVVPW\MRKTEYISTEFN RYCIFHEK\PEVKKWGSVKQQF TEEEIYKDRDSQITAIEKTFEDA QKSVIEGLGWGEARISQHYSKP RVTPVEVMPVFPDFKMWINPC AQVIFDSDPAPKDTSGAAALEM MS\QA\MIRGMMDEEGN\QFVA YFLPVEETLKKRKRDQEEEMD YAPDDVYDYKIAREYNWNVK NKASKGYEENYFFIFREGDGVY YNELETR\VRLSKRRAKA\GVQ SGTNALLVVKHRDMNEKELEA QETRKAQLENHEPEEEEEEEME TEEKEAGGSDEEQEKGSSSEKE GSEDEHSGSESEREEGDRHEAS DKSGSG\QDDSSDY*ARAARDK EEIFGSDADSEDDADSDDEDRG QAQGGSDNDSDSGRN\GGGQR TRSHSRSASPFPSGSEHSAQENG \SEAAASDSSEADSDSD
19674	50042	A	19789	1	885	
19675	50043	C	19790	164	361	
19676	50044	C	19791	22	156	

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19677	50045	A	19792	1	1344	PGRTTRSMAEDVFLSAPIPRGC ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEEE EEEEDAVLVAEAEAVAAGWM LNFLCLSLCRAFREGRSEDFRRT RNSAEAIIHGLCSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKEHDKLHE EIQNLIKIQAIAVCMENGNFKG AEEVFERIFGDPNS\HMPFKSKL LMIISQKDTFHSFF\QHFSYNHM MEKIKSYV\NYVLSEKSSTFLM KAAAKVVESKRTRTITSQDKPS GNDVEMETEANLGYKKKC*LT NSLR*LNPQRVQYPY*GSHKNL FYLKLQHGTQQQDLNKKERRV GTPQSTKKKKESRRATESRIPVS KSQPVTPEKHRARKRQAWLWE EDKNLRSGVRKYGEGNWSKIL LHYKFNNRTSVMLKDRWRTM KKLKLISSDSED
19678	50046	A	19793	1	1444	IPGSTISCLKGQYPSEPFNMAED VSSAAPSPRRCADGRDP\DPTEE QMAETERNDEEQFEC\QELLEC QVQVGAPEEEEEEEEEDAGLV AEAEAVAAGWMLDFLCLSLCR AFRDGRSEDFRRTRNSAKAIIY GLSMLTACPLRTIYICQ\FLTRIA AGKTP*MHRFENDE\RITPLGISP *MIWGSIEKEHDKLHEEIQNLIK IQAIAVCMENGNFKEAEEVFER IFGDPNSHMPFKSKLLMIISQKD TFHSFFQHFS\YNHMMG\KIKSY VNYVLSEKSSTFLM\KAAAKVV ESKRTRTITSQDKPSGNDVEME TEANLDTRKRSHKNLFLSKLQH GTQQQDLNKKERRVGTPQSTK/ RRKKEGRRATESRIPVSKSQP\V TPENDRARK\RQAWLWGRKDK ILRS\GVREFG\EGN\WS*ILLHY KF\NNR\TSVM\LKARW\RTMEG NLKLDFLQDSEDWIVFVKSFDG KGQFKYFDHCILFETCVIDVI
19679	50047	A	19794	1	1020	
19680	50048	A	19795	411	769	SHLGFPGTWTRLWPSRMSPCPP QQSRNRVIQLSTSEL/APALGN WARLPQVTEQ*FRGLRKGSRT MPGSSPPATWTKGCLLA*Q*CL CPQLGWSRVAP*CRLGALFLAC SLLLAAPLRCF

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19681	50049	A	19796	171	325	ETVAVSSAGARASSIMRIMVSS RPSETSLESVFPDSAP/PGL*PPP CLSFGL
19682	50050	A	19797	335	1536	GCSPCPPQ\QS\RNRVIQLSTSEL GEMELTW\Q\EIMSITEACRVLN APSEPSFEAPKPQLPYL\GPPPPT TY\CPC\SIHPDSGFPI\P\PPPYEL P\ASTSHVPDPPYSYG\NMAIPV SK\PLSLSGLLSEP\LQDPLALLD IGLPAGPPKPQEDPESDSGLSLN YSDAESLELEGTEAGRRRSELC RRCYPV\EYPYSLMPNSLAHSN YTL\PAAETPLALEPSSGP\VRA KPTARGE/AQGSRDERRAL\AM KISF\PTDKIVNFPVDDFNELLA RYPLTESQLALVRDIRRRGKNK VAAQNCRKRKLET\IVHLERKL ERLTNE\RERL\LRA\RGEASR\T LKVMRQQ\LQELY\REHFPSHLR E*NPGQTAYSP*KK*RACKQAC PNGDPSFPCGPRGT\KMEAHRL
19683	50051	A	19798	1	408	LNLMRWEAVQARGGAFRIPRV DPGPTPIPHNSSSRFDCNSVSTA P\RVLVSGICAAGSFVLVAFSHS VGTSLC/GYFLLLTSPEAQDPGG EEEAESAARQPLIRTEAPESKPG SSSSLSLRERWTVFKGLLWYIV PLV
19684	50052	A	19799	1	759	
19685	50053	A	19800	1	1815	
19686	50054	A	19801	1	942	MGGCAGSRRRFSDSEGEETVPE PRLPLLDHQGAHWKNAVGFW LLGLCNNFSYVVMLSAAHDILS HKRTSGNQSHVDPGPTPIPHNS SSRFDCNSVSTAP\RVLVSGICA AGSFVLVAFSHSVGTSLC/GYFL LLTSPEAQDPGGEEEAESAARQ PLIRTEAPESKPGSSSSLSLRER WTVFKGLLWYIVPLVVVYFAE YFINQGLVSEGCLFRPFPFSALN VCEVNLVKVSQHQGGWVAVV TQGKKHPISCRRLNVDGMNIIS NDGSNKLNRSRKARVSYKVQR TINASLNAATSTRAVSSNPNFV

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19687	50055	A	19802	82	1620	SLSPVADPHPSRGSPLWTLYDP GPSGDLNLMRWIGCAGSRRRFS DSEG\EETVPEPRLPLLDHEGAH WKNAEGFWLLGLCNNFSYVV MLSAAHDILSHKRTSG\NQSHV\ DPGPNGDSPTTAYSRFDCNSVF\ TGAVLL\ADILPTLVIKLL\APLG L\HLLPYRSGPRVLVSG\ICAGG KFRPGFAFSHSVG\TSLCGCWSF ASISSGLG\EVTFLSLTAFYPRA VISWWSSGTGGAGLLGALSYL GLTQAGLSPQQTLLSMLGIPAL LLASYFLLLTSPEAQ\DPERGEE AK\SQAGQPFIRTEGPE\GKPGSS SSLS\LRERWTVVKGLLWVPLF PWFEVTFPKYFITQGLFELP/LFF WTTSLSHAQQYRWYQMLYQA GVFASRSSLRS\CSIGFTW\ALAL LQCL\NL\VFLLADVWFGFLPSI YLVF\LII\LYEGAPWGSASLREK PF\HNIRPWRPSDEHREVCKWR PPCHL*HTGGFILSGASLALPLH DFLLPSSPDTRDPQDAGHIHLW ARGTGYQ
19688	50056	C	19803	270	542	
19689	50057	A	19804	271	449	CLELRNLFYGACSWEVSISSDS EKPGIFNASPASAVHC**GFARP SSWRVLGAICTFHHSVYAKTA KRKAST*RHFHH
19690	50058	A	19805	21	79	
19691	50059	A	19806	1242	1560	WATRSSCSSMMEMPPWCPCGC AGRWRRGGASRGPREAAAGH* KPRTSNQGEQPTRRPSPYAACA RRAFAGPWASLPSPSPLSAGGL AWGAPCVAHPTRPSPYLLV
19692	50060	B	19807	148	2949	
19693	50061	A	19808	1335	2173	KQAHRPREEKRREEKRKEG\PS VPETLKKKQRNFTELKIKRL\RK KFAQQML\RKAR\RKLIYEKAK HYPKE\YRKMYRT*ISNGRGWA RK\AGQLYLVLKNPKFAV\VIRN QKVSMGVSP\KLRKVVVSFLRP SSKSSNETFVKALKQRPSD*TM P*GLVRGPI*LPWGYPPQS*SPV NEP*SYK\RGY\AKIQ*EAELPLT DNALIASISWVNSAFICM\DDLI HEIYTV\GKRFK\EANNFLWPLQ IVLLPRGG\MKKKTTHFVEGGD AGTQRSDQINRLIRRMN
19694	50062	A	19809	3	186	
19695	50063	A	19810	272	428	

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19696	50064	A	19811	50	2237	RSLKAFICSILSMDKQSRDPPVK MQGSITTPGSIALAQAQAQAQV PAKAPLAGQVSTMVTTSTTTTV AKTVTVTRPTGVSFKKDVPPSI NTTNIDTLLVATDQTERIVEPPE NIQEKIAFIFNNLSQSNMTQKEE LVNNTELVQSYRQQIGNVVNQ ANLQLFWNMYNSRRDLDINRP GTVPNAKTLRCPVMLVVGDNA PAEDGVVECNSKLDPTTTTFLK MADSGGLPQVTQPGKLTEAFK YFLQGMGYMPSASMTRLARSR TASLTSASSVDGSRPQACTHSE SSEGLGQLNLKFEIEVLCKNLA LDINELKPGNLLKDKDRLKNLD EQLSAPKKDVKQPEELPPITTTT TSTTPATNSTCTATVPPQPQYS YHDINVYSLAGLVPHITLNPTA HPQLKQCVRQAIERAVQELVHP VVDRSIKIAMTTCEQIVRKDFA LDSEESRMRIAAHHMMRNLTA GMAMITC/RE/PLLMSISTNLKN SFASALRTASPLQREMMDQAA AQI*AQDNCFLL/CKVGGVDPK QLAVYEEFARNVPGFLPTNDLS QPTGFLAQPMKQAWATDDVA QIYDKCITELEQHLHAIPPTLAM NPQAQALRSLLEVVVLSRNSRD AIAALGLLQKSMENGLNYMAV AFAMQLVKILLVDERSVAHVT EADLFHTIETLMRINAHSRGNA PEGMDITTRQKVNKKREGFND
19697	50065	A	19812	1	3777	KNPEFNKMVLNETYRNIKVLLT SDKAAANFSDRSLLKNLGHWL GMITLAKNKPILHTDLDVKSLL LEAYVKGQQELLYVVPFVAKV LESSIRSVVFRPPNPWTMAIMN VLAELHQEHDLKLNLKFEIEVL CKNLALDINELKPGNLLKDKDR LKNLDEQLSAPKKDVKQPEELP PITTTTTSTTPATNTTCTATVPP QPQYSYHDINVYSLAGLAPHIT LNPTIPLFQAHPQLKQCVRQAIE RAVQELVHPVVDR

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19698	50066	A	19813	160	1002	KRLGSSAISMSKYKLIMLR\HGE GAWNKENRFCSWVDQ\KLNSE GMEEARNCGKQLKALNFEFDL VFTSVLNRAIPTARL\IL\EELGQ EWVPVESSWRLNERH\YGAL\I GLNREQ\MA\LNHGE\EQVRL\W RRSYNVTP\PPIEE\SHPY\YQEIY NRPGGIKVCDVP\LDQLPRSES\ LKDVL\ERFLPYW\NERIAPEV\L RG\KTILISAHGK*AVGALLKHL GRYPSGLKTSINIYSFLLGVPILL \ELD\ENLRAVGPH\QFLGDQEAI QAAIKKVEDQGKVKQAKK
19699	50067	A	19814	200	1155	NHYISLFQYSQDTCKLLFRNQM TISQIFLCIFSGVLMVFFLIITTSQ VSFTNFFTGLKIFFLVIKFWVSE FLHHQTGTYIHIYLLFISMKSFF LYASPLTFMILSHFQASLSSIFGF CSSLFRQSSFFSNILFF*VYTQSY REFRTYYETIPCQFDITFVIFKM CCILILC\FDLLNRRNGSIIIQKFG IYGLVKIFIF*IFTNIHLLQ*FFQV VFILQFFNIVKKSFLQPAGSKR* KFFSKVRFFSFL*F*KWEARSSA SKLFLLIY**VYR/IFSFLLVFPV V/CPVGWYLLFFFFLYLFFLFLN LSKNSFYSQWYWFKR
19700	50068	A	19815	1	168	RPWLHLHGRPGPWPAETPPPQD PEQAPPPGRAGPAGEAEGLSCV /P*APSRRPRTM
19701	50069	A	19816	1	531	PVGQGARQDDSSSSASPSVRAT SQGGHLMSDLFNKLVMRRKGI SGKGPGAGEGPGGAFVRVSDSI PPLPPPQQPQAEEDEDDWES*G AP*HLPPPDPDLGRCSDMDTAR TSCSDLLPWEGVTEPAVCGDQL QGAEGWLEATQLGRGLVCLYF MGGRLHPACATVFLRGFQRKR HTNQ
19702	50070	B	19817	61	969	
19703	50071	A	19818	60	436	RGSREYLHTGCPRSGGCRSQCP GPPTQSPKVRPPQRGAPRLRGG DFPPSRLLDTVSFPSPA*AAFPP CPVPHLPAPVQGAPREVVDPSG GWATLLESIRRAGGIGKAKLRS MKERKLEKKKQKEQ
19704	50072	B	19819	575	1666	

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19705	50073	A	19820	515	1110	MFHPTCLTCPAFANRPHVHCRP GAPAFAPSAPGTIPELPTFHTEV SPSHSRQTLQDGVT*TAPPPPPP PPPPPPAPEVLGQLQPPLPTLQP RPLLGQGAREGRTAAAA/PSPS/ GPGSSQGSGRPLRWLGHSARV HPPSWGHRQGLAAQHERKRNV EKKKQKEQEQVRATSQGGHLM SDLFNKLVMRRKGHLWEKDPG AW
19706	50074	A	19821	1	191	MQK*ITAWAPAPMKIKIIASPER KYSVWIGGSIWPQLST/FQQMW ISKQEYDESGPSIVHRKCF
19707	50075	C	19822	791	970	
19708	50076	A	19823	13	1260	INPPPLSRRCQLSHSVLPPLRRR VSLPVAMEEEIAALVIDNGSGM CKAGFAGDDAPRAVFPSIVGRP RHQGVMVG\MGQK\DSYVGDE AQSKRGILTLKYPIEHGIVTNW DDMEK\IWHHTFYNELRVAPEE HPVLLTEAPLNPKANREKMTQ\ IMFETFNTPAMY\VA\IQAVLSL* \ASGRTTGIVMDSG\DGVTHTV\ PILRGLPHCSTPFLRLGPGLARD LTDYLMKILT\ERGYSFTTHGPS GKTFRNIKGEACATSPLDFEQ\E MGT\AASSSSLEKSYELPDGQVI TIGNERFRCPEALFQPSFLGMES CGIHETTFNSIMKCDVDIRKDL YANT\ALSGGTTMDPG\IADRM QK\E\TALAAPAP*KIR\IIAPPER K\YSVWIGGSILASLSTFQQMWI SKQEYDESGPSI\VHRKCF
19709	50077	A	19824	93	534	

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19710	50078	A	19825	1	1462	WEVSAQPSPAVPRRAPLRGLSA TRSAAGTMREIVHIQ\AGQCGN QIGAKFWEVISDEH\GIDPTGSY HGDSDLQLERINVYYNEAAGN KYVPRAILVDLEPGS\MDSVRS GPFGQIFRPDNFVFGQSGAGNN WAKGHYTEGAELVDSVL\DVV RKESESCDCLQG\FQLTHSLGG RHGVPGWGTLLHQQGSGEEYP DRIHETPFSVH/VPSPKVFKTRL LEPLQRHTSRFHHLVENT\VKP YSIDNEALY\YICLPTAES*PTPT YG\ALNPPGCSATMSGVTT\CLR FP/GGQLNADLRKLA\VNMVPF PRLHFFMPGFAPLTSRGSQQYR ALTVPE\LTQQMFDSKKMIA/AP CDPPPTGR\YLTVAAIFRGRMFH GRRWDEADGSNVAGTRNRQVI SWEWVP\NNVKTA\VC\DIPPPG AWKMS\ATFIGNQPRPSRRLFK RIYE\QF\TAMFPAQGPSLHWLH GRRAMDGDGSSPEAREQHERP WCPEYQQYPGTPRPT
19711	50079	A	19826	2	180	
19712	50080	A	19827	28	185	
19713	50081	A	19828	179	307	
19714	50082	A	19829	438	663	
19715	50083	C	19830	99	335	
19716	50084	A	19831	1	320	AYADQL*LRRHKSSSSSSSSSS SSSSSSSSPLAP*LGSGDLP*EIN PPSSCSLLREKDPPTTSGPQ\PTS PRNISPISNPDPTGNRTVQLTWQ PLPQPLELWPKAL
19717	50085	A	19832	578	753	LCTPTPFPLFWKTVRKYSSNNQ KGE*NTVLMEVCPRSPRTN*KD SQ*PFELLTKMTSQGSDISGDLP WEINPLSSCSLLHEKDPPTTSGP QTDQPKKHLTNFKSETKETHFI RGPKTPVLVTDWEGRLPLVFN HSRDASLIIHPRFRGVRPRRDAC LGPSPLAASPAFLEEGQVPQPLL SMSLTPSLLFWRRGKKPSTPSSP LAASPAFLEEGQVPQPHISVPRS LISTPQPLITLHPDPFPAFLEDSK EVLKQQPKGRIKHCADGGMSK EPKNQLKGLPVTKAGNIHGIND
19718	50086	A	19833	95	259	SHRPSQ*VLQLIKVAHPELFVPP SGFVVSLTSGMKLQTLTTREW MRILLIFWNG
19719	50087	A	19834	1	939	
19720	50088	A	19835	391	792	

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19721	50089	A	19836	1	1317	
19722	50090	B	19837	1	1665	
19723	50091	A	19838	573	902	YSCLLILIRKITQNSVEVLGRRK FLGGGMEREWVMFL/EGCFKR D*GQRGNQFQIRVTAPNFMCV CVKRPPNRLCVSNKAVYFTWV QVGFQIFEKPEPIEEICKVCWRP
19724	50092	A	19839	1802	2229	GGGAEAEEELGPSSAWRGAAC PCPRKAGLVAKAEGPRQASLR GLTPLKRECIIREASLQ*LNTK/V KAAFPVRDRRWSFGFTDKTCLF CLGSEIGEVFLGLVGLRT*GRR WIFLMEQRAGGQGIDLPREVPR SKSGHQISLVSI
19725	50093	A	19840	19	4153	PPDPLPGLPCPPGGPPLPAFGGG WGGARGSWHWSSRACSRRRR LVHAPRAPLLPRAAAEKAKRP AGARQMGLKARRAAGAAGGG GDGGGGGGGAANPAGGDAAA AGDEERKVGLAPGDVEQVTLA LGAGADKDGTLLLEGGGRDEG QRRTPQGIGLLAKTPLSRPVKR NNAKYRRIQTLIYDALERPRGW ALLYH\ALVFLIVLG\CLILAVL\ TTFKEYETVSGDWLLLLETFAIF IFGAEFALRIWAAGCCCR
19726	50094	A	19841	355	640	ILDYVFSSSHLFQSKLLGRRGR ASHGTKL*AGPG\GGGEVIKGL* GGGAEAEEELGPSSAWQGAAC SFPRKAGLAAKGEGPRQASLH GLTPLKCG
19727	50095	C	19842	55	189	
19728	50096	B	19843	96	401	
19729	50097	C	19844	558	725	
19730	50098	C	19845	448	540	
19731	50099	C	19846	140	334	
19732	50100	A	19847	362	710	ILGGRKLRLEKSLGCAAQGGG AL/YEEWLELRNGCLCCS\VKD NGL*/RAIENLMQKKGKF\DYIL LETTGFADPGAVASMFWVDAE LGSDIYLDGIITIVDSKYGLKHL AEEKPDGLIQ
19733	50101	A	19848	181	543	
19734	50102	A	19849	1	594	
19735	50103	B	19850	29	746	
19736	50104	A	19851	45	362	EEQHSMLGSGFKAERLRVNLR LVINRLKLLE/KKDERARIRVEH IIREDYLVEAMEILELYCDLLLA RFGLIQSMKELDSGLAESVSTLI WAAPRLQSEVAELKIVA

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19737	50105	A	19852	344	951	EEQHSMLGSGFKAEHLRVNLR LVINRLELL/EGKKKKKTELAQ KAGKEIADYLAAGKDERARIR VEHIIREDYFVEAMEILELYCDL LLARFGLIQSMKELDSGLAESV STLILAASRLQSEVEGFPNIYSS* IPSNSPIILNL*MAIKGCKNY/RL LHQIVVPGPSQKPLQNFLLDLR LPWTTLWPIFGLEGKIPLWERIK
19738	50106	A	19853	1	1077	
19739	50107	A	19854	1	1140	
19740	50108	A	19855	1	3426	
19741	50109	A	19856	1	942	
19742	50110	A	19857	342	1499	EEQHSMLGSGFKAERLRVNLR LVINRLKLLEKKKTELAQKARK EIADYLAAGKDERARIRVEHIIR EDYLVEAMEILELYCDL/LCLA RLG/LYSSY*KELDSGLA\ESVST LIW\AAPRLQSEVA\ELKIVADQ LCAKYSKEYGKLCRTNQIGTV NDRLMHK\LSVGTPP\QILVERY LIEIAKNYNVPYEPDSV\VMAE APPGVETDLIDGGFPDDVKKR\ GPWKKEGSGGFTAPVGGPDGT VPMPMPMPMPMPSANTPFSYP LPKGPSDFNGLPMGTYQAFPNI HPPQIPATSPIRIESVRWTFNCLI KEYS/IFLAQICLGPGPKARRPF AKFP\SRPADNF*QLLFLPELPSV PDTLPTASAGASTFRHLKDIDF DDLSRRFEGAGKRKT
19743	50111	A	19858	2	255	GCISTSRLGSMPTTTLRLLQKIS *RSYSSAPASCLISIVKSASD*RA RAPTRGSYGGPLLRLSSSSSLAS GRCVTSRASLRPRS
19744	50112	A	19859	1	276	
19745	50113	A	19860	3	151	GAVPAVRLGGPLHVHLPHAR*P SNLSALQFYQDGSLRWWQTVS *RAASRSPPTRPVTIKSVCTPILP GWLSSLVANCIVKSASD
19746	50114	A	19861	1	386	DCVIATDAEVLGAPVKGKRRG RGPKGDKASDPEAGVARGIDF HHVSAVLNFDLPPTPEAYIHRA GR**CDGPGICMVGTLRDLGCA GQSLRVGDASCTVFPCRTARAN NPGIVLTFVLPTEQFHLCKI
19747	50115	B	19862	26	186	

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19748	50116	A	19863	2	1839	ARGQRVRAALLSSAMEDSEAL GFEHMGLDPRLLQAVTDLGWS RPTLIQEKAIPLALEGKDL\LAR ARTGSGKTAAYAIPMLQLLLHR K\RQVRW*NRQ*EGLVLVPTKE L\ARQAQS\LIQQLATYCCSGMS ELANVSAC*KTQSLRELCLMEK PD\VVVGTPS\RILSHFAARQPET FVTPWSFLVVERSLTFFFPFGFE EELKKSSSGKAESLAPDFNKAF LMSATFNEDVQA\LKELILHNP\ VTLKLQESQLPGARPVTAVSGG L*DLREDKFLLLYALLKLFIDSG ASLWLFCSTL*EREFTGLRLFL WEQFQ/LSPTCVLNGELPLRSR VPHHL/QQFNQGFYGLCHRQL/ NAEVLGAPVQGQASGPRAQRG Q/VPLDPEAGVARGIDFHHCVC\ VLNF*SFPPTPEA\YIHRAGR**C DGPGICMDSTR*QPRA*S*PFVL PTEQFH/CRQD*GASQWREQGA P/SLLPYKFGMEEIEGFRYR*GV HPQDAMRSVTKQAIREARL\SLI KEELLHSEKLK\TYFGRQPLGD LQA\LRHGPYLCTPQLVEAPTW GHVPDLPGSSCFSVALGAPFTK KREEACLPSCRKAQESKVPRTP LRSFKHKGKKFRPDSQALREVV
19749	50117	A	19864	3	378	TTTKFAGRRPKVTVLGQP/KAA PSVTLFPPSSEELQANKATLVCL ISDFYPGAVTVAWKRGSSPVKA GVETTTPSKQSNNKYAASSYLS LTPEQWKSHKSYSCQVTHEGST VEKTVAPTEYLLRVY
19750	50118	A	19865	1	546	MAWTPLLLLLLSHCTGSLSQPV LTQPPSSSASPGESARLTCTLPS DINVGSYNIYWYQQKPGSPPRY LLYYYSDSDKGQGSGVPSRFSG SKDASANTGILLISGLQSEDEAD YY/CGCFTVFWSTF*VLVPEHQ QSWLPLWTPGVVSLLV/CLVPS FVPPPLTKVPSSLSSPVKESAILA VDIH

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19751	50119	A	19866	2	838	RVRVSTMAWTPLLLLLLSHCT GSLSQPVLTQPPSSSASPGESAR LTCTLPSDINVGIYNIYWYQQK SGSPPRYLLYYYSDSYKGLGSG \VPSRFSGSKDASANTGILLISGL QSDDEG\DYYCATWDSSLTGQ VFGGGD/TKLTRP*GQPKACPP GVTLVPNPPS/SRSFQAQQGPQL VMSS*SDFLTPGSPLNSCPWK\A DSQPPFKAG\VETTHTPPKQSNN QVRGPAGYLSLTA\EQWEVPTE SYSCQ\VTH*RGAPWEKTVGPY RMFHRFLNPSPPHHGMT
19752	50120	A	19867	1338	1854	NSETREHNHRYVPQRETSGGTD GWKSKQPE*L*RRQLVQSWAK S*NQPKLPSSPH*ELPWVTPSA RNFRSGPYSPPPPPPPQPLPSSHL SSLHFYSPFVSYTSFDLYSSSYH SYLMDEDTVEPKELRSSQKVIG HSFTGFQPTLSANPYDRGDGKII ELLPRKAQTFPVVRT
19753	50121	A	19868	1	500	GSTYSELLSGTACVVTALHLAQ QRRHHLLGGLASRHDAPEQLA VGAPVQPRPLPAPAGAQALVG HAHVVVEGGP/PGSGGPGEGAI ARGPGAAAAAGAGPGAPRRRR LQASAGPCSRSSEPGRRSAPRA APPAPSAGPHVAFPSRRPAAGS PPRSRPPPPPGIPTGGR
19754	50122	A	19869	20	507	TRQVYSGGVRTPPCQSHPHRPR SSCRPPPPPRRPRSSRRRRGLSP RRAPAHWSSRSTRPAWWAPSR RHAPRPPWSPGPASG*CSVYFPI LPLALFPLPVHHGGVHVCGREG VGLVQEGDSHSGEWS*RSAWG STSLRAAPRSGGRPPAGGGWR YTRPPSRRC

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19755	50123	A	19870	236	1191	GSGRIPGRAGLEGPGPAFQKSR LSPASGSAGPRGASPSAVPPGR/ RPGVPAFPASNPPPVAAVPGPW VTCWGKGLQGEGKAPRAPHA GTPQR\SPGSARPTGLSPPA*PSR *RARRPSPETP\PGHGRAGPPPP DGAVQRQGPGCRAPSASRPPGS ARARRRRWPAARPPGCPARPG PRGGRPRRRPSPPAAGRARRRA PRTPAARSR*VCPRGRRSAAPP RGHGTAPCAAAAPPPPRGLGRP ADAPEQ/PRCRCARPAPPLPAPA GAQALVGHAHLLLKAALGHDF TFLWATIHEVIPKMRWGQSQC QRGGPSSHTPDLSA
19756	50124	A	19871	24	286	LRGQKVLLLGDRARLSQKKKE RKRERERE REGHGRNGR/RRNG QGRGPEGQR*NERTGQERTGH GREGRKEGRKEGRKEGRNERE
19757	50125	A	19872	43	373	PRFTDENLEMCTVIQSVQCYHR SWH/HSSPPEPAPHHQSPPAHSP VLCWFRRLGGGEDWAPSSGGR AVWRSHCSCFCCCSSSCCSCSQ SGKRTAAAPWPTTSPAPSRSCC A
19758	50126	A	19873	3387	4083	AGRSALPVDAVQVQAEGLWPP AVLLHHHHHPHHHYHHYHHH HHHHHHP*HHHPHHHHHHHHRN HHHHHHHHHLHHHHHHHHHHL YHSH\YHHH/HHHHDHHHYHH FHDHYHHHHH/HYSHH/HHPH/ HHHH*RHDHY/AHHHHHQ\HH CHHCHHPHRHGHYHYHHHGT VAFGALEDSAVARTGLPLPEGV LCGAPTAAASAAVPPPAVPAPN QGRGPQLHPGQQLRPLLHAHA ALQWPTTHL
19759	50127	A	19874	3	411	
19760	50128	A	19875	1	1095	
19761	50129	A	19876	1	471	
19762	50130	A	19877	1	554	FRGRLASPFRPVPMEALGKLKQ FDAYPKTLEDFRVKTCGGATV TIVSGLLMLLLFLSELQYYLTTE /VKGRGLMRGRGLAF*E*DL*G WEWGRRGLGLSLTEVALPQVH PELYVDKSRGDKLKINIDVLFP HMPCAYLSIDAMDVAGEQQLD VEHNLFKQRLDKDGIPVSSEAE RHVLSFVVSAD
19763	50131	B	19878	1116	1274	
19764	50132	A	19879	28	389	

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19765	50133	A	19880	75	448	
19766	50134	A	19881	276	830	QEDSCPLHPLSGIPFRRFQPTPE EAGAVVPGEGPTHDQGPSSALT RR*ACQGPLHLARTTAEPGHAH PWH*RWQRYMGKLGRDLEKV CPVWSSVACSSPGLSWAGKTE AKTSLEGGNSASASASSWAWG RSSLAPVRDILGSREFSGLLEGT FVLSVTLSADFGIGTWVDLGKV TGSSSKEGRL
19767	50135	A	19882	223	1269	APVTKRKEVFAKDSKGSALDA GRDPKRPALPETLCESGWASNT APTAPPQPGWCLCGKDFKSSCQ TPGREKERRLATMHGSCSFLML LLPLLLLLVATTGPVGALTDEE KRLMVELHNLYRAQVSPPASD MLHMRWDEELAAFAKAYARQ CVWGHNKERGRRGENLFAITD EGMDVPLAMEEWHHEA*/DTT TSAP/HSCSPGQMCGRYTQVVW AKTERIGCGSH\SCEKLQGVEET NIELLVCNYEPPGNVKGKRPYQ EGTPGSQCPSGYHCKNSLCEPI GSPEDAQDLPYLVTEAPSFRAT EASDSMKMGAEGPDKPSVVSG LNSGPGHVWGPLLGLLLLPPLV LAGIF
19768	50136	A	19883	2	281	FVPALGSSAVMLSRSRCVSRAF SRSLSAFQ/KGVSLCQGPGYPNS RKVVINNSVFSVRFFRTTAVCK DDLVTVKTPAFAESVTEGDVR WEKGKI

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19769	50137	A	19884	1	1320	MPAVTILKPNLKQIILGLKAAE VSSLPPSIVLDAKEITTQITRQIL KGNCPLGRHSLPGVSLCQGPGY PNSRKVVINNSVFSVRFFRTTTV CKYDLVTVKTPAFAEPVTEGD VRWEKAVGDTVAEDEVVCEIE TDKTLVQVPSPANGMIEALFVP DGGKVEGGTPLFTLRKTGAAP AKAKPAEAPAAAAPKAEPIAA AVPPRAAPIPT/QMPPVPSPSQPP SSKPVSAEAQNTCA\MLTIFNEI DVSNIQKMRARHKEAFLKKHN LKLGFMSASVKASAFALQEQP VVNAVIDDITKEVVYRDYIDIS VAVATPQGLVVPVIRNVEAMN YADIEQTITELGEKARKNEFAIE DMDGGTFTISNGGVFGSLF/GTP IINPP\SAILGMHGIFDKPVAIGG KVEVQPMMYVALTYDHRLIDG REAVTFLRKIKAAVEDPRVLLF
19770	50138	A	19885	1	1559	MESEALVVCINHCMAVNYGMI YQRGSSNMNILSLSLKHPEKTGI SPTANHGISDLQEGEAACGSLR TPLVGRRVLRPAPLPVVVRPYI RCPPALGSSAVMLSRSRCVSRA FSRSLSAFQKGNCPLGRRSLPED DLVTVKTPAFAESVTEGDVRW EKAVGDTVAEDEVVCEIETDKT SVQVPSPANGVIEALLVPDGGK VEGGTPLFTLRKTGAAPAKAKP AEAPAAAAPKAEPTAAAVPPPA APIPTQMPPVPSPSQPPSGKPVS AVKPTVAPPLAEPGAGKGLRSE HREKMNR\MRQRIAQRLKEAQ NTCAMLTTFNEIDMSNIQEMRA RHKEAFL\RKLKLKLRLMSAIV EGSA\FALQE\KPLLMEGIDDTT KEVVYRDYIDISVAVAHPRGLV VPVIRNVEAMNFADIERTITELG EKARKNELAIEDMDGGTFTISN GGVFGSLFGTPIINPPQSAILGM HGIFDRPVAIGGKVEVRPMMY VALTYDHRLIDGREAVTFLRKI KAAVEDPRVLLLDL
19771	50139	B	19886	239	3045	

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19772	50140	A	19887	3	809	RGRFLPPCHPAALPPCRPAALLP VVAARGAPSPPPPHVLPCVGSG LGYNMLGMIKNSLFGSVETWP WKVLSKGDKEEVAYEERACEG G\KFATVEVTDKPV\DEALTGK QLPKV\AKYAGGTNDKG\IGMG MTVPISFA\VFPN*RWLSCRKKL KVWFPDFQTNFQSDPPAPS\DKS VKI\EEREGIHCLIPCQFGGYAK\ EADYV\AQATR\LRAALGG\PAT YRGDIYFCTGYDPPMK\PYGRR NEI\WLFEDMSDPTEPRTYWEV CLCVSFLRG
19773	50141	C	19888	164	208	
19774	50142	A	19889	1542	1929	NLVPSLGSGDLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARPT\SWGRGKYPSTPS PSPLAASPAFLGGKNPPIAYFHT PTSYLCAPIPYFCAPTPSLLFWR ARTTTPTPSLCLKSFL
19775	50143	A	19890	1	208	MPEPQRPGVPPEPPPPGACYAC RKSGHWA\RNARSPGFLLSRVP SPPGPSRTPSFG*LSQWKPTCTQ VK
19776	50144	A	19891	1	1662	
19777	50145	B	19892	1	915	
19778	50146	A	19893	183	569	
19779	50147	C	19894	71	344	
19780	50148	A	19895	147	446	
19781	50149	A	19896	167	373	
19782	50150	A	19897	142	363	
19783	50151	C	19898	52	174	
19784	50152	C	19899	228	260	
19785	50153	A	19900	1	753	
19786	50154	A	19901	1	1077	
19787	50155	A	19902	500	912	LGSGDFPWEINPLSSCSL/LREK DPRTTSGPQTDQPSKHLTNLKS ASTPPPYNPFITSPPHTRSGLQFR STSSPPAPAQQFTLKKVAEAKG IVKVNAPFSLSDLSQISVRLGSFI KYEKSSPVHGSFGSNPETLYSP
19788	50156	A	19903	1	861	
19789	50157	B	19904	174	222	
19790	50158	A	19905	1	756	

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19791	50159	A	19906	1035	1852	NLVPSLGSGDLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARPT\SWGRGKYPSTPS PSPLAASPAFLGQRQVPLSWGR GRCPSTPSPSPSAASPAFLGQGQ RQVPLSWGRGRCPSTPSPSPSA ASPAFLGQGQRQVPLSWGRGR CPSTPSPSPSAASPAFLGQGQRQ VPLSWGRGRYPSTPSPSPSAASP AFLGQGQRQVPLSWGRGRCPS TPSPSPSAASPAFLGQRQVPLSW GRYPSTPSPSPSAASPTFLGQDL PLSWG
19792	50160	A	19907	1644	1981	LGSGDLPWEINPSSSCSLLREKD PPTTSGPQTDQPKKHLTNFKSA *KRTNTASYK/WHSQSRVPAPR DGLVAAPTESEVAFLPVPPHQG PPLGNLGPSTVTTSFRCWLLDP RS
19793	50161	A	19908	1011	1154	
19794	50162	A	19909	1043	1168	
19795	50163	A	19910	1328	1470	
19796	50164	B	19911	406	1191	
19797	50165	A	19912	2848	3140	SFYHLSSSHLVRLTVSFRD*PSP TCPAIYS*KGGWSQRHSQGACY TCRKSGHWA\RNARSPGFLLSH VPSVWDPTENRTVQLTWQPIPE PLELWPKAL
19798	50166	B	19913	1	941	
19799	50167	A	19914	656	1983	NLVPSLGSGDLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSEAKEICFIREPKTPAPVT DWEGSLPLVFNHCRDASLIIHS RFKGVRPRRDACLGPSPLAASPI FLGKGQRLKTDTARLPRKPPRP SRMPSFGVKHVNVTIDCLPEGA ATRGTARTSKPTTKSQKTLPST SPGHWTQSTPWASALRSSPWTE TAAPSETEETLNTGRPPELPARA TATWFSASHTLPALATRRVART QWLTADRQTWASISSVPWAQT ISEKKPGGSLWETRSSPPTTAGT EEAMNTTSLLAPAAEIMATPGS PSQASPTSGAFTHGTQTPSPTKA TAPRYPQTGNSILTFGRPFLPFA GDLFAEWPFTAGEEPVLVPRPH QVSKTRSPPSFHLTLKTVTVAL LGNGEECYVYLSVSELREIRTR LYSPDAGLNEEKMLTKLLLI
19800	50168	A	19915	117	432	
19801	50169	C	19916	122	289	

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19802	50170	A	19917	1	516	
19803	50171	B	19918	212	3302	
19804	50172	C	19919	181	444	
19805	50173	A	19920	151	485	SPRGHYQLLLSGRALADRYRRI YTAALNDRDQGGGSAGHPAS/ RSENLENTVIIPDIKLHSNPSAFN IYCNVRHCVLEWQKKEISLAAA SKNSVQSGESDSDEEEESKEPPI
19806	50174	A	19921	1	3465	
19807	50175	A	19922	1	176	
19808	50176	A	19923	114	14211	AAPVAAPGALFMPVPDGSVAA AGLGLGLPAADSPGHYQLLLSG RALADRYRRIYTAALNDRDQG GGSAGHPASRNKKILNKKKLK RKQKSKSKVKTRSKSENLENTV IIPDIKLHSNPSAFNIYCNVRHC VLEWQKKEISLAAASKNSVQS GESDSDEEEESKEPPIKLPKIIEV GLCEVFELIKETRFSHPSLCLRS LQALLNVLQGQQPEVLQSEPPE VLESLFQLLLEITVRSTGMNDST GQSLTALSCACL
19809	50177	A	19924	375	1191	SQGIPELHYTPGPRGRWCGWW PIVEPRMGASQGCCVLGHLAQ QGGGASQAVRGANGVHAGCR GDPHPRSDHYPGGRPWLPGAS QDPAVAPGGHGHPSYLARLPC AAEPGTP/PAEPPRPSSLPGAAT APAGT*\PALADAPPRRVGGAG QPGRGHV*PKLVPGWQSQDSI* PSL/PSSPARHTLAASATP*APGS GARPAW*C*WAPALAPVIPVD AHSPP\GGAGHGPGH*GPRGSV LGLRLPAGCP\GPRQPHRPGQSG PQPSSPPGGALRSASR
19810	50178	A	19925	3	543	SDDQPEKPHFDSRSVIFELDSCN GSGKVCLVYKSGKPALAEDTEI WFLDRALYWHFLTDTFTAYYR LLITHLGLPQWQYAFT\SYGISP QAKGITKATCEWGEHIIPLGSM AINSISKLTQLTQSSMYSLPNAP TLADLEDDTHEGRKGTEGSQL KCEHQLPPPMSHVGGGQRESL ARKEK
19811	50179	A	19926	1	392	FLDRALYWHFLTDTFTAYY\RL LITHLGLPQWQYAFTSYGISPQ AKITYNIKMNRRKCVHWKLAV EPLQWELRSCVSAGMGTGPKQ KVSSMKPRSCSVCSRRQSNSMG TTVSQSFLSYGKNVLFFPVRCC

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19812	50180	A	19927	1	1081	RAMEEEASSPGLGCSKPHLEKL TLGITRILESSPGVTEVTIIEKPP AERHMISSWEQKNNCVMPEDV KNFYLMTNGFHMTWSVKLDE HIIPLGEALAINKHLKTDFSFTQ SSMLFTFLIAPTLGQTWEDDTH GSQWMIQPEKPHFGLFAVLIF* GWVS\CNGSG\KVCLV\YKSG\K PALAEGHWRFLFPGTELLYWH FLTDTFTAYYR\LLIT\HLGLPQ\ WAILPFTSYGISPQAKQW\FSM Y*TYSPYNTNLV/TQKETDSFCG IKLDPSKVF*GGKNKIVIPKKKG PVQPAGG\QKGPFRDPPVPSISSI FKSSSGLWGNPTREVSTPPSNSL PAPEWWFPCTDGPRGDLQFCV WTVGLFLVE
19813	50181	A	19928	1	2835	MDALMLALGALMLALGLGDP KSAQVSDPDGAEPGPGRATGT DPLVQIHWKLGISEALSIPGGRL YRDLWSLTPVCLHIPGIAHHGP FTLGRMDVVEVAGSWWAQER EDIIMKYEKGHRAGLPEDKGPK SFGSYNNNVDHLGIVHETELPP LTAREVKQIRREISRKSKWVKM LGEWDTYKNSRKLIDRAYQGIP MNIRGPMWSVLLNIEEIKLKNP GRYQVRSARAQPTGQAVSGAQ VSSWRERQDHPGELGVKI
19814	50182	A	19929	3	142	TISSIIRKARKP\QDLLNNYTPRS SPLRSSGRTRMYKGKNVRPGNS S
19815	50183	A	19930	904	1295	WALMNGSESRFFVSSSQGRSEL VPNS/NYAVDY*PLTAHAVSSG GTSPVLARLLREKLESL\LPLHL GQVAKYAGQLRGRVKQQFAT MGERRRFWEKLFVNDR/AGAV AGKQRSESHY*NDRTVNQRTA RPSR
19816	50184	B	19932	1	1050	
19817	50185	A	19933	303	384	

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19818	50186	A	19934	375	1161	EALESAPEG/RR*GSGTKTLSPS P/PAGSWVCRIPMGRGCRHGAE R/P/PGSQESSPSNGHGKLAGPSP YLGRFKSSS*T*QSPQTPAQGVS AS*GLGAAPVLRLQGPVPP\SHC GKSRPDPC*PSPGSPDPPGERES QQESQ*WPPVGELCTDPTGNPE RGGRHLQ\SHAPSGGGLSGFPS DSFPCSCYYGSTPVARKKRFAK CRGYIYDFVYELLSLKPPSQGV AEMPPPAVGQQG\QAEPRGIPQ SPAGGRVFFQDFYSLCLENTS
19819	50187	B	19935	62	346	
19820	50188	B	19936	1	1629	
19821	50189	A	19937	1	1218	
19822	50190	C	19938	718	1053	
19823	50191	A	19939	54	212	
19824	50192	A	19940	122	451	
19825	50193	A	19941	329	398	FFSYFRPSGCILPL*ELPEARCP
19826	50194	A	19942	92	346	VGSSPSRL*SLRGQVLNKN*S/I QLGCLHIVGNPI*NS*DVPWAG WSED*GRRWISSRSSSKDRGPV S*RSPPVPGLQHQMSHASM
19827	50195	A	19943	284	374	LKNHKRSEYALPHLN**PSTTK EV*M/DRS/SALSDDITL*KSFSW LILAQKSPPLSTLQPPLLPAREQ TLFDCNSPLPTQIL*NGPTLISLR *LSQDEPGKGLSQGNVIT
19828	50196	A	19944	1	1674	MAPPLSPFADSLFGLSPPAPRDK GDTFYPWTQNSGARHGLGRQP SLGVSSLQGRLSDHSPTFQRCQ TTQGRLPWSFTLSGKSCFSEEG AIPTPSVAESFQSSFSTDPSDLSP PPQPAHRQAELSPNSSSASTPPP YNPPTTSPPHTRSGLQFSSATSS SPPAQQFPLREVAGAEGIVNAH VPFSLSDLSQISQHLGSFSSDPT KYIQEFRYLTLSYNLTWSDLNV ILTSTLSPDERERVFPVSQSHAD NRRLHEP

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19829	50197	A	19945	1746	3501	ESDPSNSTTSMDRTLL/MSSIVP RLPSACRILPTGFTIPE*SCVHRT ASLIPPLPPGSRKYSPPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTSPDISHQQAAALLRTY LKNLSPYINSTPPIFGPLTTQTTI PVAAPLCISWQRPTGIPLGNLSP SRCSFTLHLRSPTTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCISLHPWLSSPCSSDSP PRPSSCLLIPSPENNSERLLVDT RRFLIHHENRTFPSTQLPHQSPL QPLTAAALAGSLGVWVQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAGISTSVMTFRSLSNDFS ASITDISQTLSVLQAQVDSLAA VVLQNRRGLDLLTAEKGGLCIF LNEECCFYLNQSGLVYDNIKKL KDRAQKLANQASNYAEPPWAL SNWMSWVLPIVSPLIPIFLLLLF GPCIFRLVSQFIQNRIQAITNHSI RQMFLLTSPQYHPLPQDLPSA
19830	50198	A	19946	1392	1676	GFCILHIVLEPWFSAPSAPLSTSL YWLF*LYILLNFFQSFQLLCLW FECPPVAQSNLIV*SLLLSARQS HSPSSFFPLLVRNCVPLEEERCS
19831	50199	B	19947	1	1500	
19832	50200	A	19948	107	691	TTMLLIQSLFGGLFTWTRMKFG AVARIGGHPLGDQSP\SSCSLLP EKDPPTTSGPQIDQPKKHLTDF KSGTPL*LYTHVSRVSDHAGTP ALVLHP\YGKSRFSGEGATQRQ YPIPQQALKGLMPAITRLLQHG LLKPINSPYHSPILPVLKPDKPY KLVQDL\PLSTKLFCLSTPWCQT HILFYPQYLPLQPIILF
19833	50201	B	19949	1	2628	
19834	50202	B	19950	1	585	
19835	50203	B	19951	178	462	
19836	50204	C	19952	1	825	

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19837	50205	A	19953	644	1795	RPSKSQTMLNSLSTALIISKIYFL PHT*HIYFLLPGSFCYTHSLLSLP QLPLFL/CLDLNAASHIIPDTTPD PHDCISLIHLTFTFPQISFFPVSHP DHTWFIDGSSTRPN\TTHQQRQ AML*YLPHLSLRLPLCLPPLPLS KPN*LP*LKPINSPYNSPILPVQK PDKSYRLVQDLRLINQIVLPIHP VVPNPYTLLSSIPSSTTHYSMLD LKDAFFTIPLHPSSQPLFAFTWT DPDTHQSQQLTWAVLPQGFRD SPHYFSQALSHDLLSFHPSASHL IQYIDDLLLCSPSFESSQQDTLL LLQCLFSKGYRVSPSKAQISSPS VTYLGIILHKNTHALPADRWPS CLRAAAAAALILVEALKITNYA QLTLYSSHNFQNLFSSSHLTHIL SAPRLLLLYSLFVESPTITIVPGL DLNAASHIIPDTTPDPHDCISLIH LTFTFPQISFFPVSHPDHTWFID GSSTRPNHHSPAKAGYAIVSST SIIEATALPPSTTSQQAELVTLT QALTLAKGLRINIYTDSKYAFHI LQHHAVIWAERGFLTTQGSSIIN ASLIKTLLKTTLLPKEAGVIHCK GHQKASDPIALGNAYADKVAR QAASSPTSVPHSQFFSFASVTPT YSPTETSTYQSLPTQGKWFLDQ GKYLLPASQAHSILSSFHNLFH VGYKPLDRLLEPLISFPSWKSIL KEITSQCSICYSTTPQGLFRPPPF PTHQARGFAPAQDWQIDFTHM
19838	50206	A	19954	52	641	RPSKSQTMLNSLSTALIISKIYFL PHT*HIYFLLPGSFCYTHSLLSLP QLPLFL/CLDLNAASHIIPDTTPD PHDCISLIHLTFTFPQISFFPVSHP DHTWFIDGSSTRPN\TTHQQRQ AML*YLPHLSLRLPLCLPPLPLS KPN*LP*LKPSLLQKDYASISILI LNMPFIFCSTMQSYGLKEVSSL HKGPPSLMPL
19839	50207	A	19955	3	380	TTPDPHDCISLIHLTFTPFPHISFF RVPHPYHIWFIDGSSTRPN\ATH QQRQAML*YLPHLSLRLLLCPP PLPLSKPN*LP*LKPSLLQKDYA SIFILTLNMPFISCTTMQEVSSLH KGPLSLIPL

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19840	50208	A	19956	154	485	TFIRTHFLTQPQPCPRHQPSR*L SSSPPAG*TG/IFARLLIFSCLLQI LNHM/QHTLAGQSVLVKNLTP QTLQPRWTGPYLVIYSTPT/VRP PAGSSPLGSPFQSKAVSISQPA
19841	50209	A	19957	158	416	ISGTCSNLLGEEVLEERLAAAV QAFGSSRVLEMWLGFVSQWRQ VIVTQKCIAVWLLPLYYCTP*R QG*LIPVVGFEGQILIFEVFS
19842	50210	C	19958	1	1755	
19843	50211	A	19959	2	394	
19844	50212	A	19960	710	1093	KEPTQHSFSYTHSLLSLPQLPLF L/CPDFNPASHIIPDTTPDPHDCI SLIHLTFTPFPHISFFPVSHPDHT WFTDGSSTRPN\ATHQQRQDM Q*YLPHLLLTLPLCPPPLPLSKP NQLP*LRPSLLQKG
19845	50213	C	19961	1	1287	
19846	50214	A	19962	1	1293	MEEPLGFKQTLVVAQQNPLWT SGGGGHSPSGSGHRGVCITTLP VPEGSSQKETPHVSEKLKEKNE SLPGNPENSSRSSERPPRRHSKA RDSDEENDPDDEDAVVNAVGC LGKNSGFLAPELQKYQKQIKDG TAGTPAISTTTTVEIRKSSVMTT GDHLLSGKKAQRPAPGHSSCPS TETEEEKGKRLLYWVVWQVA VNSASQLEAHNSENPVSLSCRI RERPGLWHGYRPSRSPLPHSLS GSYSLWALRTDTVCD
19847	50215	C	19963	1	846	
19848	50216	B	19964	377	1172	
19849	50217	A	19965	564	1163	FPKSIFFLPPDAYTFLFPWLLQL YSLFVESPTITHCSWPRLQSGLP HYSGYHT*PS*LYLSDPPDIHPIS AYFLLSCSSP*SRLIY*WQFHQA *SPHTSKGRLCYSTSH*PAS*NL SFPFHRGNVSSRK*LLSVPSAIL LLLRDYSGPLPSLHIKLRDLPPP RTGKSA\YSTCPESGN*NTSWSR *TLICQS
19850	50218	A	19966	1382	1778	PIGTNTECVVLFQPMETGHSSR VNMSGYK*PC/PPLFGVLSWQN CWRVYPFCLLFGGPLSVMDPE GSPSGC/SNSLGLGADSVTLSTG GVFQPNVRGLNCNGKIVMGRC PLEFVPIPATSPISRKKPERSTAF

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19851	50219	A	19967	239	737	RPSFKTPENSPTLVPTWTTLFYA LFFSYPHLPTSLIRPKYFNQIICF PDYSWSTATSHCCPSSQSK/CLL CV/SLTSPQYQPLPQDLPSA*SLP L*VPTPPLIPLEAALRNIAHSLSI PPPKNFRRSNTSTLFCFICLINIR RQECQASEPRPGHRIPCDLHVYI QMA
19852	50220	B	19968	1	1321	
19853	50221	A	19969	1	1069	
19854	50222	B	19970	758	6451	
19855	50223	A	19971	53	319	CSGSMPSSSSVSRPTSPFGSPLLS SPATSSSPKTPPTSATSGSSCPTT GL*MWTWSGFTGPVKAATWR WTSATYPRWSWRPRAPLCPP
19856	50224	A	19972	1427	2103	RPVHGHLHAVPVWRDSVRGLA PSSSPRVPGRDLIKQTPRLRARV VLSPFKTADAAHSHPGLTQPGR GRMKADISAATPGPFMCRVTPL ALGVSTEPSPARLVLNFVLFCF VLRRSLALSPRLEVLWLDLG\SL QPPPP\GFKQFSCLSLPSSW\DYR CMPPWAG\QFLEF*VEDGV*H\I GQADLELLTSGDPPASASQSAG ITGVSN\RAQPQVSECGHGVAL RRQ
19857	50225	A	19973	3	320	VRMVIIKKSENNRCWRKCGEIG MLLNCW*ECKLVQPVWKT/VD PAIPLLGIYPKDYISFYGKDTCT HMFIVALFTIAKTGNQPKCPSMI DWIKKMWHIYTMEYYAAI
19858	50226	A	19974	2	79	
19859	50227	A	19975	308	630	GREKAREQVDLTLFTIAKTWN QPKCPSVIDWIKKIW/HIYTMGY YAAIKKDEFVSFAGT\WMKL*T VSVEADPHIEGRFFRFKNYASK TPSLKLQRQSRPFQETSHPTGIE KRSPPNLQKATQPHIMSAKEYA FSRKMYGKTGRKKGEVKVRER KGKGAGRSDTIYNSKDLEPTQ MPISDRLDKENMDIYTMGYYA AIKKDEFVSFAGTMDEAVNQG YSSRARTRHWSMKKILLQLAR CLPKWPLSFVLESQGLGGVGS

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19860	50228	A	19976	2	508	KTTMRYYLTPVRMAIIKKSENN RCWRGCGETRMLLHCWFECKL VQLLWKT\W*FLKDVELKIPFD PAIPLLGVYPKDYKSCYYKDTC TRMFIAALFTIAKTWNQPKCPS VIDWIKKMWHIYTMEYYAAIK KDEFVSFAGTWMKLETIILSKL SQGQKTKHRMFSLISGS
19861	50229	A	19977	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL\DPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
19862	50230	B	19978	1	1899	
19863	50231	A	19979	1	2142	MIILIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
19864	50232	A	19980	1	5127	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19865	50233	A	19981	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
19866	50234	A	19982	1	1698	MELKAKAQELREECRSLRSRC NQLEESVSVMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLTGVHESDGENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKGWVTHK GKPIRLTVDLSAETLQARREWG PIFNILKEKNFQPRISYPAKLSFI SEGEIKSFTDKQMLTDFVTTRP ALQELLKEALNMERKNRDTHR LKIKGWRKIYQANGKQKKAGV AILVSDKTDFKPTKILKDKEGH YIIVKGLIQQEELTILNTYAPSTG APRFIKQVRSDLQRDLDSHTLII GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDIYRTLHPK STEYTFFSAPHHTYSKIDHIVGS KALLSKCKRTEIITNYLSDHSAI KLELRIKKLTQNHSTTWKLNNL LLNDYWVHNEMKAEIKMFFET NENKDTTYQNLWDTFKVVCTG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKTL/QKINESRS WFFERINKIDRPL
19867	50235	A	19983	1	3450	
19868	50236	B	19984	1	2265	

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19869	50237	A	19985	1	2526	MFFETNENEDTSYQNLRDTFKV VFRWKIIALNAHKRKQERSKID TLTSKLKELEKQQQTNSKASRR HEITNIRAELKEIETQKTLQKIN ESVNWFFEKIIKIDRLLARLIKK KREKNQIDSIKNDIEDITTDPVE TQTTVREYFKHLYANKLENLEE MDKFLDTYILPSLSQEEVEPLN RPITGSEIEAIINSLPTKKSPGPD RFTAKFYQRITNTEKCLKELME/ PESQSSRTT*RMQKPQESMRST GRKGFSDGR*NE*NE*RGEWN QVGKHSAGYYPGELPQTSKAG QHSDSGNTENATKILLEKSNSK TYNCQIHQS*NEGKNVKGSQRE RNTNYHQRILQTPLRK*TRKS\K EMDKFLDTYTLPRLNEEEVESL NTPITGSEIVAIINSLPTKKSPGP DGFTAELYQRQTESQIMSELPF TIASKRIKYVGIRLIRDVKDLFK ENYKPLLSEIKEDTNKWKNIPC SWVGRINIVKMAILPKVIYRFN AIPIKLPMPFFTELEKTTLNFIW NQKRAHIANSILSQKNKAGGIT LPDFKLYYKATVTKTAWYWY QNREIDEWNTTEPSEIMPHIYN YLIFDKPEKNKQWEKDSLFNK WCWENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTIKTLE ENLGNTIQDIGIGDDFMSKTPK AMATKAKIDRWDLIKLKSFCT AKETTIRVNRQPTKWEKIFATY
19870	50238	A	19986	1	3723	
19871	50239	A	19987	1	1023	
19872	50240	B	19988	91	1596	
19873	50241	B	19989	1	3171	
19874	50242	A	19990	1	2952	MLLNQGRKLPRVFAEETLKFK GTSNKPQTLEQISTSIIAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLFEQTLNYLQEFLFTP QWHLECQQERTVHSPGKAAEA REPSVIDRHLIQESSNWHLVGA ALGQSFQRKEQAAIFAVLQPLL VIPRQTGSGVDLQKTPTDLQQR GLIVRRKTNKQKGIVHNSTTRE QNWTENEFDKLTEGGFKRWVI TNSSELKEHVLTQCKEDKNLEK SAIKLELRIKNLIQN
19875	50243	A	19991	1	1797	

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19876	50244	A	19992	1	2367	MVKGSIQQEELTNLNMYAPNT GAPRFIKQVLSDLQRDLDSHTLI MGDFNTQLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYISDHS AIKLELRIKNLTQNCSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKVVC RGKFIALNAHKRKQERSKTDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAIKNDKGDITTDPTEIQS TIREYYKHLYTNKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGAEIVAII/NNLPTKKSPGPDGF TAEFYQRK\EGILPNSFYEASIILI PKPDRDTTKKENFRPISLMNID AKILNKILANRIQQHITKLIHHD QVGFIPGMQGWFNIRKSIRVIQ HINRTKDKNYMIISIDAEKAFD KIKQCFMLKTLNKLGIDGTYFK IIRAIYDKPTANIILNGQKLEAFP LKTGTREGCPLSPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLGIQLTRDRKDLFKENYKP LLKEIKEDTNKWKNIPCSWVEK INIVKMAILPKVIYRFNAIPIKLP
19877	50245	A	19993	2	2910	WRKIYQANGK/QKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIHQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTIIMGDFN TPLSTLDRSMRQKVNKDTQEF NSALHQADLIDIYRTLHPKSTE YTFFSAPYHTYSKIDHIVQSKAL LSKCKRSEIITNCLSDHSAIKLD LRIKKLTQNHSTTWKLNNLLLN NYWVHNEMKAEIKMFFETNEN KDTTYQNLWDTFKAVCRGIFIA LNAHKRKQETS
19878	50246	A	19994	1	4729	
19879	50247	A	19995	1	1566	
19880	50248	B	19996	1	2796	
19881	50249	B	19997	127	2479	
19882	50250	B	19998	1	2907	

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19883	50251	A	19999	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
19884	50252	A	20000	1	2052	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDKTYQNLWDAFNAV CRGKFVALNAHKRKQEGSKID TLTSQLKELEKQEQTHSKASRR QEITKVRAELKEIETQKTLQKIN ESRS\ARLIKKKREKNQI/DAIKN DKRDITIDPTEIQTTIREYYKHL YANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITGSEIVAIIN SLPTKKSPGPEGFTAEFYQRYK EELVPFLLKLFQSTEKEGILPNS FYEASIILIPKPGRDTTKKENFRP ISLMNIDAKILNKILAKRIQQHI QKLIHHDQVGFIPGMQGWFNIC KSINVIQHINRTKDKNHMIISID AEKVFDKIQQRFMLKTLNKLV LEVLARAVRQEKKIKGIQLGKE ELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSEYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDVNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTSFTELEKTTFKFIWNH KGARIAKSILSQKNKAGGITLPD FKLYYKATVTKTAWY

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19885	50253	A	20001	1	2314	MDKFLDTYTLPRLNQEEVESLN RSITGSEIVAILNSLPTKKSPGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTSKKENFRPIPLMNIDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHTNRA KDKNHMIISIDAEKAFDKIQQLF MLKTLNKLGIDGMYLKIRRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAIR QEKEIKGIQLGKEEVKLSLFAD DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTLASKRIKYLG IQLTRDVKDLFKENYKPLLNEI KEDTNKWKNIPCSWVGRINIVK MAILPKVIYRLNAIPIKLPMPFF TELEKTTLKFIWNQKRARVAKS ILSQKNKAGGITLPDFKLYYKAI VTKTAWYWYQNRDIDQWNRT EPSEITPHINNYLIFDKPDKNKQ WGKDSLFNKWCWENGLAICRK LKLDPFLTPYTKINSRWIKDLN VRPKTRKTLEENLGITIQDIGMG KDFMSKTPKAMATKDKIDKW DLIKLKSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAAKKHMKKCSSSLA IREMQIKTTMRYHLTPVRMAII KKSGNN\RLFTVAKTWIQPKCA

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19886	50254	A	20002	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD

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19887	50255	A	20003	1	2502	MTELTGIQQPQIVLFEHKGHKL VQGSSSDAGKVNRIYQHYEAS DKFNYTTGLAWKTAPEQTGKT VRKQQIKLNVKKMESRSKMQE HSSSPPMEQSWRENDFDELREE AFRRSNYSELQEEIQTKGQEVK NFEKTLDEYITRITNTEKCLKEL MELKAKARELREECRSLRSRCD QLEERVSVMEDEMNEMKREG KFREKRIKRNEQSLQEKWDYV KTPNLRLIGVPESDGENGTKLE NTLQDIIQENLPNLVRQANIQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITGS EIVAIINSLPTKKSP/GPVGFTAE FCQRK\EGILSISFCEASIILIPKL GRDTTKKENFRPISLMTIDTKIF NKILANQIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVIQHINR TKDKNHMIISIDAEKAFDKIQQL FMLKTLNKLGIDGTYFKIIRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLAGAIR QEKEIKGVQLGKEEVKLSLFAD DMIVYLENHIVSAQNLLKLISNF SKVSGYKINVQKSLAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWVGRINIVK MAILSKVIYRFNAIPINLPITVFT
19888	50256	B	20004	1	2115	
19889	50257	A	20005	1	2382	
19890	50258	A	20006	1	2742	
19891	50259	A	20007	1	2250	
19892	50260	A	20008	1	2982	
19893	50261	A	20009	1	4791	
19894	50262	A	20010	1	2499	
19895	50263	A	20011	1	3259	
19896	50264	A	20012	1	3654	
19897	50265	A	20013	1	2391	

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19898	50266	A	20014	326	1158	LWICEVMVKQRSRILKICLQKQ WQKTLAMWLKPCMGTFLLQL C*LDIAWV/RAIAVHTASSNLVP SLLGLCMIDVVEGTAMDALNS MQNFLRGRPKTFKSLENAIEWS VKSGQIRNLESARVSMVGQVK QCEGITSPEGSKSIVEGIIEEEEE DEEGSESISKRKKEDDMETKKD HPYTWRIELAKTEKYWDGWFR GLSNLFLSCPIPKLLLLAGVDRL DKDLTIGQMQGKFQMQVLPQC GHAVHEDAPDKVAEAVATFLI RHRFAEPIGGFQCVFPGC
19899	50267	A	20015	1	2860	
19900	50268	A	20016	1	2956	
19901	50269	A	20017	1	3359	MNNSIKEKVKLSLTKWEMQTK PNNNTVDLKDAQEVNLTSTDY RKQHVMLPTEINSDDSLLKIGVI RLANWIKSQDPSVCCNQETHLT CRDTHRLKIKGWRKIYQANGK QKKAGVAILVSDKTDFKPTKIK RDKEGHYIMVKGSIQQEELTIL NTYAPNTGAPRFIKQVLSDLQR DLDSYTLIMGDFNTPLSTLDRS TRQKVNKDTQELNSALHQVDL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHILGSKALLS
19902	50270	A	20018	3	3130	
19903	50271	B	20019	8	2398	
19904	50272	A	20020	3	3398	SNSHITILTLNVNGLNAPIKRHR LANWIK\SQDP\SVSCIQETHLTC RDTHRLKIKGWRKIYQANGKQ KKST\VAILVSDKTDFKPTKIKR DKEGHYIMVKG*IQ*EELTILNI YAPNTGAPRFIKQVLRDLQRDL DSHPIIMGDFNTPLSTLDRSMR QKVNKDIQDLNSALHQADLTDI YRTLHPKSTEYTFFSPPHHTYSK TDHIVGSKALVSKCKRTEIITNC LSDHSAIKLELRIKKLTQNRSTT WKLNNL
19905	50273	B	20021	483	2210	

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19906	50274	A	20022	1	5316	MVKGSIHQEELTILNIYAPNTG APRFIKQVLSDLQRDLDFHTLI MGDFNTPLSTMDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFYSAPHHTYSKIDHILG SKALPSKCKRTDIITNYLSDHSA IKLELRIKNLTQNHSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYENLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAEQINKIDR
19907	50275	A	20023	2	2712	WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPTFI QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSDHSAIKLELM IKNLTQNHSTIWKLNNLLLNDY WVHKEMKAEIKMFFETNENKD TTYQNLWDTFKAVCRGKFIAL NAHKRKQERSKIDTLTSQLKEL EKQEQTLSKASRRQEITKIRAEL KEIETQKTLQKINESRSRFFERIN KIDR*\TLARVIKKKGEKNQIDTI KNDKGDITTDPTEIQTTIRESYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPITGSEIVAI VNSLPTKKSPGPDGFTAEFYQR YKEELVPFLLKLLQSIEKEGILP HSFYEASIILIPKPGRDTTKK\EN FRPISLMNIDAKILNKILANQIQ QHIKKLIHHDQVGFIPGMQGWF NTCKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQPFMLKTLNK LVLEVLARAIRQEKEIKGIQLGK EEVKLSLFADDMIVDLENPIVS AQNLLKLISNFSKVSGYKINVQ KSQAFLYNNNRQTESQIMSELA FTIASKRIKYLGIQLTRDVKDLF NENYKPLLNEIQEDTNKWKNIP CSWVGRINIVKMAILPKVIYRF

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19908	50276	A	20024	1	4461	MVASRSSRVGVFYGGQNSVDG VSRRSDGSLNELCLYRPPTGAY LAYDTLDVLPSGQFTVNTPPID VNGKSLLALLWEHTSLLTSMG GGRWAMQPLGQLGQLEHLGD RRDQVLDRSGRSRRLDAAQHL RHRPDRRPQGMVGVLTNQKEP RTRWIHSRILPEVQGGTGTVPSE TIPIDRKEGILPNLFDEASIILIPK RGRDTTKKENFRPISLMNIDAKI LNKILANRNQQHIKKLIHHDQV GFIPGMQGWFNICK
19909	50277	B	20025	1183	4247	
19910	50278	A	20026	1	2671	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTPWKLN NLLLNDYWVHNEMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDTIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEFY/PESYL*QTHSQYHTEW AKTGSIPFENWHKTGMPSLTAP IQHSVGSSGQGNQAGEGNKGY SIRKRGSQIVPVCR*HDCLSRKP HRLSPKSP*ADKQLQQSLRIQN QCTKITSILIHQKQTNREPTHE* TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQRNKRGHKQME EHSMLMGRKNQYRENGHTAQ GNLQIQCHPLQATNDFLHRIGK NYFKVHMEPKKSPHRQVNPKP KEQSWRHHTT*LQTILQGYSNQ NS\MVLVPKQRYRSMEQNRAL RNNAAYLHYSD\L*QT*EKQA WGKGIP\IYKM\AL\GKLAS\PM*

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19911	50279	A	20027	1	3159	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQ\KISES WSWFFEKINKIDRPQARLIKKK REKNQIDTIKND
19912	50280	A	20028	2	3767	HRLANWIKSQDPSVCCIQEAYL TCRDTHRLKIKGWRKIYQANG KQKKAGVAILVSDKTDFKPTKI KRDKEGLYIMVKGSIPREELTIL NIYAPNPEAPRFTKQVLSDLQR DVDSHTIILGDFNTPLSALDRSM RQKVNKDTQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHHTY SKIDHRVGSKALLSKCKRSEIIT NCLSDHSAIKLELRIKKLTQNCS TTWKLNNLLLNDYWVHNEMK AEIKMFFETNEN
19913	50281	A	20029	3311	9648	KLYVCITRITNAEKYLKELMEL KAKAQELCEECRSLRSRHDQLE ERVSVMEDQMNEMKQEEKFRE KRRKRNEQSLQEIWDYVKRPN LRLIGVPESDGENGTKLENTLQ DIIQKNFPNLARQANIYIQEIQEI QRTPQRYSPRRATPRHIIVRFTK VDMKEKMLRAVREKGFKPTKI RRDKEGHYIMVKGSIQQEELTI LNIYAPNTGGPRFIKQVLSDLQ RDLDSHTIIMGDFNTPLSTLDRS MRQKINKDIQEL
19914	50282	A	20030	2031	6332	QDSNSHITILTLNI\NGLNAPI*R HD\RNCNWIKSQDPSVCCIQET HLTCRDTHRLKIKGWRKIYQA NGKQKKKAGVAI\LVSDKTDFN PTKIKRDKEGHYIMVKGSIQQE ELTILNIYAP\NTGAPRFIKQVLS DLQRDLDSHTLI\MGD\FNTPLS TLDRSRRQKVNKDTQELNSAL HQADL\IDIYRTLHP\KSTEYTFF SAPHHTYSKIDHIVGSKALLSK CKRTGIITNYLSDHSAIKLELRI KNLTQSR
19915	50283	A	20031	2	178	
19916	50284	C	20032	88	228	

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19917	50285	A	20033	3	382	VDRTIMSDSLVVCEVDPELTEK LRKFRFRKETDNAAIIMKVDKD RQMVVLEEEFQ\FVVYSYKYV HDDGRVSYPLCFIFSSPVGCKPE QQMMYAGSKTRLVQTAELTK VQTGMWLQSVRERWCGSWV
19918	50286	A	20034	89	633	KTAELRKEEACGQNNHALPGS LRQSDSLVVCEVDPELTEKLRK FRFRKETDNAAIIMKVDKD/RG QMVVLEEEF\QNISPQREL\KMG FPRRDKPR\FVVYS\YKYVHD\D G\RVSYP\LCFIFPPRPVGCKPE\Q QMMY\AGS\KNRLV\QTAELTK GVPKSRTT*LTSLRPWL\QEKLS FLSLISGAGD
19919	50287	A	20035	78	638	WLDLTWKESSADSQLFLEKMD HSHHMGMSYMDSNSTMQPSH HHPTTSASHSHGGGDSSMMM MPMTFYFGFKNVELLFSGLVIN TAGEMAGAFVAVFLL\AMFYE GLKIARESLLRKSQVSIRYNSMP VP\GQNG\TILYGRTHKTVG\QQ\ MLSFPHLLQTVLHIIQV\VISYFL MLIFMTYNGYLCIAVA
19920	50288	A	20036	1	849	MSQKMENLIGNAHISAYEIIKEF QKEQHQAGLPGTTVPCSCQVY KCSKRPERVAREGPSEDLEPLP QTVRKCGQGCTLHGAGGSQGQ VGARPFGIGGVEALWFLASPSY WAPLIPQCQLGKLLVVRLVQL QARRELAPMLAPGAACPMVAT ACLTVQWPDPMLTHTPLTIPHL TCSLLGGNVELLFSSLVINTAGE MAGAFVAVIILAVFYEGL\IAQE SLL*PNGTILM*THKTVGQQML SFPHLLQTVLHIIQVVISYLLMLI FMTYNGSSELLFRGERPR
19921	50289	B	20037	308	568	
19922	50290	A	20038	394	528	
19923	50291	A	20039	186	856	TWGKGDILRRPRRKMSSY/SHF FVQTCRGG\HKKKHPRLLQVN\ FSEF\SKEVLQRGWRPMSCLKR KGKILKIWAKAGQGPFLERELK TLYPLPKGEDQKKKFKDPNCTP RGPPS\AFFPLLALEYPPQKSKG EHPWPVPLVDVAEENWETMW ELTLLQMDKQP\YEKKA\AKLK EKYEKDIACISSLKGKPDAAKK RELSRPEKSKKKKEEEEDEEDE EDEEEEEDE*DEEDEEEEEDE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19924	50292	A	20040	1	413	GAMRGDRGRGRGGRFGSRGGP GGGFRPFVPHIPFDFYLCEMAFP RVKPAPDETSFSEALLKRNQDL APNSAEQASILSLVTKINNGNE KL\VGSPGTLKAHIEKFTRGIPY KRGTVSRGHNVADLGGKLKIL\ PPLEAV
19925	50293	A	20041	70	1451	GAMRGDRGRGRGGRFGSRGGP GGGFKPFVPHIPSDFYLCEMAF\ PRVKPAPDETSFS*GLA*RRNQ D\LAPNSAEQ\ASILSL\VTKI\NN V\IDNLTCGSQGHFEVAKLEEV\ RQVGDPIKRGTMTTGHNVA*/L WVVIPQEFWQRLEA\VACPGGN KVVESLR/SHQDPSESFKPCLTN E\TGFEISSSDATVKILITT\VPP\N LRKLDPELHLDIKVLQSALAAI RHARWFEENASQSTVKVLIRLL KDLRIRFPG\FEPLTPW\ILDLLG\ HY\AVMNNPTRQPLGLKRWHN RALAWQISGLAGTVSCQG\SVG YSIDPCESWQL*ELHTVMTLEQ Q\DMV\CYTAQ\TFVRILP\HGGF RKILG\QEVDASYLASEIST\WD GVIVTPFRKRLYEKP\PEK\KEG EEEEENTEEPTSRRGRRK\HGN\ SGVTIPLPLLFPNPRGKTGALSC PAYWALHGDRHFPWDREDSRK
19926	50294	A	20042	253	379	
19927	50295	A	20043	284	1062	APRNYLPQRATASVRRQQISFS NEHTPHQSLHEIPNVRQRHSGL MKLNTMGAMTTSTTSAVANH* PSNKRTPLVSV/MQSASPEQRQ AVRERMQTNPKIQQRREAARE RIQSASPEQRQAVREKMQTNPQ NQQRRDAARERIQSASPEQRQV FKEKVQQRPLNQQQRDNARQR VQSASPEQRQVFREKVQESRPQ RLNDSNHTVRLNNEQRSAVCE RLSERGARRLESLYGRHMQAN PEPPKKNNDKSKKISRKPLAAK

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19928	50296	A	20044	1	2269	MSPDIPQVSPEVGLYPVANHSSI VVPTCHSLSEEDTEAQRNHELD TVKALREDAQVLKIPNQSPKDT LVTALQLAQKGTKAAAIRLGA KVGQKQSRQAKSSPALVVPGL LSFPRARFFEWQSPGLPNTAAM ENGTGPYGEERPREVQETTVTE GAAKIAFPSANEVFYNPVQEFN RDLTCAVITEFARIQLGAKGIQI KVPGEKDTQKVVVDLSEQEEE KVELKESENLASGDQPRTAAV GEICEEGLHVLEGLAASGLRSIR FALEVPGLRSVVANDASTRAV DLIRRNVQLNDVAHLVQPSQA DARMLMYQHQRVSERFDVIDL DPYGSPATFLDAAVQAVSEGG LLCVTCTDMAVLAGNSGETCY SKYGAMALKSRACHEMALRIV LHSLDLRANCYQRFVVPLLSIS ADFYVRVFVRVFTGQAKVKAS ASKQALVFQCVGCGAFHLQRL GKASGVPSGRAKFSAACGPPVT PECEHCGQRHQLGGPMWAEPI HDLDFVGRVLEAVSANPGRFH TSERIRGVLSVITEELPDVPLYY TLDQLSSTIHCNTPSLLQLRSAL LHADFRVSLSHACKNAVKTDA PASALWDIMRCWEKECPVKRE RLSETSPAFRI\LSVEPRLQANFT \IRED\ANPSSRQRGLKRFQA\NP EA\NWGPRPRSRP\GGKAADEA MEER\RRLLQNKRKEPPEDV\A
19929	50297	A	20045	1578	2356	PLRRWACNHKLRQNAHQLSSTI HCNTPSLLQLR\SALLHADFR\V SLSHACK\NAVKTDAPASALW\ DIMRCWEKECPVKRERLSETSP AFRILSVEPRLQANFT\IREDANP SSRQRGLKRFQANPEANWGPR PRARP/GVSGGKVGVGLSQGKK G*RADGVPPTPSPSHRGKAADE AMEERRRLLQNKRKEPP\EDVA QRAARLKTFPCKRFKEGTCQRG DQCCYSHSPPTPRVSADAAPDC PETSNQTPPGPGAAAGPGID

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19930	50298	A	20046	1	791	MGPSSIHHSSQHATAPQILPKVR AGPRSSGCRISECRREEKPPKGR RGLKDATRPGVNWGPDGGVQS GAGAQPWSLTPLPPGSVSPAGR AQRRSMRAAAAQERSPGRRRL GKEPLIRESWTRSAPWRCLSQD AGRAGSQVCGSSPQTRGAAAE KVAVTGAKSCSGRGKKAAAAR AKSRGGGGRKTQKAAAAKSRG C/AGQRSPKSRGSRG*IPRGRGQ KAAVAGAESNGGGGKKSRRRR HKAAKTRSSGGKNPWRQKAAS AGAK
19931	50299	C	20047	76	327	
19932	50300	A	20048	336	814	ANFSLEDPSCSPPPRLLAGSFVD SPQSLSCMRSKNPLLGSGSGPLS PTYIL*ATTPHFLLPQPLITTSPSS PSPPSPPLPPPPPSFSSSYSSSSFF E/NRVPLCCPCFGSAIRKPSPSVS TKARPQGETGRSLALLFLPQRP SSSLHRSDTLYRDCVHRI
19933	50301	A	20049	1	310	
19934	50302	A	20050	1	1482	
19935	50303	A	20051	3	2455	
19936	50304	A	20052	3	1441	

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19937	50305	A	20053	1	2322	MAEGKGEAGTFFTGQQDRLLF VFFIITIVVGLFRCSVFSSSSSSSS LSSSSSSSSSSLSSSFLHLFFIFIF VFFVFIFFVFIFVFVFAFFFIFFVF VVFFVFFFFVLLVEILMRPTISIR GQKLKISDEMSKDCLSILYNTC VCTEGVTKRLAEKNDFVIFLFT LMTSKKTFLQTATLIEDILGVK KEMIRLDEVPNLSSLVSNFDQQ QLANFCRILAVTISEMDTGNDD KHTLLAKNAQQKKSLSLGPSA AEINQAALLSIPGFVERLCKLAT RKVSESTGTASFLQELEEWYT WLDNALVLDALMRVANEESEH NQASIVFPPPGASEENG\LAHTS ART\QLPQSMKIMHEIMYKLEV LYVLCVLLMGRQRNQVHRMIA EFKLIP\G\LNNLFDKLIWRKHS ASALVLHGHNHY\CDCSPDITL\ KIQFLRLLQSFSDHHENKYLLL NNQELNELSAISLKANIPEVEAV LNTDRSLVCDGKRGLLTRLLQ VMKKEPAESSFRFWQARAVEE FPSRGTTSYADQMFLLKR\GLL EHILYCIVDS\ECKSRDVLQSYF DL\LGEL\MKFNVDAFKRFNKYI NTDAKFQVFLK\QI\NSSLVDSN MLVRCVTLSLDRFENQVDMKV AEVLSECRLLAYISQ\VPTQMSF LFRLINIIHVQTLTQENVSCLNT\ SLVILML\ARRKERLPL\YLRLL\ QR\MEHSKKYPGLL\LNNFHNL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19938	50306	A	20054	237	2033	TSPTPLPLPATMPKTISVRVTTM DAEL\EFAIQPNTTGKQLFDQV VKTIWLEGKFGFFGLQNQDT\K GFST\WLKLNRKVD*PRNVRKE \SPLLFK\FRAKFYP\EDVSEELIQ DITQRLF\FLQVKEGILNDDIYCP \PETAVLLASYAVQSKYGDFNK EVHKSGYLAGDKLLPQRVLEQ HKLNRD\QWEERIQVW\HEEHR GML/RGEDAVLEISERLLQDLE MYGVNYFSI\KNKKGSELWLG VDALGLNIYEQNDRLTPKIGFP W\SEIRNISFNDKKF\VIKPIDKK APDFVFYAPRLRINKRILALCM GNHELYMRRRKPDTIEVQQMK AQAREEKHQKQMERAMLENE RKKREMAEKEKEKIEREKEEL MERLKQIEEQTKKAQQEL\EEQ TPRAPGTLSQERKRAQSEAEKL AKERQEAEEAKEALLQASRDQ KKTQEQLALEMAELTARISQLE MARQKKESEAVEWQQKAQMV QEDLEKTRAELKTAMSTPHVA EPAENEQDEQDENGAEAS\ADL RA*S\MAKDRSEEERTTE\AEKN ERVQKHLKALTSELANARDES KKTANDMIHAENMRLGRDKY KTLRQIRQGNTKQRIDEFESM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19939	50307	A	20055	2	2230	PRVRLGAHGCPPGPRRCGCCW ANGLRSSERCVLESLRPCVQSA TRGLRCGCDSAANLDTMAKPP QGAGDRGSIHDFPGFDPNQDAE ALYTAMKGFGSDKEAILDIITSR SNRQRQEGCHSYK\SLYGK\DLI ADLK\YELTGKF\ERLIVRLMRP PAYCDAKEIK\DAISG\IGTDEK\ CLIEILASRTNEQMHQLVKRITK MPTERDLEADIIGDTSGHFQKM LVVLLQGTREEDDVVSEDLVQ QDVQDLYEAGELKWGTDEAQF IYILGNRSKQHLRLVFDEYLKT TGKPIEASIRGELSGDFEKLMLA VVKCIRSTPEYFAERLFKAMKG LG\TRDNTLIRIMVSRSELDMLD IREIFRTKY*/EKSLYSMD/IKND TSG/QSYKKTLLKLSGGDDDAA DQFFPKAAQVAYQMWELSAV ARVELKGTV\RPANDF\NP\DAD AKALR\KAMKGLGTDEDTIIDII THRSNVQRQQIRQTFKSHFGRD LMTDLKSEISGDLARLILGLMM PPAHYDAKQLKKAMEGAGTDE KALIE\ILATRTNAEIRAINEAYK \EDYHKSLEDALSSDTSGHFRRI LISLATGHREEGGENLDQARED AQVAAEILEIADTPSGDKTSLET RFMTILCTR\SYPHVRRVIQEFIR LTNYDVEHTIKK\EM\SGDIRDA F\VAIVQ\SAKTKPLFFPDK\LYK SMKG\AGTDEKTLTRIM\VSR\G
19940	50308	A	20056	3	368	
19941	50309	A	20057	1	936	MMKCEEQKEEEEETVRMFSAA SQPLDPDGTLFRLRFTAMVWW AITFPVFGFFFCIIWSLVFHFEYT VATDCGVSASSPAPGSGPG\PN YLPSVSSAIGGE\VPQRYVWRFC IGLHSAPRFLVA\FAYWNHYLS CTSPCSCYRPLCRLNFGLNVVE NLALLVLTYVSSSEDFTIHENAF IVFIASSLGHMLLTCILWRLTKK HTVSQEVRSIPSGGSKAAQKKI KDICPQDSGNGEDRKSYSWKQ RLFIINFISFFSALAVYFRHNMY CEAGVYTIFAILEYTVVLTNMA FHMTAWWDFGNKELLITSQPE

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19942	50310	A	20058	119	930	ESLFPSLAFLSPSKPLFSHPPSFH LSNKQDTSPCSCVLSSPFSLRTE ASIGVPGIKMDGGNAQEHGHFL RLPQVPNYLPSVSSAIAREVPQR YVWRFCIGLHSAPRFLVAFAY WNHYLSCTSPCSCYRPLCRLNF GLNVVENLALLVLTYVSSSEDF /TWVPG*GRSGEVFPEGTGLPLP HSDLPTSWCGHSLQCGSQSSFP PAIHENAFIVFIASSLGHMLLTCI LWRLTKKHTVSQEVRSIPSGGS KAAQKKIKDICPQDSGNGEVGT EF
19943	50311	A	20059	3	206	
19944	50312	B	20060	80	304	
19945	50313	A	20061	1	2111	MAATGTAAAAATGRLLLLLLV GLTAPALALAGYIEALAANAGT GFAVAEPQIAMFCGKLNMHVN IQTGKWEPDPTGTKSCFETKEE VLQYCQEMYPELQITNVMEAN QRVSIDNWCRRDKKQCKSRFV TPFKCLVGEFVSDVLLVPEKCQ FFHKERMEVCENHQHWHTVV KEACLTQGMTLYSYGMLLPCG VDQFHGTEYVCCPQTKIIGSVS KEEEEEDEEEEEEDEEEDYDV YKSEFPTEADLEDFTEAAVDED DEDEEEGEEVVEDRDYYYDTF KGDDYNEENPTEPGSDGTMSD KEITHDVKVPPTPLPTNDVDVY FETSADDNEHARFQKAKEQLEI RHRNRMDRVKKEWEEAELQA KNLPKAERQTLIQHFQAMVKA LEKEAASEKQQLVETHLARVE AMLNDRRRMALENYLAALQS DPPRPHRILQALRRYVRAENKD RLHTIRHYQHVLAVDPEKAA\Q MK\SQVMTHL\HVIEERRNQSLS LLYKVPYVA\QE\IQEEIDDVLQ EQRADMDQFTASISE\TPVDVR V\SSDESEEIPP\FHPFHPFPAPT* ERRILGVGRAGWGGLIGAEEK VINSK\NKVDE\NMVH*TRLLD VKEMIFNAERVGG\LEEERESV GPLREDFSL\SSSALIGLLVIAVA IAT\VIVISLVMLRKRQYGTI\SH GIVE/VVDPMLTPEERHLNKMQ

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19946	50314	A	20062	61	2634	SQPAEGKWSTGNAATATAGVL LLPAACGA*TAPALAL\AGYIEA LAANAGTGFAVAEPSNSPMFC GKLNMPCETFQTGK\WEP\DPN QAPKSCF*NQKEEVSSSYF\QEM YPRAYRSQNVMEAKPAGLRID N\WC\RRDKKQ\CKSRFCYTFSS CLVG*IL*SDVPAKFPEKVPSFF HK\ERMEVCE\NHQ\HW\HTVSQ KKAMS*PPGK*PLIIANGMPASP CGGRTSFHGTE\YVC*PSAQRLL GSCV/TKEEEEEEE\EKEEEEDE KGD\YAVYKGNFLL*ADLEDST EA\AVDEDDEDEREGEDVVEDR EYYYDTFKGDDYNEENPN\DPG SAATMSD\KEITHD\VKAVCSQE A\MTGPCRAVMPLWYFYLSKG KCVRFIYGGCGGNRNNF*SEDY CMAVCKAMIPPTPLSTNDDDVF F*TSKDDNEHARFHKAKEHVVI RPRNRMDRLK*EW*YAQL\QLK \NLPKAERQ\TLIQHF\QA\MVKA LEKEAA\SEKQQLVET/HTLARV EAMLND\RCLMALENY\LAALQ SDP\PRPHR\ILQALRRYVRAEN KDRLHTIRHYQHVLAVDPEKA AQM\KSQVM\THL\HVIEERRNQ SLSLLYKVPYVAQEIQEEIDELL QEQRADMDQ\FTASISE\TPVDV \RVS\SEGRGEIPPFHPFHPFPALP ENEDTQPV\LYHPMKKGSGVGE QDGGLIVAEEK\VINSK\NKVDE
19947	50315	A	20063	734	1049	CCPPGGTGRCLGTCGYHN/CGC SI*SSDLPQR/CCVSGRR*TFWM VWSACVCASGCLPGGNRCCCP VSLSPERIAVLGGLLPRKPPCRV VGERRSVLTLQATSQCPR
19948	50316	A	20064	6	1174	
19949	50317	A	20065	285	567	SRRRSSSYERSGSYSGRSPSPYG RRRSSSPFLSKRSLSRSPLPSRKS MKSRSRSPAYSRHSSSHSKKKR SSSRSRHSSISPVRLPLNSSLGAE LSRKKKERAAAAAAAKMDGK ESSYERSGSYSGRSPSPYGRRRS SSPFLSKRSLSRSPLPSRKSMKS RSRSPAYSRHSSSHSKKKRSSSR SRHSSISPVRLPLNSSLGAELSR KKKERAAAAAAAKMDGKESK GSPVFLPRKENSSVEAKDSGLE SKKLPRSV

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19950	50318	A	20066	214	805	LGLQAANDLHLEYAMGKRYFC DYCDRSFQDNLHNRKKHLNGL QHLKAKKVWYDMFRDAAAIL LDEQNKRPCRKFLL\TGQRDFG SN\CRFS\HMSER\DLKEL\SIQVE EGRGEPREWLL\DAPELP\EGHL GGLGLEERRAKRLELQPQVSQ G*NPFRTT/VSFQ*PRRVGQPSS GSLPPNSCGHPPPGGLALLQPR V\QWG
19951	50319	A	20067	2	418	
19952	50320	A	20068	1	1134	ATTARRRGAPGTPSLAAEGNGL SARVDEGVEEFFSKRLIQQDRL WAPEEDPATEGGATPVPRTLRK KLGTLFAFKKPRSTRGPRTDLE TSPGAAPRTRKTTFGDLLRPPT RPSRGEELGGAEGDTSSPDPAG RSRP\PTQEIARPTR*YCCLPRRR QRWVPDPTSGGPWSGEKQNWL HPLNSGYK*CCRG*ASAEAAGV PKARGSKAKMARSRKLAQMV TLWTVPRRPLPSRSSPAPT/PVS ADPSCRPGPGSQGPESATWKTL GQQLNAELRSRGWGQQDGPGP PSPGQSPSPCRTSPSPDSLGLPED PCLGPRNEERPLRLQRSPVLKR RPKLEAPPSPSLGSGLGTEPLPP QPTEPSSPERSPPSPATDQRGGG
19953	50321	A	20069	3	206	
19954	50322	A	20070	3	349	
19955	50323	A	20071	226	610	
19956	50324	B	20072	18	1306	

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19957	50325	A	20073	3	1665	LRPQGREGGDWEGGRSPFSLPY GSLRGRVVSTAQFRVPMPSASA SRKSQEKPREIMDAAEDYAKER YGISSMIQSQEKPDRVLVRVRD LTIQKADEVVWVRARVHTSRA KGKQCFLILRQQQFNVQALVA VGDHASKQMVKFAANINKESI VDVEGVVRKVNQKIGSCTQQD VELHVQ\KIYVISL\AEPRLPLQL DDAVRPEAEGEEEGRATVNQD TRLDNRVIDLRTSTSQAVFRL\Q SGICHPLRETLINKGFVEIQTPKI ISAASEGGANVFTVSYFKNNA\ YLAQSPQLYKQMCICADFEKVF SIGPVFRAEDSNTHRHLTEFVG LDIEMAFNYHYHEVMEEIADT M\VQIFKGLQER\FQTEFQTVNK QFPCEAISNFWEPTLRLEYCEAL AMLRGKLESEMG\DEDDLSTPN EK\LLG\HLVKEKYDT\DFYILD KYPIGL*RPF/HLYPCP*PPRNPQ QVPTLTNMFHEREKKYLSGAQ\ RIH\DPQL\LTERALH\HGI\DLEK IKAYIDSFRFGSPSP/HAGGGIGI/ ENRVTMLFLGLHNV\RQTSHVP
19958	50326	A	20074	3	424	
19959	50327	A	20075	178	859	
19960	50328	C	20076	304	592	

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19961	50329	A	20077	1381	2936	PTNPRPSPGLARWAESYEAKCE RRQEIRESRRCRPNVTTCRQVG KTLRIQQREQLQRARLQQFFRR RNLELEEKGKAQHPQAREQGP SRRPGQVTVLKEPLSCARRISSP REQVGRVKGHTAVCSGTLSGQ GGWV/R/RPPSLHRACRES*DNC PSSLALTLSHPIHSSLERTQ*I/SH ALTFWNSMIYPRSSRLILPQASD SSW/KGKGMKFFLNKAWASMC SHLIFLSTGKHSEGYFHLRNLEL NEKNVFEP\KAKESLQKVLEEK MNAEQQLQSTQVWGCHIDMG LGTPGSLGNKGSQLQRTLGTQH RELESQLHVLQSKLQVPGTGGG EGRQGMGRRDGDERSCSAKIE CLQGDRDLCSLDTQDLQGTLLL GGLECMAAMAK*AKKKETEAF QILKVHRVFLGSWPTKGTQVW SPKSFPNEVEPEGTGKEKDWDL RDQLQKKTLQLQAKEKEVRG* PEIVRAHLRNSRETWEAVKNCR EELNQSQQLPPRVRGSLLPIKP WMMGRFLL*PSFAHKDNLMI
19962	50330	B	20078	1	1173	
19963	50331	A	20079	16	1584	SSRFLFSLGWLWEAPEVGTRSG WLQRRPGLGAG\LGG\QEKQFL PALLSFFIYNPRFWPREGEEENK ILFYHPNEVEKNEKIRNVGLCE AIVQFTRTFSPSKPAKSLHTQKN RQFFN\EPEENF\WMVMVVRCPI IEKQSKDGKPVIEY\QEEELLDK VYSSVLRQCYSMYKLFNGTFPE SHGRRR\VKLLKERLEKFFHRY LQTLHLQSCDLLDIFGGISFFPL DKMTYLKIQSFIN\RMEESLNIV KYTAFLYNDQLIWSGLEQDDM RILYKYLTTSLFPRHI\EPELAGR DSPIRAEMPGNLQHYGRFLTGP LNLNDPDAKCR\FPKIFVNTDDT YEELHLI\VYKAMSAAVCFMID ASIHPTL\DFCRRTGTASLGPQL HSGWASGHLVEQF\NINKGDVP GLRK\EPQFKFI\YFNHMNLVEK STVHIEENAPACPLTSVHPDL\M KIPR*PSNSDLYPRV\DEDEGDH C*RALSDYW\VVGK\KSDPAGS LYVIFEIQKNAKP*LKVK*KRSK KPLCNASSNNILPSLD

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19964	50332	A	20080	85	420	LSNLFLHATNDGALTSTTIPHPP MRQPTS/S/GDGSEIFLHTELKLL EPPHAWPQSCPPRL*MTRQQLL PMTFLLKAHSKAGIESPGLNPR PGFSLHPVLPAASSAAFLLPSFR
19965	50333	A	20081	220	563	
19966	50334	B	20082	1	576	
19967	50335	A	20083	111	3586	TMFGLKPPLYFLPGSSLSSESSP VSSPATNHSSPASTPKRVPMGPI IVPPGGHSVPSTPPVVTIAPTKT VNGVWRSESRQDAGPRSSSGG RERLIVEPPLPQEKAGGPAIPSH LLSTPYPFGLSPSSVVQDSRFPP LNLQRPVHHVVPPSTVTEDYLR SFRPYHTTDDLRMSSLPPLGLD PATAAAYYHPSYLAPHPFPHPA FRMDDSYCLSALRSPFYPIPTPG SLPPLHPSAMHLHLSGVRYPPE LSHSSLAA
19968	50336	A	20084	576	1261	GDDLCSVGAPCRSTWACSTPLR CVRRSREFPGLPHAAGAARGFR LPAGRPVPARPGAAAARAAAA GEAHRPLPCGRRPGPVRRAAVP PRPRPPRRGLRGRREGPAAPAG PGGPSLLCASAGRHGPPGLRAG QGLRDSAGEAGGEPAP/AGPRP EASP*RSSLCENTCTEAGLGPRR AAGDLGSPWLTSGLLWGSFFLF FLFFFVILRQSLLLSPKTEVAVA QLMSHCSL
19969	50337	A	20085	248	356	EGEEEGDEENDPD\MTQRRIKT QQSASSSEAGCMWP
19970	50338	A	20086	1043	1191	NFYFSCKNKNKANKQQITWK\ KGLSNGCKFILSGGRQKGRTLP QRERMA

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19971	50339	A	20087	287	1401	CQNPQIPCSPFKKRLDG/LWVET PT\GYIESLP\RVVKRR\VNALKN LQVKCAQIEAKFFE/EKVHGFFE RKYAVL\YQPLFD\KRF\EIINAI YEPTE/EKECEWETR*RKDEDF GGNWKEKGQIEDEKKDE\EKE DPKG/IFPEFWLTVFK\NVDLLS DMVQEH\DEPILKH\LKDIKVKF SDA\GQPMSFVLEFHF\EPNE\YF TNEVL\TRTYRMRSEP/DTRLIL DPFSFDGPEIMGCTGCQIDWKK GKNVTLKTY*GGGRKHKGRGT \VRTVTKT\VS\NDSFSNFFPP\PE IPE/DVGDLDDDAGSLFLAGRLS EIWFTFYRERIIPRSSVNILPGEA\ IEDDDDDYDEEGEEADEEGEEE GDEENDPRLLTQR\RIKTQQSAS
19972	50340	A	20088	1	350	DNLEAEAVAPCTAAARAVAPD LFVFAA*PESVSAGGPQQPCRSP IVKPGLPSFRPSSCTQPWLTHSW AEDVDLRVNFAMNVGKARGFF KKGDVVIVLTGWRPGSGFTNT MRVVPVP
19973	50341	A	20089	1	399	
19974	50342	A	20090	1	394	
19975	50343	B	20091	82	351	
19976	50344	A	20092	3	789	CGTSRMCHTTEELA/SDPIL/YRP LAVALDTKEPEI/RNGLIKGSGT SEVELKKGATLKFTRNNAY/ME KCDENILWLDYKNICKVVEVG SKIYVDDGLISLQVKQKGADFL VTEVENGGSLGSKKGVNLPGA AVDLPAVSEKDIQDLKFGVEQD VDMVFASFIRKASDVHEVRKV LGEKGKNIKIISKIENHEGVRRF DEILEALGHWAVVPLKPTLALA LTCFSSSLGLSSLHLSPPSTQLSC SKHSTLHLPFSPTTAAPPGLLL
19977	50345	A	20093	3	424	
19978	50346	A	20094	2	173	IYHLQLFEELR/RLAPITSDPTEA TAVGAVEASFKCCSGAIIVLTK SGRSAHQQELGP
19979	50347	B	20095	1	1362	

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19980	50348	A	20096	1	1982	QRDNLEAEAVAPCTAAARAVA PDLLRLCSVRPSRSAPEDRQQP CLFSHSEAGTAFIQTQQLHAA\ MADTF/LWEHMCRL\DIDSPPIT ARNTG\IIC\TIGPGLPDQVETLK EDD*SLGMKCGSVLNFSSWEL HGVTMRETIQGMWRTANGKA FAFLTPFLLPGPLAVGFRTLKGP EIPNWGSSKGNGT\AEVGA*RK GATLKFTL\DNAYM\EKC\DENI L\WLDYKNICKV\VEVG\SKIYV DDGLISLQGKQK\GADF\LVTEV ENGGSLGI\MKGVNLP\GAAVD FACLCRRKDIQDLKFG\VE\QDV DMVF\ASFIPQSILMFHEVRKVL G\EKGKDHQGLSSKIRESMRGF RRFD\EIL\EASDGI/LWVARG*F *ALRIPAEK\VF\LAQKMIDLDRF NRA\GKP\VICATQMLESMIKKP RPTRA\EGSD\VAN\AVLDWKPT CIMLSWEKQPKGDYPL\EAV\R MQHL\IAREARWLPSYH\LQLF\ EELRPPGAQLTSDPTEATAVG\A VEASFKCC\SGAII\VLTKSGKVC SPRLARYRPRAPIIAVTRNSPGK LVRAHL\YRGIFPG\VCQGPDSR RAWA*DIG\LRVKLCHGMFGK ARGFFQERGDVVHCA*PEWRP WLPAPPNNMRVVPCCRDGPRG PSSSRPCSHPFFPKPIPFRPSNGL VELHSGAVNVATG

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19981	50349	A	20097	215	1893	TVTFSQCRFGKMLPLEKAFASP QELPSPAGSAHAGVSSRSSSRK NPRPSLRGPLLTLEFSRLRFREF VY\QEAAGPHQTLARLHELCRQ WLMPEARSKEQML/ESLLVLEQ FLGILPDKVRPWVVAQYPESCR SSLLVEGLADVLEEPGPSTVDR DAAGLPCGLILNS*RWSVREAH GPSAATRRAREPQPGPWSWGD PGTF*DTLAFSGPPVSGTEEGQ/ MKQRPKRTALP/HTEQVGGHE QVGGRSQ/RTTNVSEAEVLSRG PSAPGGVGPPGPC\EENLKSYRK LLLWEGGRRQESAGCACEEAA PAG\GCLSCLRRRPLGTPLPIPRR A\H*GGGRAAWEGPGPAGPPGR GVRLCHRIAEAVRHPAACP/ET GARRNWEPRGRTPRMGTGRAS RA/CSSSGDSAGLEAGQGPGAD EPGLSRGKPYACGECGEAFAW LSHLMEHHSSHGGRKRYACQG CWKTFHFSLALAEHQKTHG\KE KSYALGGARGPQPSTREAQAG ARAGGPPESVEGRGSPRTPRGA EVSRCAVPFRRGRFAGRESQTR HWAFPRPWVAASCGVCGRPLP
19982	50350	A	20098	5	372	
19983	50351	A	20099	1	129	
19984	50352	A	20100	1	627	
19985	50353	A	20101	1	441	
19986	50354	B	20102	1	477	
19987	50355	A	20103	2007	2156	

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19988	50356	A	20104	1	717	MKLRTLAVSVTALKVARLGSA PSDVQMCLEFLPSDSGAQLASP SGSRTGAAGGAACQSGAVRSY SSALGWSMGLGAVEQGVVLV GDARAAQEPMEWMGGSGMAG CRSRALHRGKAAKARREIEHSA GRKGLFGSARLIPATAMAPRSR LLSLGRRGNFRSRVLRRKSRPL EEAARRWRDCPTGFGALVAGA GSGRAPGVPPKRLPARTKAQVS RETRGSGEVTAQGGKGPRGLW ILLWGFYNLLPTTSHAESYPERL IQKVVSEKIARALARYLHLPFG LLGGNKTIVYSWEALRFHHQLT PSVITNTVIKVYEEPKLSQQKSR TLDVSTDEEDKIHHSSESKDDQ GLSSDSSSSLGEKELSSTVKIPD AAFIQAARRKRELARAQDDYIS LDVQHTSSISGMKRESEDDPEIS RNEETSEESQEDEKQDTWEQQ QMRKAVKIIEERDIDLSCGNGS SKVKKFDTSISFPPVNLEIIKKQL NTRLTLLQETHRSHLREYEKYV QDVKSSKSTIQNLESSSNQALN CKFYKSMKIYVENLIDCLNEKII NIQEIESSMHALLLKQAMTFMK RRQDELKHESTYLQQLSRKDET STSGNFSVDEKTQWILEEIESRR TKRRQARVLSGNCNHQEGTSS DDELPSAEMIDFQKSQGDILQK QKKVFEEVQDDFCNIQNILLKF QQWREKFPDSYYEAFISLC*RQ
19989	50357	A	20105	154	744	SQRNLCLGRVWYILFFLFAFLQ TLELVSHERRGRTGITNA*VSNS PRRELGFHVL*R*QFLLLFLFSH RLRSPAGFT*WIPHRGCRWSCL PVLRHALAFLSPWVVDGTGRR GAGGGARRGGSGHTGAHGVG GRLRHGRLQVPSPLRARSPFLLS CTLSCQLDSPCLTCSQGHQYKY QHSDKGKRLTIVTKSFDFIPS
19990	50358	B	20106	1	531	
19991	50359	C	20107	99	323	
19992	50360	A	20108	305	658	
19993	50361	B	20109	79	936	

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19994	50362	A	20110	381	1169	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPQGAPPPAPRRPVPST TQGLRSASARHGTGRQLHLQP WCGIHWVKLAGLLSLVGSQHL RGQGSRAAAALTHMHS/PHAC THAHTRAEPLRLPPPPRPLPPPL SPPPLRLCCLRSLFPCPLTESAA KAGSKKFHSVQEIPSPAVCELG VGTVLHIDPEKWRAGRENVET GGKRTGSGKDSTGRGWGQTD YGLGKKERTEEASRSCICLVCV SMRRDALCGQSVGSHFCQWSL
19995	50363	A	20111	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
19996	50364	A	20112	2	1844	
19997	50365	A	20113	746	1215	PNINRFLKHYREPVPKKRERNY STLWPLCPSTLNKIYTIMSYLSP ATKEYPFFLLLLEQEC*AE*LLA LAVSQPLLSSTTNCLKN*MVTW NGSLIPWSPCKINLTP*/PAVVL QNRRALDLLTAESGGTFLFLEE KCCCYVNQSGIITEKVKEIQGRI
19998	50366	A	20114	1	1338	
19999	50367	B	20115	1	4935	
20000	50368	A	20116	3	421	
20001	50369	C	20117	33	571	
20002	50370	A	20118	3	323	
20003	50371	A	20119	146	809	EKCRHNCSSRVWQSLVSQSVW ATEGQYGRTKNARPVQVK\DS ASFPYQRRYPLRLEAQQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINEAI VPLYPAVPNPYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESQF LFAFEDPSNPTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSYL NTLVLRYLDDLLLAAHLETLCH
20004	50372	A	20120	3	1147	
20005	50373	A	20121	2	1658	

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20006	50374	A	20122	2	211	MGIYDFSYFPPGCCLKSRRKSS RGSQE*LALSPGFSGSFGSIQDL TQV*CIQDSTPATLTAVGVDKM
20007	50375	B	20123	86	586	
20008	50376	A	20124	66	433	SSSRTEGARGKRQPMPSP/STEP RVCLTIEGQEVNCLLDTGAAFS VLLSCPGQLSSRSVTI*GVLGQP VTRYFPQPLSCDWGTLLFSNAF LIMPESPTPLLGRGILAKAGAIIH HAVLVTAAL
20009	50377	A	20125	1	459	MAVRYTDENVLRKGTREAGT MMRLRGTTECCADFAAWDVT HDALRATGGELPGAQVMLTTT ECGRHVDFCDRAVWLPRMWG YPLALPGEMRKLYTVRMAGRD ILAKAGAIIHLNIGEGTPVRCPL L/EGINPEVWKTEGQYRQAKNA RPVQVKL
20010	50378	A	20126	260	392	VEVVILPMPVPNLPSIPARITKG RMGTLLLRGLGTT*LYKSCSV
20011	50379	A	20127	1	1740	
20012	50380	A	20128	1	858	MEWEDNLPLELGRTVAKLLSD HSQTPLGIQMFLLFSLSLRKSPL VCLSYLFNFRFTLESEVQHLSG AITLTAWPKIPFLGIREAKSPRS ENTRLATILEAGHRHLGTSVSK DHPVTFWRPRRDLQSDLKQIKI DLGKFSDNPDGYIDVLQELGQS FDLTWRDIMLLLNQTLTPNERS ATITAAREFGDLWYISQVVAAV AGLVSEAVKIIQG\LTVWT/SHD VNGILTAKGDLWLSDNHLLKY QALLLEGPVLRLRTCATLNPAT FLPDNEEKIEHNCQQVIAQTYA
20013	50381	A	20129	1	6530	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
20014	50382	B	20130	1231	2065	
20015	50383	A	20131	68	372	
20016	50384	A	20132	1	1461	

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20017	50385	A	20133	1	806	AVWCTHCCAPTPSGPVLPHSAA MSFLKSFPPPGPAEGLLRQQPD TEAVLNGKGLGTGTLYIAESRL SWLDGSGLGFSLEYPTISLHALS RDRSDCLGEHLYVMVNAKFEE ESKEPVADEEEEDSDDDVEPITE FRFVPSDKSAF*FPCSVEAMFTA MCECQALHPDPEDEDSDDYDG EEYDVEAHEQGQGDIPTFYTYE EGLSHLTAEG\QATLERLEGML SQ\SVSS\QYNMAG\VRT\EDSIR DY\EDGDGRLDTTP\TVCLGQF\ EDADV
20018	50386	A	20134	225	420	RLLGDVCGRLRPRGHEEQRPG GPGARSHSRSGPRMGRDCAGA VPRVTPK*SACAAGGRGGPAT
20019	50387	A	20135	1	687	
20020	50388	A	20136	1	2979	MLRRKKQEDWAAKGSSHACG QIPEEREKGFAVGNVVANLGLD LGSLSARRFRVVSGASRRFFEV NRETGEMFVNDRLDREELCGT LPSCTVTLELVVENPLELFSVEV VIQDINDNNPAFPTQEMKLEISE AVAPGTRFPLESAHDPDVGSNS LQTYELSRNEYFALRVQTREDS TKYAELVLERALDREREPSLQL VLTALDGGTPALSASLPIHIKVL DANDNAPVFNQSLYRARVLED APSGTRVVQVLATD
20021	50389	A	20137	2	296	
20022	50390	A	20138	1187	1292	
20023	50391	A	20139	2	3250	LTSRWRPWPRPPTSASSAGWFC ASTGPWTAAPAKAPPSWASWT SRALRSSRPQTSRLWRR*PRSR AATPSSSGRGTCGIRPTSVFSTT RARSTTRPTSG**KTWTL*MTT SQ/RLLHQSTDRLTAEIWKDVE GIVGLEQVSS\RATAHQVAAPV GVCSGQWDSS/HKESLSRLMAT LSNTNPSFVRCIVPNHEKRAGK LEPRLVLDQLRCNGVLEGIRICR QGFPNRILFQEFRQRYEILTPNA IPKGFMDGKQA
20024	50392	B	20140	1	1816	
20025	50393	A	20141	500	866	QVCLYPGWQHSPGRQRVSG*A HLHTAPLWICQ*SGDCDWHES* GGGM*CVR\FEPPRTSSPPSATS GSLLK*KEKTGLSNSPCSTSTSS GGRTPSTDRMGKTRRQYPSGA GNSEDKVGFPQVF
20026	50394	A	20142	130	226	

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20027	50395	A	20143	846	1555	GRKTPSQGRRWSSPRVFLLPGG PKPCYTYPLVGEKLLFRVLPLFP HKPSASNLEKVSHCPECGKTFS RSSYLVRHQRIHTGEKPSQVPV ECGKGF**ALPT/CTAH/HYGTH TGERPYQCGQCGKSFNQSSSLI VHQRTHTGEKPYQCIVCGKRF NI\SSQFSAHRRIHTGESPYKCA VCGKIFNNSSHFSAHRKTHTGE KPYRCSHCERGFTKNSALTRHQ TVHMKAVLSSQEGRDAL
20028	50396	A	20144	93	764	AQERKALKSTPSHSSFSR/WLSR IILKNGSSSSSSSSSSSSSSLRE RERKSCENVNITRNRR/LTAETI ADTIDTSNGSVFLIWTER*EWN\ WLPKPWHQYQLQARASLSEEIL NNRWEQDPEAFRQDPEDQARS/ QWLPRGGSAPV\KQRLLLHHDS VPDHAFLRTRAAGQDLPWETV RRPPDNPDLAPADFSLFPCLGK LLAERRCFSLQRRVPWPPENQP PHRQ
20029	50397	A	20145	1	433	
20030	50398	C	20146	312	443	
20031	50399	A	20147	1	94	
20032	50400	A	20148	2	122	DLLCPQMG*GWKLTALSLQCS LQDGIERSRAKASQCCLSI
20033	50401	C	20149	25	328	
20034	50402	C	20150	157	309	
20035	50403	B	20151	33	2996	
20036	50404	C	20152	167	274	
20037	50405	A	20153	3	130	AGAVQFQALGVPNKDTKSLEL HQKPKPR*GQDDNHRMSPVYV
20038	50406	A	20154	2	453	
20039	50407	A	20155	1	1317	
20040	50408	A	20156	1	1350	

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20041	50409	A	20157	970	2559	FPLAYSLLFPP/CSRLSRELLEVV EPEVLQDSLDRCYSTPSSCLEQP DSCQPYGSSFYALEEKHVGFSL DVGEIEKKGKGKKRRGRRSTK KRRRRGRKEGEEDQNPPCPRLS RELLAEKEPEVLQDSLDRWYST PSVYLGLTDPCQPCRSAFYVLE QQRVGLAVDMDEIEKYQEVEE DQDPSCPR*L*AITDA*FCVDT WRCQVQGKQECVQFHVFNEG* ITPTDIAVGFHCSRCLGFHFFLP LSFTHLL*VDHTSKAVWQLHGI LSKFMENY*AHSFHDHCSLCVP RALTQSVL*PLHQCVTRPIR*AH FLLSLSLPLPVFLFHSFLPGPGLS QHKGNNSLPH*WICPFSF*TVPY VSHEI*LGLCGF*FPLAYSLLFPT /CSRLSRELLDEKEPEVLQDSLD RCYSTPSGYLELPDLGQPYSSA VYSLEEQYLGLALDVDRIKKD QEEEEDQGPPCPRLSRELLEVV EPEVLQDSLDRCYSTPSSCLEQP DSCQPYGSSFYALEEKHVGFSL DVGEIEKKGKGKKRRGRR
20042	50410	A	20158	2790	5320	LHLFCHKRQHGGISRALGSSKK PEMNILEISETLRPQLAEKKQQF RSLKEKCFLTQLAGFLANRQKK YKYEECKDLIKFMLRNERQFKE EKLAEQLKQAEELRQYKVVVH SQERELNQLREKLREGRDASRS LYEHLQALLTPDEPDKSQGQDL QEQLAEGCRLAQHLVQKLSPE NDEDEDEDVQVEEAEKVLESS APREVQKAEESKVPEDSLEECA ITCSNSHGPCDSNQPHKNIKITF EEDEVNSTLVVDRE
20043	50411	A	20159	394	3251	GRRVCLFSEDEECKDLIKFMLR NERQFKEEKLAEQLKQAEELR QYKVLVHAQERELTQLREKLR EGRDASR\SLNEHLQALLTPDEP DKSQGQDLQEQLAEGCRLTQH LVQKLSPENDNDDDEGVS/QVE VAEKV\QKSSAPREMQKAEEKE VPEDSLEECAITCSNSHGPYDSN QPHKKTKITFEEDKVDSTLIGSS SHVEWEDAVHIIPENESDDEEE EEKGPVSPRNLQESEEEEV\PQT PWHE*LSHLSIL

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20044	50412	A	20160	245	641	ILSVLIAVLCVVGKIPLKEPLCP AAGSAAEACVGQGMPVIQVPC SQQRPSSMCWPRNACQSSRAL GGDESYVPKNRKSFTKHPVSSC /PSPSLGWGRG*R/PGGPGRSPG LALGFPSFSGPAGFGQGTSSPRF
20045	50413	A	20161	7	194	RPLVESRGIPRSPAASFSTACPR NTASIPSAPSWWETAWTQTSS* APPVA*RPS*PSPESPL
20046	50414	A	20162	232	509	MGVLMHRRCTKAPAWAVATY EAPLHCQQLLGVVGVLAGDPS LLDLGGIHQQPQGLPITVLHQA EEADLVLLRAVTDAAALPVEQ HRP*GAPGLLPPPDGGQ*SGDP AAAGGYLQGPRGLGPQPGHPP HPGAAGSAGEPRKWLPPRRGL WCSACA*GPPSTGPGEQRGPGD SG*FISASTSASRATSACRSAFIT SQTEPPTWPSLARPQSSGLARPP APGRTAAGRD**TLPPGK
20047	50415	A	20163	3	859	SLGGNKSRPTRRCCSGSRCRCR DKSAAVSGALWRGCRESPRAP PPAPQTIPRAWPSPTAVLTHPLL AGPSRWGSSCTGAAPKPPPGRG PLRGSPALPAAPGCGGCPGWGP KPLGPWRYPPAAAGSPDHCPPS GGGSRPGAPQGGNRCSRSARRT APPSCGCSEVGSL*WSPRSGPRP PGWFGWAGACGGSGGSFAASA ALAWEGPEQSQEALQPQSPQRP APAAAAAGAGPRLSSPRRRAW SSPG*/HGIPWPTHASAALPAAG HRGSFSGILP*RAGKRSAMLST
20048	50416	B	20164	179	438	
20049	50417	A	20165	1	930	MESPWRQWRLRKVARSGGGR LSNKRKLHLKKKKKGERGGGG AEREKAAAAVAPGCKAGAGN AKKFVQNGPGTKESSASQVPTG PSAAGLLEFARGPLQTLFAWVS AAVSAEPRIFMIRECCCLIVPLE VLSQRSTWPCEFLISDCCASNQ QDSMGVGPSEPGAGYNLLVRH FLSPSEKCSIRVGVARFSRVLPP PLLGISAARAAGGAARQAAQL REGSRCPRLTDIPHAPSTPPEQG HSAEGAAKEEPKRRSARLSAKP APAKVEAK/PKKAAAKDKSSD KQVQTKGKRGAKGKQAEVAN QETKEHLPAV
20050	50418	A	20166	199	419	

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20051	50419	B	20167	969	1313	
20052	50420	C	20168	481	738	
20053	50421	B	20169	56	3476	
20054	50422	A	20170	1	2679	
20055	50423	A	20171	1	1467	
20056	50424	A	20172	208	379	NPCKKGVLIFQF*LKIHKRQFIC ADLEFVISE*CTRYPIVAFNWCK PSLLRRSTPVK
20057	50425	A	20173	1	921	
20058	50426	A	20174	197	355	
20059	50427	A	20175	1	3180	
20060	50428	A	20176	1	1309	
20061	50429	A	20177	1	2295	MFYNDVKKQQQMAALTKEKD QLSQSIVMYKSLFEASQQLLNE MKCQVEEARLKEAQLRNELKI HNIDIPTTQQVPHIEALLKRKLS EQEELKKKPRRSCTLPNYTKGS GDVLGKIAHLAQIEDDRAAMVI SWHLASDMDCVVTLTTDAARR IYDETQGRQQVLPLDSIYKKTL PDWKRSLPHFRNGKLYFKPIGD PVFARDLLTFPDNVEHCETVFG MLLGDTIILDNLDAANHYRKEV VKITHCPTLLTRDGDR
20062	50430	A	20178	3	2550	
20063	50431	A	20179	256	3680	NRGLLFCFLFLHLHLKEHERHL ATVYVFPILSCTIYRSVLLTSSQ TIIYTHVGDREAQAALKLGRWS HPRTPNAVGAPGPPEGAGGGD AVTSQSALLTFSRTRFASGAHA GAHPVLLRNEEEKGAPALVAPI FSAEGPTCSLWWTLRPASTAGL KLPAAASTRPSQRGLTADGGGP GGASVGTEEDGGGVGHRTVYL FDRREKESELGDRPLQVGERSD YAGFRAYETVKDGVTLYLLQS VNQLLLTATKERIDF
20064	50432	A	20180	8	267	RGEMPGERLKAEVFLPPSPLSPT QVVGPLHRVWS*IGNASSQRGE AQVRS*VSFSLRLEDSTPWIPGT RALRGCWLWRDFQTLQSG

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20065	50433	A	20181	1	3692	MNPIREMQVSGIALKGTMKGW TELPKSPVWTQGNKGRNYFTN LALSLLFEDDTKLNPYAGGDAI RVRISVGPFKGERFTVPGLASEC GKNSFLRFPSNSRRKQLCGRVH GSFLWFSMMSQSMGGDNLSSL DTNEAEIEPENMREKFFRSLAR LLENKSNNTKIFSKAKYCQLIK EVKEAKAKAKKESVDYRRLAR FDVILVQGNEKLIEAVNGETDK IRYYLHSEDLFDILHNTHLSIGH GGRTRMEKELQAKYK
20066	50434	A	20182	24	131	PVHKRWS*NDECYRHCTV***Q PGSEENNPALENR
20067	50435	C	20183	99	281	
20068	50436	A	20184	1	4200	MVILKDFMKFEMNSEEGDFLR TCDFFFLRHLVAVKQLAHVKV DRFFPRRQSLAESRTAGIRLQTN VQKMVSSFTTSDRKQTSPSSYS VSFIPEFHFLGPPTHCPQTAVSQ CDLLFQLHSPAEALFPARTLPG GPRSPHLRVPAAPAPLQHDPRH TGPPLPPTANRGATPPLPLGPGA LERSGRLGELNSASSFRLRRDN PQSPAARPRGSHGLAGIEGERT LINYYCQERYFHHVLLVASEGI KRYGSDPVFRFY
20069	50437	A	20185	1	1464	
20070	50438	A	20186	335	855	RIASMPRLPPRTQGRGSARLPSR ARPGLHWHHRHTMLPPKPRRW R/RALGPAEAGMLEKLEFEDEG ECAPPAAGPALPRPGRPRTGTR GDPAPHLRRCPTASCVLRKPRG RGGNRGGDAGAGELGLRGPCD LPSQNFLCFLVDVLKNGLLALQ LFSSNPTASCAESLPMLRTPVI

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20071	50439	A	20187	2	1160	SARPAASPPAGERASQLMLIAV LLLPLRRRWRRALGPAEAGML EKLEFEDEAVEDSESGVYMRF MRSHKCYDIVPTSSKLVVFDTT LQVKKAFFALVANGVRAAPLW \ESKKQSFVGMLTITDFINILHR YYKSPMVQI/YMELEDHKNLET \WRELYLQ\ETFKPLVNISP\D\AS LFGWLYTSLIKNKIHRLPVIDPIS GNALYILTHKRILKFLQLFMSD MPKPAF\MKQNLDELGIGTYHN IAFIHPDTPIIKALNIFV/EKDRIS ALP/VLWDESGKSW*IFNSPNLN VN*ILACLEENIPNNLR*STVT\Q A\LQHRSQYFEGVVKCQLSWKF LETHRWTRIVRAEGPSGLVVV\ NEADSIVGIISLSDIL\QALIL\TP AGAKQKETETE
20072	50440	A	20188	58	205	
20073	50441	A	20189	347	1581	NPSPC/WAVFFQKDAITSKIQTF LSMLHLYN**/SSPSKENTRTVE KLYKCSVDIRKIRRFKKDGVLL RR*KPYVERNCRIFYQELGAR* D\AVASI\LERCPEAIV*SPTAVN TQRKLWQLVCKNEEELIKLIEQ FPESFFTIKDQENQKLNVQFFQ DVGTKKCGH\CRLLTAAPNCFS\ NPVEKNKQMV\EFFQESYLD\L GGSEANMKSFGLLKLFKPKPFY FV*ISPTAIKETLEFLQEPRFPPA LKFLQLPIPNSKGFLFQLCPKKY TE*YFLL*KCLLNAQIFMDP/VS N*VLKWPCPFILFLFPVLEERM QGLLREGISIAQIR\ETPMVLELT PQIVQYRIRKLNSSGYRIKDGHL ANLNGSKKEFEANFGKIQAKK ALQNLLLRSLNYYDELTVGEC GNRKGRGTNVNTTL
20074	50442	A	20190	3	455	
20075	50443	C	20191	72	218	
20076	50444	A	20192	3	452	LGILLVDDFVNVLSSLAVYAED SEPESDGEAGIEAVGSAAEEKG GLVSDAYGEDDFSRLGGDEDG YEEEEDENSRQSEDDDSETEKP EADDPKE\NSAQ*QRHPGLSKL MAQLVGLRGQKNHILNMIRDV TQQPQLSLAAHTPHTPFHLQ
20077	50445	A	20193	1	334	
20078	50446	A	20194	1	687	

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20079	50447	A	20195	1	1280	RPGCGNKMAGKKNVLSSLAAY A*ISEPESDGEAGIEAVGSAAD EKGGLVSDAYGEDDFSRLGGD EDGYEEEEDENSRQSEDDDSET EKPEADDPKDNTEAEKRDPQEL VASFSERVRNMSPDEIKIPPEPP G\RCSNHLQDKIQKLYERKIKE GMDMNYIIQRKK\EFRNPSIYRE /RLIQFC\AIDELGTNYPKDMFD PHGWSEDSYYEALAKAQKIEM GQIGKRPKKERNQKFEFCDGAP KKGT/TRTNATSTTTTTCQAQL FADCFRRGKRQVGIRAIPSATKP KRTPPPKPPPNTLTTTATLPS/V VVTVTHPSASGSKDPPVISCCG APIVKERPKQVTLRGPPLGLER DRAAPVTHCPVGGAHFVYFRT GTYSPRCHLRGASVWHSRWKD RQHGSQALWTGSVHAPPGVCR LLKVPYSYLLASQKK
20080	50448	A	20196	1	542	MAYSAPEKSCTEGHESPH/HHT AGHSGWHGG*ALRQRGHSCPK EGTRGHPQTLAP/HHQCPQHAA GLPR/HNQLLHD/WFRHHHHRH WHHHHHHHQ*FPECQPSTSHQ ANPHHRPDLHDRQAPDSGYEG VSPKRVAEANFSLGSAPQAAQ GRSHGQSPGVHGFFSHGSPAAS SDIMKRLPPPGLF
20081	50449	A	20197	45	171	RKTRERIGHDVICNLL*C**SS/C GCGLS/CICS*IRHSKSSRKA
20082	50450	A	20198	277	467	GLGPHDYLYSILSIERSCCC*CC CCCCRRRRCCCCC/CV*GCSRFL CSIAESTPSGALRRLRGGR
20083	50451	A	20199	1	1080	
20084	50452	A	20200	34	119	
20085	50453	A	20201	1798	1894	
20086	50454	A	20202	363	778	GLGPHDYLYSILSIERSCCC*CC CCCCRRRRCCCCC/CV*GCSRFL CSIAESTPSGALRRLRGGRSGGS GGCCSPGGCREGGRGNTKPAT RCEVICGGGSGGGGARPAAPPG GPDASRVCWFSLNTSIVFFSCPF
20087	50455	A	20203	1	360	
20088	50456	B	20204	1	3681	
20089	50457	A	20205	1	293	
20090	50458	B	20206	38	282	

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20091	50459	A	20207	1	1124	VDTVKRLLIKKLPPVLAIQLKRF DYDWERECAIKFNDYFEFPREL DMEPYTVAGVAKLEGDNVNPE SQLIQQSEQSESETAGSTKYRLV GVLVHSGQASGGHYYSYIIQRN GGDGERNRWYKFDDGDVTEC KMDDDEEMKNQCFGGEYMGE VF\DHMMKRMSYRRQKRWWN AYILFYERMDTIDQDDELIRYIS ELAITTRPHQIIMPSAIERSVRKQ NVQFMHNRMQYSMEYFQFMK KLLTCNGVYLNPPPGVAEKTQL LKLSVPATFMLVSLDEGPGPPIK YQYAELGKLYSVVSQLIRCCNV SSRMQSSINDAETAFNKIQHRF MLKILNKQGIEETYIKITRAIYD KPTANIILNGQMLEALPLRNRT
20092	50460	A	20208	1	1053	
20093	50461	A	20209	1	7785	MTATTRGSPVGGNDNQGQAPD GQSQPPLQQNQTSSPDSSNENS PATPPDEQGQGDAPPQLEDEEP AFPHTDLAKLDDMINRPRWVV PVLPKGELEVLLEAAIDLSKKG LDVKSEACQRFFRDGLTISFTKI LTDEAVSGWKFEIHVSLAFDFK GSDLHSDACEWEERCIINNTHR LVELWCGPSCPQDWF\PLLELL AMALNPHCKFHIYNGTRPCESV SSSVQLPEDELFARSPDPRSPKG WLVDLLNKFGTLN
20094	50462	A	20210	1201	9141	ADKIAKICPVSSMTATTRGSPV GGNDNQGQAPDGQSQPPLQQN QTSSPDSSNENSPATPPDEQGQ GDAPPQLEDEEPAFPHTDLAKL DDMINRPRWVVPVLPKGELEV KLEANIDLSKKGLDVKSEACQR FFRDGLTISFTKILTDEAVSGWK FEIHRCLVELCVAKLSQDWFPL LELLAMALNPHCKFHIYNGTRP CESVSSSVQLPEDELFARSPDPR SPKGWLVDLLNKFGTLNGFQIL HDRFINGSALNVQ
20095	50463	A	20211	2	710	

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20096	50464	A	20212	1	1703	RPLDVGGPAAGTPGVLSRPCPS TAALAPKPFCAAPRPQPDAPAC AGATGGSCADFDSGVDFVRRR SSGLWGPQPPLFPVKNYTEDPV AFKDVAVNFTQEEWALLDISQ KNLYREVMLETFWNLTSIGKK WKDQNIEYEYQNPRRNFRSVT EEKVNEIKEDSHCGETFTPVPD DRLNFQKKKASPEVKSCDSFVC EVGLGNSSSNMNIRGDTGHKA CECQEYGPKPWKSQQPKKAFR YHPSLRTQERDHTGKKPYACK ECGKNIIYHSSIQRHMVVHSGD GPYKCKFCGKAFHCLSLYLIHE RTHTGEKPYECKQCGKSFSYSA THRIHERTHIGEKPYECQECGK AFHSPRSCHRHERSHMGEKAY QCKECGKAFMCPRYVRRHERT HSRKKLYECKQCGKALSSLTSF QTHIR\MHSGERPYECKTCGKG FYSAKSFQRHEKTHSGEKPYKC KQCGKAFTRSGSFRYHERTHTG EKPYECKQCGKAFRSAPNLQL HGRTHTGEKPYQCKECGKAFR SASQLRIHRRIHTGEKPYECKK CGKAFRYVQNFRFHERTQTHK
20097	50465	A	20213	3	2413	

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20098	50466	A	20214	1	2124	MGKNTPMIQLSPPGPFHNSEYR FPVLSVSAFLLYTCEMFQDPVA FEDVAVIFTQEEWALLDISQRK LYREVMLETFRNLTSLGKRWK DQNIEYEHQNPRRNFRSLIEEK VNEIKDDSHCGETFTPVPDDRL NFQEKKASPEVKSCESFVCGEV GLGNSSFNMNIRGDIGHKAYEY QEYGPKPCKCQQPKKAFRYRPS FRTQERDHTGEKPNACKVCGK TFISHSSVRRHMVMHSGDGPY KCKFCGKAFHCLRLYLIHERIH TGEKPCECKQCGKSFSYSATHR IHKRTHTGEKPYEYQECGKAFH SPRSYRRHERIHMGEKAYQCKE CGKAFTCPRYVRIHERTHSRKN LYECKQCGKALSSLTSFQTHVR LHSGERPYECKICGKDFCSVNS FQRHEKIHSGEKPYKCKQCGK ALPHSSSLRYHVRTHTGEKPYE CKQCGKATHNGEKPYACKECG KPFGSAQNLRIHERTQTHIMHS VERPYKCKICGRGFYSAKSFQI HEKSYTGEKPYECKQCGKAFV SFTSFRYHERTHTGENPYECKQ FGKAFRSVKNLRFHKRTHTGE K/PL*IHEKTHTGRKHYECKQC GKAFTSSSSFQYHERTH/S/GEK PYQCKQCAKAFISSTSFQYHER THMGEKPYECMPSGKAFISS\SS LQYHERTHTGEKPYEYKQCGK AFRSASHLQMHGRTHTGEKPY
20099	50467	A	20215	23	265	
20100	50468	A	20216	40	470	
20101	50469	A	20217	235	392	

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20102	50470	A	20218	7	1439	EGADKMATSVGHRCLGLLHGV APWRSSLHPCEMTALSQSLQPL RKLPFRAFRTDARKIHTAPART MFLLRPLPILLVTGGGYAGYRQ YEKYRERELEKLGLEIPPKLAW SLGSVALYKSVPTRLL\SRAWG RLNQVGAAHTGLRRPRFTSL\YI WTFGVNMKEARVEDLHHYRN LSEFFRRKLKPQARPVCGLHS/V GEA*PFPPAGNRTFSCLPSTAPL VSSVSGRGRMTRGGGGCLLGG GDPALPGSKPLLPFQISPSDGRIL NFGQVKNCEVEQVKGVTYSLE SFLGPRMCTEDLPFPPAASCDSF KNQLVTREGNELYHCVIYLAPG DYHCFHSPTDWTVSHRRHFPGS LMSVNPGMARWIKELFCHNER VVLTGDWKHGFFSLTAVGAT\ NWGSTRIYFDRDRNTNNPRHSK GSYNDFSFVTHTNREGVPMRK GEHLGEFNLGSTIVLIFEAPKDF NFQLKTGQKIRFGEALGSL
20103	50471	A	20219	170	1144	ARTRRLAPSPGCRRGPAVKKM RHEELLTKTFQGPAVVCGTPTS HVYMFKNGSGDSGDSSEEESH RVVLRPRVKERHKSGVHQPPQ AGAGDVVLLQRELAQEDSLNK LALQYGCKHSE*LTMA/NVADI KKVNNFIREQDLYALKSVKIPV RNHGILMETHKELKPLLSPSSET TVTVELPEADRAGAGTGAQAG QLMGFFKGIDQDIERAVQSEIFL HESYCMDTSHQPLLPAPPKTPM DGADCGIQWWNAVFIMLLIGIV LPVFYLVYFKIQASGETPNSLNT TVIPNGSMAMGTVPGQAPRLA VAVPAVTSADSQFSQTTQAGS
20104	50472	A	20220	1	626	RYSSTLTRPWTQTPRTRASPHS\ PVAGALTARPSPPRPTKPSRAG VHASRRPPQDLGPIGKGSAKTK GPRHQRKHHESITPPSRSPTKEA PPGLNDDAQIPASQESVAPLWIP VTAP*AHRVLSSCEFGAAFESA GEEEGEGEVSASQAAVQA\GTQ TRR*GATSAPCGPVPEGASVPA L*AAGAAGRAEAERPPCVPAQ AVGLSGQPLS

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20105	50473	A	20221	2492	4619	WHSWRQQGWGAHLGSSATGP GC*QGRPTCVMRPAGT/TRPGE APIGSGTGAVEMPAREPGDEKP PAPFP*QRHFVPRAHLLFGTAL RSLPELMRRAVRNPRHHLSAEE SLLFSLPGSPWKGWSSWNGQA PPLAPPAQGPLLPVPLSAGPGV AGERTVPSSPRWWRPHLFLAPT APSPPPCPTVSAPGHLLGVAQK PDCHPPASQRPRRHPLPFLPGEA FAE/SAANS*ISSISASFTFS*SSS WSLD\STKSSLPPLHLPTLTSRV PGKFSALLSQFSASFSSHGLPSE SVAIGTCST/PGERAHSRQTCGP GSSAQS*GQEEGQCPQCRDSAG TCGRPRCSRHPAGHAGSEPRPL QRRSLHCSHTG*GAGIGHKART CGRKAPPRCPSETGHHSGVGY* PWRQSQQPAARGRARCGRPCP GACPAMAPQTQSEEGRRAPR/T NPAVPSEPARP/STAGPRAGASV PPSPGPRGPAGPGAPS\AGRRRR APGATACSGGAVESG*PSL/GSA LSAQVAPEAARAPA*GPGQAA GAREEGPAWPCRSPP\GPGPSQC AALPQK/GSALRSGGRRTLGPL LSHPSFKILLAGSGGVLDNSTSS ERSRATRSSICRPVVSESWTNN NGGDTGG\SSCDFYSPGPADGL SQGHSSDHTNLLLVLSSQKRHF PA*ALVQPHPAPSPTGTEPWPP AGPRTVPRPPSASSVAPSCWWV
20106	50474	A	20222	103	538	PQLSLPLLSIRDRRRPSKCANLT LTLTVAARHGLQSLGKVGISRR MPPPANLPSLKAENKGNDPNV NIVPKDGTGWASKQEQHEEEK TPEVPPAQPKPGVAAPPEVAPA PKSWASNKQGGQGDGIQVK*Q FQQEFPSLQAAGDQK
20107	50475	C	20223	1	569	
20108	50476	A	20224	1	1095	

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20109	50477	A	20225	1	1970	MWKGFTILDSFKNISDSWEDVR ISTLTGVWKKLIVTLMDDLEEF KTSVEEITLTQRKLFFVMESPV GPISPPQPPSVSAWNKPLTSFGS APSSEGAKNGQESGLEIGTDTIQ FGAPASNGNENEVVPVLSEKSA DKIPEPKEQRQKQPRAGPIKAQ KLPDLSPVDNK\EHKPGPIGKER SLKNRKVKDAQQVEPEGQEKP SPATVRSTDPVTTKETKAVSEM STEIGTMISVSSAEYGTNAKESV TDYTTPSSSLPNTVATNNTKME DTLVNNMESARKAWENSPNVR EKGSPVTSTAPPIATGVSSSASG PSTANYNSFSSASMPQIPVASVT PTASLSGAGTYTTSSLSTKSTTT SDPPNICKVKPQQLQTSSLPSAS HFSQLSCMPSLIAQQQQNPQVY VSQSAA/ATLTTACLS*WSTAQI PAFYMDTSHLFNTQHARLAPPS LAQQQGFQPGLS\RSQPAFMQS SLSQPSVVLSGTAIHNFPTVQH QELAKAQSGLAFQQTSNTQPIPI LYEHQLGQASGLGGSQLIDTHL LQVTVPLPASQLSLPNFGSTGQ PLIALPQTLQPPLQHTTPQAQA QSLSRPAQVSQPFRGLIPAGTQ HSMIATTGKMSEMELKAFGSGI DIKPGTPPIAGRSTTPTSSP\SGL LLQVRTASPAK
20110	50478	A	20226	260	8485	VSTEMSEKSGQSTKAKDGKKY ATLS\LFNTSKGKSLETQKTTVA ARHGLQSLGKVGISR\RMPPPC* PPKFLKPE*QRANDPNVNIVPK DGTGWASKQEQHEEEK\TPEVP PA\QPKPGVAAPPEVAPAPKSW ASNKQGGQGDGIQVNSQFQQE FPSLQAAVDQEKK\EKETNDDN YGP*PSLRPPNVACWRDGGKA AGSPSSSDQDEKLPGQDESTAG TSEQNDILKVVEKRIACGPPQA KLNGQQAALASQYR
20111	50479	A	20227	330	485	RQGDRVSLCCLGRS*TPGLK*F SHLDLLNCWDYRCETVHLAEI AQVSEKQI
20112	50480	C	20228	1189	1413	

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20113	50481	A	20229	1	407	MPFSLADCDSQHCLLFAVVDL GTAKATSCMSDTFDFYSSSGNS ANLKEGGKSPPAGPGKGPRGA QKRKYSGPWNRKESCKKHEGV KGAEGRGGTVASVRES/REPRF KMAAFSMHPC*RLSRHRGHLA QRCFCFCR
20114	50482	A	20230	1	408	HMDLAQPSQPVDELELSVLERQ PEENTPLNGADEVFPSLDEEVPP AEANKESPWSSCNKNVVGRCK LWMIITSIFLGVITVIIIGLCLAA VTYVDEDENEILELSSNKTFFIM LKIPEECVAEEELPHLLTERL**S L**HLGKWR**SST/GLHLPTTF LLQELQGLSLLASAGGTSSSKE GKTSSAPLRGVFSSGCRSSTESS SSSTGCEGWARSM
20115	50483	C	20231	144	383	
20116	50484	A	20232	1	530	AKDSESRRMLRGYNPQQMSEG HRQKSEFYNRTASESNVYLNSF HYPDHSYKDQAFDTLSLDSSDS METSISACSPDNIS\SASTSNIARI EEMERLLKQAHAEKTRLLESRE REMEAKKRALEEEKRRREILEK RLQEETSQRQKLIEKEVKIRERQ RAQARPLTRYLPVRKEDFDL
20117	50485	B	20233	10	543	
20118	50486	A	20234	370	556	
20119	50487	A	20235	3	3160	TELQQLGQKTADGSPGLKRALI FALNFHSSPPGKDMAAVQRTL MALGSVAVTKDDGCYRGEPS WFHRKAQQNRRGFSEEQLRQG QNVIGLQMGSNKGASQAGMTG LSDPTPWTAHLGMYVQGNAKF VSPVRRIVVHEYYNSQTFDYDI ALLQLSIAWPETLKQLIQPICIPP TGQRVRSGEKCWVTGWGRRH EADNKGSLVLQQAEVELIDQTL CVSTYGIITSRMLCAGIMSGKR DACKKRKLGTERPGTQAAP
20120	50488	A	20236	231	873	KKFRALGSVGPGFRASGVQVA DEV\CRIF\YDMKVR\KCS\TPEE DQDKERSAVIF\CLSADKKCIIV E\EG\KEILVGDVGWNP*TDPF\R HFVG\MLP*KKIVRYAFVMDGK LLETKGFQKRKSLMFFFV/WAP EL\APLKK*K*SYCKLQGMAFK KNFQGIKHECQA\NGPEDLNRA\ CIAEKL\GGSLIVAFEGCPCVDH HSVPQIEKLPMFNCYPLAI

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20121	50489	A	20237	915	1255	GHGQKPAGKKKKILAVRSGSEP AGGFQGY/RGGHGTAS/GSPGD DDSPGALWEQSPGPL*AWPGA VSEEPMVCAEPVQEQSGPQLPP PRHSRSPSGDSGQPGVPAERRRI MGMADA
20122	50490	A	20238	3	227	LLMDTF/FQIVIYL/GETIAQWR KAGYQDMPEYENFKHLLQAPL DDAQEILQARFPMPVKLRIQPG NATVSDCVQNV
20123	50491	A	20239	1	642	RRDTIARNWANVQSQVRHIEQ AFDQEAAA\VLMARLG\VFEPK SKEGPDVLRWLDRQLIRLCQKF GQYTKEDPTSFRLSDSFSLYPQS MFHLRRSPFLQVFNNSPDESSY YRHHFARQDLTQSLIMIQPILYS YSFHGPPEPVLLDSS\RFPMPRYI NTEHGGSQARFLLSKVNPSQTH NNLYAWGQETGAPILTDDVSL QVFMDHLKKLAVSSAC
20124	50492	B	20240	20	277	
20125	50493	A	20241	1	3030	

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20126	50494	A	20242	1	2677	MAEVKVKVQPPDADPVEIENRI IELCHQFPHGITDQVIQNEMPHI EAQQRAVAINRLLSMGQLDLL RSNTGLLYRIKDSQNAGKMKG SDNQEKLVYQIIEDAGNKGIWS RDIRYKSNLPLTEINKILKNLES KKLIKAVKSVALGIPAGCSVCP KCGASNHLSARFCGSCGICVKS LVKLSLDRSLALAAEEPRPFSES LNIPLPRSDVGTKRDIGTQTVGL FYPSGKLLAKKEQELASQKQR QEKMSDHKPLLTAISPGRENIG ENLQVIGLVKNFLSNIPQAPAT QAKMGKWDPRQRGAQSPLIFL YVVDTCLEEDDLQALKESLQM SLSLLPP\DALVGLITFGRMVQV HELSCEGISKSYVFRGTKDLTA KQIQDMLGLTKPAMPMQQARP \AQPQEHPFASSRFLQP\VHKID MNLTDLLGELQRDPWPVTQGK RPLRSTGVALSI\AVGLLEGTFP NTG\ARIMLFTGGPPTQGPGMV VGDELKIPI\RSWHDI\EKDNARF \MKKATKHYEMLANRTAANGH CIDIYACALDQTGLLEMKCCAN LTGGYMVMGDSFNTSLFKQTF QRIFTKDFNGDFRMAFGATLDV KRVQVGERGREAKNKLWTVH AHSSWRALNTGLRSFDFIPGTV REPVKILGRRLTSDLQIRNSPLE AAVQGGVSKTVSTVSLAHAMR AHPHLLMEDLRILVIDLDPQSS
20127	50495	B	20243	453	3318	
20128	50496	A	20244	2	1367	

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20129	50497	A	20245	1	1459	MLEGKYGPPPGSFQTRRTALAR SHTNTSPSTSPAANRLNALGIGE RDASPSWLGETQDQVKRQPGL SGSRKIPRCAMTYGSLGQQAA QAAGVHAPNVFVASLLCQFLQ FVYRNSMGWTGGADFSYSCQE GETKELWSSGHHLKACRAVAF SEDGQSEYWGRQPAMWWKGA VSSTMTLGTFSPELITVSKDKAI HVLDVEQGQLERRVSKAHGAP INSLLLVDENVLATGDDTGGIC LWDQRKEGPLMDMRQHEEYIA DMALDPAKKLLLTA\TYCSTLY SGDGCLGIFNIKRRRFELLSEPQ SGDLTSVTLMKVQLVMWGKK VACGSSEGTIYLFNWNGFGATS DRFALRAESIDCMVPVTESLLC TGSTDGVIRAVNILPNRVVGSV GQHIGEPVEELALSHCGRFLAS SGHDQRLKFWDMAQLASCGG G*LPSAQKKGRTTAGSEQQDLE HR*LLRRTEARGRSLHGSQKKR RRLGMTVTEGMN
20130	50498	A	20246	221	847	RHIFSFFSGHVLAVSLGKFIFEST LFPSERAARRRRRPVQQWPRFK ARDLRGKKKEELLKQLD\DLKV EAV/SQLRVAKVTGR\AASKLS KIR\VVRKSIARVLTVI\NQTQKE NLRKFYKGKKYKPL\DLR\P*GR HRAMRPPASNQARRENLEGPK EAGSGKGAAFTRCGK*RGSRA LRGRLCQ*KHKENLKTKKQQR KERLYPLRKYAVKA
20131	50499	A	20247	1	415	FFFFFECG*SFTNSFSVTIHRRIH NGEKSYECSDCGKSFNVLSSVK KHMRTHTGKKPYECNYCGKSF TSNSYLSVHTRMHN/TANVNSI TVGKAFIDLSCLR*HEQTLTRC MNHLLLCNKLPPKILWLQTKTL VISKFL

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20132	50500	A	20248	196	1768	RRSVLLPGCPVAVGVTGWRLSS CPQLPLCLPCSQPLSEKDTQRA ESWLMSS*KAG/YKGLVTFEDV AVEFTQEEWALLDPAQRTLYR DVMLENCRNLASLGNQVDKPR LISQLEQEDKVMTEERGILSGTC PDVENPFKAKGLTPKLHVFRKE QSRNMKMERNHLGATLNECN QCFKVFSTKSSLTRHRKYSILGE RPYGCSECGKSYSSRSYLAVHK RIHNGVKPYECNNCGKTFSSRS YLTVHKRIHNGEKPYDCSYCG KTFSNS*YLRPHLRIHTGEKPYK CNQCFREFRNQSIFTRHKRVHT GEGHYVCNQCGKAFGTRSSLSS HYSIHTGEYPYECHDCGRTFRR RSNLTQHIRTHTGEKPYTCNEC GKSFTNSFCLTIHRRIHNGEKSY ECSDCGKSFNVLSSVKKHMRT HTGKKPYECNYCGKSFTIGQGD GFEIVLPPPQLQQLIKAFFLGNT HCLSDRLSVQCIHYSIRYLHLNI HYLHYSIHYLHYSICYLHYSIM DPPQQSPHPLQHPLQNPLQ
20133	50501	A	20249	2	408	
20134	50502	A	20250	1	280	
20135	50503	A	20251	2	469	RGIREGEEFDVDLAGMEVAVG GWGRGLWLHRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFLSSNTTCQQFRDPGFR GRYPASPHTLSLPPETAHL*LLL CLPAAGVLPHTWPLLDRQGWH RGHAR

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20136	50504	A	20252	1	1762	FRMAAPLVLVLVVAVTVRAAL FRSSLAEFISERVEVVSPLSSWK RVVEGLSLLDLGVSPYSGAVFH ETPLIIYLFHFLIDYAELVFMITD ALTAIALYFAIQDFNKVVFKKQ KLLLELDQYAPDVAELIRTPME MRYIPLKAALFYLLNPYTILSCV AKSTCAINNTLIAFFILTTIKGKA LKGEYKGSAFLSAIFLALATYQ SLYPLTLFVPGLLYLLQRQYIPV KMKSKAFWIFSWEYAMMYVG SLVVIICLSFFLLSSWDFIPAVYG FILSVPDLTPNIG\LFWYFFAEM FEHFSLFFVCVFQINVFFYTIPLA IKLKEHPIFFMFIQIAVIAIFKSYP TVGDVALYMAFFPVWNHLYRF LRNIFVLTCIIIVCSLLFPVLWHL WIYAGSANSNFF*GITLTFNVG QLPHELFIMVPEGGGPGALMA AIERNVDRAVPGGSAERDPIER STLHILLISDYFYAFLRREYYLT HGLYLTPQGIAPEAMLVLQSRP GWHRASWTLRGLVGPEAGPKL SSPELPAGECLGRRGSSPRVTSS LVPKRDPWLTDSKAYGEELGA PQLGPPPCGSAHQGAPSQTGRR
20137	50505	B	20253	102	406	
20138	50506	B	20254	200	408	
20139	50507	B	20255	347	458	
20140	50508	A	20256	2	430	
20141	50509	A	20257	3	567	
20142	50510	B	20258	1	1317	
20143	50511	A	20259	928	2067	
20144	50512	A	20260	2	4498	VHELQSLSEMLKPEVLSPTVKG KLLTGIKSPRSYTPKPNPVTHVI STGIQKIWIGATVGSTEVSVAV TPDGYADAVRGDRFMMPAERR LPLSFVLDVLEGRAQHPGVLYV QKQCSNLPSELPQLLPDLESHV PWASEALVHKHHYENLYCVVS GEKHFLFHPPSDRPFIPYELYTP ATYQLTEEGTFKVVDEEAMEK VSVLFLGSREGEGQKPGSEEQA QKIWGVEAAVQRLGMLEAGIL PQEGRFQALAEIADI

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20145	50513	A	20261	3	3137	DTPAWHGDANRTKAALEAARS DYLEFPPAARELCVPLAVPYLD KPPTPLHFYRDWVCPNRPCIIRN ALQHWPALQKWSLPYFRATVG STKVSV\AVTPDGYADAVERGI RF/M*LPVERRLPLSFVLDVLEG RAQHPGVLYVQKQCSNLPSELP QLLPDLESHVPWASEALGKMP DAVNFWLGEAV*VTFLHKDHY ENLYCVGSGEKHFLFHPPSDRP FIPYELYTPATYQLTEEGTFKVV DEEAMEKAEVSRTC
20146	50514	A	20262	164	1236	AQSRRSRDRGQAFSNHHAAEHI TCTPGSGSGSRVSSGQAARRRL SGRAGLWAAVTNPPPHPTWLE VSRSAAATARAALCRRSACLLP RTPHLSAMISASRAAAARL/VG AAASRGLRAARHQIRSNQGTV VGIDLGTTNSCVAVMKKNVPF KIVRASNGDAW/VEAHGKLYSP SQIGAFV/LMKMKETAD**LFLS SEPPQPGQRAGFLQPSCCGAYY LYPWLRERQSSILWSGGAAAPQ RKSGPLGRSDQPPPSPHVVGGF QKRCRHRSRSSLPSERLFAASYS SFIRHDKCQPSCSSPSRGAAASR GLRAARHQIRSNQGTVVGIDLG TTNSCVAVMKKNVPFKIVRAS NGDAWVRLMGNCILRVRLEHL CDEDERDCRLIVALPEGMEEPE FDYQNDMGNSQDLERRRGCAA EPWEEGVGQSLALPLVSLCLKC RWYRSPCTQGQHPATFSGPAEG VISERSMLEHWHEEINQCKAYN EDVFSTMRTNPARISSEAMAPA DIIDHSSQRPDFTSGKMLADEF GTASNIKSRVNAFQSWEPLHLY NKDSNL
20147	50515	A	20263	216	728	

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20148	50516	A	20264	1	2519	MAPSSRSGAGNTSTPGGCARAR APPGNAGVHSGTQTGAVRDTA FISPSSPGLFLSSEPPQPGQRAGF LQPSCCGAYYLYPWLRERQSSI LWSGGAAAPQRKSGPLGRSDQ PPPSPHVVGGFQKRCRHRIAQL FAVGALVCCLVLLHLSAMISAS RAAAARLVGAAASRGPT\AAR HQDSW\NGLSHEAFRLVSRRDY \AS\EAIKGAVVGI\DLGTTNSCV AVMEGNQAK\VLENAEGAKTT PSVVAFTADGERLGGMPAKRQ AVTNPNNTFYATKRLIGRRYDD PEVQKDIKNVPFKIVRASNGDA WVEAHGKLYSPSQIGAFVLMK MKETAENYLGHTAKNAVITVP AYFNDSQRQATKDAGQISGLN VLRVINEPTAAALAYGLDKSED KVIAVYDLGGGTFDISILEIQKG VFEVKSTNGDTFLGGEDFDQAL LRHIVKEFKRETGVDLTKDNM ALQRVREAAEKAKCELSSSVQT DINLPYLTMDSSGPKHLNMKLT RAQFEGIVTDLIRRTIAPCQKA MQDAEVSKSDIGEVILVGGMT RMPKVQQTVQDLFGRAPSKAV NPDEAVAIGAAIQGGVLAGDV TDVLLLDVTPLSLGIET\HGAVF SKLINRKTNIPTKKSQVFSTAAD GQTQVEIKVCQGEREMAGDNK LLGQFTLIGIPPAPRGVPQIEVTF DIDANGIVHVSAKDKGTGREQ
20149	50517	A	20265	1	168	LERERRKRSRKELLNFYAWQH RESKMEHLR/QLRKKFEEDKQR IELLRAQRKFRPY

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20150	50518	A	20266	3	1085	ARAGAEPQLPATPALPGGKMV ARSLAGLSSG*PGHPSPPISFPAI PIKFSEKQQASHYLYVRAHGIQ QGTKWREALGWP/SRMLTLGF P/PPCS/EESLSCLQSTCGLVQSV ELKFPDLPHPCTSCLAFSVPC*S SRTVSAGHLQGLPRLPSCFPTE GAPSPGLGAGSPGALLFRDLVP DVGRSPQPLTSLSLQGFQVAYV VFQKPSGVSAALAVGPKCQA* GSPVSLAPFSSEWISDYADSVPD PGWRLREVPGAHRTMGSPSLQ EEAKAKEEEGVPDEEGWVKVT RRGRRPVLPRTEAASLRVLERE RRKRSRK\ELL\NFYAWQHSRE/ SKMEHS*GKCARSFEEDKQRIR ACCGPKRKIPDRN
20151	50519	A	20267	2	334	SLQVQPFASLISKAPLSTPRLLIN KEKAGQSDPFLGMIMGLGGGM DFDSKKA/YAELLGWKKELEDL VRREHASIDAQSGAGVPNPSTS ASPKKSPPPAKDEARTTEREKP Q
20152	50520	A	20268	124	407	QSDPFLGMIMGLGGGMDFDSK KAY/RVRPRRGLGQPGMDRVR WERGHEGR*EEQAGASPPGNS DLLLHRRDVAWLGECDQGCLA LAELLGWKVRS
20153	50521	A	20269	193	458	
20154	50522	A	20270	55	1165	RDRAVGDSLKGFSTAPMAEPD PSHPLETQAGKVQEAQDSDSDS EGGAAGGEADMDFLRNLFSQT LSLG\SQKERLLDELTLEGVA\R YMQSERCSQSSSCLVGAGISTS AGIPRLFASPSTGLLLNNLEK*P SFPNPEAIF*DSAIFKKH\PEPFFA LAK\EL\YPGAVSRPTICSIISCGL LERDKGGLLLR/CVKRREH*VT WERIAG\LEQEDLVEAHGTFYT SHCVSASCRHEYPLSWMKEKIF SEVTPKCEDC\QSLVKPD\IVFFG ESLGARFFSCYCSSDFLKV\DLL L\VMGTSL\RDVAWLGECDQGC LALAELLGWKKELEDLVRREH ASIDAQSGAGVPNPSTSASPKK SPPPAKDEARTTEREKPQ

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20155	50523	A	20271	3	357	FGFNGCSKRIIKLQELSDLEERE NEDSMVPLPKQSLKFFCALEVV LPSCDCRSPGIGLVEEPMDKVE EGPLSFLMKRKTAQKLAIQKAL SDAFQKLLIVVLG/QDCLDHP*S TSVSVSK
20156	50524	A	20272	696	1123	IPLKMMNFLQSLKSPQLSHQLR L*LPQEVEPSLTQQNFPAQTP/V PPMEAEPSPNQQEATVQASEPP KNIELSSQQMVPENIFPPTMENS NQLPEPPTEVVAQLPPRYEVTIP TQGQDQAQLSTLASVTLQPLDL GFIITPESTTEIELSPTMQETPTQ PPKEFVPQPPV/LSRESSEETGPL PVQQETSAESPEPTKDENPSPIQ *EAAFSEISSQGSSWHQT
20157	50525	A	20273	1	727	GIPAADR\EASLELIKLDISRTFP NLCIFQQGGPYHDMLHSILGAY TCYRPDVGYVQGMSFIAAVLIL NLDTADAFIAFSNLLNKPCQMA FFRVDHGLMLTYFAAFEVFFEE NLPKLFAHFKKNNLTPDIYLID WIFTLYSKSLPLDLACRIWDVF CRDGEEFLFRTALGILKLFEDIL TKMDFIHMAQFLTRLPEDLPAE ELFASIATIQMQSRNKKWAQVL TALQKDSREMEKGSPSLRH
20158	50526	A	20274	3	435	CGGIPKMEESAEYEAARHKRE KRMENINLAGSKRGKEDGKDS EFAAIENLPGFELLSDREKVLCS SLNLSPARYVTVKTIIIKDHLQK RQGIP/CQKPPS*LPGQSPKEKD FEFPHRKRLDLQGRVLKLRRFE SQGDAQTVCQPK
20159	50527	A	20275	46	513	

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20160	50528	A	20276	3	1084	NQEWKRSPPITVAKATQGAYL NILKDTLRAQKEQKEGKEEVIH KGAKLHPNGYRMAQGSETLVA RGGPCRSVEPSAASPQELRGW WEAQALKRWGLMGGVWVME VDPSWLGAISAIVSSSASRLLKS VWHIPCPHFLLLRPQLKEAQRR KKQLEERCRVEESIGNAVLTW NNEILPNWETMWCSRKVRDLW WQGIPPSVRGKVWSLAIGNELN ITHELFDICLARAKERWRSLSTG GSEVENEGLCVAVCAQQGHVG VMGFGSDEPSAVSPCEKGKSLA AWVLIFVDFRVGLQKSFQKRK ERESTKLQQLWSWCLMLTYFA AFEVFFEENLPKLFAHFKKNNL TPDIYLID/W*FRLLVGC
20161	50529	A	20277	60	556	EDSEMAPPAPGPASGGFGEVYE LFDVKNAFYIGSYQQCINEAQR VKLSSPERDVERDVFLYRAYL\ RRDSIVAELDREMSRSVDVTNT TFLLMAASIYLHDQNPDAALRA LHQGDSLECTAMTVQILLKLDR LDLARKELKRMQDLDEDATLT QLATAWVSLATGG
20162	50530	A	20278	1	628	FFYKSVLAQKEVRCVLDE/ISPL GPPELKPVRMFADL/LPHESRR DSSVPELAEKMSRSVDVPTPPS LLMAASIYLHDQNPDAALRAL HQGDSLECTAMTMQDAYYIFQ EMADKCSPTLLLLNGQAACHM AQGRWEAAEGLLQEALDKDSG YPETLVNLIVLSQHLGKPPEVT NRYLSQLKDAHRSHPFIKEYQA KENDFDRLVLQYAPSA
20163	50531	A	20279	1	884	RKFGVVLDEIKPSSAPELQAVR\ MFADYLAHESRRDSIVAELDRE MSRSVDVTNTTFLLMAASIYLH DQNPDAALRALHQGDSL\ECTA MTVQILLK\LDRL\DLARKELKR MQDL\DEDATLTQLATAW\VSL \ATGGEKLQDAYYIFQEMADKC SPTLLLLNGQAACHMAQGRWE AAEGLLQEALDKPPHGCSCERK LVSPFMVETEAQKSPVCKKVPC HGPPWAGRALGASSLDSGYPE TLVNLIVLSQHLGKPPEVTNRY LSQLKDAHRSHPFIKEYQAKEN DFDRLVLQYAPSA
20164	50532	B	20280	512	903	
20165	50533	A	20281	18	413	

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20166	50534	A	20282	1	1195	MKHPNINSALQAPHPFVPGRPH LVAGVAPPALSNHPQARATAA AGKPHPRCAEAAGIGLACTAPG SHWLKMGELPLDINIQEPRWD QSTFLGRAP\HFFTVTDPRNLLL SGAQLEASRNIVQNYRAGVVTP GITEDQLWRAKYVYDSAFHPD TGEKVVLIGRMSAQVPMNMTI TGCMLTFYRQGSKDEGHCRRG RSECLCSLRKTPTVVFWQWVN QSFNAIVNYSNRRW*HFPSLVR QLGT\AYVSAT\TGAVATALGL KSLTKHLPPLVGRFVPFAAVAA ANCINIPLMRQRELQVGIPVAD EAGQRLGYSVTAAKQGIFQVVI SRICMAIPAMAIPPLIMDTLEKK DFLKRRPWLGAPLQVGLVGFC SIHISNLEPELRAQIHEQNPSVE VVYYNKGL
20167	50535	B	20283	24	51	
20168	50536	C	20284	1	1182	
20169	50537	B	20285	1	372	
20170	50538	A	20286	1	4610	ELAQNHSRPAPASAPGGGGGG DPNMATARTFGPEREAEPAKE ARVVGSELVDTYTVYIIQVTDG SHEWTVKHRYSDFHDLHEKLV AERKIDKNLLPPKKIIGKNSRSL VEKREKDLEVYLQKLLAAFPG VTPRVLAHFLHFHF\YET*VIHA A\LAEELFEKGEQLLGAGEVFAI GPLQLYAVTEQLQQGKPTCAS GDAKTDLGHIL\DFTCRLKYLK VSGTEGPFGTSNIQEQLLPFDLS IFKSLHQVEISHCD
20171	50539	A	20287	1	4670	MAAQRAAGATGGGGRGASAP GGGGGGDPNMATARTFGPERE AEPAKEARVVGSELVDTYTVYI IQVTDGSHEWTVKHRYSDFHD LHEKLVAERKIDKNLLPPKKIIG KNSRSLVEKREKDLEVYLQKLL AAFPGVTPRVLAHFLHFHFYEI NGITAALAEELFEKGEQLLGAG EVFAIGPLQLYAVTEQLQQGKP TCASGDAKTDLGHILDFTCRLK YLKVSGTEGPFGTSNIQEQLLPF DLSIFKSLHQVEISH
20172	50540	A	20288	2	227	ERFRPPIARVIDVSNGKVHVAE/ SCLEETGGLGVDIVLDAG\LDPP DSHCLFLKGATLAFLNDEVWN LSNVQQGRYL
20173	50541	A	20289	3	487	

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20174	50542	A	20290	2	222	
20175	50543	A	20291	1	296	HLSPGKSV\LIMDGASA\F\GTIAI QLAHHRGAKVISTACSLEDKQC LERFRPPIARVIDVSNGKVHVA ESCLEETGGLGVDIVLDAGGYI FQHSSYIFT
20176	50544	A	20292	353	512	
20177	50545	A	20293	2	396	VRLYSKDDEPAVKLQLLPHKH DIITLLGVGGHWVTTEENLQLD PPDSHCLFLKGATLAFLNDEVW NLSNVQQGKYLS*QSFQLRILK DVMEKLSTGVFRPQSDEHIPVF EARI\SLEIVEKNQGR*NKLHF
20178	50546	B	20294	1	1182	
20179	50547	A	20295	1	1189	PTRPDQWEQGAGSLTKDWKV AVVKVQAVGAAQRQVTMKGL YFQQSSTDEEITFVFQEKEDLPV TEDNFVKLQVKACALSQINTKL LAEMKMKKDLFPVGREIA\GIV LDVGSKVSFFQP\DDEVVGILP\ LDS*KTPGL\CESLLRVHEPLLG FINPEKVTW\TEAAGSISGMGV RAYYSFLHLS/YLHLLSWGKSV LIMGGS/ASAFGTIAIQLAHHRG AKVISTACSLEDKQCLERFRPPI ARVIDVSNGKVHVAESCLEETG GLGVDIVLDAGVRLYSKDDEP AVKLQLLPHKHDIITLLG\VGGH WVTTEENLQLDPPDSHCLF\LK GATLAFLNDEVWNLSNVQQGK YLCILKDVMEKLSTGVFRPQLD EPIPLYEAKVSMEAV\QKNQGR
20180	50548	A	20296	3	115	FFKFSFFNGC*SIKRQSQGQALD RDIICFVDICTKDC

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20181	50549	A	20297	1	1401	MKEEELTRQIVLVQEAGKGVV RTKDGACAEVWQALEELEKGL CAGIVRVEGMAAAPPSYCFVAF PPRAKDGLVVFGKNSARPRDE VQEVVYFSAADHEPESKVECT YISIDQVPRTYAIMISRPAWLW GAEMGANEHG\VCIANEAINTR EPAAEIEALLGMDLVRL\GLER GETAKEALDVIVSLLEEHGQGG NYFEDANSCHSFQSAYLIVDRD EAWVLETIGKYWAAEKVTEGV RCICSQLSLTTKMDAEHPELRS YAQSQGWWTGEGEFNFSEVFS PVEDHLDCGAGKDSLEKQEESI TVQTMMNTLRDKASGVCIDSE FFLTTASGVSVLPQNRSSPCIHY FTGTPDPSRSIFKPFIFVDDVKL VPKTQSPCFGDDDPAKKEPRFQ EKPDRRHELYKAHEWARAIIES DQEQGRKLRSTMLELEKQGL* AMEEILTSSEPLDPAEVGDLFY
20182	50550	A	20298	1	356	QTPKIVADKDYSVTANS\KIVV VTAGVRQQEGESRLNLVQRNV NVFKFIIPQIVKYSPDCIIIVVSNP VDILTYVTWK/ARFRYLMAEKL GIHPSSCHGWILGAHGDSSVAV WSGVNLAG
20183	50551	A	20299	1	322	
20184	50552	A	20300	25	1086	
20185	50553	A	20301	1	864	
20186	50554	A	20302	13	190	

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20187	50555	A	20303	1	1350	MEKPKRLRWLWGPAPSSLLAE PAPEETHAADFVFSARLLQRSP EPSLSWGGRALAEEQKAEGSSC GSAERLVAFAAKTRPYLSLCK MATLKEKLIAPVAEEEATVPNN KITVVGVGQVGMACAISILGKS RAMEHTTAGAPYTPRQQTCQC NMMSLADELALVDVLEDKLKG EMMDLQHGSLFLQTPKIVADK DYSVTANSKIVVVTAGVRQQE GESRLNLVQRNVNVFKFIIPQIV KYSPDCII\IVVSNPRDI\LTYGT WKLSGLPKHRVIGSGCNLDSAR FRYLMAEKLGIHPSSCHGWILG EHGDSSVAVWSGVNVAGVSLQ ELNPEMGTDNDSENWKEVHK MVVESA\YEV\IQA*KGYTH\WA IGLSVA/EILNESMLKNLSR\IHP VSTMVKGMYGIENEVFLSLP\CI \LNAGGLTSVINP\KVKDDEVAQ LKKSADTLWDI\QKDLKDL
20188	50556	B	20304	1337	1706	
20189	50557	A	20305	178	344	
20190	50558	A	20306	2	297	TKMTVNNLHPRVTEEDIV/GQP MKCNLHMNGNVITSDQPILLRL SDSPSMKKESELPRRVNSASSS NPPAEVDPDTILKALFKSSGAS VTTQPTEFKIKL
20191	50559	B	20307	8	478	
20192	50560	C	20308	146	391	
20193	50561	A	20309	3	735	HRQKDARFRIKGKVQDAREML NSRKQQTTVPQKPRQVADARE KISLKRSSPAAFINPPIGTVTPAL KLTKTIQVPQQKAMAPLHPHPA GMRINVVNNHQAKQNLY\DLD EDDDGIASV\PTKQMKFAASGG FL\HHM\AGLSSSKLSMSKALPL TKVVQNDAYTAPALPSSIRTKA LTNMSRTLVNKEEPPKELPAAE PVLSPLEGTKMTVNNLHPRVTE EDIVELFCVCGALKRARLVHPG VAEVG

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20194	50562	A	20310	1	1763	MEIASFVGPNVNTVGNLRPAQS AAGDGDEVQSVHSQRQDCQAT GSLSNGENNEKNAFTTYQQET KNTTTPQSVYFLGVNKMSSQH REGSRGTSPPLPVLACFELAVA RVGPRTPEVVRRSLAAEGAGSR GLDCFRLARRIKMADISLDELIR KRGA\AAKGRLNARPGVGGVR SRVGIQQGLLSQSTRTATFQQR FDARQKIGLSDARLKLGVKDA REKLLQKDARFRIKGKVQDAR RDV*TFRKQQTT\VPQKPRQV\A D\ARERIQLGRGRSPAAFLNPPI GTGTPALKLTTTIQRMHVDPVG WILTTECFQVPQQKAMAPLHP HPAGMRINVVNNHQAKQNLY DLDEDDDGIASVPTKQMKFAA SGGFLHHMAGLSSSKLSMS\KA LPLTKVVQNDAYTAPALPSSIR TKALTNMSRTLVNKEEPPKELP AAEPVLSPLEGNKMTV\NNLHP RVTEEDIV\EVFCVCGGL/RRRA RLVPSGG*PKVVFCEKRDDAIT AYKKYNNRCLDGQPMKCNL\H MNGNVITSDQPILLRLSDSP\SM KKESELPRRVNSASSSNPPAEV DPDTILKALFKSSGASVTTQPTE
20195	50563	A	20311	1	915	
20196	50564	A	20312	3	3238	LDTDDDLNSDDYEYEDEAKLVI FPDHYEIALPNIEELPALVSECA RLLARCAWLCVSLKLSTLLTDD TGLLTVRNKEEVLARSAKVTIA CDAVLSSKSPYRKQDPDTWEN ELPVSKYANNLTQLDNGVRIPP SGWKCARCDLRENLWLNLTDG SVLCGKWFFDSSGGNGHALEH YRDMG\YPLAVKLGTITPDGAD VYSFQEEEP\VLDPHLAKHLAH F\GID\MLHMHGTENGLQ\D\NDI KLRVSEWEVIQES

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20197	50565	A	20313	2	2716	AEFRGIPRRRRQTPRSGSGSAR SAPVRAEAMQRRGALFGMPGG SGGRKMAAGDIGELLVPHMPTI RVPRSGDRVYKNECAFSYDSPN SEGGLYVCMNTFLAFGREHVE RHFRKTGQSVYMHLKRHAREK VRGASGGALPKRRNSKIFLDLD TDDDLNSDDYEYED*AFLVIFP DHYEIALPNIEELPALVTIACDA VLSSKSPYRKQDPHTWENELPV SKYANNLTQLDNGVRIPPSGW KSARCDLRENLWLN
20198	50566	A	20314	2	322	
20199	50567	A	20315	1285	3331	GAGAPRDWRLRRRGGAALCLK VLFDVRSFPREAAALTPHRLLQ FPRSSESPGDQMMAAARLLPVP AGPQPLSFQAKLTFEDVAVLLS QDEWDRLCPAQRGLYRNVMM ETYGNVVSLGLPGCKPDIIFHLE LRGISLGPVPEWG*EEPGPVE*L L/ENVETKGESQNTDLSPKPLIS EQTVILGKTPLGRIDQENNETK* SFCLSPNSVDHREVQVLSQSMP LTPHQAVPSGERPYMCVECGK CFGRSSHLLQHQRIHTGEKPYV CSVCGKAFSQSSVLSKHRRIHT GEKPYERNRACISLYSE\PHLAH LSLIHTGEKPH*CLECPKAFTQL SHLIQHQRIHTGERPYVCPLCG KAFNHSTVLRSHQRVHTGEKP HRCNECGKTFSVKRTLLQHQRI \HTREKPYTCSECGKAFNDRSV LIQHHNVHTREKPYECSECGKT FSHRSTLMNHERIHTEEKPYAC YECGKAFVQHSHLIQHQRVHT GEKPYVCGECGHAFSARRSLIQ HERIHTGEKPFQCTECGKAFSL KATLIVHLRTHTGEKPYECNSC GKAFS\RTQLLIQHQRIHTGEKP YECGECGGAFNQHGHLIQHQK SAQKSCDPWLTQE/CPFSQKLH VEPTSSLQPKRSLC*LYRKLFFG DSVSQNNSRKKHLACCSCGKTS ETTCFIFLNHLEV/HVGE*SYNC
20200	50568	A	20316	1	319	
20201	50569	A	20317	1	2433	
20202	50570	A	20318	2	293	GELAGTQCTRGACPHSP*PLHR Q/HTTVTHITAFDPDSTGQQVW QDLLQDGQLDSPTGDGGSDWE MVGREVVPVLGPGVGGLVISRP CFHVRDPYPWG

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20203	50571	A	20319	1	537	GGGTITRGWRGQFCRWQLNPG MYQHRTVIADQMRTLRSREV** HAQGHKFTVCLRREGQTVYQQ VLSLERPSVLRSWNWGLCGYF AFYHALYPRAWTVYQLPGQNV TLTCRQITPILPHDYQVRPPHLY LPLPSLPQDLPLLETAWPARRG SHACNPNTLGGKAGGSRDQEIE TILANT
20204	50572	C	20320	3	170	
20205	50573	A	20321	278	1018	RVGVSRRPEVRNWATRDCRAQ ERMTHCLLHGMGRAGAASLTP KPMSLISAYCGGLWLAAVAVM VQMAALCEGTGQSRISFLLSSA GAKKPMRDCCGMVSSGSLSSL KAAERTPGALFFSSSTPGRYYN YDSSSRPQSRSVMSDQVCWTV GVPEGLWP*EKGDTEVREEEEQ PERKMGFPWRWEVFPTQHVVR ALQTIFELNVQAFAGGAMGAV NGMQPHGVPDKSSVQSDEVW VGVVYGLAATMIQE
20206	50574	A	20322	3	627	

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20207	50575	A	20323	270	2945	NTSSFKLSPTTGPPGRYLTTTGA RIWNRLARYLVSEGSGLGAIEV MGTQDPGNMGTGVPASEQISC AKEDPQVYCPEETGGTKDVQV TDCKSPEDSRPPKETDCCNPED SGQLMVSYEGKAMGYQVPPFG WRICLAHEFTEKRKPFQANNVS LSYMIKHIGMGLRYLQWRDRK THVEKKTPFIDMNKSVPPIQSYF \VPLGGLRGGTSTRGWRGQFCR WQLNPGMYQHRTVIADQFTVC LR\REGQTVYQQVLSL\ERPSVL RSWNWGLCGYFAFYHALYPRA WTVYQLPGQNVTLTCRQITPIL PHDYQDSSLPVGVFVWDVENE GDEALDVSIMFSMRN/GTGWW RRCPRGFVGMSPSVWSVGVQT VRGLLLHSSNPSKPLHDGLWLA RSSRAATTVNPH/CTAFDPG\RT GAA\VWQDLLQDGQLDSPTGQ RTPTQKGVGIAGAVCVSSKLRP RGQCRLEFSLAWDMPRIMFGA KGQVHYRRYTRVFGAG\GDAP PALSHYALCRYAEWEERISAW QSP\VLDDRSLPAWYKSALFNE LYFLADGGTVWLEVLEDSLPEE \RAETSVTSAPTLRDYRRFG*LE GQEY\RMYNTYDVHFYASFALI MLWPKLELSLQYDMALATLRE DLTRRRYLMSGVMGTCEKEGT FIPHDIGGPRWMEPWASAFNAY \LIHDTADW\KDLNLKFVACRFI
20208	50576	C	20324	123	359	
20209	50577	A	20325	1	259	KPVGEKDTWSGMRTTGQLRPA HGVRLKANKDSLYKPILRQKK HFNSLHIPKALQKALPFKNKPK TQAKAGKVPKDRRR*TVSNITV
20210	50578	A	20326	297	585	
20211	50579	A	20327	182	374	PDFRIAAT*VVLDLDKSIKIVKK LKLTGFPYKIFKNTSFIKACISIY SHIYKSPYCLRKGMKYL

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20212	50580	A	20328	1	1267	MAANRKDFIHRRCGPELSQSEA VPQGLCRAERSSALAMLSGSVP RRTQLRPCKGTQRRCRRGGEA DSGGEAVGGGAAERRSAAARR RGGRRRGGGEAVGGGAAERRS AAARRRRGGRRRRGGGEAGGG GAAEARRAAAARRAAAARRA AAARRAAAARRAAAARRIAES GGEAHSRGEAHSGGEAHSGGA GAERRRPRLHSPALKTHPGQSS EGHVEYKLNHVEFEDQDDEAR VQYEGFRPGMYVRVEIENVPCE FVQNFDPLYPIILGGLGNSEGNV GHVQMRLKKHLWYKKILKSQ DPIIFSVGWRRFQTILLYYIEDH NGRQRLLKYTPQHIHCGAAFW DIVFMRT\WYLVSIPAFYNPVTS LLKPVGEKDTWSGMWTTGQL RLAHGVRLKTTKDSLYKNIHMI VETDTYSDHEEINTS
20213	50581	A	20329	66	1414	KEELYGDFEDLETGDVHKGKS GPDTQNEDVEK\KEEIDPDEEES AKKKHLDKKRKLKEMFDVEY DEGESTYFDDLKGEMQKQAQV N/RHTRFPPRAPRHVQLNHAEF EDQDDEARVQYEGFRPGMYVC VEIENVPCEFV*NLDPRYPIILG GLGNSEGNVGYVQVGPFAAYL VPEALWISPPSIILPSHPPQMRLK KHRWYKKILKSRDPIIFSVGWR RFQTIPLCYIEDHNGRQRLLKY TPQHVHRGAAFRSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSR IAATGVVLDLDKSIKVVKKLKL TGFPYKIFKNTSFIKGMFNSALE VAKFEDAVIRTVSGIRGQIKRA L*APEGAFQDSLEDKLRMSDIV FMRTWYPVSIPAFYNPVTSLLK PVGEKDTWSGMWTTGQLRLA HGVRLKTNKDSLYKVLVVCVL VEMKPVLYRQ

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20214	50582	A	20330	4210	5099	AKDQKKHRKKNSGPKAAKKK KRLLQDLQLGD\EEDAWKRNP KAF\AFQSAVWMARSFHRTQD LKTKKHHIPVVD\RTPLEPPPI\V VVVMGPPKVGKSTLI*CLI\RNF TRQKLTEI\RGPVTIVSGKKLRL\ TIIDCGCDINMMIDLG\EVADLV LMLIDASFGFEMETFEFLNICQV HGFPKIMGVLTHLDSFKHNKQL KKTKKRLKHRFWTEVYPGAKL FYLSGMVHGEYQNQEIHNLGH FITVMKFRPLTW
20215	50583	A	20331	56	467	
20216	50584	A	20332	282	452	
20217	50585	A	20333	1	1356	
20218	50586	A	20334	80	1096	GLGVRVLRCPGVYRGPCTRAA YLGWLWTTLSPYCCLRSADMN PIVLVHGGGAGPISKDRKERVH HGMVRATTVGYGILREGGSAV DAVQGAVVALEDDPEFNAGCG SVLNTNGEVEMDASIMDGKDL SAGAVSAVQCIANPIKLARLVM ENFPHCFLTDQGAAHFAGAMG VPEIPGKKLVTERNKKRLEKEK HEKGAHKTDCQKNLGTVGAV ALDCKGNVAYATSTGGIVNKM VGRVGDSPSLGAGGYADHDF* AVSTTGHGE\SFLKVNLARLTLF HIEQGKTLEEAADPIG/CG*MKS RVKGLGGLIVVSKTGDWVAK WTSTSMPWAAAKDGKLPLRN
20219	50587	A	20335	1	1416	
20220	50588	A	20336	3	277	

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20221	50589	A	20337	235	2811	VKMEAPLRPAADILRRNPQQD YELVQRVGSGTYGDVYKARNV HTGELAAVKIIKLEPGDDFSLIQ QEIFMVKECKHCNIVAYFGSYL SREKLWICMEYCGGGSLQDIYH VTGPLSELQIAYVCRETLQGLA YLHTKGKMHRDIKGANILLTD HGDVKLADFGVAAKITATIAKR KSFIGTPYWMAPEVAAVEKNG GYNQLCDIWAVGITAIELGELQ PPMFDLHPMRALFLMSKSNFQP PKLKDKTKWSSTFHNFVKIALT KNPKKRPTCLKDF*HHTF\VAQ PGLSRALAVELLDKVNNPDNH AHYTEADDDDFEPHAIIRHTIRS TNRNARAERTASEINFDKLQFE PPLRKETEARDEMGLSSDPNFM LQWNPFV*WWQITGKSTSKR\A IPPPLPPKPRISSYPEDNFPDEEK ASTIKHCPDSESRAPQILRRQSS PSCGPVAETSSIGNGDGISKLMS ENTEGSAQAPQLPRKNDKRDFP KPAINGLPPTPKVLMGACFSKV FDGCPLKINCATSWIHPDTKDQ YIIFGTEDGIYTLNLNELHEATM EQLFPRKCTWLYVINNTLMSLS EGKTFQLYSHNLIALFEHAKKP GLGCPIFQTHRFPDRILPRKFAL TTKIPDTKGCHK\CCIVRNPYTG HKYLCGALQSGIVLLQWYEPM QKFMLIKHFDFPLPSPLNVFEM LVIPEQEYPMVCVAISKGTESN
20222	50590	C	20338	365	389	
20223	50591	A	20339	1	350	FDVTELCGQWLSRGGEIEGFRL SAHCSCDSRDNTLQVDINGFTT GRRGDLATIHGMNRPFLLLMA TPLERAQHLQSS/RAPCCVPQAL EPLPIVYYVGRKPKVEQLSNMI VRSCKCS
20224	50592	A	20340	1	708	
20225	50593	B	20341	229	1249	
20226	50594	B	20342	49	375	
20227	50595	A	20343	42	305	GARAHAPVLVQEEDLHGPHPL RPERL/PSVPSGRSSPPASR/PVG PGG/DQLRPSPDRQQQVSGME WC/PWSGRSPGLSPTVGPRGGC HPTST
20228	50596	B	20344	8	1990	
20229	50597	A	20345	1	1512	

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20230	50598	A	20346	1	1663	SGRDRRGRAWRKRNREPPTRG RSPDPQGPSARPLPSLGARISAA DRLSGLAARLIGNSRPVAGANA GVGPDLSHAGLVPTCARRLRR KNGLGRRRRRPPPSPPRPSLESS SRLTTLGTSQPLKFNFFPCDLRI FQTFNC\WGI\PVL*AKHR\ADR MRRFGRPF*TQESFDLALLEEV WSEHDFQYLRQKLSPTYPAAH HFRSGIIGSGLCVFSKHPIQELT QHIYTLNGYPYMIHHGDWFSG KAVGLLVLHLNGMELNAYVTH LHAEYNRQKDIYLTHLVG\QA WELAQFIHHTSKKADVVLLCG DLNMHPEDLGCCLLKEWTGLH DAYLETRDFKGSEEGNTMVPK NCYVSQQELKPFPFGVRIDYVL YKAVSGFYISCKSFETTTGFDPH SGTPLSDHEALMATLFVRHSPP QQNPSSTHGP\AERSPL/MCVCL KEALDGSLGLGMA\QARWWA\ TFA\SYVIGLGL\LLLALLCVLA AGGGAGEAAILLWTPSVGLVL WAGAFYLFHVQEVNGLYRAQ AELQHVLGRAREAQDLGPEPQ LYALL\LGQQEGDRTKEQ
20231	50599	A	20347	175	544	RLRCQKGIPPSLRGRAWQYLSG GKVKLQQNPGKFDQ\LDMSPG DPTWLDVIERDLHRQFP\FHEM FVS/RGGH/GQQDLFRVLDAYT LYRPEGSYCKTQAPIAAVLLMH MP\AEQAFWCLVQICEKYL
20232	50600	A	20348	1	434	CAAGIRHELRRRARLGWRTAT ERMGRACPRPGKACREPGRA* ARALTPQPPTNSALSGLTRRPT ASPS\PHRQVRLDRGLAGRQGR AGGSTPGGAEAEGVQVAGHAQ AMVVAAARDACPPQHVPPKDS APKDSAPQDLAPQVSAH
20233	50601	A	20349	3	510	

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20234	50602	A	20350	1	1669	MAKSNGENGPRAPAAGESLSG TRESLAQGPDAATTDELSSLGS DSEANGFAERRIDKFGFIVGSQ GAEGASILGQTVPSPHGRVGEG PPIRSYTASSTGTGNRLEEVPLE VLRQRESKWLDMLNNWDKW MAKKHKKIRLRCQKGIPPSLRG RAWQYLSGGKVKLQQNPGKF DELDMSPGDPKWLDVIERDLH RQFPFHEMFVSRGGHGQQDLF RVLKAYTLYRPEEGYCQAQAPI AAVLLMHMPAEQAFWCLVQI
20235	50603	A	20351	1	243	
20236	50604	A	20352	70	382	
20237	50605	A	20353	2	322	
20238	50606	A	20354	86	215	
20239	50607	B	20355	1	735	
20240	50608	A	20356	92	1104	MSSPQAPEDGQGCGDRGA\PPG DLRSVLVTTVLNLEPLDEDLFR GRHYWVPAKRLFGGQ\IVGQA M\VAAATSV\SEDVHV\HS\LHC YF/VFRAGDP/KSLPVLYQVERT RTGVEA\FRLRSVKGP*NMGKPI F\ICQ\ASFQQA\QPSP\MQHQFS MP/TLLPTTEELV*IVRTLFDQY LRDPNLQKRYPLALNRI\AAQE VPIEIKPVNPSPLRPAAEEWEPK QMFW\VRARGY\IGKSTPWKM\ HC\CV\AAYIS\DYAFLGTALAA LTQWPSTRCHFHGPPLD/HNPM W\FHAPFRAD\HWMLYECESPW AGG\SRGL\VHGRLWRQDGVLA VTCAQEGVIRVKPQVSESKL
20241	50609	A	20357	3	1106	LRRQLQPLLPLPKSPPRSGAHL GSLFRSPQPSYPVRPPGSAGTPP PACLPPAQPCQGSPAMNLFRFL GDLSHLLAIILLLLKIWKSRSCA GISGKSQVLFAVVFTARYL\DLF TNYISLYNTCMNV\VYIACSFTT VWLIY\TKFK\ATYDG\NH\DTFR SGSSRVV/VPQAILGVSWSNHD FTPL\EILW\TFSIYLGVSGPSLPQ LFHG*GKTGRGRETHSPATYLF CAKAFNPHALSLSNW\IWR\YHF \EGFFD\LIAIVAGPGPRQSSYCD FF\YLYYSPKFLKGERKFEFCRH RPRFLSISSPRAAAGRAGGKAG RKMKSFSHPRGDFFKNPTSLCS PIPPSCPGLKGNSARIPGLWGAQ RLGAVCSFLAF

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20242	50610	A	20358	356	1356	TPTTSGRTRKMWPRPGT*PP/A NCSANINLTHQPWFQVLEPQFR QFLFYRHCRYFPMLLNHPEKCR GDVYLLVVVKSVITQHDRREAI RQTWARAAVRGWGPSAVRTLF LLGTASKQEERTHYQQLLAYE DALYGDILQWGFLDTFFNLTLK EIHFLKWLDIYCPHVPFIFKGDD DVFVNPTNLLEFLADRQPQENL FVGDVLQHARPIRRKDNKYYIP GALYGKASYPPYAGGGGFLMA GSLARRLHHACDTLELYPIDDV FLGMCLEVLGVQPTAHEGFKTF GISRNRNSRMNKEPCFFRAMLV VHKLLPPELLAMWGLVHSNLT CSRKLQVL
20243	50611	A	20359	221	1579	CCVDEGLEPTCFERTEDIGGVW RFKVSEIFLGLEQVVLLFQGESQ LMSCFSDFPMPEDFPNFLHNSK LLEYFRIFAKKFDLLKYIQFQVL YFWGNGFLCISSAHI*IENTQSN GKEQSAVFDAVMVCSGHHILP HIPLKSFPGETRWDSQLFGVGF QVLYM*FEGKRILVIGMGNSGS DIAVELSKNAAQV*CSLLTMYL EGRKWGCHTGDWDSVFHTRFR SMLRNVLPRTAVKWMIEQQM NRWFNHENYGLEPQNK*SYFA FLMVYSLVSKVV*RCLKVKST VKELTETSAIFEDGTVEENIDVII FATGYSFSFPFLEDSLVKVENN MVSLYKYIFPAHLDKSTLACIG LIQPLGSIFPTAELQARWVTRVF KGLCSLPSERTMMMDIIKRNEK RIDLFGESQSQTLQTNYVDYLD ELALEIGAKPDFCSLLFKDPKLA VRLYFGP\CNSY
20244	50612	A	20360	3	200	
20245	50613	A	20361	292	570	
20246	50614	A	20362	2	511	RLRSGPLRLPGADSGSGPKAVC SPPFIVAPTGRGYCGDHESSFGA MEEPGVTPQPYLGLLLEELRRV SPGAMSVTWP/EGSREPPGEGSS RPALGSKPPWSEVPKPVLVCCP APAR\FEAVVRLVGRLSGFCVM EEDLGLWEGREKKLALMLSGLI EEKSKLLEKFSLVQKE

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20247	50615	A	20363	2	3262	FLSDLEENFENNIFSFQVCDVVL NHAPDFRRVYLPYVTNQTYQE RTFQSLMNSNSNFREVLEKLES DPVCQRLSLKSFLILPFQRITRL KLLLQNILKRTQPGSSEEAEAT KAHHALEQLIRDCNNNVQSMR RTEELIYLSQKIEFECKIFPLISQS RWLVKSGELTALEFSASPGLRR KLNTRPVHLHLFNDCLLLSRPR ESVTGVAGQGTRGEGDEERGG SEREREGSEKLRWISALAMPRE ELDLLECYTAE
20248	50616	A	20364	2	2339	TGRGYCGDHESSFGAMEEPGA TPQPYLGLLLEELRRVVAALPE GMRPDSNLYGFPWELVICAAV VGFFAVLFFLWRSFRSVRSRLY VGREKKLALMLSGLIEEKSKLL EKFSLVQKEYEGYEVESSLKDA SFEKEATEAQSLEATCEKLNRS NSELEDEILCLEKELKEEKSKHS EQDELMADISKRIQSLEDESKSL KSQVAEAKMTFQIFQMNEERL KIAIKDALNENSQLQESQKQLL QEAEVWKEQVSELNKQKVTFE DSKVHAEQVLNDKESHIKTLTE RLLKMKDWAAMLGEDITDDD NLELEMNSESENGAYLDNPPK GALKKLIHAAKLNASLKTLEGE RNQIYIQLSEVDKTKEELTEHIK NLQTQQASLQSENTHFENENQ KLQQKLKVMTELYQENEMKL HRKLTVEENYRLEKEEKLSKV DEKISHATEELETYRKRAKDLE EELERTIHSYQGQIISHEKKAHD NWLAARNAERNLNDLRKENA HNRQKLTETELKFELLEKDPYA LDVPNTAFGRGSRGPGNPLDH QITNERGESSCDRLTDPHRAPS DTGSLSPPWDQDRRMMFPPPG QSYPDSALPPQRQDRFCSNSGR LSGPAELRSFNMPSLDKMDGS MPSEMESSRNDTKDDLGNLNV PDSSFP\AKKEATGPGFVPPPLA PVRGPLFPVDARGPFLRRGPPFP

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20249	50617	A	20365	160	2810	GLRVPLSPSSPRSRLRSGPLRLP GADSGSGPKAVCSPPFIVAPTG RGYCGDHESSFGAMEEPGATP QPYLGLLLEELRRVVAALPEG MRPDSNLYGFPWELVICAAVV GFFAVLFFLWRSFRSVRSRLYV GREKKLALMLSGLIEEKSKLLE KFSLVQKEYEGYEVESSLKDAS FEKEATEAQSLEATCEKLNRSN SELEDEILCLEKELKEEKSKHSE QDELMADISKRIQSLEDESKSL KSQVAEAKMTFQIFPMNEERLK IAIKDALNENSQLQESQKQLLQ EAEVWKEQVSELNKQKVTFED SKVHAEQVLNDKESHIKTLTER LLKMKDWAAMLGEDITDDDN LELEMNSESENGAYLDNPPKG ALKKLIHAAKLNASLKTLEGER NQIYIQLSEVDKTKEELTEHIKN LQTEQASLQSENTHFENENQKL QQKLKVMTELYQENEMKLHR KLTVEENYRLEKEEKLSKVDEK ISHATEELETYRKRAKDLEEEL ERTIHSYQGQIISHEKKAHDNW LAARNAERNLNDLRKENAHNR QKLTETELKFEL\LEEDPYALDV PNTAFGREHSPYGPSPLGWPSS ETRAFLSPPTLLEGPLTLSPLLP GGGGRGSRGPGNPLDHQITNER GESSCDRLTDPHRALSDTGFLS PPWDQDRRMMFPPPGQSYPDS ALPPQRQDRFCSNSGRLSGPAE
20250	50618	A	20366	131	461	

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20251	50619	A	20367	1	1761	MARGYGATVSLVLLGLGLALA VIVLAVVLSRHQAPCGPQAFAH AAVAADSKVCSDIGR\AILQQQ GSPVDASIAALVCTSVVNPQSM GLGGGVIFTIYNVTTGKVEVIN ARETVPASHAPSLLDQCAQALP LGTGAQWIGVPGELRGYAEAH RRHGRLPWAQLFQPTIALLRGG HVEAPVLSRFLHNSILRPSLQAS TLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRL GQMLVEDIAKEGSQLTLQDLA KFQPEVVDALEVPLGDYTLYSP PPPAGGAILSFILNVLRGFNFST ESMARPEGRVNVYHHLVETLK FARGQRWRLGDPRSHPKLQNA SRDLLGETLAQLIRQQIDGRGD HQLSHYSLAEAWGHGTGTSHV SVLGEDGSAVAATSTI\NTPFGA MVY\SPRTGIILNNELLDLCERC PRGSGTTPSTVSGDRVGGAPGR CWPPVPGEPSPSSMEPSILINKA QGSNLVIGCAGGELIISAVAQAI MSKLWLGFDLRAAIAAPILHVN NKGCVEYEPNFSQEVQRGLQD RGQNQTQRPFFLNVVQA[illegible]DE GACVYAVSDLRKSGEAAG

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20252	50620	A	20368	341	2239	LCASSCPFICPPIRPSVCPPAAPL LLGCRAMARGYGATVSLVLLG LGLALAVIVLAVVLSRHQAPCG PQAFAHAAVAADSKVCSDIGR AILQQQGSPVDATIAALVCTSV VNPQSMGLGGGVIFTIYNVTTG AQWIGVPGELRGYAEAHRRHG RLPWAQLFQPTIALLRGGHVVA PVLSRFLHNSILRPSLQASTLRQ LFFNGTEPLRPQDPLPWPALAT TLETVATEGVEVFYTGRLGQM LVEDIAKEGSQLTLQDLAKFQP EVVDALEVPLGDYTLYSPPPPA GGAILSFILNVLRGFNFSTESMA RPEGRVNVYHHLVETLKFAKG QRWRLGDPRSHPKLQNASRDL LGETLAQLIRQQIDGRGDHQLS HYSLAEAWGHGTGTSHVSVLG EDGSAVAATSTIYTPFGAMVYS PRTGIILNNELLDLCERCPRGSG TTPSPV/SGDRVGGAPGRCWPP VPGERSPSSMVPSILINKAQGSK LVIGGAGGELIISAVAQAIMSKL WLGFDLRAAIAAPILHVNSKGC VEYEPNFS/QETVSCFVALAVL KLLASSDPATLAPKWLRL*EVQ RGLQD\RGQNPDPEGPFFLDVV PACV/SQEGACV*RPSRT*RKSG EAAGLLKTLLCPELEVLAPP
20253	50621	A	20369	203	1518	RCYLQFLALLLTSTSARAAAAI AAAEEPAGSPSVMTRAGDHNR QRGCCGSLADYLSSAKFHL*LG HSLSTWGDRMWHFAVSVFLVE LYGNSLLLTAVYGLVVAGSVL VLGAIIGDWVDKNARLKVAQT SLVVQNVSVILCGIILMMVFLH KHELLTMYHGWVLTSCYILIITI ANIANLASTATAITIQRDWIVV VAGEDRSKLANMNATIRRIDQL TNILAPMAVGQIMTFGSPVIGC GFISGWNLVSMCVEYVLLWKV YQKTPALAVKAGLKEEETELK QLNLHKDTEPKPLEGTHLMGV KDSNIHELEHEQEPTCASQMAE PFRTFRDGWVSYYNQPVF/LGW HGSCFPLYDCPGL*LHHHRVRL HSGTEWFHPQYFDGSISYNWN NGNCSFYLATSKMWFGSDRSD LRIGTAFLFDLVCDLCIHAWKP
20254	50622	A	20370	1	497	
20255	50623	A	20371	1	1575	

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20256	50624	A	20372	251	1351	SLKSTDGVKCGLSINIFHKRREN ILFGMGNPLLDISAVVDKDFLD KYSLKPNDQILAEDKHKELFDE LVKKFKVEYHAGGSTQNSIKV AQWMIQQPHKAATFFGCIGIDK FGEILKRKAAEAHVDAHYYEQ NEQPTGTCAACITGDNRSLIAN LAAANCYKKEKHLDLEKNWM LVEKARVCYIAGFFLHVSPESV LKVAHHASENNRIFTLNLSAPFI SQFYKESLMKVMPYVDILFGK* DRSWPTFAREQGFETKDIKEIA QKDTSPCPKMNSKGQRIRDLHP KGRDDT\IMATESEVTAFAGLGI KTQKEINDTNEAGDAFVGGFLS QL\VSDKPLTECIRAGHYAASIII RRTGCTFPEKPDFH
20257	50625	A	20373	1	201	
20258	50626	A	20374	15	304	
20259	50627	A	20375	51	283	TWVKEAQNDGLCVCYIFIFNCQ MTGLDIEKD\QIIEMACLITDSD LNILAEVRDAHVIQSYFLKGTG NITIIFSSFFI
20260	50628	A	20376	2	520	QRRLRDWGRGCWSRVMLGGS LGSRLLRGVGGSHGRFGARGV REGGAAMAAGESMAQRMVW VDLEMTGLDIEKDQIIEMACLIT DSDLNILAE/GNSVHEDKKFLD KYMPQFMKHLHYRIIDVSTVKE LCRRWYPEEYEFAPKKAASHR ALDDISESIKELQFYRNNIFKKK
20261	50629	A	20377	2	206	EFGTRRHVPPCLINFFKDQGSP* LARLVSNSWPQVIHPPWPPTVL GLRGVGHCPWPRLGNSSWVW GGH

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20262	50630	A	20378	1	1401	MRSQKTSLYFSLEAKFYCSLRN ERIASCDIINDAGIQTKTLMKRS HVAYALKKPVEQGDSFELESK GFMAITIAVCIEQNLRHSSSLFIC MSSTGQSGTTNNASSLIPSYVFT PPHFNLLDKQGRTAGKSHCGE DRKEHNNACHQEEEAPDVNPL HGLQASGSPGKTQRIKSQALEG TRLYSHSEETRSGLIRLLRLRQR RLRDWGRGCWSRDMLGGSLG SR\LLRGVGGSHGRFGARGVRK RGAAMAA\GESMAQRMVWVD LEITGLDI*KVQIIEMACLITDSD LIILAEGPNLII\KQPDELLDSMS\ DWCK\EHHGKSGLTKAVKEST NYHCQQAE\YEFPALWYDQPD SLPGLCPTCQEIKFHE\DKKFP* QNTCPQFMKHLHYRII\DVSHC* KELCQTAGYPEEYEFA\PKKAA FSIGPLDD\ISENL\KKVPFFPEN NHLPRKKIRMKRKEGKL*KMG ENEKTVS
20263	50631	C	20379	180	248	
20264	50632	A	20380	455	1133	GIEGWRGEADTLPAEGQDGGR RVSKGDIFSGGAETAQGWGVM GPFQAAPSKRAGREHRGGQRR VQHVGWYPRPGSDKGHGKGT QDSRVPQLPPHPPPIHLVSRHRG KLRHGFLRPMPEPRGLESGKTG NCFGELQH/RTSP*GRSGPREGG PRNIAQQGGCRGSACGRRSH\E ALRPRVWCGEGPQWTW\CAVC P\NRSAPGAGLAD\RQHPGESRA WGETRLGEAGGAE
20265	50633	A	20381	214	412	
20266	50634	A	20382	3	257	PATVIITVNTTWSAALISRESAL RSFPVKAAALSPSREGGSVTAT PNVRSMTSAVPIMRVSVQ\SKR *PEEQN*QETYPQTTSCR
20267	50635	A	20383	1	1569	
20268	50636	B	20384	15	1744	

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20269	50637	A	20385	2	7205	QASGSCWSSPFFSASTPSAAAT GVPGPTDMAAVLQQVLERTEL NKLPKSVQNKLEKFLADQQSEI DGLKGRHEKFKVESEQQYFEIE KRLSHSQERLVNETRECQSLRL ELEKLNNQLKALTEKNKELEIA QDRNIAIQSQFTRTKEELEAEKR DLIRTNERLSQELEYLTEDVKR LNEKLKESNTTKGELQLKLDEL QASDVSVKYREKRLEQEKELL HSQNTWLNTELKTKTDELLAL GREKGNEILELKCNL
20270	50638	A	20386	120	7384	GWTRFPRVPPRESPAGGRARAT ERGDRGGGPGVWVLLVFAFLL RFYPVGRCHWGPWAPPTWAA VLQQVL\ERTELNKL\PKSVQNK LEKFLADQQ\SEIDGP*RGGHGE I*RWESEQQYFEIEKRLSHSQER LVNETRECQSLRLELEKLNNQL KA\LPEKNKELEIA\QDRNIA\IQ SQFTRTKEELEAEKRDLIRT\NE RLSQELEYLTEDVKRLNEKLKE SNTTKGELQLKLDELQASDVSV KYREKRLEQE
20271	50639	A	20387	2	433	
20272	50640	A	20388	2	181	GFRRVSLEF*FPGVRWGMRKL GAPDLAPFSQM*SGGRAPCVAS *PPCRGLRLMRTGSRR

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20273	50641	A	20389	1	2422	MAGALAGLAAGLQVPRVAPSP DSDSDTDSEDPSLRRSAGGLLR SQVIHSGHFMVSSPHSDSLPRRR DQEGSVGPSDFGPRSIDPTLTRL FECLSLAYSGKLVSPKWKNFK GLKLLCRDKIRLNNAIWRAWYI QYVKRRKSPVCGFVTPLQGPEA DAHRKPEAVVLEGNYWKRRIE VVMREYHKWRIYYKKRVSGG GPGRPQSFPPAAAGYRPPRKIPG KGILTPELAPLGPSIQSRADSAT VWPQRLLAASLPRGRLRKPSRE DDLLAPKQAEGRWPPPEQWCK QLFSSVVPVLLGDPEEEPGGRQ LLDLNCFLSDISDTLFTMTQSGP SPLQLPPEDAYVGNADMIQPDL TPLQPSLDDFMDISDFFTNSRLP QPPMPSNFPEPPSFSPVVDSLFSS GTLGPEVPPASSAMTHLSGHSR LQARNSCPGPLDSSAFLSSDFLL PEDPKPRLPPPPVPPPLLHYPPP AKQETVPEFPCTFLPPTPAPTPP RPPPGPATLAPSRPLLVPKAERL SPPAPSGSERRLSGDLSSMPGPG TLSVRVSPPQPILSRGRPDSNKA LLGSFLGSPNSLLPETENRRITHI SAEQ\KRRFNIKLGFDTLHGLVS TLSAQPSLKVSKATTLQKTAEY ILML\QQERAGLQEEAQQLR\DE IEEL\NAAINLCQQQLPATGVPI\ THQRFDQMRDMFD\DYVRTRT LHNW\KFWVVSSLKPMAGGLQ
20274	50642	A	20390	315	387	
20275	50643	A	20391	570	1017	FCLHILQVPHTLAGHSPCAHG/R PPLPRF/HDRLPEEIQQQIVRETF HLVLKRDDNICNFLEGGSLIGG SDYKLIYRHYATLYFVFCVDSS ESELGILDLIQLEQFKKDNEETG FGSGTRALEQALEKTKANIKW VKENKEVVLQWFTENSK
20276	50644	A	20392	1	1128	
20277	50645	B	20393	62	130	

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20278	50646	A	20394	99	718	ENRGWQSMIQAILVVNNHGKP RLVRF\YQRFPEE\IQQQIVRETF HLVLKRDDNI\CNFLEGGS/L*L GGSDYK\LIYRHYATLYFVFCV DSSESELGI\LDLIQVFVGNSWIS CFENVV*IWI*TFH\MDK\VHYIL QEVVMGG\MVLETNMNEIVAQ IEAPNRLEKSEG\GLSAAP\ARA VSAVKNINLPEIPRNINIGDLNIK VPNLSQFV
20279	50647	A	20395	3	370	SLHLAAILGETSTVEKL/YAAGA GLCVAERRGHTA/LHLACRVG AHACARAL/LQPRPRRPREAPD TYLA/QGPDRTPDTNHTPVAL/Y PDSDLEKEEEESHTPLHVAVIH K/DVEMVRLLRDAGADLDK
20280	50648	A	20396	2	1097	SRQSPATGGRLRWAPDAALAM AVVACLGQAADSDKWGDSRLS SLGPDAAAPGGPGLGAELGPGL SWAPLVFGYVTEDGDT\FSAGT EYMDLQNDLRQVSHEGWCRA WGPGFPV*LPTACPLLLQTALH LAAILGETSTVEKLYAAGAGLC VAERRGHTALHLACRVGAHAC ARALLQPRPRRPREAPDTYLAQ GPDRTPDTNHTPVALYPDSDLE KEEEESEEDWKLQLEVENYEG HTPLHVAVIHKDVEMVRLLRD AGA\DLDKPEPTCGRSPLHLAV EGPRQADVLELL\LRAGANP\A A\RMYGGRTP\LGSAMLRPNP\I LAR\LLRA\HGAPEPEGEDEKSG P\CSSSSDSDSRLSPSAWSPLPPG
20281	50649	A	20397	47	478	LRLRKLKAIMLAFGRGKTRNSE ESSDSQEVIWKDTWMFTALGH CGISMFGLWDRELTLTNYELFIS SSPTPS*VPQRLCYVVSTFLMYL SLDHLYTGEMKAFLHVLDTQS VNSDFAFFVRLSFQYFYKLLCV LWQGTVNKEFI

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20282	50650	A	20398	1	1992	METFVIGWQPAVTVWTIGVAP PPTLEITSQHEIWVAQHPNYIIS VKQESPAPMPWTAVALDSHRS MNTIVNCAREGSTLHAPYESLM PDDLRWNSFILKSSPSPHSRSME KLSSMKLVPGAKYIRDHCLVK EALTIHKSPILLAAIDLLGNLSG FTDYQSYVIHGCLENNPTLERSI ALFNGISKWVQLMVLSKPTPQ QRAEVITKFINVAKGATAELNL WQHPKIIMLSQVVPGVFSQEHS LIRSLHANLHFTVCFPEDPLAM VAGMVQESTCPCEILQLPTTGQ LANWNEMTELVSSNGNYCNYR KPFPTCDGLKIPILGVHLKDWIA VHVNFPDWTEEIKVNIVKMHQ LSVTLSELVSLQNASHHLEPNM DLINLLTV/DGLQPADLMHAISL FRTSHRPQGLFL*IKGTSPAEHS DRSCQHFRV*KCSSWESWHGG/ WLSLEE*MSSFLLRSF*KI/YCSR KNVACQTRAVCTNLDALLSSS QMSNNHHPFSLPAQDEVFEFPG VTAGHRDLDSRAITLVTGSSRK ISVRLQRATTSQATQTEPVWSE AGWGDSGSHTFPKMKSKFHDK AAKDKGFAKWENEKPRVHAG VDVVDRGTEFELDQDEGEETR QDGEPAEAVSVGAVAAPGMSE KELLQVDGRTPTRVLRMADLV GISEFRGEPAFV
20283	50651	A	20400	1	417	
20284	50652	A	20401	2	94	

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20285	50653	A	20402	190	2189	AFCPAGTRSAPCPRPRTMTMTL HTKASGMALLHQIQGNELEPLN RPQLKIPLERPLGEVYLDSSKPA VYNYPEGAAYEFNAAAAANA QVYGQTGLPYGPGSEAAAFGS NGLGGFPPLNSVSPSPLMLLHPP PQLSPFLQPHGQQVPYYLENEP SGYTVREAGPPAFYRPNSDNRR QGGRERLASTNDKGSMAMESA KETRYCAVCNDYASGYHYGV WSCEGCKAFFKRSIQELPTLC*I GWYWYQNRDIDQWNRTEPSEI IPHIYNHLIFDKRDKNKKWGKD SLFNK*CWENWLAICRKLKLD HFLTPYTKINSRWIKDLNVRTK TIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIK LKSFCSLLGYLKTENTAKETTIR LNRQPTEWEKIFAIYSSDKGLIS RIYKELKQIYKKK/GNPINKWV KDMNRHFSKEDIYAANRHMKK CSSSLAIREMQIKTTMRYHLTP VRMVIIRKSGNDRCWRGCGEIG TLLHCWWDCKLVQPLWKTVW RFLRDLQLEIPFDPAIPLLGIYPK DYKSCCYKDTCTRMFIAALFTI AKTWNQPKYPTTIG*IKKMWHI YTMEYYAAIKKDEFI/SLVGTW MKLETIILSKLTQEQKTKHHMF SFITGSRTMRTHGCREGNITHW GLLRDSVNMVTQAH
20286	50654	A	20403	2	907	RVPAMATSSFALPRILGAGARA PSRWLGFLGKATPRPARPSRRT LGSATALMIRESEDSTDFNDKIL NEPLKHSDFFNVKELFSVRSLF DARVHLGHKAGCRHRFMEPYI FGSRL\DHDIIDL\EQTATHLQLA LNFTAHMAYRKGIILFISRNRQF SYLIENMARDCGE\YAHTRYFM GGMLTNARLLYGPTVRLPDL\II FLHTLNNIFEPHVAVRDAAKM NIPTVGIVDTNCNPCLITYPVPG NDDSPLAVHLYCRLFQTAITRA KEKRQQVEALYRLQGQKEPGD QGPAHPPGADMSHSL
20287	50655	B	20404	70	1477	

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20288	50656	A	20405	153	688	AHPLLRSSPEETSRSRKPRCATT NGFLRIPEKTTPWSPEVAIHRNR \ITPNKPPTVKSLEKVFC*LDKE AQKEKESQK*KGPVRMPTKT\L RITT\RKTP\CGE\GSKDRWDRF\ QIEISQSRLH*LCTSPF*DLFKQI TFHQYLSPGV*GEKSPFADALS QISIHTIDDQFVKKKKKKKKW
20289	50657	A	20406	26	603	RPRGTLREYKVVGRCPAHSHK CHTPPL\YR\MRNFAP\N\HVVA KS/RAFWYFVSQLKKDEESLPG EIVYCGQGV*ESSPCGSKNFGI WLRY\DSRSG\THN\MYRE*PGP *PTAGGCSPSCYPRHGVARHAG PEAHFHFRFIERLEEI\AGQQNC RRPGCSKQFPRISRFKFP\LAPPG SLRRQDKPRF\TTKRPNTFF
20290	50658	A	20407	161	418	
20291	50659	A	20408	1	2580	
20292	50660	A	20409	3	264	
20293	50661	A	20410	3	302	ALALLSPWVVDGTRHRGAGGG AHPGGSGRTGAHRGGGRLRHG GLQVPSPAPREGS*GPARNRAQ RRAVDRTQ*ECSSKEVYT*RLV PPPPLGHSHSSPE
20294	50662	A	20411	2	415	
20295	50663	C	20412	1	1230	
20296	50664	A	20413	238	1765	VTAYHAATMNEVSVIKEGWLH KRGEYIKTWRPRYFLLKSDGSF IGYKERPEAPDQTLPPLNNFSV AECQL\MKTERPRP\NTFVIPCP QLTNIIRGTL/HTLVSPNQRE\EW NPPYQVVPQQPSRGGPKARTP WNNKCGSPK*LSHD*ENGSGGS ASHG/RKVTMNDSTYLNLLGK GTFGKV\ILFRKKATGR*FA\MK \IFRKKVINAKD*VAHNIQPRAG VLPEHPGNPFLQLR*KYAFPDP TTRPVPL*MEYA\NGGELFF\HL S\RERV\FTEERA\RFYGAEIVSA SEVTWHSRGRGNTRDNQSWKT LMLEQKMAHIK\ITDFGL\CKRG ASSDGAT\MKTFCETP\EYLAHE \ILEDNDYGRAVDWWGLGVVM YEMMCGRLPFYNQDHERLFELI LMEEIRFPRTLSPEAKSLLAGLL *\KDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKKLLPPFK PQVTSEVDTRYFDDEFTAQSITI TPPDRYDSLGLLEAGPADPASP QFSYSASIRE

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20297	50665	A	20414	192	866	LSCRMRMLVLGQNPTLDSIDRS GVRSKCRIFNKLRESFHYNSAE LTISVNMSYNCCSGNFSSRSCG DYLRYPASSRGFSYPSNLVYST DLCSPSTCQLGSSLYRGCQEIC WEPTSCQTSYVEVQAPAKTSC YRPKNLPCSASPCKTTYS\GSLG FGSSSCRSLGYG*GSCYSVGCG SSGFRSLGYGGCGFPSLGYGVG FCRPTYLASRSCQSSCYRPTCGS
20298	50666	A	20415	312	1420	RSHSNAVPSVWNLTLPLDSGPH QSPASTTGPCTNTERSSVPMSCS PPACPTQCVLCSCTEGQIYCGL TTCPEPGCPAPLPLPDSCCQACK DEASEQSDEEDSVQPLHVVRHP QDPCSSDAGRKRGPGTPAPTGL SAPLSFIPRHFRPKGAGSTTVKI VLKEKHKKACVHGGKTYSHGE VWHPAFRAFGPLPCILCTCEDG RQDCQRVTCPTEYP\C\RHPREK WPGKCCKICPEDKADPGHSEIS STRCPKAPGRVLVHTSVSPSPD NLRRFALEHEASDLVEIYLWKL VKDEET*GSGEVKYLAQGHTA RIFHLTQIKKVRKQDFPERGTA LPTARWPPRRSLERLPSPDPGAE GHGQSRQSDQDITKT
20299	50667	A	20416	17	1008	KSGARSLQPQFLRAPEDGGPLS LPNAAMARGPKKHLKRVAA\P KHWMLDKLTGVFAPRPSTGPH KL\RECLPLIIF\LKDQTLSNALT GD\EVKKI\CMQRFIKI\DGKVRT DITYP\AGFMDVI\SIDKTGREFP VL/YLIDTQGVRFCL*HRIYTLR EGQSTSLCKVRKILLWAPKGIP\ HL\VTH\DAR\TIR\YPDP\LIQGE MNTHSRLI*KTGK\IT*FPSKFDH LVTCVMVT\GGA\NLGRNWVLI TQQRRSTLGSF*PLVHVK\DAN GNKLLATSDFSNIF/VVIGKGNK PW\ISL\PRGKGIPPHHLLEERDK RLAAKQSSWVKWGPWVTWSD
20[illegible]	50668	A	20417	1	1377	
20[illegible]	50669	A	20418	1	2178	
20302	50670	A	20419	158	250	

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20303	50671	A	20420	1	860	MDQTVKSLMASEEEYSTKEEK YEKEMKLLEEKLKEAETRAEF VERSVAKLEKTTDDLEETLASA KEETWRFIRPGTRPYWNSATCF LLPGHKMAAEVHKLNPNVSEH DQERWHDAFGNGGADNHSKL QASTRRGGPLSQELLQSLAASL AAGGLTALSAEFTIGKGELMAH DVLWGCAPDEYDDLISGTCSHL PKGKTHDVLTGSDDGRHSNTS LAWGAGVQFNPTESVAIDIAYE GPGSGDWRTDGFIVGGLFCGV NMAVKIS\GVLKDGTGKPVQN* TIQLKAKRNSTTVVVNTLASEN PDEAGRYSMDVEYGQYSVILL VEGFPPSHAGTITVYEDSQPGTL NDFLCAMTES\DARPEALGRFG LYWWKEVARNAS\AVGQNTA AAKKSASDASTSAREAATHAV DAGGFKNAQARTSSPDKAGSA GFKQGFPRGGNGINKRAT*RIK KVACR*SLMASEEEYSTKEEKY EKEMKLLEEKLKEAETRAEFVE RSVAKLEKTTDDLEETLASAKE ETWRFIRPGTRPYWNSATCFLL PGHKMAAEVHKLNPNVSEHDQ ERWHDAFGNGGADNHSKLQA STRRGGPLSQELLQSLAASLAA GGLTALSAEFTIGKGELMAHDV LWGCAPDEYDDLISGTCSHLPK GKTHDVLTGSDDGRHSNTSLA WGAGVQFNPTESVAIDIAYEGP
20304	50672	B	20421	34	800	
20305	50673	A	20422	130	368	RQVITTLYIPYRRRHLSPPDPEQ PLNHKQNRKVNHGGTEFQVVV LPFPKMKINCYRRNQFFLFFFST VKVPVGWSMVPLQAATAGAR L*NSDISPLKSQQTQDKFPSSKP PHIYIKK
20306	50674	A	20423	1	57	

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20307	50675	A	20424	85	874	GPRGLVSMAGGSVEVTPSTFTC YLRPPSASPPTPPSHPGLLPRSPA LCSLHTGARTLPLFGGGRCSSA VLPPRPGP/RAGSGSGQRERFHR FQPTYPYLQHEIDLPPTISLSDG EEPPP*QVPCHLQVR\DPKQQL\ ELNRE\SVGAPPNRTIFDSDLMD SARLGGPCPPSSNSG/ISAPTCYG \SGGRMEGPPP\TYSEVIGHLPG GPSFQH\Q\QSSGPPSLLEGTR\L HPHTHSRP*RSAAIWSKEKDKQ KGHPSLGSPGGPGLGLRR
20308	50676	A	20425	3	250	ESVSATEDLAPDAAQGEDNSEI KELL\RENEPLPACNGPAQAQPS PTTERAKSQEEVLPSSTTPSPGG ALSPSGQPSSSVDAA
20309	50677	A	20426	2	393	
20310	50678	A	20427	1066	1824	
20311	50679	A	20428	3	902	
20312	50680	A	20429	1	2163	
20313	50681	A	20430	1	1890	
20314	50682	A	20431	1	2882	MKQQLPVSYLQVIFNHWASRIS GARGAGWGPVRLGRLCADRAL DGESRPGGGGQSGVPASEASQ KAAHGRRLPVPARLLRCAHSA LEPGRGSASSPRNSTTSDNDQPP DYSFSKRCDSHSLGFSLVWESR NLTLPPTSKLLHFSAFHFFIYKC RAEGHKLYKDLKNFLSAVKVM HESSKRVSETLQFIYY\SEWYGH EELKAIVWNNDLLWEDYEEKL ADQAVRTMEIYVAQFSEIKERI AKRGRKLVDYDSARH

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20315	50683	A	20432	1	1791	MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEKVLQKLG KAVETKDERFEQSANNFYQQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSETLQEIYSSEWDGHE ELKAIVWNNDLLWEDYEEKL\ ADQAVRTMEIYVAQFSEIKE\RI AKRGRKLVDYDSARHHLEAVQ NAKKKDEAKTAKAEEEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMSKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPTSPSTLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEEDEPLPA CNGPAQAQPSPTTERAK\SQEE VLPSSTTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPPRRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSPRAS LGTGTASPRTSLEI*PNPE\PPEK PVRTPEAKENENIHNQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE

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20316	50684	A	20433	158	1830	QLQSKMKLFWLLFTIGFCWAQ YSSNTQ/SKGRTSIVHLFEWRW VDIALECERYLAPKGFGGVQVS PPNENVAIYNPFRPWWERYQP\ VSYKLCTRSG\NEDEFRNMVTR CNNV\GVRI\YVDAVINHMCG\N AVSAGTSSTCGSYFNPWKLRTF PAIP\YPGWDFNDGKC\KTGSGD IENYNDATQVRDC\RLTGLLDL ALEKDY\VRSKIA\EYMNHL\IDI GVAGFRLDASKHM\WPGDIKAI L\DKLHN\LNSNWFPAGSKPFI\F QEVIDLRVGEPNLKASDYFGNG RVTEFKYGAKLGTVIR\KWDGE KMSYLKKWG\EGWGF\MPSDR ALVFVDNHDNQRG\HGAGGASI LTFW\DARLYKMA\VGFMLAHP YGFTRVM\SSYR/WAKHSFKKG NDVNDW\VGPTQINNG\VIKEV TINPRH*LVGND\WV\CEH\RWR \QIRNM\VNFRNGSGMAQPFLQ NWYDNGSNQVAF\GRGNR\GFI VFNK*WPVIFI*LCKPGLPAGSY CDVISGDKVIGNCSAIKIPVSVD GKAHFSMSNSAEDPFLAIHAES KIVKFKIKCKSAKQKKKKKKG RPF
20317	50685	A	20434	3	383	
20318	50686	A	20435	1	378	CASGSSGWRPVLWAGAFTMAS AELDYTIEIPDQPCWSQKNSPSP GGKEAETRQPVVILLGWGG\SK DKNLVKYSAIYHKRKLLELLFD YEIEKEPPAFSLSSATVASCCTA TCWSSCRPVASAACV
20319	50687	A	20436	1	558	CASGSSGWRPVLWAGAFTMAS AELDYTIEIPDQPCWSQKNSPSP GGKEAETRQPVVILLGWGGCK DKNLAKYSAIYHKRGCIVIRYT APWHMVFFSESLGIPSLRVLAQ KLLELLFDYEIEKEPLLFHVFSN G/VRHAVPLTCWELLQTRRFCR LRVVGTIFDSAPGDSNLVGGSA GLGSHPGARG

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20320	50688	A	20437	78	1237	CWSHSDTYWPRTPRPPPPGRPG PVVHLAQPVLHPEAGIPEFWES GSPGQTRGAALVLTVHICVSEN SPSPGGKEAETRQPVVILLGWG GCKDKNLAKYSAIYHKRNTAT LQPPLTYMRGWGLFLTGAPAD QYLIQIKRISQWLRGCIVIRYTA PWHMVFFSESLGIPSLRVLAQK LLELLFDYEIEKEPLLFHVFSNG GVMLYRYVLELLQTRRFCRLR VVGTIFDSAPG*QQPG*GL\SGP GQPSWERRARPMLRLLLLVAF ALGGSSCFHVLLAPITALFHTHF YGQAYRTRALAWPELYLYSRA DEVVLARDIERMVEARLARRV LARSVDFVSSAHVSHLRDYPTY YTSLLCRTSMRKLRPLLKAIAPS HLCSQKINALKPSP
20321	50689	A	20438	3	427	
20322	50690	B	20439	101	1099	
20323	50691	A	20440	733	2228	

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20324	50692	A	20441	582	2595	PPPPVRRRDPGPAVRPAGAMA KKSAENGIYSVSGDEKKGPLIA PGPDGAPAKGDGPVGLGTPGG RLAVPPR\ETWTRQMDFIMSCV GFAVGLG\NVWRFPYLCYKNG GGVFLIPYVLIALVGGIPIFFLEIS LGQFMKAGSINVWNICPLFKGL GYASMVIVFYCNTYYIMVLAW GFYYLVKSF\TSTLPWATCGNY/ TWKHSPTCVEIF\RHEDC\ANAS LANLTCDQLANR\RSP\VIEFWE NKVLKLSGGLE\VPGALNWE\V TLGLLACWVLVYFCVWKGVK STGK\IVYFTA/THYPYVVLVVL LVRGVLLPGALDGIIYYLKPDW SKLGSPQVWIDAGTQIFFSYAIG LGALTVLGSYNRFNNNCYKDA IILALINSGTSFFAGFVVFSILGF MAAEQGVHISKVAESGPGLAFI AYPRAVTLMPVAPI\WAALFFF MLLLLGLDSQFVGVEGFITGLL DLLPASYYFRFQREISVALCCA LCFVIDLFMG\TDGGMYVFQLF DYYSASGTTLLWQA\FWECVV VAWVYGADRFMDDIACMIGY RPCPWMKR\CWSFFTPLVC\MGI FILNVVYYEPLVYKQN/TYVYP WWGE\AMG\WPFALS\SMLFVP L\HLLGLPSLRAKGHPWLKRW QH\LT\QPIWGLHPL/EELPRFRD ADVQGTLTHP*TPVSESSKVV\V
20325	50693	A	20442	1	363	MGKRGLILLIEACIAIAQPLQRW FVVPPRAGMPVTYD/HSNSAAG SPPV*NARLCSPGEKVLCRSQT GNFPHTPQEQAVPSAWNALPV QP*SH/GPSPMLVPCRCVCPMET RVQGSASPGGQG
20326	50694	A	20443	747	1389	LGAVQLCPPPCRPCHRAALPGG LFPPPRPPHSPQAGPLHPQWTQ* PGSVGSPTQLSPEASRPQWPPT A\GSPRAGVHPGHGQA*SADISS AKQWTQVGPAGQGGSKFGKT KVPWQSGPLGWDPGARAGQG VG*ETRGPSLQLAWSDGEGV/P GWRGSYRGHRRGP*PPAPWPW SGGHPGSPMEWPCPGTELQMR NRAGSRDLHSLGRAPPAATAPS

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20327	50695	A	20444	90	1181	RAEPHLQVPGVPGSAQKPQGT QMAPVSPRRGPQRGWHTLGAQ RLLPQAALSSPAFPQHPGGRWA PRRRGQSSQGHSPESLPSERAQP HWNHPQLLSPCTPLSCP*GGPR QA/EQAGDSGSGTWVGLGAAP SERGAPMSARHWLRAPGRRPIF LLSALW*TPAWGGGPAASRSP GGPSSRVVGCPLCPLAPGPVPS VE*RPMSTKDLPPPSPR*KP/PA GPAPV*/SPKAVGIPAWERPPTR PETEGAGGSCAERLLAPVEMAP VSRGQRRDPEPGSRHG/DPPTDT AALGGPRPPQHLPRTRQHWEI* GPGAPPTDTAALGDLRPQSPGL LMELG\PISRDPHGRGPWQGPV GKLWPGGQGSCPQSPPV
20328	50696	A	20445	2	957	IPSRKDHEKAEFEVHEVYAVDV LVSSGEGKVRRVPELAKRGD*E CSPDQMLLKLLFQAKDAGQRT TIYKRDPSKQYGLKMKTSRAFF SEVERRFDAMPFTLRY*AMIVL GTSLTHRPYTQEHFFLSLPA*TC SVHVLTPSLSLPISFSLKVM*KS NPKHDFCLRVGAILKYEQNGK T*WGVKDTSEYHLPCQ\AFEDE KKARMGVVECAKHELLQPFNV LYEKEGEFQKELHFGFPDYKISF L*VQKS*V*QRNFLSKHIFIFAIG EFVAQFKFTVLLMPNGPMRITS GPFEPDLYKSEMEVQDAELKA LLQSSASRKT
20329	50697	A	20446	85	266	

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20330	50698	A	20447	207	1759	LSQRALRLSPRARSFSLSPACPL PCLLALSLALSSRIEGTLTTACG WGRETEAAAAQGKRGCSGGSR KMSGEDEQQEQTIVD/DSLVVT KYKMGGDIANRVLRSLVEASSS GVSVLSLCEKGDAMIMEETGKI FKKE\KEMKKGIAF\PTSISGTIN *PI/CHFSPFERSD\QDYIPPRKGD LVK\IDLGVPCWMGFIANVASH/ SFVVDVAQGTQVTGRK\ADVIK AAHLCAEAA\LRLVKPGNQNT QVT\EAWNKVAHSFNCTPI\EG MLSHSLKQHVIDGEKP*FQNPT DKQK\RAHEKADFEV\HEVYAV DVLVKPQERARPKDAGQRTTIY KRDPSKQYGLKMKTSRAFFSE VERRFDAMPFTLRAFEDEKKA RMGV\VECA\KHELLQPF\NVLY EKEGEFVAQ\FKFTVLLMP\NGP MRITS\GPFEP\DFYK\SEMEV\Q DAELKALLQ\SSAKSEKPQKKK KK\KASKTAGEWPLVAFSAVLE TFRRKWKLGGLEVGPISPACCS CLHPPSHQTPRLCEVQFFFST
20331	50699	A	20448	1	3825	
20332	50700	A	20449	1084	2429	ARERSLRGSPAREREKERKCTA LSE*GEQMERKTNS*TKQTE*N RNEIGPRGAGPPGDAGSGRQPA LRPHVHKQTEKTTRVRTVLNE KQLHTLRTCYAANPRPDALMK EQLVEMTGLSPRVIRVWFQNK RCKDKKKSILMKQLQQQQHSD K/SGEQPLGRRLESGGGCASAA VSACPFLGEPWEIQGELGAPDG VCLYLHSKASLGFEASYFVWD RGFSLSQWQPRVAGSGRCAEP KAAWQCAAPASRAGGLCTPSA AAERSPVEKEGSSDAIECAPPR KAMQTLNHSRPGAPVSKVAEK ARPNSSTYCLLLAPQSLQGLTG TPLVAGSPIRHENAVQGSAVEV QTYQPPWKALSEFALQSDLDQP AFQQLGLLSAGGRSPRDTFRLG ARGPGAPARVPLHLPLPGVSAA P\VSFSESGSLGNSSGSDVTSLSS QLPDTPNSMVPSPVET
20333	50701	A	20450	133	276	
20334	50702	A	20451	2	205	WDTSS*SLRTPRSRQVSTRPRR KKEKLPSKGMFSSVSLPQVLTQ RHQRPTCSWSLCWQPQHLILLR S

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20335	50703	A	20452	182	411	GRAWPAPPTSVTPRLRSPAESP RWPSAEERSSLP/VRGRRPGYG* VSCCGPRAPPGVNGDALRSARP AQLPA*RPQRH
20336	50704	A	20453	786	1208	GVHRGTHGRQKWRPCAPRAQ HSWGPGGRLPAGCRG*AGSCA/ PSLGL*CGAGPQGWGRRDP*TR RRTPRRPPRGPRPRVWMAPPAR SHPWRAAPRSAGAAPRPLGLG GRSGRETRPAPGGELQRPAAAG PPLMSCGWRVVLA
20337	50705	A	20454	385	727	KAMSPVFPRHSKWDLDLSRPLF TSAALLSACKILKLKVDKNKM VATSGVKKSYI*STV*TTREDW TAGRQRTWRCIYSTTEEKEDSG *SPSKGNGEGRGDAT*TTER*RS DTGL
20338	50706	A	20455	568	3382	HPGWVARGPGAGEGHAAGCG PARCQAGGPLQDGGCGGQGHR FGGGHVPEIKGGGFPHAGACAL EERQPR*QP*GVGKRGGGLFHA SSSPSSGGSRTEPAEG*GGAVCR AGDLGHIDDAGDHGDSGK\KE RVEEEGGKPKHVLSTSGVQSD AREPGEESQKADVLEGTAERLP PIRASGLGADPAQAVVSPGQGD GVPGPAQAFPGHLPLPTKVEAK APETPSENLRTGLELAPAPGRV NVVSPSLEVAPGAGQGA
20339	50707	A	20456	762	1245	LRQYSVKMRIVPTILLNFGADP DLRDIRYNTVLHYAVCGQSL\S LVEKL\LEYEADLEAKNKDGYT PLLVARY*QLIPKLVKFLLE\KG ADVNASDNYQRTALILAVSGEP PCLVKLLLQQGGEICNEG\MVD SQLRNMFISMVLLHRYPQFTAS HGK\QKHAK
20340	50708	A	20457	346	608	PKRRGAPLPVIPQSAS*KPKLPM GRPPPPVPSVSPGPLPGSLAIAP HSLEPHLVQSSCLVVPPKTKQS KRKPGRGAQAPTLPNATEFSVC RNDPKEGGRRSP*FPNRLLEPE APPRPSAGESPRPAAA/SPLPCSE EK/PTPQLCARERLAPSAAPPPP PRCGPAPLLEPSAWTPELARRA

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20341	50709	A	20458	340	889	SAPFSSGERTPGCPEASPFPGGG GGNARPSGPAPHPPSSAS*KPKL PMGRPPPPVPSVSPGPLPGSLAI APHSPEPQLVQSSCLVVPPKTK QSKRKPGRGAQAPTLPNATEFS VCRNDPKEGGRRSP*FPNRLLE PEAPPRPSAGESPRPAAA/SPLPC SEEK/PTPQLCARERLAPSAAPP PPPRCGPAPLLEPSA\EAEEGGW GAGPLGRALPPPPPGKGLASGQ PGVRSPDEKGADQRQPSGPRLC SAPAPPRRS/PPRRRRPSNFVPED QPHYVPGSASAGPRRSPRPPRR ELGAPSHLP
20342	50710	A	20459	148	397	GHKELVTGTEAIELAHAYETCH AVPRTIAKLVPKTH\LMSESEW RNLGVQQE/RQGWVH\YMIHEP E\P*HFGCSRRPLTQGTQRK
20343	50711	A	20460	139	272	VLKPGGSYSFGSPSCNSSH*LIG FQKWKDVPCEDKFSFVCKFKN
20344	50712	A	20461	440	1167	ARDSLQLSMAQTSSYFMLISCL MFLSQSQGQEAQTELPQAR\ISC PEGTNAYRSYCYYF*WKTRET W\VDADLYCQNM\NSGKLGVC GSPRAEGCLFWPQLI*GGVGT* WTFNVLDLGLQ*PPKRTRRW\H WEQWGPLVSLQSSWGHWEPPS RCLNPG\Y\CVSLDLQSTRISRN WKDVPFVKDK\FSF\VCKVQKT RGQAGKIQCLELTPAITNGVQK LNRTISPTQLNLVTLFSAEFALLI FNSFT
20345	50713	A	20462	3	322	
20346	50714	A	20463	1	420	DLYELVQYAGNIIPRLYLLITVG VVYVKSFPQSRKDILKDLVEMC RGVQHPLRGLFLRNYLLQCTR NILPDEGEPTDEETTGDISDSMD FVLLNFAEMNKLWVRMQHQG HSRDREKRERERQVSW\RCKCG TLQ\QIVLTG
20347	50715	A	20464	1	1446	

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20348	50716	A	20465	3	2564	LGAGAACCRLWGVAMPTTQQ SPQDEQEKLLDEAIQAVKVQSF QMKR\CLD\KNKRIGVRHKTML RNMLG\ELRTSMLSPKSYYELY MAISDELHYLEVYLTDEFAKGR KVADLY\ELVQYAG\NIYPQGF YLLVHSLSCNNVKSFPQSR\RDI LKDLVEMCRGVQH\PLRGLFLR NYLLQCTRNILPDEGEPTDEETT GDIRDSMDFVLLNFAEMNKLW VRMQHQGHSRDREKRERERQE LRILVGTNLERLSQVE/WCKCG TL\RQIVLTGILEQVVNCRDALA QEYLMECIIQVFPDEFHLQTLNP FLRACAELHQNVNVKNIIIALID RLALFAHREDGPG\IPADIKLFDI FSQQV\ATVIQSR\QDMPSE\DV VSLQVSL\INL\AMKCYPDRV\D YV\DKVLGNNSGRIFNKLNLEHI ATSSAVSKGNFTRLLGKLPVGH FTNNILT\VL\KLKHFHPLFGYFD YESRK\SMSCYVLS\NVL\DYNT EIVSQDQVDSIMNLVSTLIQ\DQ P\DQPVEDPDPEDF\ADEPEALV ARFIHLLRSEDPDQQYLILNTAR KHFGAGGNQRIRFTLPPLVFAA YQLAFRYKEI\SKVDDKWEKKC QKIFSFCPTKTI\SALIKAEL/AQE LPLRTFSFKGGT*LA/AGELGFG NHG\TVAY\EFMSQGIFSVWKD/ EKSGDFPKAQLGWPFTFGSIGA LFERVEVLSVEEDSWNPLR\TQ
20349	50717	C	20466	23	385	
20350	50718	C	20467	16	435	
20351	50719	A	20468	1	436	
20352	50720	A	20469	1	747	
20353	50721	A	20470	1	864	

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20354	50722	A	20471	2	2138	VGRAAAAAAAVAVPLAGGQE GSPGGGRRGSRGTTMVKKRKG RVVIDSDTEDSGSDENLDQELL SLAKRKRSDSEEKEPPVSQPAA\ SSDSETSDSDDEWTFGSHKHKK KGQARTLEQKGTMKKQANKT ASSGSSD/RTDSSAESSAP\EEGE VSDSDSNSSSSSSDSDSSSEDEE FHDGYGEDLMGDEEDRARLEQ MTEKEREQELFNRIEKREVLKR RFEIKKKLKTANKKEKKEKKK* QEEEQEKKKLTQIQESQVTSHN KERRSKRDEKLDKKSQAMEEL KAEREKRKNRTAELLAKKQPL KTSEVYSDDEEEEEDDKSSEKS DRSSRTSSSDEEEEKEEIPPKSQP VSLPEELNRVRLSRHKLERWCH MF\FFAKTVTGCFVRIGIGNHNS KPVYRVAEITGVVETAKVYQL GGTRTNKGLQLRHGNDQRVFR LEFVSNQEFTESEFMKWKEAM FSAGMQLPTLDEINKKELSIKEA LNYKFNDQDIEEIVKEKERFRK APPNYAMKKTQLLKEKAMAE DLG\D\QDKAKQIQDQLNELEE RAEALDRQRTKNISAISYINQRN REWNIVESEKALVAESHNMKN QQMDPFTRRQCKPTIVSNSRDP AVQAAILAQLNAKYGSGVLPD APKEMSKASVGQGKDKDLNSK SASDLSE\DLFKVHDFDVKIDLQ VPSSESKALAITSKAPPAKDGAP
20355	50723	A	20472	438	709	FLSQSWIFKQIRASRTLFLVAFS SNTFTSCRSFCSSSEAMGAGSG RSPELQPRRRRNRKPRAEPSNR AQTPTRTS/LRRCSLRPHRPCAR SR
20356	50724	A	20473	2	1315	ILQKRIGGFLDALVRNSQPARYI NDYQLSNYGLDMLGPSLDPAP MASEELQKDLEEVKVLLEKAT RKTEKSKIETEIKNKLQQKSQK KAELLDNEKPAAVVAPITTGYT KGGGGEERGGEAPTSNEAQAT EVRGGAGGGKDKDDGDRER\P RKTRGGRARTE*NNRHEQ*IQI KKRRETEKERRNEKGRRRHKT ATQKRRREERRARRVGEGTRK REQPAHEQEHATTTHTRPPAP/R RTRKTQTHNRKERKKEE
20357	50725	C	20474	43	162	

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20358	50726	A	20475	2	363	YEPLDSNKRIGTSSSSYVLCLCS SLAIFSNFMGNLLSFCGVLKLK SLACIH*RFFFN*A**VFIHISSRE Q*FINVCSSCPAFFNPERRNELY ASLLSFVPSALVPIFEDNVSYLF VKSF
20359	50727	A	20476	505	2294	VYSDAKSIYCLLFAHSQRPPCV FNENDPQNSGTVHTVFLVGLTD HRHARAKIESWAGEAAPFTLV AASADKLFGDLHISKYCGRIAV SVFQFQQYCGLCDSTS/SLQQY CGLCGST*HSGSTVASVAGLHI VAVPWPLWQDFTLWQYRGLC/ AQDFTLWQYHGLCGRTSRVAV PWPLWQYFTLWQYCGLCGRTS HC/GQYRGLCGRTSHCGSTVAS VAGLHVWQYCGLCGSTSRC/E QYHGLCGRTS/RLWQYHGLCG RTSYC/EQYRGLCGSTSRCG/MY RGLCGRTSH/WWQYCGLCSSTS YCSRTVA\LWQYFIL\CSTSY/W QQYHGLCGNTSYCGIL\QLQQY SGLCSSTSYWGSTVASVAVLHI AAVLWPLRQYFILQQNRGFCG NTSYCG/SYFILWQYHGLCGST SYCG/SYFILQQYHGLCGSTSYC /EQYRGLCGSTSYC/TQYCGLCG SSSYC/AQNCGFCGNTSYCGSTS /VLQQYHGLCGSTSYCGRTV/V FCGSTSYWGSTSYCGSTVASLA VLHIVAVLCPL*QYFTTNKTKN KTKPGSCHLTYFGGAAGGPSL* APGGVAGTVGSASRSASWGLP EWICCLRDPKSLSFPYWGFEVW
20360	50728	A	20477	2	554	LSSTGGLHAGRLCCSPCLLVIPL KSSQHIF\RVL\NTNIRLGRRKNS PLPITAHLRVWARRYA\HVVLR KADIDLTK\RAGEL\TEDE\VER VITH/ILQNPRQYKDPKTGFFEQ DKKDVK\DGKYSQVPSQLVWD NKLP*KTWEPTERRFRAH*/RGL RHFLGAFRVRGQAHQEPLGRR GRHRWVCPRRK

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20361	50729	A	20478	50	774	LFGVVYTGFCLGVWTAGVGGV PGPNFPRPILTLVRGP*GKGVG WVAGPGQLRPTGPWSI*VSHPT PPGPLSISYRAQAAGGQGPAP\I THPQGRQEP*RQLPPGGPLA/RH PPKAPDPARPHP/RQHRGPS/ST APKGRCWQHKQEPSGHPAGHT PGRPG/PPQAPPRPSPWVGPGPQ TPTPCP*DEPHRPPGLQPWRPFS PLAMAPMGRLQALPGLDQRGQ TVSPLRLLGALESLAWLPSAFIA
20362	50730	C	20479	156	908	
20363	50731	B	20480	1	804	
20364	50732	C	20481	278	551	
20365	50733	A	20482	169	1144	INYSLEKHVGALGRVLFSL*RA GCPGMGSTRERGLYLGKHRGS GGIW*ALAGP*KSRGDSVSLTQ GHTHVCSRSPR*ADSPPG/SHLS PVPHSVEVAGHVLVPATRAAV PCSASAGA*QSTYRTGVHQGNP TV*TK/PSRRPSGGVAK*FLPSA VRGEPGAKPLVDDLLPGWSLA THGQPPLVAAPGSGLWGRPAD A*GCETAGGSPCPRSTSRPSGPS GVQGCPLG*AGSGASASRSEPP GSTSCCPRAP\T*PAAPCVPDWP AGDQWRSHGYLPPSREL*G/W MPPSRPATLPQLAFARQRQGNR FDAAFESSGEDFHQMPRVGRM
20366	50734	C	20483	31	90	
20367	50735	B	20484	48	197	

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20368	50736	A	20485	5447	5642	PRDMESCYNPGLDGIIEYDDFK LNSSIVEPKEPAPETADGPYLVI VEQPKQRGFRFRYGCEGPSHGG LPGASSEKGRKTYPTVKICNYE GPAKIEVDLVTHSDPPRAH\AHS LVGKQCSKLGICAVSVGPKNM TAQFNNLGVLHVTKKNMMGT MIQKLQRQRLRSRPQGLTEAEQ RELEQEAKELKKVMDLSIVRLR FSAFLRASDGSFSLPLKPVTSQP IHDSKSPGASNLKISRMDKTAG SVRGGDEVYLLCDKVQKDDIE VRFYEDDENGWQAFGDFSPTD VHKQYAIVFRTPPYHKMKIERP VTVFLQLKRKRGGDVSDSKQF TYYPLVEDKEEVQRKRRKALP TFSQPFGGGSHMGGGSGGAAG GYGGAGGGGSLGFFPSSLAYSP YQSGAGPMRCYPGGGGGAQM AATVPSRDSGEEAAEPSAPSRT PQCEPQAPE\MLQRAREYNARL FGLAQRSARALLDYGVTADRR ALLAGQRHLLTAQDENGDTPL HLAIIHGQTSVIEQIVYVIHHAQ DLGVVNLTNHLHQTPLHLAVIT GQTSVVSFLLRVGADPALLDRH GDSAMHLALRAGAGAPELLRA LLQSGAPAVPQLLHMPDFEGLY PVHLAVRARSPECLDLLVDSGA EVEATERQGGRTALHLATEME ELGLVTHLVTKLRANVNARTF AGNTPLHLAAGLGYPTLTRLLL
20369	50737	A	20486	3	346	PQTITDTELWVTLTVEVWDIST/ LFPGN*SHA/TLPSH*NLITLTPL NANI/AIPQHALKGLKPVITRLL QHGLLKPINSPYNSPILPVQKLD KSYRLVQNLRLINKIVSPIHPVV PN
20370	50738	A	20487	1	808	YGTSLLLPWQLITCPLPSH*NLI TLTPLNANI/AIPQHALKGLKPVI TRLLQHGLLKPINSPYNSPILPV QKLDKSYRLVQNLRLINKIVSPI HPVVPNPPAFTSQITQAVSQAL GIQWNLHIPYHPQSSGKVERTN GLLKVHLTKLSLQLKKDWTVL LPLALLRIRACPRDATGYSRFEL LYGRTFLLGPNLIPDTSPLGDYL PVLQQARQAANLLLPTPDPQPH EDTLAGRSVLVKNLTPQTLQPR WTGPHFIIYSTPTAVCLQDPPH

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20371	50739	A	20488	2	513	CCPIASEAQ*TITDAELWVTLTV EAQSLLRVFLSYLPTLTHKYGT SLLLPWQPITCPLPSR*NLITLTP LN/GQYPIPQHALKGLKPVITRL LQHGLLKPINSPYHSPILPVLKP DKAYKLVQNLRLIYQIVLPIHP VVPNPYTLLSSVPPSTTHYSVL DLKHAFFTIPLQP
20372	50740	A	20489	1	1893	
20373	50741	C	20490	1	1806	
20374	50742	A	20491	1	645	MTSGPQINQPKKHLTNFKSEPS DL/FPSSPGCSLPAED*RCPIALE AP*TITQA\RVTLIVEGKSVPLV NTEATQSTLPSFQGPVSLASITV VGIDGQASKPLKTPLLWCQLG QHSFMHSFLVIPTCPVPLLGRDI LTKLSASLTIPGLQPHLIATLLP NPKPPSCLPLLSPHLNPQVWDIS TSLATDHMPITIRLKPNHPYPAQ RQYPIPQHALKD
20375	50743	A	20492	113	328	LGSGAWGGGDLPWEINPLSSCS LLREKDLLTTSGPQT\TSPRNISP ILNRDPTVQLTWQPLPEPLELW PKAL
20376	50744	C	20493	183	254	
20377	50745	A	20494	1	511	MWKGPKGLDMYGKSSVSPKTS DILGRDTLLLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLPWEINPLSSCSLLHE KDPPTASGPQT\TSPRNISPILNR VSEVSDHAGTPALVLHP
20378	50746	A	20495	1	1108	MWESLELPGNIFNGFDQNADN DMDDEIQAEVISDGDEEFVGN WNKPRDLVPCILATLALTKRGQ DTAQTMASEGARPKHWQLPGG VGPVGAQKSRIEVWEPLPIFRR MYGKACMSRQKFAAGAGFSW YVPVAVVGAKVHDVNLHMLS FPSKWKLHTCMKFGAVTQIVTS LGRSSCSLLLEKDPPMVLRPTSP RNISPISNLTKETRFIRGPKTPAP VTDWEGSLPLVFNHCRDASLII HPGFRGVRPRRDACLSPSPLAN LINLTFKVYNNRKKLQFLAFTV RQTSAMSPAHKNFQTPEPQRPG IPPEPPPPGACYKC/HEIRPPGQG MPAAQDSS*ATS/LSVRDPTGN WTVQLTWHPLPEPLELWPKAL

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20379	50747	A	20496	128	302	TAAARHSSRTSSPRSLLQVLEI WPSGQGMPAAWDSS*AASHL WQPLPEP\LELWPKAL
20380	50748	C	20497	80	106	
20381	50749	A	20498	196	575	
20382	50750	A	20499	1	505	TKETRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIIHPGFRGVR PRRDACLSPSPLANLINLTFKVY NNRKKLQFLAFTVRQTSAMSP AHKNFQTPEPQRPGIPPEPPPPG ACYKC/HEIRPPGQGMPAAQDS S*ATS/LSVRDPTGNWTVQLTW HPLPEPLELWPKAL
20383	50751	A	20500	372	563	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT\TSPRNISPILN/PEK KETRFIRGPKTPAPVMD
20384	50752	A	20501	96	505	WS*QP*GLGSHRHHRRRHHRSS SSSSSSSSSSSKSNSDWQPLPEPL ELWPKAL
20385	50753	A	20502	79	207	
20386	50754	A	20503	583	736	
20387	50755	A	20504	99	246	DLIFHQRHSVSAESLTMHGLNN *QTSAKRVVQG\TWQPLPEPLE LWPKAL
20388	50756	A	20505	654	719	
20389	50757	A	20506	71	951	LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQT\TSPRNISPISNPR/ PKETRFIRGPKTPAPVTDWEGS LPLVFNHSRDTSLIIHPGFRGVR PRRDACLGPSPLAASPTFLGKG PAAPRQTELGPNSSSASAPPPYN PFIASPPHTWSGLQFPSMTSPPP PAQQFTLKKVAGAKGIVKDLIN LTFKVYNNRKKLQFLASTVRQ TPATSPAHKNFQTPELQQPGVP PEPPPRGACYKFQKSGHRAKEC LQPRIPPKPHPICVGPHWKSDCP THLAATPRAPGTLAQGSLTPSQI

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20390	50758	A	20507	1	1010	CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGDSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKKNGEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQT\TSPRNISPISNPRQRRQV LSMDPKLRHRSRTGKAAFPWC LIIAGTPL
20391	50759	A	20508	3	539	IVDDCGGAFTMGVIGGGVFQAI KGFRNAPVCRLLSEAPLFIYSCS RSVSPTVNVSSERAESRPTLFM AVSLHMAWCLAHIGIRHRLRG SANAVRIRAPQIGGSFAVWGGL FSTIDCGLVRLRGKEDPWNSITS GA\LTGAVL\AARSAPLAM\VGS AMMGGILL/ALIEGVSILL/TR*T ATV
20392	50760	A	20509	3	778	GEQRAALPPAPKECTHPNVTNT LVQAESSDAGVRLRWGRGLTA RPDASAMEEYAREPCPWR\IVD DCGGAFT\MGVIGGGVFQAIKG FRNAPVGIRHRLRGSANAVRIR APSTTGSFAVWGGLFSTIDCGL VRLRGKEDPWNSIT\SGA\LTGA VL\AAP\SGPLAMGGLQQ*WGG ILSAPHLRAFGILL\TR*TA\QQF RKWAPNSLEDP\SQ\LPPKDVT\P APGYP\SYQQYHLRKPLATMGA TSSVPFPDGSTLKGRAGFPG
20393	50761	A	20510	1	231	LRWRVWSLSLLMFRCVRSFFLL VGSWSRWFRSEAADLCGECYS S*GSTSGVVRFSRWACGLAGLR SEAADLAPPTSC
20394	50762	A	20511	318	494	

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20395	50763	A	20512	1	1234	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPQQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGSLLRSQM PCADLSILKEAAETLDSTSTRNS AFLGNTHDEAPIVHVFIPSLAYS TNIWSLIFNPTTMIMMCSRDWL SSCENKRVDLAFGLVYSGTPVQ KLEQMKFSPQLGCNHFESKDR NDFLFAPEEIEKDPQGESLLCDF MTKTPKAMATKAKIDKWDLIK LKSFCTAKETTIRVNKQPTEWE KNFAIYPYDKGLISRIYKELKQI YEKKIKQPHQKVDERRLLNLTT DRLTGEKAYRFIKVQVLRVTQ GMKIQRRARSKELQGDGDEIQR WKRLHSPPRLLGEEPHRIIFKLD SANDMHKSAPFSSLQSPLWHQP VMQEVERQYKEKKDLVREGG KCRCQGRPGKVVLTELSLEAR GGWMEDIPSRRTSKCGPWELV SHCVQNWWVLGLTDFKNEAS DPRGVKLQTFTVSVTALKAAR LELLVLPGGLVVSLASGVKLQT FAVSVTAHKRSVDPKTEGAGS GLGQPRKGLSQCSSGPKG*YPE STKNLNKFTRKKSNNPIKRLMK
20396	50764	B	20513	1	531	
20397	50765	A	20514	1139	1562	GALQPTAALWEPLSGLAKARA GTLSLQGSVEGVA*AGTGAAC GACGPDGVPGGRGLGGPRTGS SRPALSHFITEEDKDQRVQDQL GGVWHRMEIHEQHVGKQQEE GDVEDHIPGEDHEGGGEERHIV PKQLLVLVDRFLPK
20398	50766	A	20515	1	1597	
20399	50767	A	20516	461	1601	

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20400	50768	A	20517	1	914	MNNLRRAALRAVTLTAKVCSF TPEPARPQTHQKEETPNTSEHQ KEQTPDTPPLRTVTLTARVHGFI LEVSETKNPPIPDTPATREAEGL RSRLAVYSTRDSPCVACSGSYT QAQGSLGRKFQDPVSLFEDLTK NTPEPNLRPITSKPVLVQETLSN FALFLKESNGP\VKVWGSH/IKG LT*KALHGF\HVH\EFG\DNTAR LYQVQGPHF\NPLSQKTTVGPK\ DEESHC*DLGQCDCLTKNGVA DVSI*RFCESHSSGDHCIIG\RTL VVPWKKPDDFGQRVGNE\ESSK T\GNAGKSVWPCGVNWIAQ
20401	50769	B	20518	8	173	
20402	50770	C	20519	13	180	
20403	50771	A	20520	3	486	VTETWKCAGIPHRYRSFESC/IW NPVINSDRMDYAGPVCFKNADI GRCAHEKLRED*DGAAPGEIGI QPEADATPYFATPTPVLTHGPC AAESEPALLIGSKQFGLSRNSHI AIAFDDTKVKNRLTIELEVRTE AEFRLLFYMARINHADFATVQL RNGLPY
20404	50772	A	20521	1	459	
20405	50773	A	20522	2	239	SDSSGSREVDPVAATTMPGAA GVLLLLLLSGGLGGVQAQRPQ QQRQSQAHQQRGLFPAVLNLA SNALITTNATCGEKGPEMYCKL VEHVPGQPVRNPQCRICNQNSS NPNQRHPITNAIDGKNTWWQS PSIKNGIEYHYVTITLDLQQVFQ IAYVIVKAANSPRPGNWILERSL DDV\EYKAWQ*H\AVT\DTEAL TP*PN*SPELGHRQNAQD*\EVI CTSFYSKIHPLENGEIHISLINGR PSADDPSPELLE
20406	50774	A	20523	2	445	
20407	50775	A	20524	1	2765	MGRRRLLVWLCAVAALLSGA QARGTP\PWRGLR/LPGASRYSL YTTGWRPRLRPGPHKALCAYV VHRNVTCILQEGAESYVKAEY RQCRWGPKCPGTVTYRTVLRP KYKVGYKTVTDLAWRCCPGFT GKRCPEHLTDHGAASPQLEPEP QIPSGQLDPGPRPPSYSRAAPSP HGRKGPGLFGERLERLEGDVQ RLAQTYGTLSGLVASHEDPNR MTGGPRAPAVPVGFGVIPEGLV GPGDRARGPLTPPLDEILS

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20408	50776	A	20525	2	363	RFTKVEMKEK\MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAKL
20409	50777	A	20526	1	1566	
20410	50778	A	20527	1	1604	MAILFEMRLGQQSSAKFPGFQS SFFPVIPVNKPSGKFKRDRAHFS STRLLWPDCQISQLWGGYLRK KGSSPSQGLIDKTPSPWKKAPR ERGGCGRSFSRFKHPCLTALKR AADLPAQHSSSAKDTSQKGPTD TSYRRALAGIWQVPPLGRSFQK KDQAAIFAVVQPLQVIPRQTGS GVDLQQTSADWQQRGLTVRR KTNKQKGIACSLKDPIRGHQHQ RPKDHNFSPAREQNWTENEFD KLTEVGFRRWVITNSSELKKHV LTQCKDAKNLERSLEELLTRIPS VEKNINDLMELKNTARELREA YTSFNSPIDQAEERISVIEDQFN KINREDKIREKRIKRNKQSLQEI WDYVKRPNLQLIGVPESDKEN GTKLENTLQNIIQENFPNLAREA NIQIQEI\QRTPQRYSLRRATPRH IISV/RFTKVEMKEK\MLKAVRE KGR\VTHKGKPIRLTTADLSAET LQARRQSGGQYFNIL*RKGIFQP R\ISYPA\KLSFISEGEIKYFIDK\Q MLRDF\VTTRDWPALKEHQAC
20411	50779	A	20528	58	1081	SSMAKPC\GVRLSGEARKQVEV FRQNLFQEAE\EFLLR\FLPQKII Y\LNPASFQEDFPFNVA*/LLNLS SGAPLGHPPIPRPLHPKDDEM\E TDKAGRRKEVP*SVGFFPWGN* GKFL\SLVCPGLKPE\VWDFSKR NCILGDLHWIQTPDSPRFEDGN DFGGSQSRKKVLEKG*MPVKT KV\EAF\QTTISKY/FSSERGDAC GPRPPKETHVMDYRALVHERD EAAYGELRAMVLDLRAFYAEI VKSSGIGAHVSFKVQNIHSSYC SGPTVSPTCVTGLPASQSPDSG AQLASSSGSHTCAAGGAACQS RALRLHSSALGWSMGLGTVEQ GAALIEEVQAAQEPTEG

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20412	50780	A	20529	1632	1932	KEGCELCRCCCRPGPPASSHGQ PHHVFPH/VLSMASPWAVSPSS VNVSQFFIC/TCQDAKTEWLDC KHVVFGKVKDGMNIVEVMEH LGSKNGKISNQQEDHHC
20413	50781	A	20530	245	740	GAWKARSDCSSNP*NYVNRLE LFADKVPKTAEKF\QALSTGEK GFGYKGSL\FHRIIPGF\TCQSGD FTRPYSIGGKSHLPGRNLMTRT FILKHTGPGILSMANAGPSVNV SQFFI\CPAKMPRTEW\LDCKHV VFGKVKDGMNIVEVMEHLGSK NGKISNQQEDHHC
20414	50782	A	20531	135	1427	GKPTFASRQQPLAEECPASSAL QRRWLWRWRWWLRRRRRQR RSSGSCQGQPAGPLGGPPANRG AAPQGSMAMNYNAKDEVDGG PPCAPGGTAKTRRPDNTAFKQQ RLPAWQPILTAGTVLPIFFIIGLI FIPIGIGIFVTSNNIREIEIDYTGT EPSSPCNKCLSPDVTPCFCTINF TLEKSFEGNVFMYYGLSNFYQ NHRRYVKSRDDSQLNGDSSAL LNPSKECEPYRRNEDKPIAPCG AIANSMFNDTLELFLIGNDSYPI PIALKKKGIAWWTDKNVKFRN PPGGDNLEERFKGTTKPVNWL KPVYMLDSDPDA*WIHK\DDFI VWMRTAALPTFRKLNRLIQRK SDLHPTLPAGRYSLNV\NAYYP VHYFDARKRMIMSAISWMGGK NPFLGMAYFAVGAISFHLGVAL LGINHKYRNSSNTADITI
20415	50783	A	20532	1	370	
20416	50784	A	20533	1	1104	LREFANFDFDIWRKKYMRWM NHKKSRVMDFFRRIDKDQDGK ITRQEFIDGILSSKFPTSRLEMSA VADIFDRDGDGYIDYYEFVAAL HPNKDAYKPITDADKIEDEVTR QVAKCKCAKRFQVEQIGDNKY RFGDSQQLRLVRILRSTVMVRV GGGWMALDEFLVKNDPCRAK GRTNMELREKFILADGASQGM AAFRPRGRRSRPSSRGASPNRST SVSSQAAQAA\SPQVPATTTPK GTPIQGSKLRLPGYLSGKGFHS GEDSGLITTAAARVRTQF\ADS KEGLPSRPGSSSLEAKFGSR\AS SRRGSDASDFDISEIQSVCSDVE TVPQTHRPTPRAGSRPSTAKPS KIPTPQRKSPASKLDKSSKR

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20417	50785	B	20534	527	4627	
20418	50786	A	20535	37	315	
20419	50787	A	20536	1314	1577	HGSGSAPTCRWPRTQGRCREIC ADGFSGVMRNCTG*EAASGR* CKSFVHVYLQLRCACSVCHSA GSDSFQLQRSPHTPSTCTHALV
20420	50788	A	20537	1	1652	MQATKTESGRNGKPGQPSNRC HYLLNQGWVANSGKGGRTNIP DKELKSGDDPENVHITSFQYLA LAAFPRGRARDLQLAMTEPPHP SVGSCAARASLTSAAPCSTAPSP INHPKAEECGCTARDWQAAPP AARVRDPLGEASWAPESEYVC NCSVVGSLNVNRCNQTTGQCE CRPGYQGLHCETCKEGFYLNY TSGLCQPCDCSPHGALSIPCNSS GKCQCKVGVIGSICDRCQDGY YGFSKNGCLPCQCNN\RSARCD ALTGACLNCHENSKGNHCEEC KEGFYHSPDATKECLRCPCSAV TSTGSCSIKSSELEPECDQCEDG YISPNCNKCENGYYNFDSICRK CQCHGHVYLISTPKICKPESGEC INCLHNTTGFWCENCL*GYVH DLEGNCIKKEVILPTPEGSTILVS NASLTTSVPTPVINSTF\TPT\TL* TIFSVSTSENSTSALADVSWTQF NIIILTVIIIGVVLLMGFEGAGY MYRENQNRKLNAPFWTIELKE DNISFSSYHDSIPNADVSGLVED DGNEVAPNGQMTLTTPIHNYK
20421	50789	A	20538	1	177	
20422	50790	A	20539	1	480	
20423	50791	A	20540	410	896	FSCLKRMHIKAMPEDAKGQDW IALVKAAAAAAAKNKTGSKPR TSANSNKDKDKDERKWFKVPS KKEETSTCIATPDVEKKEDLPTS \SETFGLHVENVPKMVFPQPEST LSNKRKNNQGNSFQAKRARLN KITGLLASKAVGVDGAEKKED YNETAPMLEQV

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20424	50792	A	20541	1	1526	LKDEEDFFDFKAGEEVLARWT DCRYYPAKIEAINKEGTFTVQF YDGVIRCLKRMHIKAMPEDAK GQVKSQHPLSWCCPIDPAGSCN QSMGSEDWIALVKAAAAAAA KNKTGSKPRTSANSNKDKDKD ERKWFKVPSKKEETFNLLLATP DVE/RRKEDLPTSS/EKHL*GLH VRRNVPKMVFPQPESTLSNKRK NNQGNS\FQAKRARLNKITGLL ASKAVGVDGAEKKEDYNET\A PMLEQA\ISPKPQSQKKNEADIS SSANTQKPALLSSTLSSGKARS KKCKHESGDSSGCIKPPKSPLSP ELIQ\VEDLTLVSQLSSSVINKTS PPQPVNPPRPF\KH\SERRRRSQR LGTLP\MPDDSVEKVSSPLSSPL D/EGKVFS/LSSSSKISQESSS/IPE VPDVA/HICPLEKLGPCLP\LDLS RGSEVTAPVAS\DSSYRNECPRA EKEDTQMLPNPSSKAIADGRGA PAAAGISKTEKKVKLEDKS\STA FGIRSWDFSALLMKIPSYSPISLS GLPES
20425	50793	A	20542	363	1187	FHITMCGICCSVNFSAEHFSQDL KEDLLYNLKQRGPNSSKQLLKS DVNYQCLFSAHVLHLRGVLTT QPVEDERGNVFLWNGEIFSGIK VEAEENDTQILFNYLSSCKNES EILSLFSEVQGPW\AFIYYQASS HYLWFGRDFFGRRSLLWHFSN LGKSFCLSSVGHPNIWNWQISG KKFQHLDFFRIDLKSTVISRCIIL QLYPWKYISRENIIEENVNSLSQ ISADLPAFVSVGSQMEGQTVSL EKPVVPLNMDVATSWHWETH AVFFPCATYR

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20426	50794	A	20543	1140	2372	CCHKLHWRLIAVIFPMCHLQER YFKSFLLMYT*KEVIQQFIDVLS VAVKKRVLCLPRDENLDSQME VLENV**GKANVGNPVFWGGL D/CPWLLATLLDRHIPLDEPLVL LNVAFIAEEKTMPTTFNREGNK QKNKCEIPYPKNFSKDVAAAA ADSPNKTCQC\PDRITGRAGLK ELQAVSPSRIWNFVEINVSMEE LQKLRRTRICHLIRPLDTVLDDS IGCAVWFASRGIGWLVAQEGV KSYQSNAKVVLTGIGCRWSNL QGYSPSSVSAFKSHGLGRIGIKE IMMELGRISSLEILGRDDR\VIG DHGKEARFPFLG*/RMLSPFLNS SARFGEKANLDFTPRGIGEKLPF NALQPVELG\LTASALLPKRAM Q\FGSRIAKMEKINEKASDKCG RLQIMSLENLSIEKGTKL
20427	50795	B	20544	70	464	
20428	50796	A	20545	18	552	
20429	50797	A	20546	1	1257	
20430	50798	B	20547	223	342	
20431	50799	A	20548	9	5293	KIHRHRLSPATEKGAASSGEGD KDPPPPAHEDIAVKGTATAAGT GPGTGAAAAAAAAAVPPPHPNI RALQTQAPQQIPRGPVQQPLED RIFTPAVSAVYSTVTQVARQPG TPTPSPYSAHEINKGHPNLAATP PGHASSPGLSQTPYPSGQNAGP TTLVYPQTPQTMNSQPQTRSPF FPKGLKIQPP\RATIPNSKSFPFV PGAQTPTAVYQG*FRHIM\M\V NHLPLPYPVPQGPQYCIPQYRH SGPPYVGPPQ
20432	50800	A	20549	1	78	
20433	50801	A	20550	1	2805	MAKGFYISKSLGILGILLGVAA VCTIIALSVVYSQEKNKNANSS PVASTTPSASATTNPASATTLD QSKAWNRYRLPNTLKPDSYRV TLRPYLTPNDRGLYVFKGSSTV RFTCKEATDVIIIHSKKLNYTLS/ QGHRVVLR\PPDIDKTELVEPTE YLVVHLKGSLVKDSQYEMDSE FEGELADDLAGFYRSEYMEGN VRKVVATTQMQAADARKSFPC FDEPAMKAEFNITLIHPKDLTAL SNMLPKGPSTPLP
20434	50802	A	20551	1	239	
20435	50803	A	20552	1	654	

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20436	50804	A	20553	161	3193	GSLSRLPTITMAKGFYISKSLGI LGILLGVAAVCTIIALSVVYSQE KNKNANSSPVASTTPSASATTN PASATTLDQSKAWNRYRLPNT LKPDSYQVTLRPYLTPNDRGLY VFKGSSTVRFTCKEATDVIIIHS KKLNFP\LSQGHRVVLRGVGGS QPPDIDKTELVEPTEYLVVHLK GSLVKDSQYEMDSEFEGELAD DLAGFYRSEYMEGNVRKVVAT TQMQAADARKSFPCFDEPAMK ARF\NITLIPPQGT
20437	50805	A	20554	3	429	
20438	50806	A	20555	3568	4012	VLSTSFPGTELNPPISPLAVNSTE LLKGELSLSSLGVLSLSDTSVPN SVSNSFLLGLRKRLGRGVGISCS NALSALDLAACNFSLMRPLME NSAKPVLEVEGIGG/TAFDAGA GIALSDHFIKLISWYDNEFGYSN RVVDLMAHMASKE
20439	50807	A	20556	1	1211	QTAASSFASPGEPHRSNTMGKV KALVNGFDRIGRLVTRAAFNSG KGDIVAINDPFIDLNYMVYMFQ YDSTHGKFHGTVKAENGKLVI NGNPITIFQ\ERDPSKIKWG*H\G AEYVV\ESTG\VFTTM\EKAGAH FAGGSQKGHSSFAPSTEAIMFM MKVNYEKYDNSLKIISNASCTT NCLAPLAKVIHDNSGIVERLMI TVHVITTTQKTVDGPCRKLRPD GHRALQNIIPASTSTAKAMVKV IPELNKKLTGMASHVPTAKVLV VDPTCH/LGKPAKYYDIKKMM KQASEDPIKGILGYTEHQIVSSD FNSDTQSSTFDAGAGITLNDHF VK\LISWYDNEFGYSNSVVDLM AHVASKELSGYSLKVSFAVQK LFSLIRSNLSIIAFDAIVFGVFVM KSLPVSICRM
20440	50808	A	20557	1	300	PTANVSVVDLTCRL*KPAKYD DIKKVVKQASEGPLKGILGYTE HQVVSSDFNSDTHSSTFDAGAG IALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
20441	50809	A	20558	1	3399	
20442	50810	A	20559	1	3126	
20443	50811	C	20560	298	435	
20444	50812	A	20561	1	888	
20445	50813	B	20562	1	4536	

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20446	50814	A	20563	37	3900	LGLGLSMLVGQGAGPLGPAVV TAAVVLLLSGVGPAHGSEDIVV GCGGFVKSDVEINYSLIEIKLYT KHGTLKYQTDCAPNNGYFMIP LYDKGDFILKIEPPLGWSFEPTT VELHVDGVSDICTKGGDINFVF TGFSVNGKVLSKGQPLGPAGV QVSLRNTGTEAKIQATATQ\PG GKFAFFKVLPGDYEILATHPTW ALKEASTTVSVTNSNANAASPL IVAGYNVSGSVRSDGEPMKGV KFLLFSSLVTKED\A
20447	50815	A	20564	1	310	EEETVPTTAGASPGPPRNKKNR ELRPQRPKNAYILKKSRISKKPQ VPKKPREWKNPEPSAAAS*GGE GQAHGGPAICPGQICALSQTPG LPGNSLSPRSPVGK
20448	50816	A	20565	3	267	
20449	50817	B	20566	267	560	
20450	50818	A	20567	1	429	LIGLDPEPLAEVDVISLEQGRRK QIERLGYDPQAKAPFQPKPKQK GRSSTASLVKRKRKVMDEE\NR VK*TIGNGPGLPKGCTLPACAL CPCQPAHFLTLCPVSLPSPVPQD KVRQSLQQQHHKEAK/APKPTG ARPSALDRFVR

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20451	50819	A	20568	2	1951	FKPTVWQLRGVLHVDRLFVWA SMETAPKPGKDVL\SKKDKLQT KRKKP\RRYWEEETVPTTAGAS PGPPRNKKNRELRPQRPKNAYI LKKSRISKKPQVPKKPREWKNP ESQRGLSGAQDPFPGPAPVPVE VVQKFCRIDKSRKLPHSKAKTR SRLEVAEAEEEETSIQSLLRSEL LLAEEP\GFLEGEDGEDTAKICQ ADIVEAVDIASAAKHFDLNLRQ FGPYRLNYSRTGRHLAFGGRRG HVAALDWVTKKLMCEINVME AVRDIRFLHSEALLAVAQNRW LHIYDNQGIELHCIRRCDRVTRL EFLPFHLLLDTASETGFLTYLDV SVGKIVAALNARAG\RLDVMSQ NPYNAVIHIGHSNG\TASLWESS YGREPLAK\ILC\HRGLGSGAVA \VDSYRHVTWATSGP*DHQLED LFDFARGRY\QPLEHSGPCPMG AGHLAFSQRELL/VLAGLGDVV NIWAGQGKASPP\SLDRPYFTH RV*GPVHGLQFCPFEDVLGVG HT*G\ITSML\VPGAGEPNFDGL\ ESNP\YRSRKQRQ\EWEVKALL EKVPAELICLDPRALAEVDVISL ETGKRRKQIERLGYDPQ\AKAP F\QPKPKQKG\RSSKA\TLVKRK RKVMIEDHKG/DKVRQSLQQQ HHKEAK\AKPTG\ARPSALDRF
20452	50820	A	20569	1	437	
20453	50821	A	20570	157	425	

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20454	50822	A	20571	207	1562	LVIVFFYPQHTAPGPPLTVLNQ AMHARGPHGQLSPALPLASSVL MLLMNLAHLGQPWMLGPLTW HISPFSLPVHRLLTHALGHTALP GLLLSLLLLPTVGWQQECHLGT LRFLHASALLALASGLLAVLLA GLGLSSAAGSCGYMPVHLAML AGEGHRPRRPRGALPPWLSPW LLLALTPLLSSEPPFLQLLCGLL AGLACILCLSPGPVGMCGFCG WVPGKEVAQRGEGPSNTKEPC THIAWPVAWAHPWLLLVFLDR PPCPGQTDAAGAFRWLEPSERR LQVLQEGVLCRTLAG\GMPVQ VVGTVAGLPVRPSSLP/SSSRPPI PGPPYVASPDLWSHWEDSALPP PSLRPVQPTWEGSSEAGLDWA GASFSPGTPMWAALDEQMLQE GIQASEVGSPGIGAGVALTLPTS PPTPNRLQQLERMGFPTEQAVV ALAATGRVEGAVSLLVGGQ
20455	50823	A	20572	460	916	AHSPRDHPWTVLNQAMHARGP \HGQ\LSPALPL\ASSVLMLLMST LWLVGAGPGLVLAPELLLDPW QVHRLLTHALGHTALPGL\LLS LLLLPTVGWQQECHLGTLRFLH ASALLALASGLLAVLLAGLGLS SAAGSCGYMPVHLAMLAGEG HRPRRPRGALPPWLSPWLLLAL TPLLSSEPPFLQLLCGLLAGLAY AAGAFRWLEPSERRLQV\LQEG VLCRTLAGCWPLRLLATPGSLA ELPVTHPAGVRPPIPGPPYVASP DLWSHWEDSALPPPSLRPVQPT WEGSSEAGLDWAGASFSPGTP MWAALDEQMLQEGIQA\SLL\D GPAQEPQSAPWLS\KSSVS*MR LQ\QLERMGFP/TTEAAVVALA\ ATGRVEGA\VSLLVGGQSGT\ET LVTHGKGGPAHSEGP\GPPWAN CPQHCLLASSVLMLLMSTLWL VGAGPGLVLAPELLLDPWQVH RLLTHALGHTALPGLAPEPAAP AHCGLAAGVPPGHAEIPACLSP ARPGFWAAGSAAGRPWAVQCS RQLWIHACPPGHAGWGRTPP
20456	50824	A	20573	174	401	CTVVFSVLAELSCTSRFCPNMW TPLREPMTENGRWGLSVRVLE HGGNQSNSACGPEPPEGEMGS* LEED*LPALIP

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20457	50825	A	20574	450	1029	ATQLPPQPWQTPAALGWAAAT SLMPYRAPSPPARAQHPPALCL APPPPLWLQLPHLEASHSLVEA RPNPPVSTLAQQGIQPSPRHLPR CPSLRPRQQPPQQVP/PQPAAPT PTATITSTGPSLFASIATAPTSSA TTGLSLCTPVTTAGAPTAGTQG FSLKAPGAA\PAPPQQHPPLPPP PPPPPPAAAPPALP
20458	50826	C	20575	115	276	
20459	50827	A	20576	3	307	ASRLGPREGGARKNPGGPCSAT QYISVPSP\GAASFPVLGSQSLLT TVSPPLPA*P/LAMAL*PRPLCA PGPSPRSPRLRSPLPPSFFSRGRR RLSLLQPWSE
20460	50828	A	20577	2	388	
20461	50829	C	20578	244	487	
20462	50830	B	20579	5	569	
20463	50831	A	20580	204	676	RTDQYPQRGETEEGLEGQLLPH RQLPGGLGAHRGPDPACGLRD SSRGVPLAGSPLRVR*GRGHDL RQSGGVRPGGGSNRGLVVAGD ARGRAAPLAGGVPAAADRSRL PGVPAAREPHGPTPAPDPDSAA EPGAVSTLRAEPTPQPVVSTGC CSSTWN
20464	50832	B	20581	1	1413	
20465	50833	B	20582	60	224	
20466	50834	B	20583	8	2469	
20467	50835	A	20584	841	1436	HHQVPLPVGRERGGKRGPGSW ETCLSVLGPAIPPSEPWPVSPSW VHSLVPGEQALPLICSQPPMAP QWPETGPGPHLVHRTCRVCLN WQGMTRTRGYQAGPSSRRTIPT PAQLPAPLASLPPRQDPPSSPAE PPSGRFSMEPWWEPARHPPGSP AAPCSSHRIT/APPTPSLAAQPG/ PVGSNPPLSPEGLCLAGTPACG W
20468	50836	A	20585	1799	5195	SKGNGSPSTTQTQTPRAAPDGS LSEETPAGPPTCSVPPASALPRQ QYAKSLPVSVPVWGFKEKRTE ARSSDEENGPKPKPASVDANTK LTRSLPCQGSLKRATSCERAGK AVGEEVSGYSLHGCSKERRRRP RLKKEGGSGEPGVGYLFISVLV NSNSELIRLINNAIKNDLASRNP TFMCLALHCIANVGSREMGEA FAADIPRILVAGDSMDSVKQSA ALCLLRLYKASPDLVPMGEWT ARVVHLLNDQHMGV

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20469	50837	A	20586	8	268	SRSSRTWSPIPEKEKTKLQKQR EDELIQKIHKLVQKRDFLVDDA EVERLREQEEDKEMADFLRIKL KPLDKVTKSPPI*QSQRAHL
20470	50838	C	20587	50	196	
20471	50839	A	20588	16	1263	SLSSRCMMVAEQGCALEPCQG LSHGAALGVLMVVFP/VSSLQQ DQLDIIS\MAETT\MMP\EEIELE MAKIQRLREVLVRRESELRFMS FEEQYNEDHKKGVIDLFTADSL KTMTRLVTGVWLAYLAATASN PLQEGEHAGEQIGAGGCRSRLE GGALTWDPVLLPPVRISRMLLL LLIPGELPGIAFKLMNPTKAEPM HMFIILEPFDLRKLMDDIQLCK DIMDLKQELQNLVAIPGCTRSM MLVSAQLLEGLRKLIIMAEDKG ADMSRAQSRSKRPPKMLICLLV DVFFPEKEKTKL\QKQREG*AN PRRFHKLVQKRDFLV\DDAEVE RLR\EQE\EDKEMADFLRIK\LKP LDKVTKSPASSRAEKKAEPPP\S KPTVAKTGLALIKDCCGATQC NIHVSPHVGCPGPWGPPPTLLS
20472	50840	A	20589	31	339	
20473	50841	A	20590	1	1179	
20474	50842	A	20591	1	1167	PARSMAATSLMSALAARLLQP AHSCSLRLRPFHLAAV/RGNLSL GQVGVQCCNHGLLQP*PPGLK* SSHLSLNEAVVISGRKLAQQIK QEVRQEVEEWVASGNKRPHLS VILVGENPASHSYVLNKTRAAA VVGINSETIMKPASISE\EELLNL INKL\NNDDNVDGLLVQLPLPE HIDERRICNAVSPDKDVDGFHV INVGRMCLDQYSMLPATPWGV WEIIKRTGIPTLGKNVVVAGRS KNVGMPIAMLLHTDGAHERPG GDATVTISHRYTPKEQLKKHTI LADIVISAAGIPNLITADMIKEG AAVIDVGINRVHDPVTAG\PGL VGNVDFEGVRQKAGYIT\PVPG GVGPMTVAMLMKNTIIAAKKG AEA*RSEKVLKSKELGVATN

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20475	50843	A	20592	1	1963	MAASDVNCGACFAELQGNATA NTPGGTSHHTHLAIHGSCHDSQ AKEAGRKRQPWPPPDGRSEPAP DSHPHLSPEALGYFRRALSALK EAPETGEERDLMVHNIMKEVE TQALALSTNRTGSEMLQELLGF SPLKPLCRVWAALRSNLRTVAC HRCGVHVLQSALLQLPRLLGSA AEEEEEEEEDGKDGPTETLEEL VLGLAAEVCDDFLVYCGDTHG SFVVRTLLQVLGGTILESERARP RGSQSSEAQKTPAQECKPADFE VPETFLNRLQDLSSSFLKDIAVF ITDKISSFCLQVALQVLHRKLA QFCAHICNAVIGYLSARGSSVD GKPLLLFLRDQTSFRLLEQVLL VLEPPRLQSLFEEHLQGQLQTL AAHPIANFPLQRLLDAVTTPEL LSPVFEELSPVLEAVLAQGHPG VVIALVGACRRVGAYQAKVLQ LLLEAFHCAEPSSRQVACVPLF ATLMAYEVYYGLTEEEGAVPA EHQVAMAAARALGDVTVLGSL LLQHLLHFSTPGLVLRSLGALT GPQLLSLAQSPAGSHVLDAILTS PSVT\PSCAAVCLQNLKGTNIVA LACKSP*QPRVLKCHLEWSSLE GP/RRKIAAELGEQNQEL\KEPP FGHHVARNVALTTFLKRREAW EQQQGAVAKRRRALNSILED
20476	50844	A	20593	55	393	
20477	50845	A	20594	150	379	

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20478	50846	A	20595	1	2408	MGVWGIRTPFMVVGLESPVGS SPRGQGSCVRLPQRRPDKSHAG ARTGPETLRERAQQSNKLPEW AEKGSHPARWSPNRGGRWTLP TARERRPSRALKARAAGRRQA KVADFRLPAAAPPEGAAQLRLE SERLPHQDEKEPSSYRGSCGSCP VTLRKMPYLGSEDVVKELKKA LCNPHIQADRLRYRNVIQRVIR YMTQGLDMSGVFMEMVKASA TVDIVQKKLVYLYMCTYAPLK PDLALLAINTLCKDCSDPNPMV RGLALRSMCSLRMSKLDQWGQ AEVLNFLLRYQPRSEEELFDILN LLDSFLKSSSPGVVMGATKLFLI LAKMFPHVQTDVLVRVKGPLL AACSSESRELCFVALCHVRQIL HSLPGHFSSHYKKFFCSYSEPH YIKLQKVEVLCELVNDENVQQ VLEELRGYCTDVSADFAQAAIF AIGGIARTYTDQCVQILTELLGL RQEHITTVVVQTFRDLVWLCPQ CTEAVCQALPGCEENIQDSEGK QALIWLLGVHGERIPNAPYVLE DFVENVKSETFPAVKMELLTAL LRLFLSRPAECQDMLGRLLYYC IEEEKDMAVRDRGLFYYRLLLV GIDEVKRILCSPKSDPTLGLL\ED PAERPVNSWASDFNTLVPVYG KAHWATISKCQGAERCDPKLP KTSSFAASGPLIPEENKERVQEL PDSGALMLVPNRQLTADYFEK
20479	50847	B	20596	330	2458	
20480	50848	A	20597	2	171	
20481	50849	A	20598	32	1040	LQLAKLGDWRMQALRHVHCR FTEG*FMYSL*LTFPPAGYQVT GVFMKNWDSL\DEHGV\CTAD K\DCE\DA\YRVCQIL\DIPF\HQV SYGTEVIFFYSSDFLNEYEKGRT PNPDIVCNKHIKFSS*SLCSKNL TGADAIATGHYARTSLEDEEVF EQKHVKKPEGPASWRNCLSVG WFLYTLGQRANIGGLREPWYV VEASPPSHSILQAPRTDHPALYR DLLRTSRVHWIAEEPPAALVRD KMMECPPPRAPLFYPVPCVLTL NQDGTVWVTAVTPDARVSPLQ FAVFYKGDECLGSGKILRLGPS AYTLQKGQRRAGMATESPSDS PEDGP\GLSPLL
20482	50850	A	20599	12	432	

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20483	50851	A	20600	2	509	RLHSLLGDYYQAIKVLENIDLS TKSMYSRVPEC\QVTTYYYVGF AYSMMRCYQDAIRVFASILLYI HRTNSMFQRTKYKYEMIIMLN EQMHALLAIALTMYPMRI\DESI YLHLREKYVDKMLRMQNGDL QVYEELFRYSCTKFL*PVPPNY DTVHAHYHTESFLQSLRR
20484	50852	B	20601	8	1188	
20485	50853	A	20602	1	257	
20486	50854	B	20603	210	312	
20487	50855	C	20604	49	288	
20488	50856	A	20605	13	446	IPVRPTRPADDYESEAAYDPYA YPSDYDMHTGDPKQDLAYERQ YEQQTYQVIPEVIKNFIQYFHKT VSDLIDQKVYELQASRVSSDVI DQKVYEIQDIYEN\DAVFLILYK ELYYRHIYAKVSFQSFSQYRCK TAKKSEEEIDFL
20489	50857	B	20606	77	611	
20490	50858	A	20607	1	1956	SLVDPRVRPRVRVLASEAAMS YPAD\DYESEAAYDPYA\YPSD YDMHTGDPKQ\DLAYE\RQYEQ \QTYQVIP\EVIKNFIQYFHKTVS DLIDQK\VDELQASPCLQVIVID QERLYEDSRTIY*EQAWTKL\TE RFF\KNTPWPGGWKPLVPQGLA MDA/VSFLDFYPKNYTYRHIYA KVSGGPSL\EQRFESYYNYCNL FNYILNADGSRSPLNYPNQW\L WGYLSMEFIYPVFSHF\SQYRW *DLPKKSEEEI\DFLRSNPKIW\N VHSVLNVL\HSLVDKSNINRQL GGYTQAGGDP*ECGWGSMGR HSLYMM\LHYFSLVR/GFSRLHS LLG\DYYQAIKVLENIELNKKS MYSRVPRVPRSPTYY\YVGFAY LM\MRRY\QDAIRVFANILLYIQ RTKSMF\QRT\TYKYEMI\NKQIE QMHAL\LAIALT\MYPMR\IDESI HLQLREKYG\DK\MLRMQK\GD PQVYE*LF\SYSCP\RFLAA\VVP TYDNVHPN\YHKEP\FLQ\QLKG VFLDEVQ\QQGPAFKPIRSFLKL\ YTTHALLAKPGLASLDPHRGRE FRDPRFLCLSNHQG*RNLVLGP AGISSPWIGEISVSPQRVDLPTL NKDMIPHRGTPKVPQAVMGDF LHPVRSHKFGGA*SEPLKEGWG QRPWMIFTTHFREPVFDVIIGQG
20491	50859	A	20608	2	413	

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20492	50860	A	20609	232	621	
20493	50861	A	20610	1	3590	MAPRKRGGRGISFIFCCFRNND HPEITYRLRNDSNFALQTMEPA LPMPPVEELDVMFSELVDELDL TDKHREAMFALPAEKKWQIYC SKKKDQEENKGATSWPEFYID QLNSMAAGILEGVFVHIVITHC LQNQQQLLHDKQGNRHFICCL RSHQHPMLPACSNVHLSSFDRK TLCKDALCPLPASHVSRYLRKS LLALEKEEEEERSKTIESLKTAL RTKPMRFVTRFIDLDGLSCILNF LKTMDYETSESRIH
20494	50862	A	20611	203	3480	SHQEIEQNSAMAPRKRGG\RGI AFIFCCLRNNDHPEITYRLRNDS NFALQTMEPALPMPPVEELDV MFSELVDEL\DLPDKHREAMFA LPAEKKWQIYCSKKKDQEENK GATSWPEFYIDQLNSMAARKSL LALEKEEEEERSKTIESLKTALR TKPMRFVTRFIDLDGLSCILNFL KTMDYETSESRIHTSLIGCIKAL MNNSQGRAHVLAHSESINVIAQ SLSTENIKTKVAVLEILGAVCLV PGGHKKVLQA
20495	50863	A	20612	1	338	PGGALRVPDAPAGAEGQELCR SDFPVGGAGVGDEEGVQCPAP AAHRDDTDLRGAH*EVQDAAG RRKQPDREQPAGAEEGAPHLPE RVPPG*RHGTCTDRGQARACG GPLAPE
20496	50864	B	20613	610	6429	
20497	50865	B	20614	28	280	

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20498	50866	A	20615	160	1397	VKMSAQESCLRLIKDFLFVFNL FFFALGSLIFC\FGIWILIDKTSFL SFVGL/AAFVPLQIW\SKVL\AIS GNLSPWGIALLGLCWGALK\EL RCLLG\LYFG\MLLLLFATQITLE KSSSSNQR\AQLERSLR\DVVGK TI\QKYGINPE\ETAPEEN\WDYV QSNLRWCGWHYGRDWFKVFIL RGNGSEAH\RVTRS*YNFMAT* NSTILNKVIVHQLTRLEHLARSR HSAD\ICAVPAESHITRKG\CAQ GIQK\WLHNTLIFP*WAICLGVG LLE\LGFMTLSNIPVEETVDHGL PTGSARYRLGPAPPQSRAPPPVS VRWALPVLPVNICLIPRLAVEPS GVHISPGDTTWLRAPAAVTSPT GPGAFVHSFLSPSVGLPPPTRLF FTQTSNKPPAFLVNDHKKGGRS KKALEGPNVTRA
20499	50867	A	20616	290	492	
20500	50868	A	20617	1164	2134	NNYNHHHHHHHHHDYYNHH/ HHYHHHHHHHHNYNHHHHDH HHNYKHHHHHYHQHHHNYNH HHHHHHSYNHHHHHHHHHHN YNHYHHHHHHHHHHHREYHH HH/HHHHYHHHHHHNYNYHH HYHHHHHQHYHHNHHHHNHH YNHHY\HHNQYHYHHYHHHD YYHHH/HYHHHNYYYLYNRYH HYHHYHQSNHYRHHHHHHQY HHN/HEPFA/HHT*ILFCS*KQDR NLHCAWPFFFPFFNCHHHCHH HHQQQQHSGVKTKQSRPESLLP ERCIYLHQKHHPLHRPGAPQHQ KTASWRGQAREAAGSSPGSLSS HTADHEVEAFKRCFYSRF
20501	50869	B	20618	164	1526	
20502	50870	A	20619	1	762	

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20503	50871	A	20620	69	1054	AISCHVVHAGHQQTQITGNDPF PVVTYSKGPNLQSSRSDMDDST EREQSRLTSCLKKREEMKLKEC VSILPRKESPSVRSYKDGKLLA ATLLLALHACCLTEVSFYQVAA LQGDLASLRAELQGHHAEKLP AGAGAPKAGLGGSSSCSPRDLK IF*TTSSREKAIP/GSEQQK*GVP FQGPEETVTQDCLQLIADSETPT IQKGSYTFVPWLLSFKRGSALE EKENKILVKETGYFFIYGQVLY TDKTY\AMGHLIQRKKVHVFG DELS\LVTLFR\CIQNMPETLPNN SCYSAGIAKLEEGDELQLAIPRE NAQISLDGDVTFFGALKLL
20504	50872	A	20621	3	855	LQNSHGHTMIRTLLLSTLVAGA LSCGDPTYPPYVTRVVGGEEAR PNSWPWQVSLQYSSNGKWYHT CGGSLIANSWVLTA\AHCISSS\R TYRVGLGRHNLYVA\ESGSLA/ MSSVSKIVVHKD\WNFNQISKG\ NDI\ALLKLANPVSLTDKIQ\LA\ CFPPAGTILPN\NY\PC*VTGLGE SCRTNG\AVPDVL\QQGR\LLAV DYATCS\SSA\WWGSSVKTSMIC A\GGDGVISSCNGDSGGPLNCQ A\SDALWQVHGIVSFGSRLGCN YYHKPSVFTRVSNYIDWINSVI AYN
20505	50873	A	20622	19	414	SVCWEDRYLKARMEESPLSRA PSRGGVNFLNVARTYIPNTKVE CHYTLPPGTMPSASDWIGIFKP/ GYLPKPGAQLYQFRYVNRQGQ VCGQSPPFQFREPRPMDELVTL EEADGGSDILLVVPKATVLQNQ
20506	50874	A	20623	1	393	AKSWQEEQSAQAQRLKDKVA QMKDTLGQAQQRVVSEAPWQ QETGNSKGKL*RSLRV*REGER HG*RLNNTTPSPNAVEWRER/IT SLADE*FTRNCDLHLLLSPEAEL EPLKEQLRGAQELAASSQQKAT LY
20507	50875	A	20624	56	416	NRPLLALVASDTQPLHTHTHTH TPLSDAPKPIPGA/HLP/CSYLEF PLTSVPHPSLFHNLRYSVWRGF LYF*GFLYSVSSPRISSHGKK*CI CAFCEEWGEQVVPGIPISKAPLP LQVPPQQ
20508	50876	A	20625	115	392	
20509	50877	B	20626	1	3388	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20510	50878	A	20627	3	1889	SSPREKTSDSSHRPSRHGFLFLR LVGLSPFSYLCVPPSRPVPGSPR SLSAMRLLPLAPGRLRRGSPRH LPSCSPALLLLVLGGCLGVFGV AAGTRRPNVVLLLTDDQDEVL GGMTPLKKTKALIGEMGMTFS SAYVPSALCCPSRASILTGKYPH NHHVVNNTLEGFCSSKSW\QKI QEPNTFPAILRSMCGYQTFFCR GNI*MKYGAP\DAGG\LG\HVPL GLGVTWYALEKNS\KYYNYTL FYSMGKARKHGENY\SVDYLT DVLANVSLDF\LDYKSNF*PFF MMIATP\APHSPWTAAPQYQKA FQNVFAPRNKNFNIHGTNKHW LIRQAKTPMTNSSIQFLDNAFR KRWQTLLSVDDLVEKLVKRLE FTGELNNTYIFYTSDNGYHTGQ FSLPIDKRQLYEFDIKVPLLVRG PGIKPNQTSKMLVANIDLGPTIL DIAGYDLNKTQMDGMSLLPILR GASNLTWRSDVLVEYQGEGRN VTDPTCPSLSPGVSQCFPDCVCE DAYNNTYACVRTMSALWNLQ YCEFDDQEVFVEVYNLTADPD QITNIAKTFDP\ELLGKMNYRL MMLQSCSGPTCRTPGVFDPGY RFDPRLMF\SNRGSVRTRRFSQT SSCSDPHTASADGSLHALFLMK
20511	50879	A	20628	132	253	
20512	50880	A	20629	1	1269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20513	50881	A	20630	1	1920	MDEAEFSSFVVRTNTCGELRSS HLGQEVTLCGWIQYRRQNTFL VLRDFDGLVQVIIPQDEVIENFL LLSKSFFDAIAGSAASVKKILCE APVESVVQVSGTVISRPAGQEN PKMPTGEIEIKVKTAELLNACK KLPFEIKNFVKKTEALRLQYRY LDLRSFQMQYNLRLRSQMVMK MREYLCNLHGFVDIETPTLFKR TPGGAKEFLVPSREPGKFYSLP QSPQQFKQLLMVGGLDRYFQV ARCYRDEGSRPDRQPEFTQIDIE MSFVDQTGIQSLIEGLLQYSWP NDKDPVVVPFPTMTFAEV\RPP YGTDKPDTRFGMKIIDISDVFR NTEIGFLQDALSKPHGTVKAICI PEGAKYLKRKDIGSIRNFAADH FNQEILPVFLNANRNWNSPVAN FIMESQRLELIRLMETQEEDVV LLTAGEHNKACSLLGK\LRTGN VAGPSRKQEGVVLRDPTLFSFL WVVDFPLFPGQRRKIQESWDR GQHPF\TAPHPR*IT\LLYTEPKK ARSQHYDLVLNGNEIGGGSIRI HNAELQRYILATLLKEDVKMLS HLLQALDYGA\PPHGGIALGLD RLICLVTGSPSIRDVIAFPKSFRG HDLMSNTPDSVPS*GTEALSYP SLQANRLQSRKSSLNHAYHAES
20514	50882	A	20631	1	425	KEPVGCVNNISFLASLAGSTSR NRLQSTRGAGRLQNSGTGLSTN LQHFQEENFRKSSPQLEHT/WSF FGECTTHHLPPVKAPLQTKKKT TNHCFLCGKKTGLASSYECRQ VGELEKLRCFLCDNPAWGLCKI KYLNCLFITSL
20515	50883	A	20632	1	1647	
20516	50884	A	20633	1	3096	
20517	50885	A	20634	1	419	
20518	50886	A	20635	558	1070	SFRFGHSHGLWKRKKVA*GSN AIQHNMLQGKQNFHGAALWY KGNSTQSKRPQRAP*ESSTTKR GLQLSRQTLQLDPGGTVPCSEE YCICQ*EGPASRNRYNGVPSHF PSPTCIRESSHSGKILKSRLRCW GWPTDPWSVLPMDPRTSPLCA AGSQAVVAHSGRQQKYPAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20519	50887	A	20636	3887	4573	KKTTLLTLSKTRNILNPFKVVK KKAYGSRKHLRQ/HLAINPAAL LPTAASQISEVKPVLPELAFPSS EHRRSHGLESVPVLPGSGEAGV SFDLPAQADTLHSANKSRVKM RGKRRPQTRAARRLAAQESSEA EDM\RSPEDPLHSGLMAPFPQM AIGHSSEQPVEKTALRRPWQLP LHLGKVVLCLEWTQAPLQSLW VIPEGRLTFLILGTFFPRALDLSP WREQNPRQR
20520	50888	A	20637	1	2988	MATAPSPPMLTLAPAWLCPAT TTPRDHSEASLEALPGDPPAHP AAAATAAAVIPALEPPHTPVYA IFVNHSLLDLYIDRPLPYLIGSK LFMEQEDVGLGELSSEEGNADE QSSGLEGACKVNLELLLTNAD KGLKAPEQHLKHVAGVLNGES VETSVLNYRELSPHKNRLLSPL RCSAPMSLHNSLVKPERQSKCF EFGKLQPSSSQSLDVQNITDSSF SRTTCFQGVKVDSLGKRSDVIS KVEARDITEMTNKA
20521	50889	A	20638	1	1176	
20522	50890	A	20639	2	367	
20523	50891	A	20640	124	441	RYPRVPENRCFSELLFFQAPLG VGMARGNQR\ELARQKNLKET\ QEI\SRGKGKEDSLTALSRKQRD S*IIAKKQKAA\NEKKS\MQTRE NVMTGYLENPGATAQLGVS
20524	50892	A	20641	32	232	
20525	50893	A	20642	1	256	
20526	50894	C	20643	133	509	
20527	50895	A	20644	88	685	QKRGRLFKIILKVVLYLMKVIVI HRKMFQRAQELRWRAEDYHK CKAFSDHPLCKKASLQLGQNG GSGASSFFRIALLALPHS*NFKK QDGPPATSSNSTTFYN**LPEPQ DTSRMSSYSLSTLSSSTLRG**S QDSSLSYSGGRGRKITETQEAE VE*AENRSLHSSLGNKKKSVSG TKEKNQKTKQNPHSKNKLTKN
20528	50896	A	20645	42	946	
20529	50897	C	20646	1	453	
20530	50898	C	20647	771	1223	
20531	50899	C	20648	324	659	
20532	50900	C	20649	427	654	
20533	50901	B	20650	343	1774	
20534	50902	B	20651	23	525	
20535	50903	B	20652	2354	5689	
20536	50904	B	20653	448	3506	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20537	50905	B	20654	12	182	
20538	50906	C	20655	210	422	
20539	50907	C	20656	145	357	
20540	50908	B	20657	1	327	
20541	50909	B	20658	1	2595	
20542	50910	B	20659	122	472	
20543	50911	B	20660	163	418	
20544	50912	C	20661	86	517	
20545	50913	B	20662	334	2946	
20546	50914	B	20663	11	700	
20547	50915	B	20664	184	2372	
20548	50916	C	20665	267	467	
20549	50917	B	20666	131	268	
20550	50918	B	20667	18	255	
20551	50919	B	20668	100	356	
20552	50920	B	20669	120	839	
20553	50921	B	20670	355	504	
20554	50922	B	20671	1	1524	
20555	50923	B	20672	175	366	
20556	50924	B	20673	436	792	
20557	50925	B	20674	94	1347	
20558	50926	B	20675	865	1189	
20559	50927	B	20676	241	423	
20560	50928	B	20677	124	352	
20561	50929	B	20678	1	847	
20562	50930	B	20679	262	4624	
20563	50931	C	20680	76	297	
20564	50932	B	20681	1	702	
20565	50933	B	20682	1	1347	
20566	50934	B	20683	78	2874	
20567	50935	B	20684	133	7317	
20568	50936	B	20685	294	1449	
20569	50937	C	20686	139	367	
20570	50938	C	20688	154	445	
20571	50939	B	20689	1	1086	
20572	50940	B	20690	111	440	
20573	50941	B	20691	303	462	
20574	50942	B	20692	1	2905	
20575	50943	C	20693	349	453	
20576	50944	C	20694	233	376	
20577	50945	B	20695	1	2016	
20578	50946	B	20696	1464	3022	
20579	50947	B	20697	1	1059	
20580	50948	B	20698	1	933	
20581	50949	B	20699	1	930	
20582	50950	C	20700	129	215	
20583	50951	C	20701	283	408	
20584	50952	B	20702	1	1134	
20585	50953	B	20703	1	525	
20586	50954	B	20704	146	556	
20587	50955	B	20705	1	675	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20588	50956	B	20706	1	1107	
20589	50957	B	20707	1	774	
20590	50958	C	20708	52	156	
20591	50959	C	20709	1	420	
20592	50960	B	20710	1	1347	
20593	50961	C	20711	1	411	
20594	50962	B	20712	169	248	
20595	50963	B	20713	63	1321	
20596	50964	B	20714	1	359	
20597	50965	C	20715	1195	1674	
20598	50966	B	20716	964	1290	
20599	50967	B	20717	51	389	
20600	50968	B	20718	108	232	
20601	50969	B	20719	425	3545	
20602	50970	C	20720	35	226	
20603	50971	B	20721	1	387	
20604	50972	B	20722	1	1926	
20605	50973	B	20723	523	1242	
20606	50974	B	20724	42	2346	
20607	50975	B	20725	63	287	
20608	50976	B	20726	59	200	
20609	50977	B	20727	1	1176	
20610	50978	B	20728	1	769	
20611	50979	B	20729	1	2009	
20612	50980	B	20730	219	3045	
20613	50981	B	20731	195	1739	
20614	50982	C	20732	126	435	
20615	50983	B	20733	2752	4108	
20616	50984	B	20734	1	1104	
20617	50985	B	20735	24	230	
20618	50986	B	20736	1	1292	
20619	50987	B	20737	1	7977	
20620	50988	B	20738	157	2627	
20621	50989	C	20739	165	533	
20622	50990	B	20740	35	87	
20623	50991	C	20741	68	202	
20624	50992	B	20742	83	2670	
20625	50993	B	20743	162	276	
20626	50994	B	20744	104	245	
20627	50995	B	20745	66	2768	
20628	50996	B	20746	14	3115	
20629	50997	C	20747	69	203	
20630	50998	B	20748	1	2152	
20631	50999	C	20749	114	387	
20632	51000	C	20750	56	250	
20633	51001	B	20751	53	3398	
20634	51002	B	20752	642	2386	
20635	51003	B	20753	1	1242	
20636	51004	B	20754	51	601	
20637	51005	B	20755	192	463	
20638	51006	B	20756	125	1254	

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20639	51007	C	20757	208	333	
20640	51008	B	20758	155	4443	
20641	51009	B	20759	1	2529	
20642	51010	B	20760	63	321	
20643	51011	B	20761	226	645	
20644	51012	B	20762	1	1395	
20645	51013	B	20763	258	475	
20646	51014	C	20764	126	263	
20647	51015	B	20765	1	1429	
20648	51016	B	20766	51	3256	
20649	51017	C	20767	83	403	
20650	51018	B	20768	1	621	
20651	51019	B	20769	1	463	
20652	51020	B	20770	1002	3594	
20653	51021	C	20771	107	403	
20654	51022	B	20772	51	401	
20655	51023	C	20773	46	398	
20656	51024	B	20774	1	513	
20657	51025	B	20775	1	531	
20658	51026	C	20776	1	423	
20659	51027	B	20777	52	670	
20660	51028	C	20778	43	375	
20661	51029	B	20779	1	1629	
20662	51030	B	20780	1	1713	
20663	51031	B	20781	1	5154	
20664	51032	B	20782	37	585	
20665	51033	B	20783	1	3789	
20666	51034	C	20784	149	367	
20667	51035	C	20785	89	234	
20668	51036	B	20786	113	278	
20669	51037	B	20787	1	1632	
20670	51038	B	20788	1	762	
20671	51039	B	20789	230	3411	
20672	51040	B	20790	95	1150	
20673	51041	B	20791	1	1230	
20674	51042	B	20792	74	3123	
20675	51043	B	20793	1	1719	
20676	51044	C	20794	206	402	
20677	51045	B	20795	302	424	
20678	51046	B	20796	60	80	
20679	51047	B	20797	1	1248	
20680	51048	B	20798	8	1910	
20681	51049	B	20799	124	807	
20682	51050	B	20800	43	618	
20683	51051	B	20801	7	328	
20684	51052	B	20802	244	385	
20685	51053	B	20803	850	970	
20686	51054	C	20804	97	360	
20687	51055	B	20805	551	3159	
20688	51056	B	20806	861	1110	
20689	51057	B	20807	1	876	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20690	51058	B	20808	1	849	
20691	51059	B	20809	1	1443	
20692	51060	B	20810	508	2398	
20693	51061	B	20811	53	185	
20694	51062	B	20812	50	633	
20695	51063	B	20813	1	444	
20696	51064	B	20814	58	262	
20697	51065	B	20815	27	1005	
20698	51066	B	20816	1	4860	
20699	51067	B	20817	1	3489	
20700	51068	C	20818	52	363	
20701	51069	C	20819	347	499	
20702	51070	B	20820	1	4140	
20703	51071	B	20821	85	3930	
20704	51072	B	20822	848	3116	
20705	51073	B	20823	41	1211	
20706	51074	B	20824	248	4307	
20707	51075	B	20825	67	3180	
20708	51076	C	20826	229	467	
20709	51077	B	20827	71	1827	
20710	51078	B	20828	1	1045	
20711	51079	B	20829	1279	1479	
20712	51080	B	20830	1	2460	
20713	51081	B	20831	62	3691	
20714	51082	B	20832	1	1062	
20715	51083	B	20833	1	873	
20716	51084	B	20834	1	1041	
20717	51085	B	20835	161	5445	
20718	51086	B	20836	199	343	
20719	51087	C	20837	86	229	
20720	51088	C	20838	1	225	
20721	51089	C	20839	34	165	
20722	51090	C	20840	238	455	
20723	51091	C	20841	200	322	
20724	51092	B	20842	59	164	
20725	51093	C	20843	1353	1793	
20726	51094	B	20844	1	1329	
20727	51095	C	20845	43	324	
20728	51096	C	20846	223	435	
20729	51097	C	20847	212	307	
20730	51098	C	20848	386	529	
20731	51099	B	20849	300	995	
20732	51100	B	20850	876	3312	
20733	51101	B	20851	153	306	
20734	51102	B	20852	39	3131	
20735	51103	B	20853	29	136	
20736	51104	B	20854	112	333	
20737	51105	B	20855	31	474	
20738	51106	B	20856	26	1716	
20739	51107	B	20857	27	1234	
20740	51108	B	20858	1	6390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20741	51109	B	20859	1	1014	
20742	51110	B	20860	128	837	
20743	51111	B	20861	1	931	
20744	51112	B	20862	357	4629	
20745	51113	B	20863	1	1017	
20746	51114	B	20864	1	1908	
20747	51115	B	20865	224	9448	
20748	51116	B	20866	1	1209	
20749	51117	B	20867	138	359	
20750	51118	B	20868	1	1567	
20751	51119	B	20869	226	9033	
20752	51120	B	20870	20	2689	
20753	51121	B	20871	1602	2647	
20754	51122	C	20872	72	452	
20755	51123	C	20873	64	423	
20756	51124	B	20874	33	363	
20757	51125	B	20875	131	1675	
20758	51126	B	20876	37	219	
20759	51127	B	20877	1	564	
20760	51128	B	20879	1	651	
20761	51129	B	20880	44	424	
20762	51130	B	20881	28	202	
20763	51131	B	20882	1	3403	
20764	51132	B	20883	110	970	
20765	51133	B	20884	70	485	
20766	51134	B	20885	482	2943	
20767	51135	B	20886	469	1480	
20768	51136	B	20887	156	308	
20769	51137	C	20888	218	348	
20770	51138	B	20889	1	5130	
20771	51139	B	20890	21	1139	
20772	51140	B	20891	1	1302	
20773	51141	B	20892	1	1028	
20774	51142	B	20893	1	858	
20775	51143	B	20894	1	2001	
20776	51144	B	20895	1	546	
20777	51145	B	20896	1	1167	
20778	51146	B	20897	1	1299	
20779	51147	B	20898	1	1260	
20780	51148	B	20899	1	771	
20781	51149	C	20900	155	337	
20782	51150	B	20901	1	1251	
20783	51151	B	20902	106	543	
20784	51152	B	20903	57	2279	
20785	51153	B	20904	905	1120	
20786	51154	B	20905	145	2277	
20787	51155	B	20906	1	1384	
20788	51156	B	20907	1	4775	
20789	51157	C	20908	99	251	
20790	51158	B	20909	1	693	
20791	51159	B	20910	77	2173	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20792	51160	B	20911	140	313	
20793	51161	B	20912	1	392	
20794	51162	C	20913	1	222	
20795	51163	B	20914	1	951	
20796	51164	B	20915	45	1244	
20797	51165	B	20916	166	2544	
20798	51166	C	20917	279	449	
20799	51167	B	20918	1	1250	
20800	51168	B	20919	229	2094	
20801	51169	B	20920	94	434	
20802	51170	C	20921	253	336	
20803	51171	B	20922	1	1314	
20804	51172	B	20923	6	327	
20805	51173	B	20924	163	3060	
20806	51174	B	20925	20	385	
20807	51175	B	20926	22	58	
20808	51176	C	20927	141	287	
20809	51177	B	20928	37	1063	
20810	51178	C	20929	261	401	
20811	51179	B	20930	66	3148	
20812	51180	B	20931	223	4149	
20813	51181	C	20932	21	278	
20814	51182	B	20933	158	1283	
20815	51183	B	20934	8	896	
20816	51184	B	20935	240	387	
20817	51185	C	20936	312	512	
20818	51186	B	20937	451	611	
20819	51187	C	20938	160	428	
20820	51188	B	20939	110	294	
20821	51189	B	20940	121	1764	
20822	51190	B	20941	1	423	
20823	51191	C	20942	74	316	
20824	51192	C	20943	136	255	
20825	51193	C	20944	79	381	
20826	51194	B	20945	282	1180	
20827	51195	B	20946	63	371	
20828	51196	C	20947	193	672	
20829	51197	B	20948	85	898	
20830	51198	B	20949	35	1055	
20831	51199	B	20950	1	870	
20832	51200	B	20951	103	1189	
20833	51201	B	20952	501	594	
20834	51202	B	20953	39	1694	
20835	51203	B	20954	489	4797	
20836	51204	C	20955	31	153	
20837	51205	B	20956	259	699	
20838	51206	B	20957	4	231	
20839	51207	B	20958	50	520	
20840	51208	C	20959	322	456	
20841	51209	B	20960	163	1152	
20842	51210	B	20961	33	745	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20843	51211	B	20962	210	3519	
20844	51212	C	20963	34	294	
20845	51213	C	20964	301	381	
20846	51214	B	20965	71	675	
20847	51215	B	20966	1	873	
20848	51216	B	20967	118	1618	
20849	51217	B	20968	424	2415	
20850	51218	C	20969	106	231	
20851	51219	B	20970	71	756	
20852	51220	B	20971	1	1049	
20853	51221	C	20972	94	327	
20854	51222	B	20973	339	2589	
20855	51223	B	20974	89	273	
20856	51224	B	20975	1	2514	
20857	51225	B	20976	472	5831	
20858	51226	C	20977	247	300	
20859	51227	B	20978	1	2487	
20860	51228	B	20979	55	243	
20861	51229	C	20980	207	377	
20862	51230	B	20981	642	4117	
20863	51231	B	20982	44	2127	
20864	51232	B	20983	48	1127	
20865	51233	B	20984	1	3411	
20866	51234	B	20985	74	469	
20867	51235	B	20986	39	1251	
20868	51236	B	20987	223	378	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20869	51237	A	20988	1	2577	MPPNRHRMRGETTLWNPGCDH AGIATQVVVEKKLWREQGLSR HQLGREAFLQEVWKWKEEKG DRIYHQLK\KLGSSLDWDRACF TMDPKLS\AAVTEAFVGLHEKG IIYRSTAFVNWPCTLNSAISDIE VDKKELTGRTLLSVPGYKEKV EFGVLVSF\AYK\VQGSD*/DDE EVVVANKLGSKT\MLGDVAVA VPPPKDTR\YQHL\KGKNVIHP\F LSRSLSPLSSDEFVDMDF\GTGA VKDHPPRHDQNDYEVGQRHGL EAISIMDSRGA\PIKCASAFPGPA AGLRPGKRCWWR*RNRGLFRG IEDNPMVVPLCNRSKDVVEPLL RPQWYVRCGEMAQAASAAVT RGDLRILPEAHQRTWHAWMD NIREWCISRQLWWGHRIPAYFV TVSDPAVPPGESEDLSVFYPGT LLETGHDILFFWVARMVMLGL KLTGRLPFREVYLPCPSCENAH GRK\MSKSLGNVIDPLDVHL/Y GISLQGLHNQLLNSNLDPSEVE KAKEGQKADFPAGVPECGTDA LRFGLCAYMSQGS*K*TWNVN RIMG*RQFCNKLW[illegible]FALR GLGKGFVPS\DTSN[illegible] DR*IRNLLTEAVRLS[illegible] DFPAVTTAQ[illegible] LECLKPVLNGVDQV/A[illegible] QTLYTLPWTLGLRLLS[illegible] TEELFQRLPRRMPQAPP[illegible]
20870	51238	A	20989	2	4083	SQRGEHVGAGCRGGDLRELGS PGEPPTVSARSTPPPGPLGGSQP RPAPGCEVDSPAQSDHLPPVFP LRSDLLITMSTLYVSPHPDAFPS LRALIAARYGEAGEGPGWGGA HPRICLQPPPTSRTSFPPPRLPAL EQGPGGLWVWGATAVAQLLW PAGLGGPGGSRAAVLVQQWVS YADTELIPAACGATLPALGLRS SAQDPQAVLGALGRALSPLEE WLRLHTYLAGEAPTLADLAAV TALLLPFRYVLDPPAR

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20871	51239	A	20990	1	756	MDMGAIKEGESRRPGDRMTVA GTKLLHLQSTHLDFISLSGAPSG ALELSKAQPAHAQDTRVLMKM VIIWDLSQVPLQPGHDGHSFRIH DYLYFQVLSPGDIRYIFTATPAK DFGGIFHTRYEQIHLVPAEPPEA CGELSNGFFIQDQIALVERGGCS FLSKTRVVQEHGGRGGDHL*Q RS*QMTASTW/QMIQDSTQRTA DIPALFLLGRDGYMIRRSLEQH GLPWAIISIPVNVHQHSPPLSCC NRPFLFW
20872	51240	A	20991	2	393	
20873	51241	A	20992	1066	1824	
20874	51242	A	20993	3	902	
20875	51243	A	20994	1	2163	
20876	51244	A	20995	1	1890	
20877	51245	A	20996	1	2882	MKQQLPVSYLQVIFNHWASRIS GARGAGWGPVRLGRLCADRAL DGESRPGGGGQSGVPASEASQ KAAHGRRLPVPARLLRCAHSA LEPGRGSASSPRNSTTSDNDQPP DYSFSKRCDSHSLGFSLVWESR NLTLPPTSKLLHFSAFHFFIYKC RAEGHKLYKDLKNFLSAVKVM HESSKRVSETLQFIYY\SEWYGH EELKAIVWNNDLLWEDYEEKL ADQAVRTMEIYVAQFSEIKERI AKRGRKLVDYDSARH

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20878	51246	A	20997	1	1791	MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEKVLQKLG KAVETKDERFEQSANNFYQQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSETLQEIYSSEWDGHE ELKAIVWNNDLLWEDYEEKL\ ADQAVRTMEIYVAQFSEIKE\RI AKRGRKLVDYDSARHHLEAVQ NAKKKDEAKTAKAEEEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMSKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPTSPSTLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEEDEPLPA CNGPAQAQPSPTTERAK\SQEE VLPSSTTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPPRRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSPRAS LGTGTASPRTSLEI*PNPE\PPEK PVRTPEAKENENIHNQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE
20879	51247	A	20998	3	273	RRPRQRPTDQTQWFSILPDFSLD LQEGPSVESQT\HSDPHIPPVDP TTHLTFNHLSIVCVSLTLSLPHL GSPCLWSPALVSQEAASHQDRR
20880	51248	A	20999	309	1310	RHQRAPEQGPDASWKMLDSLL ALGG\LVLL\RDSVE\WEG\RSLL K\ALVKKSALCGE\QVHILGCE\ VSEKEFREGFDS**STIRLVYHD F\FRDP\LNWSKTEEGL/VPGGPL GALRS\MCKR\TDPVPVTIALDS LS\WLLLRLHCT\TLCQ\ALHAV EPSRTLVLGDSSSVGKVSVLGL LHERLPRPAPVVALSSLAQTKV TLGGYHGARPSAHIL\CRRPRQ\ RPN\YQTQWFSI\LPDFSLGSPRG ALCRVPALIPIPHITPGGIPHNSF *PFNLHL\SKKEREARDSLILPFQ FSSEKQQA\LLRPRPGQATSHIF YEPDAYDDLDQEDPDDDLNILP

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20881	51249	A	21000	418	1304	GLVMEIGMHHHEHHHLQAPNK EDILKISEDERMELSKSFRVYCII LVKPKDVSLWAAVKETWTKH CDKAEFFSSENVKVFESINMDT NDMWLMMRKAYKYAFDKYR DQYNWFFLARPTTFAIIENLKY FLLKKDPSQPFYLGHTIKSGDLE YVGMEGGIVLSVESMKRLNSL LNIPEKCPEQGGMIWKISEDKQ LAVCLKYAGVFAENAEDADGK DVFNSQICWAFY*R/WQ*LITPN QVVEGCCSDMAVTFNGLTPNQ MHVMMYGVYRLRAFGPYFSM MHWFSYLQMVLTMTEKW
20882	51250	A	21001	1	1092	
20883	51251	A	21002	130	397	EGVHSQVNLFPIKGNQTHVPAS HGTDSALPPTLQMDYRALVHE PD*AAYGELRAMVLDLRAFYA ELYHIISSNLEKIVNPKGEEKPF
20884	51252	A	21003	11	805	SSMAKPC\GVRLSGKGRKQVEV FYRNLFQEAEEFLLR\FLPPESHI P*NRLLQEDFPFNVA*/LLNLSS GAPLDIPPSPDP\PP\KDDEMETD K\QEKKEVPKCDFLP\GNEKCPC PCLPLVKPRSLDLSKEKC\ILVI\ TWGSRHLDPPRFEDGK*FWG* AIPGEGAWRG*NA\VKDPKWE AFPATPISQVLSSERGDACGPRP PQETHV\MDYRALVHERDEAA YGELRAMVLDLRAFYAELYHII SSNL\EKIV\TPRGEEKPIYVLEP
20885	51253	A	21004	352	670	AKRSRIHVGVVIVDSDGAELGR DAAALSEKPPSLTIGLHMELVG MGGEPALTATPANCPEYPAKPS SI/EQQ*QSQVQ**Q*QVRHGSG PLHRTPRQLFLCSRQFAL
20886	51254	A	21005	3	222	SPEESPPACPRQVFPLYHLQRG QGKRVQVG*GGSLWITTKTRLL PGGVGDNEVAPGSWHLALVFR LLSSGRP

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20887	51255	A	21006	1	3639	MSEETLQSKLAAAKKKIQDILN VLVSDLNRSNGVVLPTLDKWK DAPEAWDLCLALRSICGLAIQL LGAAPLTRAANFSVAEVTDVR DSARRWETRKAPYLSCRIALRM NEAAVFRHLVPGVYFPRCDQG CQLTAALGCGAGVQSHVGPVT VTTGPDSVTAADAAGLCRVLR AVGWGGSECRLTPHPYKFHVE PYGGRLVPPRLSVDPGSSRREA TSKVAVDLLVLDAAGADGPVS QSPVWKEAAGVVSQLRGGRQ
20888	51256	A	21011	137	944	KPRCCHSATMFEVPLVQGSILK KVLEALKDLINEACWDISSSGV NLQSMDS/SHVSLLQFTLPSEGF DTYRCDCNLAMGVNLTIMSKIL KCAGNEDIVTLRIEDNVNTLVL VFEASNQEKVSDYEIKLMDLD VEQLGIAEQEYHYVVKMLSGE FASIC*DLSHIGDAVVISGVKDG IIFSASGDLGN\KNKLSQTSTVD KEEEAVTMEMNEPVQLTFALR YLNFLTKATPLSSMVTLNMSA DIHLVVDYKIADVGHLKYYLA PKMEDEEGP
20889	51257	B	21012	205	1309	
20890	51258	A	21013	189	410	
20891	51259	A	21014	1767	2158	RAQPHLYPEAARTRGRK*LHFC APSSAPRAPVSERR/CAGRFLSW CPVAAWDPARWARRARRRRR AAARRRRPPRWRRRCLSARGR RRSLNSSKTKNTKCLNSINQRL KILSLQKDLMCGTAGRCKTLTE Q
20892	51260	A	21015	1	1710	
20893	51261	A	21016	132	522	
20894	51262	A	21017	1	1386	
20895	51263	A	21018	331	3101	SFSEANISTAKKTFLYNELYVY NTRKDTWTKVDIPSPPPRRCAH QAVVVPQGGGQLWVFGGEFAS PNGEQFYHYKDLWVLHLATKT WEQVKSTGGPSGRSGHRMVA WKRQLILFGGFHESTRDYIYYN DVYAFNLDTFTWSKLSPSGTVP TPRSGCQMSVTPQGGIV\VYGG YSKQMPPHSGQSRGRKPGSCLL LLLLLLLLLLLLLLCVLPLGYSL IELSSSYRLHGNEPVPATFHGLN SHMGLVATILDNVNP

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20896	51264	A	21019	2	2911	VRGPRARCRRRSSKTEPRKGPS RTSTRKRLELGAGSDSISVRRAP PHEHLFPSGERGPFSFLVSRRGL GPGKMGKKGKKEKKGRGAEK TAAKMEKKVSKRSRKEEPGVC RRIRPDLGVECSAAAAHGFPNR GQFYGLPCARHSSLGFTPHEQE DLEALIAHFQTLDAKRTQTVEV PCPPPSPRKCRGSQFVVTEDSVR KGTALRLNASLSVHPEKDELIL FGGEYFNGQKTFLYNELYVYNI RKDTWTKVDIPSP
20897	51265	A	21020	1	208	DGYRHEMLPASLIQAQRDYFG AH/TYELWAKPGQFIH/TNWTG HGGTVSSSSYNAFALFSVQFFK SVVRDS
20898	51266	A	21021	3	316	
20899	51267	A	21022	2	578	LIGLAVMGQNLILNMNDHGFV\ TVSKVDDFLANEAKGTKVVGA QSLKEMVSKLKKPRRIILLVKA GQAVDDFIEKLRRCRDLKAKGI LFVGSGVSGGEEGARYGPSLMP GGNKEAWPHIKTIFQGIAAKVG TGEPCCDWVGDEGAGHFVKM VHNGIEYGDMQLICEAYHLMK DVLGMAQDEMALCPIFCSVF

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20900	51268	A	21023	3	1758	AYANLGTRFWREPLRVFPSLVL RASPLFGSALSAAMAQADIALI V\LFVMGHNLILNMKDHGFEVC AFNRTVSKVDDFLANEAKGTK VVGAQSLKEMVSKLNKPPRDQ YLLC/VKAGQAVDDFIEKLVPL LDTGDIII\DGGNSEY*GTPQDG CRDLKAKGILFEGS\GVSAGEE GD\RYGP\SLMPGGNK\EAWPHI KTIFQGIA\AKVGTGEPCC\DWV GDEGAGHFVKMVHNGIEYGD MQLICEAYHLMKDVLGMAQD EMAQAFEDWNKTELDSFLIEIT ANILKFQDTDGKHLLPKIQGTS AGARRGNRGSGT/WPFSGPGKY GVPV\TLI\GEAVF\ARCLSSL\KD ERI\QASKKLKGPQK\FQFDGD* EIISWEDIRKALYASKIISYAQGF MLLRHAA\TEFGWTLNYG\GIA LMWRGGCIIRSVFLGKIKDAFD RNP\ELQNLLLD\DFFKVQLFEN CQ\DSWR\RAVSTGVQGWAFP MPLFYRLPLSI*TGTSHEMLPAQ PSSRLQRGLLSGAHTL*NSWAK PGAVLFHTNWTG\HGGTVSSSS YQCLDHAAPVTLHDSTVPGHSI GLNGTAHLALCPIFCSVFFKSV
20901	51269	A	21024	317	885	MRWRSKSAWRAEPKSRTNSGT ASNVSPSRPLEC*R/FLRLVSGE LILALIAFICIETIMACSPCEGLY FFEFVSCSAFVVTGVLLIMFSLN LHMRIPQINWNLTDLVNTGLSA FLFFIASIVLAALNHRAGAEIAA VIFGFLATAAYAVNTFLAVQK WRVSVRQQSTNDYIRARTESRD VDSRPEIQRLDT
20902	51270	A	21025	4761	5127	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQT\TSPRNISPISNPHTR TSKRLNRSGQAFLQNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL

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20903	51271	A	21026	174	2238	LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQT\TSPRNISPISNPRQR RHILSMDPKLRRRSWTWVGSLP LVFNHCRDASLIIHPGFRGVRPR RDVCLGPSPLATITDAELYVTL TVEGKSIPFLIDTEATHSTLPSFK GPVALASIHVQNVQIKRDKEGH YIMVKGSIQQEELTILNMYAPN TGAPRFIKQVLNDLQRDLDSHT IIMGDFNTPLSTLDRSTRQKVN KDIQDLNSALHQADLIDIYRTL HTKSTECTFFSAPHRTYSKIDHI VGSKALLSKCKRTEIIINCLSDH SAIKLELRIKKLTQNHSTTWKL NNLLLNDYWVHKEMKAEIKM FFEINENKNTTYQNLWDTFKAV CRGKFIALNAYKRKQERSKIDT LTSQLEELEKQEQTRSKASRRE EITKIRAELKEIETQKTLQKINES RSWFFEKINKIDILLARLIKKKR EKNQIDAIKNDKGDIATDPTEIQ TTIREYYKHLCPNKLENLEEMD KFLDTYTLPRLNQEEDESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AKFYQRYKEELVPFLQKYKEEL VPFLLKLFQSIEKEGILPNSFSEA SIILIPKPGRDTTKKENFRPISLM NIDAKILNKILANQIQQHIKKLI HHDQVGFIPGMQGWFNIRKSIN VIQHINRTKDKNHMIISIDAEKA FDKIQQPSC
20904	51272	A	21027	1	181	MEEKEERKRRRKRKRRREEGR DGERKRMEKQKENQDPKDPPT TSGPQT\TSPRNISPISNP
20905	51273	A	21028	167	408	LGSRTFPWEINPPSSCSLLREKD PPTTSGPQT\TRPRNISPISNLVS GLFLLSSPTSLTIPQPLSSFNLDD TLQSLPSLNF
20906	51274	A	21029	449	663	LGSGDLPWEINTQSSCSLLCEK DPPTTSGPQT\TSPRNISPISNPDP TGNRTVQLTWQPVPEPLELWP KAL
20907	51275	A	21030	79	381	LGSGDLPWEINPLSSCSLLREKE PPTTSGPQT\TRPRNISPISNPELA TLAGNLATGPRNARSPGFLLSH VLSVWDPTENQTVQLTWQPLP QPLELWPKAL
20908	51276	A	21031	122	334	LRSGDLLWEINPLSS*SLLHEKD PPTTSSPQT\TSPRNISPISNPDPT ENQTVQLTWQPLPEPLELWPK AL

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20909	51277	A	21032	109	320	LGSGDLP*EINPPSSCSLLREKD PPTTSGPQT\TSPRNISPISNPDPT GNRTVQLTWQPLPQPLELWPK AL
20910	51278	A	21033	620	717	
20911	51279	A	21034	3	678	GGGFSDRDRTIALQPGQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGEKFYFIPKAMG AMEGSGQRRTLPDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLRE/KD PPTTSGPQSNQPRKHPPISNPEL VHVPEIWPLGQGMPAARIPPKP RPICVGPH*KSTVQLTWQPLPEP LELWPRLSD
20912	51280	A	21035	339	1098	LGSGDLPWEINPLSSCSLLREKD PPTTSGPPT\TSPRNISPISNPGET KETRFIRGPKTPAPVTDWEGSL PLVFNHCRDASLIIHPRFKGVRP RRDACLGPSPLAASPTFLGKGQ RLKTDTARLPRKPPRPSRTLSFS TAPRILSIVVPGSGHTLAFLDVT RHRLYRESKPVVGEEVDYSEW LSDVGKSEWSFSTCASSTSVNK HDTGRRLLGKRGGGMECSKGL CNFITMTKNIRSLAQMTIWQYL SPCREPV
20913	51281	C	21036	1	438	
20914	51282	A	21037	174	483	LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQT\TSPRNISPISNPRQR RHILSMDPKLRRRSWTWVGSLP LVFNHCRDASLIIHPGFRGVRPR RDVCLGPSPLA
20915	51283	A	21038	590	824	PNSSWMRGEPKKDPPTTSGPQT \TSPRNISPISNPGRLSDYSPRFQ RCQTTQGRLPWSFTLSGKSRFS GEGATWGLKT
20916	51284	B	21039	1	1596	
20917	51285	B	21040	155	2206	
20918	51286	B	21041	1	831	
20919	51287	B	21042	75	474	
20920	51288	B	21043	38	1009	
20921	51289	C	21044	335	481	
20922	51290	B	21045	66	652	
20923	51291	B	21046	1	673	
20924	51292	B	21047	1	451	
20925	51293	B	21048	74	3516	
20926	51294	B	21049	783	3463	
20927	51295	B	21050	1	807	
20928	51296	B	21051	41	1700	

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20929	51297	C	21052	18	381	
20930	51298	B	21053	1	3147	
20931	51299	B	21054	1	2586	
20932	51300	C	21055	756	1403	
20933	51301	B	21056	42	205	
20934	51302	B	21057	40	420	
20935	51303	B	21058	303	1170	
20936	51304	B	21059	1	2631	
20937	51305	B	21060	19	3093	
20938	51306	B	21061	23	241	
20939	51307	B	21062	84	1775	
20940	51308	B	21063	68	1542	
20941	51309	B	21064	74	2566	
20942	51310	C	21065	730	1023	
20943	51311	B	21066	67	1159	
20944	51312	B	21067	294	929	
20945	51313	B	21070	68	336	
20946	51314	B	21071	1	1992	
20947	51315	B	21072	1	4188	
20948	51316	C	21073	44	535	
20949	51317	B	21074	983	2636	
20950	51318	B	21076	289	1693	
20951	51319	B	21077	364	2393	
20952	51320	B	21078	471	590	
20953	51321	B	21079	1	1026	
20954	51322	B	21080	343	4253	
20955	51323	B	21081	1	819	
20956	51324	B	21082	648	894	
20957	51325	B	21083	1	1236	
20958	51326	B	21084	1	822	
20959	51327	B	21085	211	363	
20960	51328	B	21086	193	264	
20961	51329	B	21087	1	1260	
20962	51330	B	21088	143	3158	
20963	51331	B	21089	85	353	
20964	51332	B	21090	221	598	
20965	51333	B	21091	1	4878	
20966	51334	B	21092	171	362	
20967	51335	C	21093	320	408	
20968	51336	B	21094	1	1218	
20969	51337	B	21095	1	1761	
20970	51338	B	21096	315	1224	
20971	51339	B	21097	526	3482	
20972	51340	B	21098	41	4858	
20973	51341	C	21099	38	250	
20974	51342	C	21100	157	225	
20975	51343	C	21101	191	415	
20976	51344	B	21102	42	507	
20977	51345	C	21103	71	367	
20978	51346	C	21104	231	439	
20979	51347	C	21105	207	459	

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20980	51348	A	21106	1	429	
20981	51349	A	21107	184	544	VRLLKILQLQRFKMYVQQLDL TYFLRKIKCTLENGIVMSNTEA ESGVQLKPGRWGASALYSSHHI IH*A*LLVPR*VSNVVCSRNDT* TKNKDTKNRRC*PKSSTRRGK* KRERKEKEVT
20982	51350	A	21108	3	1200	LSQKEEEEDTFIEEQQLEEEKLL ERERQRLHEEWLLREQKAQEE FRIKKEKEEAAKKRQEEQERKL KEQWEEQQRKEREEEEQKRQE KKEKEKTFMWKPSVDLFSHLA SLRTPIICQDKGNAYQEHFPEK KKKRSSQLAIPEGAFGYPHHLL AILGLRCSRKHNFPTSSPTLLIKS MFTTFGMEQCRRDDYDPDASL EYSEEETYQQFLDFYEDVLPEF KNVGKVIQF/KGLFEIQQCPRGK HCNFLHVFRNPNNEFWEANRDI YLSPDRTGSSFGKNSERRERMG HHDDYYSRLRGRRNPSPDHSY KRNGESERKSSRHRGKKSHKRT SKSRERHNSRSRGRNRDRSRDR SRGRGSRSRSRSRSRRSRRSRSQ SSSRSRSRGRRRSGNRDRTVQS
20983	51351	A	21109	789	907	
20984	51352	A	21110	236	1823	CPIQRQSPGPAQTGRWEPLPCT VPITLRMSEGSGGAGKMAALE KMTFPKKMTFPEKPSHKKYRA ALKKEKRKIRRQELARLRDSGL SQKEEEEDTFIEEQQLEEEKLLE RERERLHEEWLLREQKAQEEFR IKKEKEEAAKKRQEEQERKLKE QWEEQQRKEREEEEQKRQEKK EKEEALQKMLDQAENELENGT TWQNPEPPL\DFRVMEKDGVN CPFYSKTGACRFGDRCSRKHYF PTS\SPTLLIKSMFTTLGMEQC\R RDDYDPDASLEYSEEETYQQFL DFYEDVLPEFKNVGKVIQFKVS CNLEPHLRG\NIYVQYQSEEEC QAALSLFNGRWYV\AGRQLQC EF*TGDRWKMAICGLFEIQQCP RGKHCNFLHVFRNPNNEFWEA NRDIYLSPDRTGSSFGKNSERRE RMGHHDDYYSRLRGRRNPSPD HSYKRNGESERKSSRHRGKKSH KRTSKSRERHNSRSRGRNRDRS RDRSRGRGSRSRSRSRSRRSRRS RSQSSSRSRSRGRRRSGNRDRT
20985	51353	A	21111	289	366	

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20986	51354	A	21112	1	1289	
20987	51355	A	21113	60	367	EELGYAGRGMGARQPPPARKA VSPLQERAEPVGSPG*GWRSRP STHGIASHGGPACSLCSLHFTFF VDFPSLFSPICLPEGWDWQQEQ PCLLYLSSPRCTQA
20988	51356	A	21114	1	653	RRRGSAAGGRAAERKAEVGA MNMAGGKAGKDSGKAKAKA V\SRSQR\AGLQFPVGRIHRHLK TRT\TSHGR\VGATAAVY\SAAI L\EYLT\AEVLEL\AGYAS\KDLQ SKSVSLPRHLQLAIPWVIEELDS LIQGLP*AGGGVIPSHPHKS\LIG KEGDSKKTALEGMLLTQPLSLP RHLYCNWDKKNNGDMWNFLP PVKWKSIDNYCRHDKRNICMF LDSEV
20989	51357	A	21115	1	1019	SVCWAGGAPRAHSTRTHAWLG RPAMEPGSVENLSIVYRSRDFL VVNKHWDVRIDSKAWRETGRP EP\QVASVEESGSDSGLC/HHSR FCHQLDFSTSGALCVALLVLGG LPGSTGLPRELRAILPLLQLRGH IQESRVSIVRWGGPGPRVSPTNL TPAFCAPGCENPKPSLTGSWSG R*VWIGPAPSLIRHRPHPAGRTH QLRV\HCSALGHPVVGDLTYGE VSGREDRPFRMMLHAFYLRIPT DTECVEVCTPDPFLPSL\DACWS PHTLLQSL\DQL\VAGLKGQPPD P*TRG*GGPRPGSPSALLPGHGR PPPPTTKPPETEAQRGPCLQWL SEWTLEPDS
20990	51358	A	21116	698	1472	RWAPRRGLSVDLDGGSSAPLCP PATTARLDAEPHGSLPNSCLWE CSCLLQGIWAAGPSGLSLHYPP LSSPLGSSPPSRPQRLVLIRAGR GGWVGSVGETMTSSYGHVLER QPALGGRLDSPGNLDTLQAKK NFSVSHLLDLEEAGDMVAAQA DENVGE\SSRTRGGGAGLGKGL SGVQTQRASAVWESSRLKMLS RVGRASLGQRMTA*GRLQLYP HAPKSVTDRSPCSSQVTKSWNR GALQHSMIFTKRCLFQTLKE

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20991	51359	A	21117	50	1226	KMAEEVVVVAKFDYVAQQEQ ELDIKKNERLWLLDDSKSWWR VRNSMNKTGF\VPSTYVGR\EN SARKASIVKNLKDTLGIGKVKR KPSVPDSASPADDSFV\DPGERL Y\DLNMPA\YVKFN\YMAERED ELS\LIKG\TKVIVMEKCS\DGW WRGTYNGQVGWFPSNYVTEE\ GESPLGDHVGSLSEKLAAVVN NLNTGQVLHVVQALYPFSSSN DEELNFEK\GDVMDVIEKPEND PEWWKCRKINGMVGLVPQKL W*PLLQSIQLTSGLGTLTFQCGF IRPYIPGKFVGNPWYYGKVTRH QAEMALNERGHEGDFLIRDSES SPNDFSVSLKAQGKNKHFKVQ LK\ETVYCIWQRKSCTME*LVE HYK\KAPNFYNVNKGEKLYLV
20992	51360	A	21118	132	428	
20993	51361	A	21119	3	337	AKLAGAAVPVCARGRAAPLAA AALPAARL\PSGAGPAGLVSDV RRRPFARE/PEPRVP/SQPPALSA LGALALKLFSSPPSCWSFSVKT GVLVPWIMCISWPYFLSGNLLT MMW
20994	51362	A	21120	438	1066	LNQKGKGGRGEALKNDLVVAP PPSPRRGVR*EALHVPDTGPFK KPRKRK*NQRQREAERK*TFPR EEEARRETHGPLPAPRPPPPLCP/ PAASSAPRPGPKGAR*LSLSAE GRARRRSAGASGGAGAAATAA AAAAPEHPRGSEPRQPASPAPQ RERPRRPAPRLPPQCPRPSKGRA WTLQTTTGQKVCTGAGTRRA WRRAGAVRRAFWA
20995	51363	A	21121	1	924	
20996	51364	A	21122	1	435	
20997	51365	A	21123	1	524	
20998	51366	A	21124	1	602	MGKGSPAHAQGPGSFLHGGAG DQGRGRPITLYEDRGFQG\RHY ECSSDHPNLQAYLSRCNSVRVD SGCWVLYEQPNYSGLQ*FLRR GDYADHQQWMGLSDSVRSCR LIP\HASSHRLRIYEREDYRGQM VEITEDCSSLHDRFHLSEIHSFN VLEGSWVLYELPNYQGRQYLL RPGDCRWCQDWGATDARVGS LRRAVELY
20999	51367	A	21125	1	1239	
21000	51368	A	21126	298	408	
21001	51369	C	21127	92	241	

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21002	51370	A	21128	33	191	RDDPRVRPPPNSHT*PQQEPGL* LIKCTSPPQAPAPRTVHGPYFY MRLIKMF
21003	51371	A	21129	3	1285	
21004	51372	A	21130	3	3468	QPGHTIYLLPTVVICNLLPCELD FYVKGMPINGTLKPGKEAALH TADTSQNIELGVSLENFPLCKEL LIPPGTQNYMVRMRLYDVNRR QLNLTIRIVCRAEGSLKIFISAPY WLINKTGLPLIFRQDNAKTDAA GQFEEHELARSLSPLLFCYADK EQPNLCTMRIGRGIHPEGMPGW CQGFSLDGGSGVRALKVIQQG NRPGLIYNIGIDVKKGRGRYIDT CMVIFAPRYLLDNKSSHKLAFA QREFARGQGTA
21005	51373	A	21131	3	451	
21006	51374	A	21132	2	107	LEGLEES/VRDRCKKEFTDLMIE MDSRLLGPTSKVK
21007	51375	A	21133	2	158	PGIPVL/DYRTYTDGFFSLPSKD GDKDVMITGKLDILKPQNQHR VFTVESRVI
21008	51376	A	21134	2	5632	FVRRTCRESRCWPGAETELDH WSLGEGVRGAMALQLWALTL LGLLGAGASLRPRKLDFFRSEK ELNHLAVDEASGVVYLGAVNA LYQLDAKLQLEQQVATGPALD NKKCTPPIEAS\QCHEAEMTDN VNPLLLVDPPRKRLVECGQLLK GI\CALRALSNISLRLFYEDGSG EKSFVASNDEGVATVGLVSSTG PGGDRVLFVGKGNGPHDNGIIV STRLLDRTDSREAFEAYTDHAT YKAGYLSTNTQQFVAAF
21009	51377	A	21135	168	5568	AREKCGGAMGAGSSTEQRSPE QPPEGSSTPAEPEPSGGGPSAEA APDTTADPAIAASDPATKLLQK NGQLSTINGVAEQDELSLQEGD LNGQKGALNGQGALNSQEEEE VIVRQVDHIDSEDVSDRDSDTE MTTKSAVVHDITDDGQEETPDI IEQIPSSESNLEELTQPTESQAND IGFKKVFKFVGFKFTVKKDKTE KPDTVQLLTVKKDEGEGAAGA GDHQDPSLGAGEAASKESEPK QSTEKPEETLKREQ

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21010	51378	A	21136	807	1162	ISYHGGRRRRPQ/PVGPLGSCRS *SSRRWSTTGRTTFRAGWKSCS TPPSTSSLPTSTGTW*GPGTSAL LPPTPLPPPRAAATPCACACASE SRMPAARALGLRVRRRLLEGRS GKDTQG
21011	51379	A	21137	1	562	
21012	51380	A	21138	1	423	
21013	51381	A	21139	1	1871	MTTFKEAMTFKDVAVVFTEEE LGLLDLAQRKLYRDVMLENFR NLLSVGHQAFHRDTFHFLREEK IWMMKTAIQREGNSGDKIQTE METVSEAGTHQEWSFQQIWEKI ASDLTRSQDLVINSSQFSKEGDF PCQTE/ARTICNSHKTEI/FPRA/I GYKPSFSDVSHFDFHQQLHSGE KSHTCDECGKNFCYISALRIHQ RVHMGEKCYKCDVCGKEFSQS SHLQTHQRVHTGEKPFKCVEC GKGFSRRSALNVHH
21014	51382	A	21140	1056	2988	FCILIGDKIQTEMETVSEAGTHQ EWSFQQIWEKIASDLTRSQDLV INSSQFSKEGDFPCQTEARTICN SHKTEIFPRAIGYKPSFSDVSLF DFHQQLHSGEKSHTCDECGKN FCYISALHI\HQRVHMGEKCYK CDVCGKEFSQSSHLQTHQRVH TVEKPFKCVECGKGFSRRSALN VHHKLHTGEKPYNCEECGKAFI HDSQLQEHQRIHTGEKPFKCDI CGKSFCGRSRLNRHSMVHTAE KPFRCDTCDKSFRQRSALNSHR MIHTGEKPYKCEECGKGFICRR DLYTHHMVHTGEKPYNCKECG KSFRWASCLLKTSSESHSG\EKP FKC\EECGKGFYTISQCYS\HQR SHSGEKPYKCVECGKGYKRRL DLDFHQRVHTGEKLYNCKECG KSFSRAPCLLKHERLHSGEKPF QCEECGKRFTQNSHLHSHQR\V HTGEKPYKCEKCGKGYNSKFIL YMHQ\RVHTGERPYNCKECGK SFGWASCLLKHQRLHSGENPFK CEECGKRFTQNSQLHSHQRVH TGEKPYKCDECGKGFSWSST\R LTHQR\RH\SRETPLKCEQHG\K NIV\QNSFS/EKLPEKVHQC*KK PYKCEDL/CGKGYNRRL*IL\DM HQR\VHMGEKTWKCRECDMCF \SQAS\SLRLHQNVHVGEKP

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21015	51383	A	21141	154	1470	KDGDHMGYTYKVIERILEIGAF RPHMSLGQLQSARGVACLGCK GTCSGFEPHSWRKICKSC\NAA KRTTA*HLT*KNDRKLGRWLR DSKYSTLHLLG*KAGTASGFYK RNP\MI\LTNPIATGKDPTFDTIT YEWGSPWEFTQETGDCSYMGA HSPREEGSQLTGHQRGAFYRA ARPAHAPGLPIYD\QDPLALPVD FWRNELKTEWKEFVK\KYKSE GPSALGEVALPGQGWLAPRKE GE/GSRKKPEGGRRP/PAATTNG SLSDPSKEVEYVCELCKGAAPP DSPVVY\SDRAGYNKQWHPTCF VCAKCSEPLV\DLIYFWKDGAP WCGRHYCESLRPR/CAPACDEI\ IFAEDYQRVEDLAWHRKHFVC EGCEQLLSGLGVHRHPGVQLL VPQLAASPKRSLKGCPTPQPESP GIPTEKDKPGCARDPSLRVPDV TSKPSEINQ
21016	51384	A	21142	1	1332	
21017	51385	C	21143	147	272	
21018	51386	A	21144	160	374	ETPVSSRCEKHVSSPHLCPGIHR AVSLSSH\STCGRSWRSELHGPQ STNLSGNTELPLHFLFGAWQTG VFKM
21019	51387	A	21145	3	4366	LGAQQRELQEALGARAALEAL LGRLQAERRGLDAAHERDVRE LRARAASLTMHFRARATGPAA PPPRLREVHDSYALLVAESWRE TVQLYEDEVRELEEALRRGQES RLQAEEETRLCAQEAEALRREA LGLEQLRARLEDALLRMREEY GIQAEERQRAIDCLEDEKATLT LAMADWLRDYQDLLQVKTGL SLEVATYRALLEGESNPEIVIW AEHVENMPSEFRNKYYHYTDS LLQRENEWNLFSRQKAPLAS
21020	51388	A	21146	1	4617	RVIDCLEDEKATLTLAMADWL RDYQDLLQVKTGLSLEVATYRI VEHVAVEGVSKLWKPLWQKS QSLVISSGVSFTGGRLNLERLRR GPTPLASTESVKQVLVNNRMII DDEMVKTLAMSRTCSAPNPLT ADVKTWSRSYRSEDAATGPVL GVASTVALLEGESNPEIVIWAE HVENMPSEFRNKSYHYTDSLL QRE\NERNLFS\RQKAPLASFNH SSALYSNLSGHRGSQTGTSIGG DARRGFLGSGYSSSATT

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21021	51389	A	21147	2	435	
21022	51390	A	21148	1	1233	MCEEETTALVCDNGSGLCKAG FAGDDAPRAVFPSIVGRPRHQG VMVGMGQKDSYVGDEAQSKR GILTLKYPIEHGIITNWDDMEK KKEAEELARNMAIQQELEKEK QRVAQQKQQQLEQEQFHAFEE MIRNQELEKERLKIVQEFGKVD PGLGGPLVPD/SGEALLRCVPHL NSLIHTAFRLSHNCKAS*ATCG GQVLETWSTEQLRKYSHNRWI APCGGAWAAVPTVSPVSQCQH CPGSGDMWNSLWKTDEE*IYH YPCSHPQAKCWV*LLQHRERR RTFPHTGSAGPHHTGLDSCKQF *AVREHGVR\GIHETTYNSIMKC DIDIRKDLYANNVLSGGTTMYP GIADRMQKEITALAPSTMKIKII APPERKYSVWIGGSILASLSTFQ QMWISKPEYDEAGPSIVHRKCF
21023	51391	A	21149	2	1273	PRVRPRVRPRVRSLGEEPLIPSV LRSPAHSATHTMCEEETTALVC DNGSGLCKAGFAGDDAPRAVF PSIVGRPRHQGVMVGMGQKDS YVGDEAQSKRGILTLKYPI\EHG \IITNWDDMEKIWAPLLLTMEL RVSTWKRHPTLLTEAPLNPKAN REKMTQIMFETFNVPAMYVAI QAVLSLYASGRTTGIVLDSG\D GVTHNVPIYEGYALPHAIMRLD LAG\RDLTDYLMKIL/AKRGGY SFVTTAEREIVRDIKEKLCYVAL DFEK*\MATAASSSSLE\KSYELP DGAGLSPIGKWTLP\CPETLFQP YFISNGVPLEFNDDNLTIPSMK\ CDIDIP*GLICPTMFLSGGTTHV PWALLDRIQKENPSPGPPGTMK IKI\IAPPEREVTSVWD/LGGSILA SLSTFQA\MWISKPEYDDAGPSI VHRKCF
21024	51392	A	21150	95	674	

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21025	51393	A	21151	1	1536	MGGGEQGTLRTAENQGLQVCP GEAGSSLGFSGNTPTNGLPARG DQTSYRDFWSGPQFPDTSLRTA APGAREQCGTHGGEGSTLEGSR PDVPQDLFSPTLGFYGSTYPELE QGMLGGH*G/PAENQGLQVCP GEAGSSLGFSGNTPTNGLPARG DQTSYRDFWSGPQFPDTSLRTA APGAREQCGTHGGEGSTLEGSR PDVPQDLFSPTLGFYGSTYPELE QGMLGGHVEASREYQMLSHV GNPDYPHALATEQATSPSTESG SAGFKGVALAMLSKITMCVRIG ILVFQQDQGSMCKAFSTTGMG LVTYLLTCRAWSRLQCGASYR AHDVNVLPGCSGPAALLLGDW FSLHSSDAVLPAQGQGMLSQG EADACITLPHLFPSREVVFLLGL EAGGLIPGAEGPPEDMGLVRGP PAVAAGPPPRWLSPEFCLLQYS EEEGCKEPLWLKVEAEVSTLYR FMPTGFTRGPFNIEHREWGNTT ATWTRMISNHNKHSQRGRKMT ARLPCGGAPHFSDRTDDKWRR SSLLTRSGCQTERLLTSQTEPLP AGGSPHFSNGETGQRRSSPPQR GCDRPQALLTSKTEQQRKSASH ISYDERPGKDAPHFLDGMVAG KRRSSLSRLGSQA

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21026	51394	A	21152	689	2176	PATSPTSRAMAQPSAPAASMLL PCPECPSGPRFMTCCLSVSTFCS PSLRRPPGSIKGSSGLGGG\SSRT SCRLSG\ALGAGSCRLGSAGGL GSTLGG\NSYSSCYSFGSGGGY GSSFGG\VDGLLA\GGEKA\TMH NLIDF\LASYLDKVPCPWKEAN TELEV\KIRD\WYQRQ\APGPAR DYSQYYRTIEELQNKILTATVD NANILLQIDNARLAC/ADDFRT K\F\ETEQALRL\SVEADINGL\R RVL\DELTLARADL\EMQIENLK EEAWPTLKERTTEGRRLNALR GQVGW*RSMLEMDAAPGVDL SRILNEMPSCVDHRVTRCINRP GAELKLGSGGWTEELKREVAT NSELVQSGKSKISEL\RRTMQAL EIELQSQLSMKA\SLEGNLGGD RATAYCVQLS\QIQGL\IGSGED QL\AQLR\C\EMEQQ\NQDYKILL DVKTRLEQEIATYRRLLEG\ED AHLT\QCKKEPVTTRQV\RTIVG KRSRD\GKVILLPRSRFHQTTR
21027	51395	C	21153	58	252	
21028	51396	A	21154	2	190	
21029	51397	A	21155	2	432	KMADGVDHIDIYADVGEEFNQ EAEYGGHDQIDLYDDVISPSAN NGDAPEDRDYMDTPPPVPGYG PPPGPPPPQQGPPPPPGPFPPRPP GPLGPPLD/TLAPPPHLPG\PP\PG \APPPA\PHVEPSFLFLPPINSGH GLHSDRPRFH
21030	51398	A	21156	1	1070	MGGIGARAAAAGKGRRRRARA PPGLPPPTSDGGGGAAAASSLR RLHAAPPPGPSAAGSASRVPPTI GSEAAPAREDRRQLHSGRVRAS GSPRLTRPRPVKRRGRTRGGGA PRQGSAARPRGGKGAHSAVAS ARAAAGPGSASRPHGAASAAG TWALTYLVELFADIRVNVYVV HAVRHLPSACAAAAAAASCRF ALVGVGSEASSKKLMDLLPKR ELHGQNPVVTPCNKQFLSQFE MQSRKTTQSGQMSGEGKAGPP GGSSRAAFPQGGRGRGRFPGA VPGGDRFPGPAGPGGPPPPFQD PSVNSDPVCGTFG/EH*PPGYQT PSNLSVRPMAKPKPEGTDLSRS REGFFKSRFAPN

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21031	51399	A	21157	63	1750	MKMAGGVNHIDIYADVGE*FN QEA\EYGGHDQIDVHDDAISPS ANNGDAPEDRDYMDTLPPTVG DDVGKGAAPNVVYTYTGKRIA LYIGNLTWWTTDEDLTEAVHS LGVNDILE\IKFFENRANGQSKG FALVGVGSEASSKKLMDLLPK RELHGQNPVVTPCNKQFLSQFE MQSRKTTQSGQMSGEGKAGPP GGSSRAAFPQGGRGRGRFPGA VPGGDRFPGPAGPGGPPPPFPA GQTPPRPPLGSFQGPPG\PPGPPP PGQVLPPPLAGPPNRGDRPPPPV LFPGQPFGQPPLGPLPPGPPPPV PGYGPPPGPPPPQQGPPPPPGPF P\PRPTGSNLGHPLTLAPPSASFP GP\PP\GAPPPSPHVNPAFFPPPT NSGMPTSDSRGPPPTDPYGRPPP YDRGDYGPPGREMDTARTPLS EAEFEEIMNRNRAISSSAISRAV SDASA/GVDYGSAIETLVTAISLI KTIPKYPADD/RCTKFLISSLQD CLHGIESKSYGSGSRRRERSRER DHSRSREKSRRHKSRSRDRHDD YYRERSRERER\HRDRDRD\RD RERDREREYRHR
21032	51400	A	21159	1	96	TNFKSGLLGLAAED*HCPIASE AP*TITDAEL
21033	51401	A	21160	1	1056	MWKGPKGLDMYGKSSVSPKTS DILGRDTLLLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLPWEINPLSSCSLLHE KDPPTASGPQTDQPKEHLTNFK SGFRGVRP/LQGRLPWSFTLSGK SRFSGEGASTPTPSLCVSTPSPPF WGARNTQPLLLHPEWQ/CPLF* RSKYPNLVSLCPSPLFPRPDLLS L/SAQSLISAPQPLISLCPNPLFPC PDLLSLHPNPLFPRPNPFPAFLE GACYKCQKSGHQAKECLQPGI PPKLRPICAGPHWKSDCPTHLA ATPRAPGTLAQGSLTASQIFLA
21034	51402	C	21161	283	408	

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21035	51403	A	21162	3	505	ILNPVSGLFLFSSPLSLNLSSLSL NLFLLSILAPHFNLSILLISIPFIFP LEIELSNSPGSHSQSPWNSGPRL SDSFPDLLGLAAEE*HCPIASEA FSQTYRAYLSLSLSLSLSPEPPT AGDGVT/HSSPVASTTITVLGQT /SKPAQCWPLPKVCCHHSLTSD YVHPRP
21036	51404	A	21163	164	420	LANFCEESGAGEPGSHSQSPWN SGPRLSDSFPDLLGLAAEDRHC PIASEAPLLQRKSLYKSPCTSSTI S*CCIPRSGISESLSVN
21037	51405	A	21164	50	298	
21038	51406	A	21165	49	433	SSSGIWPSHSQSPLRSSPAKLLS RFRCSLSSLLLCLATLLLVWQP LPEPLELWPKA/HLTDSFPDLLG LAAED/W/HCPIPSEAP*TLTDAE LRVTLTVEGKSIPFGAGKEVTL ESYWVSLTLSFLICYMII
21039	51407	A	21166	282	374	CDLFLPHPN*SMYFVISPTPKKV LCNSPHT
21040	51408	A	21167	71	333	LRSGDLPWEINPLSSCSLFREED PPTTSGPQTNQPKEHLTNFKSA AED*RCQFASEAP*TITDAKLRV SLTAEGLLATLFLNPKPEY
21041	51409	A	21168	113	342	AFGCFTTGVGRVTDSDGPLYTG PWAPGSHSQSPWNSGPRLSDSF PDLLGLAAED*HCPIASEAPFLT LIFLLCVIQ
21042	51410	A	21169	301	608	TFTPLKSYIKAPSSAGPVAEQE MTPEGKVGAGPE*LTWKNQFL FY
21043	51411	A	21170	2	724	FLVSLMLPPAVVMLNHCYSLIF TNALVKRLFAWNMLSELATCA GNLATGPRNARSPGFLLSCVPS VRDPTGNQTVQLTWQPLPEPLE LWPKA/HLTDSFPDLLGLATED *HSPIASEAPWAIMDAELRVTL TVEDRDSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSQSSSSSSPCD LFLPHPN*SMYFVISPTLKKVLY NVTHP*EVSL*FSPPLRMYFVRS IPCPQNIALNSTAYP
21044	51412	A	21171	442	501	

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21045	51413	A	21172	266	1003	SCMCLALDPCNHGEGHQPDFS GVKFRRHGADNHEASAATATT AAATTVAAAAAAAAAAAAAR VTLTGSHFQSPWNSGPRLSDSF PDLLSLATED*RCPIASEVPWTI TEAELRVTLTVEGKSIPCLIDTG ATHSTLPSFQGPVSLAPITVVG\I DGQASKPL\KTPPLW\CQLGQH SFMHSFLVIPHL/CPIFLIRGRNIL TKLS\ASLTIPGSTANISLVAFFP NPKPPLCPLTSPQYHPLPQDLPS A
21046	51414	A	21173	2	245	LTALLRKSLDPRLISTGENTQTA ETMGPLSAPPCTQHITW\KGLLL TAETPKPSISSSNLNPRGGHGRL CALILLILEDSG
21047	51415	A	21174	3	324	
21048	51416	A	21175	3	552	
21049	51417	A	21176	3	435	
21050	51418	A	21177	3	1459	GAVRTWGRGFQTEKCQASLLN FWNPPTTAQVTIEAEPTKVSKG KDVLLLVHNLPQNLAGYIWYK GQMKDLYHYITSYVVDGQIIIY GPAYSGRETVYSNASLLIQNVT REDAGSYTLHIVKRGDGTRGET GHFTFTLY\LIPWTLLYL*RSLA QVSHYETPGKTAPPCGSTA**L N*PPDLTLFSPVLFLLKYPVPGQ AFQYPKGLKTIGSSITHL*DVLG KGSCRENIPRAAK*D*N*EDSST ACSK*GPQVETPKPSISSSNLYP REDMEAVSLTCDPETPDASYL WWMNGQSLPMTHSLQLSKNK RTLFLFGVTKYTAGPYECEIRN PVSASRSDPVTLNLLPKLPKPYI TINNLNPRENKDVLAFTCEPKS ENYTYIWWLNGQSLPVSPRVK RPIENRILILTQCSREMKQGPY\ QCEIQ\DRYGG\IRSYPVTLECP/ HITTKHSGLYACSVRNSATGME SSKSMTVKVSAPSGTGHLPGLN

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21051	51419	A	21178	3	1445	IRADPAHELENCSCPGKRLSTE RGRTAQLTAVLREFLDPRLISTE ENTQAAETMGTLSAPPCTQRIK WKGLLLTASLLNFWNLPTTAQ VTIEAQPPKVSEGKDVLLLVHN LPQNLTGYIWYKGQMRDLYHY ITSYVVDGEIIIYGPAYSGRETA YSNASLLIQNVTREDAGSYTLH IIKGDDGTRGVTGRFTFTLHLET PKPSISSSNLNPRETMEAVSLTC DPETPDASYLWWMNGQSLPMT HSLKLSETNRTLFLLGVTKYTA GPYECEIRNPVSASRSDPVTLNL LPKLPKPYITINNLNPRENKDVL NFTCEPKSENYTYIWWLNGQSL PVSPRVKRPIENRILILPSVTRNE TGPYQCEIRDRYGGVRSDPVTL NVLYGPDLPRIYPSFTYYRSGE VLYLSCSADSNPPAQYSW\TINE KFQL\QGQKLFIP\HITTKHSGLY V\CSVRNSATGKESSKSMTVEV SGKWIPASLAIGF
21052	51420	A	21179	3	1380	TAQLTAVLREFLDPRLISTEENT QAAETMGTLSAPPCTQRIKWK GLLLTASLLNFWNLPTTAQVTI EAEPTKVSEGKDVLLLVHNLPQ NLTGYIWYKGQMRDLYHYITS YVVDGEIIIYGPAYSGRETAYSN ASLLIQNVTREDAGSYTLHIIKG DDGTRGVTGRFTFTLHLETPKP SISSSNLNPRETMEAVSLTCDPE TPDASYLWWMNGQSLPMTHSL KLSETNRTLFLLGVTKYTAGPY ECEIRNPVSASRSDPVTLNLLPK LPKPYITINNLNPRENKDVLNFT CEPKSENYTYIWWLNGQSLPVS PRVKRPIENRILILPSVTRNETGP YQCEIRDRYGGIRSDPVTLNVL YGPDLPRIYPSFTYYRSG\EVLL LVLFCGTLNPP\AQYSWTINEKF QLPGQKLFIRHITTKHSG\LYVC SVRNSATGKESSKSMTVEVSAY SSSINYTSGNRN

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21053	51421	A	21180	2	1341	TEGGRTAQLTAMLRQLLDPRLI STEENTQAAETMGPLPAPSCTQ RITWKGLLLTASLLNFWNPPTT AEVTIEAQPPKVSEGKDVLLLV HNLPQNLPGYFWYKGEMTDLY HYIISYIVDGKIIIYGPAYSGRET VYSNASLLIQNVTRKD\AGT\YT LHIIK\RGDETREEIRHFTFTLYL ETPKPYISSSNLNPREAMEAVR LICDPETLDASYLWWMNGQSL PVTHRLQLSKTNRTLYLFGVTK YIAGPYECEIRNPVSASRSDPVT LNLLPKLPIPYITINNLNPRENK DVLAFTCEPKSENYTYIWWLN GQSLPVSPGVKRPIENRILILPSV TRNETGP\YQCEIRDRYGGIRSY PVTLNVLYGPDLPRIYPSFTYYR SGENLDLSCFTESNPPAEYFWPI *GKFQQSGQKLFIPQITRNHSG LYACSVHNSAAGKEISVSLFRH
21054	51422	A	21181	1	1532	MTQFPMDKRQGRSRSVAITNT AVTSLEWVPFHAFAIPRSTLVS QQRLSTERGRTAQLTAVLREFL DPRLISTEENTQAAETMGTLSA PPCTQRIKWKGLLLTASLLNFW NLPTTAQVTIEAEPTKVSEGKD VLLLVHNLPQNLTGYIW\YKGA MR\DLYHYVTSYVVDGQIIKYG \PAYSGRETAYSNASLLIQNV\T RED\AGSYTLHIIKGDDGTRGVT GRFTFTLHLETPKPSISSSNLNPR ETMEAVSLTCDPETPDASYLW WMNGQSLPMTHSLKLSETNRT LFLLGVTKYTAGPYECEIRNPV SASRSDPVTLNLLPKLPKPYITI NNLNPRENKDVLNFTCEPKSEN YTYIWWLNGQKPP/VSSPRVKR PH*KTGSLIPTPVFTRNETGP\YQ CEIRAR\YGG\IRSDPVTLNVLY GPDLP\RIYPSFTYYRSGGKSSY LSCFCGTSNPP\AQYSW\TIN*K VFSLPGTKALYSRHITTKHSGL YVCSVRNSATGKESSKSMTVE VSDWTVP
21055	51423	B	21182	28	29751	

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21056	51424	A	21183	158	1660	EASLLEDDDGMVYLRPLTSHQ YRTAQLRAMLRKFLDPRLSSTE ENTQAAETMGPLSAPPCTQRIT WKGLLLTASLLNFWNPPTTAQ VTIEAEPTKVSKGKDVLLLVHN LPQNLAGYIWYKGQMKDLYH YITSYVVDGQIIIYGPAYSGRET VYSNASLLIQNVTREDAGSYTL HIVKRGDGTRGETGHFTFTLYL ETPKPSISSSNLYPREDMEAVSL TCDPETPDASYLWWMNGQSLP MTHSLQLSKNKRTLFLFGVHK VHCRDPMECEIREPS*VASRS*P SSPWNLLPKL\PKPYITI\NN\LNP REKKDVLAFT\CDP\KSRNYTYI WWLNGQSLPVSPRVKRP\IENR DPSFLP\SVTRNETGP\YQCEIRD \RYGG\IRSYPVTLNVLYG\PDLP RIYPFISPIYHFREENLRTLSCFC GTFNPPGRVFLGTINGGSFQVIQ GQKALYSPRITTKHSGA/LYAW LCSVTSRPLAWESSQIPWTV\KV SGSFQGTGTSSWGLNPL
21057	51425	A	21184	927	1378	QPPTLRSWDCWFAWGKRQLM SSP/STEPQVCFTIEGHEIDFLLG TGMAFSVLISCPG*LSSRSVTIR GILG*PVTRYFSHLLSCNWETLL FSHNAKTQGGGTLTLPKPSKSH RPWAVRGLAPGPAAAVLNFSP GLSCLPTGQGLGPAAHHA
21058	51426	A	21185	1	221	ILLAQLESQDGDILRQRDEFDLL VAGEICRFSALIEELE\EKNERPA RELLTVRPEPEPCPTCAVLRLLH LCLA

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21059	51427	A	21186	335	1963	VCDPALPPWAKQREWALEGSH SSRTSMGLLVASVTSLGRWKF NCPI/CVQGTLKEAGSLSNCG/H KNFCRACLT\RYCEIP\GPD\LEE SP\TCP\LCKEPFRP\GSFRPNWQ LANVVENIERLQLVSTLGLGEE DVCQEHGEKIYFFCEDDEMQL CVVCREAGEHATHTMRFLEDA A\APYREQIHKCLKCLRKEREEI QEIQSRENKRMQVLLTQVSTKR QQVISEFAHLRKFLEEQQSILLA QLESQDGDILRQRDEFDLLVAG EICRFSALIEELEEKNERPAREL LTDIRSTLIRCETRKCRKPVAVS PELGQRIRDFPQQALPLQREMK MFLEKLCFELDYEPAHISLDPQ T\SHPKLPLVPRTIQR\AQFS*QM GRTSPDNPQ\RF\DRATCVSRPT LGITGGRHTWVVSIDLAHGGSC TVGVVSEDVQRKGELRLRPEE GVWAVRLAWGFVSALGSFP\TR LTLKEQPRQVRVSLDYEVGWV TFTNAVTREPIYTFTASFTRKVI PFFGLWG\RGS\SFSLSSLRRSSY LLSSKYRTHINPSTMWT
21060	51428	A	21187	217	397	
21061	51429	A	21188	529	1526	YCGRVGELAAGELVFLWSRVG PQNPRSSRLPPPTLAMFLTRSEY DRGVNTFS\PEGRLFQVEYDIEA IKLGSHSQLAPRHREGV\ALAV\ EKRIYLPHLMGAQAGI*GKLLG DLMLHIGLLPIEWGLICLMLKT FNSIKSRVGRHR/YPWGSPYNG GH*QWESFEPKLCPNLGFSSFG EEDAESRVPMS\RPLGSSHLFIW EELYEKGTPSLFP*GTPFWGPFV PVWMARSQFGSGFQRGAPRAP LPRKFPPTSPMTFERSPSSPSPHP SLKQVMGGRKLNANQTIEPRPT VPALAENFPHCSQRKKLEEVIQ GHFKESWILRTSLGTISVLNNVP
21062	51430	A	21189	211	382	TSVSPSVPPLPC*RHPGEPQTGN NASNGTSSSRDESRPPVRVVPPP QTAVAITLSTA
21063	51431	A	21190	3	96	FFFPPQKYD*DR*EHPRFHKTLR NWRVGAQ
21064	51432	A	21191	1	1320	
21065	51433	A	21192	1	339	

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21066	51434	A	21193	289	3694	MAFVPVIPESYSHVLAEFESLDP LLSALRLDSSRLKCTSIAVSRK WLALGSSGGGLHLIQKEGWKH RLFLSHREGAISQVACCLHDDD YVAVATSQGLVVVWELNQERR GKPEQMYVSSEHKGRRVTALC WDTAILRVFVGDHAGKVSAIK LNTSKQAKAAAAFVMFPVQTIT TVDSCVVQLDYLDGRLLISSLT RSFLCDTEREKFWKIGNKERDG EYGACFFPGRCSGGQQPLIYCA RPGSRMWEVNFDGEVI
21067	51435	A	21194	2	128	
21068	51436	A	21195	1041	2238	LLHPAQRSLSKDGTKESLEDAA LMGEEGKPEINQQLSLESMELD ELALEKYPIAAPLVPYPEKSSED GVGNPEAKILSGTPTYKRRVISL LVTIENHTPLVELSEYLGTNTLS EILDSPWEGAKNVYKCPECDQ NFSDHSYLVLHQKIHSGEKKHK CGDCGKIFNHRANLRTHRRIHT GEKPYKCAKCSASFRQHSHLSR HMNSHVKEKPYTCSICGRGFM WLPGLAQHQKSHSAENTYEST NCDKHFNEKPNLALPEETFVSG PQYQHTKCMKSFRQSLYPALSE KSHDEDSERCSG\CGDNFFSFSK FKPLQCPDCDMTFPCFSELISHQ NIHTEERPH*\CKTCEESFALDSE LACHQKSHMLAEPF\KCTVCGK TFKSNLHLITHKRTHIKKHHVK
21069	51437	C	21196	156	389	

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21070	51438	A	21197	1	2466	MLSRLFRMHGLFVASHPWEVI VGTVTLTICMMSMNMFTGIAG LFTIFSSFVFSTVVIHFLDKELTG LNEALPFFLLLIDLSRASTLAKF ALSSNSQDEVRENIARGMAILG PTFTLDALVECLVIGVGTMSGV RQLEIMCCFGCMSVLANYFVF MTFFPACVSLVLELSRESREGR PIWQLSHFARVLEEEENKPNPV TQRVKMIMSLGLVLVHAHSRW IADPSPQNSTADTSKVSLGLDE NVSKRIEPSVSLWQFYLSKMIS MDIEQVITLSLALLLAVKYIFFE QTETESTLSLKNPITSPVVTQKK VPDNCCRREPMLVRNNQKCDS VEEETGINRERKVEVIKPLVAET DTPNRATFVVGNSSLLDTSSVL VTQEPEIELPREPRPNEECLQIL GNAEKGAKFLSDAEIIQLVNAK HIPAYKLETLMETHERGVSIRR QLLSKKLSEPSS\LQYLPYRGY\ NYSLW*WGACCENVIGYMPIP VGVAGPLCLDEKEFQVPMATT EGCLVASTNRGCRAIGLGGGAS SRVLADGMTRGPVVRLPRACD SAEVKAWLETSEGFAVIKEAFD STSRFARLQKLHTSIAGRNLYIR FQSRSGDAMGMNMISKGTEKA LSKLHEYFP*NCRF*AV\SGNYC TDKKPAAINWIEGRGKSVVCET VIPAKVVREVLKTTTEAMIEVN INKNLVGSAMAGSIGGYNAHA
21071	51439	A	21198	236	3022	GEGSFRSATALTGARLSVGAGV RWPLVRSGGSKDSVATMLSRL F\RMHGLFVASHPWEVILGTVT LTICMMSMNMFTGNNKICGWN YECPKFEEDVLSSDIIILTITRCIA ILYIYFQFQNLRQLGSKYILGIA GLFTIFSSFVFSTVVIHFLDKELT GLNEALPFFLLLIDLS\RASTLA KFALSSNSQDEVRENIARGMAI LGPTFTLDALVECLVIGVGTMS GVRQLEIMCCFGCMSVLANYF VFMTFFPAC
21072	51440	A	21199	1	450	CKSRGSNLRVHFKNTRETAQAI KGMHIRTATKYLKDVTLQKQC VPFRRYNGGVGRCAQAKQWG WTQGRWPKKSAEF\LVIEHIQV NKAPKMRRRTYRAHGRINPYM SSPCHIEMILTEKEQIVPKPEEEV AQKKKISQKKLKKQKLMARE

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21073	51441	A	21200	1	876	
21074	51442	A	21201	1	1725	
21075	51443	A	21202	278	889	SVKMVRYSLDPGGTPRKSCK/S QRGSNLRVPFKDHS*KLPQAHQ RVCHIRKSPTKY\LKDVHLTRN QCVPIPDRYNG*QLGQVCRRHK QMGPGTTKGR\WPQKGVLKFL PAHALKTAE\SNAEL\KGLDVDS LVIEHI\QVNKAP\KM\RRRTYR AHGRINPYMSSPCH\IEM\ILTEK EQIVPKPEEEVAQKKKISPEETE RNKNLLARE
21076	51444	A	21203	1	1923	
21077	51445	A	21204	1	280	
21078	51446	A	21205	1	109	
21079	51447	A	21206	1	638	
21080	51448	A	21207	1	396	
21081	51449	A	21208	26	969	HGVGCRDGLPMECRFLCQIFM AFMQMNSYCARHKKATRRTV* /CRNQDMTESSQKWTGKGSAV EHLVESGEWTMHPARPVSACR CPSDCHVPLSPGACWPKLECLS EGSSYISDGKEYLFYLNVCGET EIQFCNKKQAAVCQVKKSDTS QVKAAGRYHNQTLRPSESSWS LLFVVLVFFPGVHSPFSLDEALT LCPQNCLPPGTVSAPLNCVYPL ALSAAVALAAGSELMECHRLV NSLEVSTAAQGQSSKTQFYACL CRLSTHLWKYSEESGRRLVCSF YQPSELNPALNLSFLVGTRLQE GAALLFIQSGFTIV
21082	51450	A	21209	1	465	
21083	51451	A	21210	217	453	
21084	51452	A	21211	1	840	
21085	51453	A	21212	1	663	
21086	51454	A	21213	176	957	DEPIGVPLLSAPPAGTTKIKADQ LHLQGAAPKICPCLQDGSLGQH YCPFVSFSRYYINLCQKIYKGPL GCSERASICRRTTTGDVQVLG\L VHTQK\LGVIGPRVVVTTSKRY PCGGNKTASSVIELTCTKPVGR PAFKRFEIDSCTYYFSWDSGAA CAVKPQEVQMVNGTITNPINGK SFSLGDIYFKLFRASGDMRTNG DNYLYEIQLSSITSSRNPACSGA NICQVKPNDQHFSRKVGTSDKT KYYLQGNPWLPTKFHI

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21087	51455	A	21214	3	7616	SPVEPRSPRAPAPSPPPPLPWRR DPVPGAAPSSRAPLASRPPRSSG PGAMGAAAGRSPHLGPAPARR PQRSLLLLQLLLLVAAPGSTQA QAAPFPELCSYTWEAVDTKNN VLYKINICGSVDIVQCGPSSAVC MHDLKTRTYHSVGDSVLRSAT RSLLEFNTTVSCDQQGTNHRVQ SSIAFLCGKTLGTPEFVTATECV HYFEWRTTAACKKDIFKANKE VPCYVFDEELRKHDLNPLIKLS GAYLVDDSDPDTS
21088	51456	A	21215	2	184	VNCQPLGMISLMKR\PPGFSPFR SSRIGEIKEETTSHLRSCEYKGR PPKAGAEPASEREVS
21089	51457	A	21216	1	203	
21090	51458	A	21217	1	1107	
21091	51459	A	21218	1	915	
21092	51460	A	21219	1	1932	
21093	51461	A	21220	2	746	

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21094	51462	A	21221	1	2157	MGFPLRPSPAHLSSGRQQFPAK EERLLLSLTQESQSEEIDCNDKD LFKAVDAALKKYNSQNQSNNQ FVLYRITEATKTVGSDTFYSFK YEIKEGDCPVQSGKTWQDCEY KDAAKAATGECTATVGKRSST KFSVATQTCQITPGGWFILWHC PGGKLTISDYPNSSRVLHCTQC VQGLNRRTRRHKTCPPLQAAS QIEERIGFEGRPGLESFRAPCLL ASPFPCLEKGAEGPVVTAQYDC LGCVHPISTQSPDLEPILRHGIQ YFNNNTQHSSLFMLNEVKRAQ RQAAP/GREFSSMDTFEGYEGA EDMEKLAGPFPVG*QSRNLFLQ IRFPGEERKHPGRKRRTR*GSN GDRQHQEGACWGVHAG*LLR GRRLVSRRGRGARGPPPRRAAL PAVAPAPRLQSARIPERGDGDD GVRRWGHREAIGS*GQS/LS/CN GIIILIKEERLPCPFHCISLMKRPP GFSPFRSSRIGEIKEETTVSPPHT SMAPAQDEERDSGKEQGHTRR HDWGHEKQRKHNLGHGHKHE RDQGHGHQRGHGLGHGHEQQ HGLGHGHKFKLDDDLEHQGGH VLDHGHKHKHGHGHGKHKNK GKKNGKHNGWKTEHLASSSED STTPSAQTQEKTEGPTPIPSLAK PGVTVTFSDFQDSDLIATMMPPI SPAPIQSDDDWIPDIQIDPNGLSF NPISDFPDTTSPKCPGRPWKSVS
21095	51463	A	21222	207	424	HHINCVLLYLQSHLRS\CEYQG\ RPPKAGAEPASE\REVSLTNWA ESSTPRHIAPTTSASNLEMEGQE ERWDRI

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21096	51464	A	21223	170	1487	IMKLITILFLCSRLLLSLTQESQS EEIDCNDKDLFKAVDAALKKY NSQNQSNNQFVLYRITEATKTV GSDTFYSFKYEIKEGDCPVQSG KTWQDCEYKDAAKAATGECT ATVGKRSST\KFSVATQT\CQITP AEGPVV\TAQLRTCLG/CVWHPI IQRQSPDLEPILRHGIQYFNNNT QHSSLFTLNEVKRAQRQVVAG LNFRITYSIVQTNCSKENFLFLT PDCKSLWNGDTGECTDNAYIDI QLRIASFSQNWD\IYPGKDVVQ PPTKICVGCPRDIPTNSPELEETL THTITKLNAENNAISYFKIDNVK KARVRVVAGKKYFIDFVAR\ET TCSK\ESNEELTESCETKKLG\Q RLG\CNAE\VYVVPW\EKKIYPT/ VFNCSTTGEWIFT*WKRPPRVF SPFRS\SRIGEIKEET\TSHLRSCE YKGRPPK\AGAEPASEREVS
21097	51465	C	21224	21	281	
21098	51466	A	21225	204	441	QISQVLIICNQK*VILTGNFLDT YF*TTFINKKIDELRLCA/CAVA HSYNTTLCKKPRWKDCLRPAV QDQPVQHSETLSL
21099	51467	A	21226	333	604	SSDRITKPPSAEFLPLQRTFLHSL QDTVIELLH*DLETPPLTVLQNH PSLPRPIPAPPTLCPQTRWPHLR GHQGILAASHILETALAAIF

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21100	51468	A	21227	846	3269	GFMEVLRDPIKKNSSESKPAQS GFSRGNSPLSCPESVEASPAVNE KSVYSTHNYGTTQRHGCRGLP YADHNYGAPPPPTPPASPPVQTI IPRSDLNGLPSPVEERCGDSPNS EGETVPTWCPCGLSQDGFLLNC DKCRGMSRGKVIRLHRRKQDN ISGGDSSATESWDEELSPSTVLY TATQHTPTSITLTVRRTKPKKR KKSPEKGRAAPKTKKIKAFREG SRKSLRMKNSPSEAQNLDENTT EGWENRIRLWTDQYEEAFTNQ YSADVQNALEQHLHSSKEFVG KPTILDTINKTELACNNTVIGSQ MQLQLGRVTRVQKHRKILRAA RDLALDTLIIEYRGKVMLRQQF EVNGHFFKK\PYP\FVLFLLQNL NGVEMCVDARTFGNDARFIRR SCTPNAEVRHMIADGMIHLCIY AVSAITKDAEVTIAFDYEYSNC NYKVDCACHKGNRNCPIQKRN S*CYRTATPTTSSKPTHHWSRD *T*KS\RRKELEMEQQNEASEEN NDQQSQEVPEKVTVSSDHEEV DNPEEKPEEEKEEVIDDQENLA HSRRTREDRKVEAIMHAFENLE KRKKRRDQPLEQSNSDVEITTT TSETPVGEETKTEAPESEVSNSV SNVTIPSTPQSVGVNTRRSSQA GDIAAEKLVPKPPPAKPSRPRPK SRISRYRTSSAQRLKRQKQANA QQAELSQAALEEGGSNSLVTPT
21101	51469	A	21228	2	197	CRPPSPRPVRAARPARPQASFSR EPPPRRMAP*SKRRRQSARGPV RPSRVWARIKAKPYSCCCQL
21102	51470	A	21229	4	488	GSYDINRQDTFQKDRQRVGPSG ASQKTEGFLLRLLYSGLIIAHCS LEILGRNDPPASASKVAETTDS GSLSLANT*PPTPR/VTSQTANA TSQAAPALPLGSVPGRRAADPR PLLAWAPAPPGPGTSRNTHPAP DGLDMLVPIGDGVLGGNCFRN QCKSVSTS
21103	51471	A	21230	124	293	

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21104	51472	A	21231	239	1393	IYPQISFQKKFVMFFFSEALCTA RAEECDPIGLLNNPRTSRYSRL KPNSSLGGSESRKTQMGPLPPP PKSPDGARPVPGCIKEAGPARG RSRLAPNPGALRRG/VGLGR*S ARI*GLVSKAAAGQGEARRGE AT*ARGALGRTTAGSFNAGWL TLDGARQQPGRQTPTRIPSCVA DNAAGPSRTTTPD/EALRPLRG GPACTAPASFDSRAPYSASSAPS EGRWPSRGFPPIS/PLYSQLPETR SHEWQAASKIQPRKASTSQ*SA RMEAT*QQWAGPPAEP*SLWFP RLARRSVVHWRTPY/ISSSITSLP PVAAGIPEDSGPGSTQSSSRPGN TSSSSRPPPPPPPPPP/QPLPPPPA GLASPRPVRARRPARPQASFSR EPPPRRMAP
21105	51473	A	21232	107	234	
21106	51474	A	21233	224	227	LPQPGPGRRRACLRQASPRQYS RLPGRPPPSG*SW
21107	51475	A	21234	67	607	QRSWAGPGAGPEAGTRPPARG RRRQPGNVDPRRRAPQLRSQM QVAMARATTATGNRLWPGLLI MLGSVCHRGSPCGLSTHVEILL LEHQDAYQAGIVFPDCFYPSIC KGGKFHDVSESTHWTPFLNAS VHYIRENYPLPWEKDTEKLVAF LFGITSHMAADVSWHSLGLEQ GFLRTMGAI
21108	51476	A	21235	54	193	
21109	51477	A	21236	1275	1764	STKCQYFSHLLLLFSASESKQLL LYSAFFRYVPVKDLLGIYEKLYI CFISLLQTGL*RYQE*YHIHFIFS FSLP*LYPTYSTKSPFLVEQFQE YFLGGLDDR*NSCL*RSR*MAN SFDCFLSDSVLQGVVFSVVTSL FLFLFNSSKMQKNDFHRNLTTS
21110	51478	A	21237	297	428	QCQRGPGCSRGHGI*I*EHWTA FGLLDLRQWFARGSWASGHGP

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21111	51479	A	21238	3247	5958	QRSWAGPGAGPEAGTRPPARG RRRQPGNVDPRRRAPQLRSQM QVAMARATTATGNRLWPGLL MIVMASLCHRGSSCGLSTHIEIG HRALEFLHLHNGHVNYKELLL EHQDAYQAGTVFPDCFYPSLC KGGKFHDVSESTHWTPFLNAS VHYIRENYPLPWEKDTEKLVAF LFGITSHMVADVSWHSLGIEQG FLRTMGAIDFHGSYSEAHSAGD FGGDVLSQFEFNFNYLARRWY VPVKDLLGIYEKLYGREVITEN VIVDCSHIQFLEMYGEMLAVSK LYPSYSTKSPFLVEQFQEYFLG GLDDMAFWSTNIYHLTSFMLE NGTSDCSLPENPLFIACGGQQN HTQGSKMQKNDFHRNLTSSLT ENIDRNINYTERGVFFSVNSWT PDSMSFIYKALERNVRTMFIGG SQLSQKHVSMPLRHHYFLSFPY ARLGW\AMTSADL\NQDG\HGD LRGWGAPGLTAAPAHIPHSGR VYLIYGNDLGLPPVDLDLDKEA HRILEGFQPSGRFGSALAVLDF N\LDGV\PDLAVGAPSVGSEQLT YKGAVYVYFGSKQGGMSSSPN ITISCQDIYCNLGWTLLAADVN GDSEPDLVIGSPFAPGGGKQKG IVAAFYSGPSLSDKEKLNVEAA NWTVRGEEDFSWFGYSLHGVT VDNRTLLLVGSPTWKNASRLG HLLHIRDEKKSLGRVYGYFPPN
21112	51480	A	21239	2	403	VVAEEDTELRDLLVQTLENSGV LNRIKAELRAGVFLALEEQEKV ENKTPLVNESLKKFLNTKD\LQ GLEGRENLARDLGIIEAEGTVG GPLLLEVIRRCQQKEKGPTTGE GALDLSDVHSPPKSPEGKTSAQ
21113	51481	A	21240	3	1699	

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21114	51482	A	21241	3	1812	APRLKMGLHPNKPIVSQSRVVN DGQCKLHAAVDSRDPPDGTKR RVSSGGTGLPGPGRGPGLPAGA WLSAEGRGAGGSGDCGPSSGS AEPTQRPPRPSALPGAIPPLHLG LAPFRLASEAVAEQAPPPAPTLS FGAQWSGAPQGSVSSVNPEGA GPARCASGRGFGCVGRVARAR SVPCCGRWPLARLRRLSWRSK MAATAAAV\VAQEDTELRDLL VQTLENSGVLNR\IKAELRAAV FLALEEQEKVENKTPLVNESLK KFLNTKDGRLVASLVAEFLQFF NLDFTLA\VFQPETS/TIF*LLF*L QGLEGRENLARDLGIIEAEGTV GGPLL\LEVIRRCQQKEKGPTTG EGALDLSDVHSPPKSPEGKTSA QTTPSKIPRYKGQGKKKTSGQK AGDKKANDEANQSDTSVSLSE PKSKSSLHLLSHETKIGSFLSNR TLDGKDKAGLCPDEDDMEGDS FFDDPIPKPEKTYGLRKEPRKQ AGSLASLSDAPPLKSGLSSLAG APSLKDSESKRGNTVLKDLKLI SDKIGSLGLGTGEDDDYVDDFN STSHRSEKSEISIGEEIEEDLSVEI DDINTSDKLDDLTQDLTVSQLS DVADYLEDVA
21115	51483	A	21242	419	651	TNIFSRLNPQTKNVFCARQLSS* SVTI*GVLGQAVTRYFSQALSC DWGTLLFSRAFLIMPESPTPLLG RDILAKAGA
21116	51484	A	21243	555	888	RTSSRRTPNPCSRIRKNYFKFH MEPKKSP/S*PRQC*AKRTKLEA SCYLTSNYTTRLQ*PKQHGWG TIRSFSSHEAIFQTITWGKTLDN TRLSRTEVPAAFHSALCPWFIET
21117	51485	A	21244	728	1428	
21118	51486	A	21245	238	505	INVGRHHVILQGLSCPGQLSSRS VTI*G\VLGQAVTIYFSQPLSCD WRTLLFSHVFLIMPESPTPLLGR DILLYVCIGRFPIFRADCRT
21119	51487	A	21246	940	1434	QLAPCTLTEPRVCLTIEGQEVN CFLDTRAAF\VLLSCPRQLSSRS VAIRGVLGQAVT*YFSQPLSCD WGTLRFSHAFLIMPKSPTPLLG RDILAKAGAIIHEKRKAFMRKR EIKKQARSSKVHTSAASSCART APLGESFAEHLIKIADFTPPSSSS PCTTLFFS

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21120	51488	B	21247	747	1138	
21121	51489	A	21248	1685	2051	SSSRTEGARGKRQPMPSP/STEP RVCLTIEGQEVNCLLDTGAAFS VLLSCPGQLSSRSVTI*GVLGQP VTRYFPQPLSCDWGTLLFSNAF LIMPESPTPLLGRGILAKAGAIIH HAVLVTAAL
21122	51490	A	21249	2	1014	GGAGPVVLRRRAACSPGPAPR AARPPAMEPGPDGPAASGPAAI REGWFRETCSLWPGQALSLQV EQLLHHRRSRYQDILVFRSKTY GNVLVLDGVIQCTERDEFSYQE MIANLPLCSHPNPRKVLIIGGGE GG\VL\REVVKHPSVESVVQCEI DEDVIQVSKKFLPG\MAIGYSSF EADTYMWGDGF*VSWKQKQ\D AFDVI\IIDSSDPMGPA\ESLFKES YYQLMKTA/LLREDGVL\CCQG \ECQWLH\LDLIKE\MRQFC\QSL FPV/VLAYAYCTIPT/YTPSGQIG FMLCSKNPSTNF\QEPVQAVDN SSKVAKMQLK\Y\YNSERATAA AFVLPE\FARQGLE
21123	51491	A	21250	3	418	FSYEKLLNWQEFAVDLEHHSY RSFLGLTCLKQISTRTEDFIIDTL ELRRDMYILNESLTDPAIVKP\L AEEMLSYARDDTHYLLYIYDK MKLQMRERGNRQTVQLHVVW QRSRDICLKKFIKPI\FTDESYLE LYRKLKK
21124	51492	A	21251	1	1704	
21125	51493	A	21252	1	3104	MFDTHQAARLLNLGRHSLDHL LKLYCNVDSNKQYQLADWRIR PLPEEMLSYARDDTHYLLYIYD KMRLEMWERGNGQPVQLQVV WQRSRDICLKKFIKPIFTDESYL ELYRKQKKHLNTQQLTAFQLL FAWRDKTARREDESYGYVLPN HMMLKIAEELPKEPQGIIACCN PVPPLVRQQINEMHLLIQQARE MPLLKSEVAAGVKKSGPLPSAE \RENVKSQPVQVHL*QRPVLTA GRKLLPACTFYMPACWGL

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21126	51494	A	21253	2	2775	QALARRAVQAEKMAPPSTREP RVLSATSATKSDGEMVLPGFPD ADSFVKFALGSVVAVTKASGG LPQFGDEYDFY\RSFPG\FQAFC ETQGDR/LCFQCMSRVMQVPM GC\RSN\IKDRSKV\TELEDKF\D LL\VDAN\DVILERVGILLDEAS GVNKNQQPVLPAGLQVPKTVV \SSWNRKAAEYGKKAKSETFRL LHAKNIIRPQLKFREKIDNSNTP FLPKIFHSNPMVQ\KPLPQALSK ERRERPQDRPE
21127	51495	A	21254	3	2668	QALARRAVQAEKMAPPSTREP RVLSATSATKSDGEMVLPGFPD ADSFVKFALGSVVAVTKASGG LPQFGDEYDFYRSFPGFQAFCE TQGDRLLQCMSRVMQYHGCRS NIKDRSKVTELEDKFDLLVDAN DVILERVGILLDEASGVNKNQQ PVLPAGLQVPKTVVSSWNRKA AEYGKKAKSETFRLLHAKNIIR PQLKFREKIDNSNTPFLPKIFIKP NAQKPLPQALSKERRERPQDRP EDLDVPPALADFIHQQRTQQVE QDMFAHPYQYELNHFTPADAV LQKPQPQLYRPIEETPCHFISSL DELVELNEKLLNCQEFAVDLEH HSYRSFLGLTCLMQISTRTEDFII DTLELRSDMYILNESLTDPAIVK VFHGADSDIEWLQKDFGLYVV NMFDTHQAARLLNLGRHSLDH LLKLYCNVDSNKQYQLADWRI RPLPEEMLSYARDDTHYLLYIY DKMRLEMWERGNGQPVQLQV VWQRSRDICLKKFIKPIFTDESY LELYRKQKKHLNTQQLTAFQL LFAWRDKTARREDESYGYVLP NHMMLKIAEELPKEPQGIIACC NPVPPLVRQQINEMHLLIQQAR EMPLLKSEVAAGVKKSGPLPSA ERLENVLFGPHDCSHAPPDGYP IIPTSGSVPVQKQASLFPDEKED NLLGTTCLIATAVITLFNEPSAE DSKKGPLTVAQKKAQNIMESFE
21128	51496	A	21255	98	286	HARPRHGPRLRCEVGLRCAPG YAGASARPTCECGDTRYCPQDP NQT*SRPVPIIAHRYCLTG
21129	51497	A	21256	1020	1280	
21130	51498	B	21257	153	3804	

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21131	51499	A	21258	159	579	PNVRWCPS\CYRNQDDHELQIT HGNKILCGIVWKKIAQVEQMR KFSRLEKQRTHVLSCSDLQAVR RFRGVVSEGSFEMGEKVYKRK DMFQLSLLTEQHGDSTLGSGSS YTQMPAENGSLVHTLVTAAPPF FAEKPHSITAG
21132	51500	A	21259	1	1290	MGASRSQKPGPSRDYSYTAGC DVDQRRRGAQKLSRSDTKRIV MSYGKKALKNDKFEIRAFSSSL EVRYRNQDDHELQIHTGTRFY VELCGFAVTRLRDPPMLRHAA MALLPWRPPDYSASLLPDWLP VPSSKVVITYPGFTSIWAFSNTE T/LCSEYKYYCEECRSKQE/AHK RRKV*KLPMILAP/HLKRFKYK DQLHRFTKLFTRASLRGPRDER LKRVSRQLFSLVVVTSRVFDVL LRILHRLGQYVSSEYYVALMCS EGHGPGAEDVTELLQSHEKTE WMRSCFFWMTKSGVFDGIYLW NAFNQEGEDLYKENCKTLMKE VEDAQINGKTSYAHGSEEYCK MSILPRILLQKISRDDCFKIVLKF CVDHQKTKKCCMITLKSSVVQ LAFTIKISVSEMCAREDFVVVIS FQHSEVPSRQLARCTFKEGYT
21133	51501	A	21260	3	142	
21134	51502	A	21261	1	1368	

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21135	51503	A	21262	1	2420	MEEVAEAPQPIDPKPLATQPQSI IITTITTIITITTTTITTTTTTITTTIT IITTTITITTTITTTTTITIITTTITITT TITITTIITITTTITITTIITTTTITTT VITIITTTITTIITITTITPSSSSSPSS QADECWGEAEPLMSRQAHVW LRYRTGCREERPDQELTGSWG HGPRSTLVRAKAMAPPPPPLAA STPLLHGEFGSYPARGPRFALTL TSQALHIQRLRPKPEARPRGGL VPLAEVSGCCTLRSRSPSDSAA YFCIYTYPRGRRGARRKATRTF RADGAATYEENRAEAQRWAT ALTCLLRGLPLPGDGEITPDLLP RPPRLLLLVNPFGGRGLAWQW CKNHVLPMISEAGLSFNLIQTER QNHARELVQGLSLSEWDGIVT VSGDGLLHEVLNGLLDRPDWE EAVKMPVGILPCGSGNALAGA VNQHGGFEPALGLDLLLNCSLL LCRGGGHPLDLLSVTLASGSRC FSFLSVAWGFVSDVDIQSERFR ALGSARFTLGTVLGLATLHTYR GRLSYLPATVEPASPTPAHSLPR AKSELTLTPDPAPPMAHSPLHR SVSDLPLPLPQPALASPGSPEPL PILSLNGGGPELAGDWGGAGD APLSPDSTAGFTSWLSQGSSTLT RLRRGPRNSPILWAPTSHP*CPG RGLH\RGPPDHLLPPLGTPLPPD WVTLEGDFVLMLAISPSHLSAD LVAAPHARFDDGLVHLCCVRS
21136	51504	A	21263	573	1025	RKQSHEDEWRSTNKTVGHPSA RLYEPPWWAHTWTPPGGSKAP SDP/PLSHQLSPPAGQPHFASPEP TSKTPDPWPGNVFSSFPLPQSLP ELRHTLYLPMGTKKPPGSSMIF YT*AQYPGTNSSATICRLLSYKS GQVYPNTGQAPPQQRRGR
21137	51505	A	21264	48	327	EELEALRR\QRLAELQAKHGDP GDA\AQQEAKHREAEMRNSILA QVLDQSARAR\VSEQGLIEILKK VSQQTEKTTTVKFNRRKVMDS DEDDDY
21138	51506	A	21265	1	400	
21139	51507	A	21266	786	905	VSEQGLIEILKK*CQLTEKTSTV KFNRRKVMDSDEDDDY

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21140	51508	A	21267	907	1327	PRLLQRSTPSPWRTEELEALRR\ QRLADAAGQNTGDPGDAA\QQ EAKAPGQAEMRNSILAQVPGSS PAPAPRLSNLSHLVKP*KNLKP V\ENYPYTRLARYWTT*VMTGI RNQGFN*KSLKKVKAQ\QTEKT TTVKFNQKKK
21141	51509	B	21268	1	828	
21142	51510	A	21269	317	2390	KWPKMNPQQQRMAAIGTDKE LSDLLDFSAMFSPPVNSGKTRP TTLGSSQFSGSGIDERG\GTTSW GTSGQPSP\SYDSSRGFTDSPHY SDHLNDSRLGAHEGLSPTPFMN SNLMGKTSERGSFSLYSRDTGL PGCQSSLLRQDLGLGSPAQLSS SGKPGTAYYSFSATSSRRRPLH DSAALDPLQAKKVRKVPPGLPS SVYAPSPNSDDFNRESPSYPSPK PPTSMFASTFFMQDGTHNSSDL WSSSNGMSQPGFGGILGTSTSH MSQ\SSSYGNLHSHDRLSYPPHS VSPT\DINTSLPPMSSFHRGSTSS SPYVAASHT\PPINGSDSILGTK GNAAG\SSQTGDALGKALASIY SPDHTSSSFPSNPSTPVGSPSPLT GTSQWPRPGGQAPSSPSYENSL HSLQSRMEDRLDRLDDAIHVLR NHAVGPSTSLPAGHSDIHSLLG PSHNAPIGSLNSNYGGSSLVASS RSASMVGTHR\EDSVSLNG\NH SVLSSTVTTSSTDLNHKTQENY *RWPCKSQSGT\VVPQEIKT\EN KEKDENLHEPPSSDDMKSDD* SSQKDIKVSSRGRTSSTNEDEDL NPEQKIEREKERRMANNARERL RVRDINEAFKELGRMCQLHLKS EKPQTKLLILHQAVAVIL\SLEQ QVRERNLNPKAACLKRREEEK VSAVSAEPPTTLPGTHPGLSETT
21143	51511	A	21270	2	153	QNASSPSKGSQLLTSKGTKLDG E*V**INRSRLQKVANNKLLWR KLKGQF

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21144	51512	A	21271	1	1230	MRKTQCKNAESSKNQNASFPP KDHNSLTAREQNWIENEFGELT EVGFRRLNQEEVEFLNRPITGSE IEAIINSLATKK\GPEGFIAEFY*R KTQCKNAESSKNQNASFPPKD HNSLTAREQNWIENEFGELTEV GFRRLNQEEVEFLNRPITGSEIE AIINSLATKKRTRGIHSRILLEVI TSFYVERGGNAMSFMGKGVTK STILCLLHLSHEMMAQAGSLE WMSLWFLPLGSHSEEHIPTQQG LAWLIPLWVDRDPEVRFTSLGL GSALTTLETGCVALANSCQNIS GGLWGTVVNILLDQSECSMVR RESQHHVDVAKVYHLHPPEW WPKLYLGPLDHSRELRSSVLEC MEQRLEVTLGTTPYFSVPISKFI QAVTTKCLRLGASRFSVCLAGL SAAPEQKIHPPPPTQQFQQLPHD SVGFLQFSLHPKGNFGSGISSPD RSGDASHYSYPSLWQIRGTSRV KKQTWGSGNLKKWGIHKVQP QRLMMQNDTDEESI
21145	51513	A	21272	1	987	
21146	51514	A	21273	180	466	ARGSERAAASFSASMYEGKKT KNMFLTRALEKILADKEVKKA HHSQLRKACR\VALEGNKAETE KQSPPHGEAKAGISTLPPVKSK TNFIEADKYF
21147	51515	A	21274	1	1224	
21148	51516	A	21275	251	5986	SCRCPPRLQSPTSTPSPFSLLFLP LLLLPSSRWEPRVGRAAASFSA SMYEGKKTKNMFLTRALEKIL ADKEVKKAHHSQLRKS/CGRV ALEEIKAETEKQSPPHG\EAKAG SSTLPPVKSKTNFIEADKYFLPF EL\ACQSKCP\RIV\STSLDCLQK L\IAYGAL*LGNAPDSTTPGKKL IDRIIETICGCFQGPQTDEGVQL QIIKALLTAVTSQHIEIHEGTVL QAVRTCYNIYLASKNLINQTTA KATLTQ
21149	51517	A	21276	46	214	KLRLTTTSVYAIPNRRRYDGFK LVQSCIFI*NFRS*DLRPPQYMPF LIEGGMTVSNSCRAAFSFTSLC RHFRSEAWLQNTNTGGFGSTF
21150	51518	A	21277	306	616	
21151	51519	B	21278	47	927	

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21152	51520	A	21279	660	890	GGKITASGSPVPRPSGA*ALPSG RCSTPRTSSCPRQLPEPPGL\PSP PSAPANTTPDDSHAAP*GTRAH THRPPPHT/PTAPSRPPTSPPVAT RTAPKAPQ/HHP/PTSCPTQRPT DSPSVHEPSQPLATQHSTQPI*P VIVTQ
21153	51521	A	21280	3	213	
21154	51522	A	21281	349	2616	TTAMAHRKLESVGSGMLDHRV RPGPVPHSQEPESEDMELPLEG YVPEGLELAALRPESPAPEEQE CHNHSPDGDSSSDYVNNTSEEE DYDEGLPEEEEGITYYIRYCPED DSYLEGMDCNGEEYLAHSAHP VDTDECQEAVEEWTDSAGPHP HGHEAEGSQDYPDRQLPIPEDE PSVLEAHDQEEDGHYCASKEG YQDYYPEEANGNTGASPYRLR RGDGDLEDQEEDIDQIVAEIKM SLSMTSITSASEASPEHGPEPGP EDSVEACPPIKASCSPSRHEARP KSLNLLPEAKHPGDPQRGFKPK TRTPEERLKWPHEQVCNGLEQP RKQQRSDLNGPVDNNNIPKTK KVASFPSLVAVPGPCEPKNLID GIIFAANYLGST\QLLSERNPSK NIRMMQAQEAVSRVKRMQKA AKIKKKANSEGDAQTLTEVDLF ISTQRIKVLNADTQETMMDHAL RTISYIADIGNIVVLMARRRMPR SASQDCIETTPGAQEGKKQYK MICHVFESEDAQLIAQSIGQAFS VAYQEFLRANGINPEDLSQKEY SDIINTQEMYNDDLIHF\SNSEN CKELQLEKHKGEILGVVVVESG WGSILPTVILANMMNGGPAAR SG\KLSIGDQIMSINGTSLVGLPL ATCQGIIKGLK*PDHR*SFNIV\S CPPV/TPRFLYSKRPDLKYQLGF SVQNGIICSLMRGGIAERGGVR

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21155	51523	A	21282	20	771	TTPNKQHMMQTRAGSAWYLR SRGCSQGAPQKASSGSGGSSW NRSVATVPGIVLGWRRPELLSE RGCAEARGAGVAGRQRLQLTG VQGKSVVRGRGLLGRREWCRR GGGAAPRPTPAGTPVPRRPGTR AGPEEGEGAGAGARAAPEPRP HALSPPAAFGADGQLRPLLLTS LRAHHPGRGGLLLTSPGTHQPR RGRQGTPPPASPSPA/PEEGALP GVLPL*PPPSPPSP/SSESPRPHPG GGALAVTRRTAAA
21156	51524	A	21283	1615	1985	LGSTRQAAPGQLRGHQAPAPN SDATAGQGRCRRSAD*GWGSR EQI*ALPLPSGPAPLLPPLLPPLL PVPPSPPPPSPPSPPSPLPPP\GPP* PPLTFSVVTPGGLWCPPHRKSL NPTSKGVNEY
21157	51525	A	21284	3	501	
21158	51526	A	21285	1	2646	
21159	51527	A	21286	31	319	VIQDLHVPPREESAEQVDDPPE PVY\RT*RGSPGPLHRAPLQPPF PARCGRRTRTRAPGAPTTTTQT RELPPGSRPLRLPRVPPAQPPPL PRWTAT
21160	51528	A	21287	3	147	
21161	51529	A	21288	20	600	PVTPRRTILPWALSVSPALPLP* PHPPAGLVMSARTSRCSTPTTS LRSSG*GWRTPTGSHTSTIQRTP LFDGSCPRSLSLPLEASINPARM VTPQPRPALQRRRSQQSWMRL GAGRKSLLPQLL*GPRPWTRQG CSIAPRRQTRESGSGRSTGVPPG LCWRVAS*HSSRTQRPRLQAA* GSLPSFPPLSTQWS

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21162	51530	A	21289	383	1800	TCSTQTSLRNPPRRPRAASLPQT CSRSPRPSRAHSLTGRPPRFQSQ MPSRSPCC*IC*NIRIDLCGS\TH SDGRFELVFSGKKLALRASSQD EAEDWLDRVREALQKVRPQQE DEWVNVQYPDQPEEPPEAPQG CLSPSDLLSEPAALQGTQFDWS SAQVPEPDAIKESLLYLYMDRT WMPYIFSLSLEALKCFRIKNNE KMLSDSHGVETIRDILPDTSLG GPSFFKIITAKAVLKLQAGNAE EAALWRDLVRKVLASYLETAE EAVTLGGSLDENCQEEKNNTK HTTARNAFEENDFMENTNMPE GTISENTNYNHPPEADSAGTAF NLRPTVKQTETKWEYNNVGTD LSPEPKSFNYPLLSSPGDQFEIQ LTQQLQSLIPNNNVRKLIAHVIR TLKMDCSGTHVQVTCAKLISRT GHLMKLLSGQQEVKASKIEWD TDQWKIENYINESTEAQSEQKE KSLEAASGTQDGVHVQEPRPQ APSPLDLQQPVESTSSQQPSSTV SETAREVGQGNGLQKAQAHDG AGLKLVVSSPTSPQQVCKLWW SAGLHTPPPVTSLGTVGLQGPQ QRFPKFPDFFHPLEISCGKVA
21163	51531	A	21290	2	667	
21164	51532	A	21291	84	377	RMGKHCFENLLFRDGKAQRAC MGYTVCHSHIVGSGQKCWPA WPQVNLQPSRHQQVCCSLPRC AKCKTVFHQSCQAV\VKKGCPR CAR*RKYQQQNVFA
21165	51533	A	21292	2	1168	FVLPVVSGRETASSARRLRGCR SREPPSPRSSLRLVSCDSLREQL REWRCFQWWRMDWTPRLPSR HIISELEHLTFVNMDVGRCRAW LRLALNNGLMECYLKLLLQ\EQ ARLREYYQPTALLRDAEEGEFL LSFLQGLMSLSFELSYKSAILNE WTLTPLALSGLCPLSELDPLSTS GAELQRKESLDSISHSSGSEDIE VHHSGHKIRRNQKPTASSLSLD TASSSQLSCSLNSDSCLLQENGS KSPDHCEEPMSYDSDLGTANA EDSDQSLQEVLLEFSKAQAASG TQDGVHVQEPHPQAPSPLDLQ QPVESTSGQQPSSTVSETAREV GQGNGLQKAQAHDGAGLKLV VSSPTSPNISSMIQSTRPVHFCIV STKHCTWEKVGMDE

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21166	51534	A	21293	263	813	
21167	51535	A	21294	130	1094	NQPHRTKGCPNSSTECKNGSLT CDFMQVPILEMGKLRPEGERRV QDRDSNPSLSPSAGLFQARWS* PPRPSFLLPAGKRRGCDGGGRG GGRVRAGGAPLRVHRQGRAPP QSTEHWWHVRRKPGGRPFYLP AQYVRELPALGNPAADAPPGPP IGTRSP*AARLRLPVRERGCGSG PQRPPSGAPRRGQLPVRPCAAR RREP/RAAAWRPACPPACTCGP\ GARAARAVPGRPDARRRLASR RQPRKQRQLQGLQRSGLLGVP AAPVAQRLRERLRGHPGGTRP AAVGDREAGTTPGAEAGRLAE DSARREPGLEENHSAQRRA
21168	51536	A	21295	2	3676	
21169	51537	A	21296	432	3453	DLAGEVLLCGGAADYGTLGFS SPAVQEANRGALCSSIERGHIIS ELEHLTFVNTDVGRCRAWLRL ALNDGLMECYLKLLLQEQARL HEYYQPTALLRDAEEGEFLLSF LQGLTSLSFELSYKSAILNEWTL TPLALSGLCPLSELDPLSTSGAE LQRKESLDSISHSSGSEDIEVHH SGHKIRRNQKLTASSLSLDTASS SQLSCSLNSDSCLLQENGSKSP DHCEEPMSCDSDLGTANAEDS DRSLQEVLLEFS
21170	51538	A	21297	64	2996	LCPPAQPAASQPQVELPAGWPQ PHALPLPHDHRAQHLLGCAHP GRAKPELQQHHDCACAAQIPHI PVRQPYQHPDPPLCQPRRPACP ALPIHGRQLLLQEPLQAGTGGG PGCPPWPGQPHPPVTQVQQPHC GAPQPAFQPGVSAVVLRGRIVK LAPEDLANLTALRVLDVGGNC RRCDHAPNPCMECPRHFPQLHP DTFSHLSRLEGLVLKDSSLSWL NASWFRGLGNLRVLDLSENFL YKCITKTKAFQGLTQL
21171	51539	A	21298	1	320	PVRTPPIPAFSPLKTLRIMSLHQF LLEPNCGRPQLCRGTMARKPAP RKH*KHISRQCRVVLFEYKIGES VGFFKAVIFLFVFLRFHSILDQS FSLSSLLWKIVTLT
21172	51540	A	21299	1	443	
21173	51541	A	21300	1	1059	

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21174	51542	A	21301	116	1559	PRTARPSCAHARTVRAVATRRR RVHFRDLSAAPSGLSVLRPRPT EPVRVDCPESANPPVRARPDSP DPRMFELLAASDARINGPFCAP RVLLAPLLGAFVTVSKIVSKIAL SPK*SRRSHLLRRNGSQW\VKV H\ELKEHNG\HITGID\WAPKSD RICH/CLGADRNCLMVWS\QK\D GVWKPNPG*FLRNLIGGGNFL* KWVPPRRTKFGCGGSGARLISV CYFESENDWWVSKHIKKPIRST VLSLDWHPNNVLLAAGSCDFK CRVFSAYIKEVDEKPASTPWGS KMPFGQ\LMSEFGG\SGTG\GW VHGVSFS\ASG\DRLGWGSATD ST\VSVA*CLQKVVQVSTLKT\E FLAAP*VVSFVSREPASGLPAH DC\CPMLFNYG*PRAALTFRLP KLDIPK\QSIQRNMSAHGNAFG NM\DKRATTED\RNTAL\ETLH\ QNSITQVLYLLRWDKQD\CRKF CT\TGI\DGEPWTIWDFQDPRSL PSQGLRIM

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21175	51543	A	21302	1	2223	MKHYTRVQSSISPPAERQETHA WASPAVTSLESAACHELQEAD LSESLSYPRIVSSSSLQQYVAQG GSFPCFGMPWNFISGGAESTNA VISFANATTAVPMAVLSRRESS LANNPGVVNYSALPENENVGP EMPERPANSSKNSTETANYPTL MGNYNGQNTASLSVFIPPYFAE KIILTEMPGTTETNVENNSQTV YYPALSGNTSAPYPASSYLPITS NFVLERVAEMPETAGTNVKNN TQTVNYPPSSGRGRSQGNASLS LSIPPKFGIERHLGCFLVLAIRSK AAMN\IIYHIGFV*TQAFISLRY/ MPKSAVAGSYGNALQNVLHIE MLFKTESGPQMSYGTMSYSTE MKNNCDQDDASASACLTPDFA LLPLNILVKVDTNTENSVNTMN RSTLLDSDSGQDSSSSSVCIPPK YGYLGDPKRNVRVLKIHLLAV QNMAKPKQAACYLVRILFSKEI LISSSVDIHLKDSQSLDPNKMA ALREYLATTFPTCDLHEHGKD WQDCISGINSMIYCLCSEGKSTP KTVRKNKKRTNRVASASADRN DQRGRDGGEGCSWMFQPMNN SKMREKRNLQPNSNAIPEGMRE PSTDNPEEPGEAWSYFGRPWRN IRMPCSVLTLAKTKSCASLSAR YLIQKLFTKDVLVQSNVYGNL KHGLCALDPNKISALREFLQEN YPICDLSENGRDWKSCVTSINS
21176	51544	A	21303	1	297	
21177	51545	A	21304	1	162	
21178	51546	A	21305	11	212	KGKNCVAIAADRRFGIQAQMV TTDFQKIFP/MGAQRLKFRLNL YELKEGRQIKPYTLMSMVANL LYEK
21179	51547	A	21306	37	554	SSIKFGRSNPDYWIALPSRNLDP AIMSIMSYNGGAVMAMKGKN CVAIAADRRFGIQAQMVTRDF* KFFPMG*PACTPGMAGFAIDVQ TVAQRLKFRLNLYELKEGRQIK PYTLMSMVANLLYEK/RDPDHL FETISQAMLNAVDRDAVSGMG VIVHIIEKDKITTRTLKARMD

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21180	51548	A	21307	51	741	YTAIMSIMSYNGGAVMAM\KG KNCVAIAADRRFGIQ\ARLLTTN FQKIFPMGDRLYIGLGGASPLD VQTS/VAQRLKFRAEPVMS*RE GRQI\KPYTLH*AMGGQPSLL*E KVFGPLTYTE\PVHLPGLGPERP FKALSICFSKTLIRVGPMGDLN DFCGSSGNLAPNKMYG\MCESL WGGPTWDPDHLF*KPFSQGHG *MLWDRDGS/VSGMGSSLFHIIE KDK\IPPRTLKARMD
21181	51549	B	21308	150	404	
21182	51550	A	21309	199	395	
21183	51551	A	21310	100	182	SFLFWIKR*SFPDALYFSSKSGA CSCN
21184	51552	A	21311	203	289	KCLALDIALATRRSAI*FPSVKG PGRGV
21185	51553	B	21312	166	411	
21186	51554	A	21313	232	317	KCPALDIAVATRRSAI*FPAVKG PGRGV
21187	51555	A	21314	129	278	FYSSVSGVSSKDDRRFGCSGYS AAVISFRQC*SQLPGCSATYQR ESTFS
21188	51556	A	21315	789	962	
21189	51557	A	21316	477	599	
21190	51558	A	21317	86	577	ATEPLAPSERREVSIPLLVPAPL PPPPRPPVPSRTRTRPWRRP*AC FPMTLAASCGPTRSPWPSQQPIP QPAPVG/PGNIKTLGDAYEFAV DVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNTFAHKCQLPE DVDPTAV\TSALRKDGSLTIRAR RDPHTEHV
21191	51559	B	21318	312	466	
21192	51560	A	21319	886	1338	GFWQVIRALRGGEVHREGTSA PGRHRRRCGCRSAWNRCCTAC SHVWPPRQMWPQG/PDVAMKT GNIKTLGDAYEFAVDVRDFSPE DIIVTTSNNHIEVRA/REA/ERPD GTVMNTFAHKCQLPEDVDPTS VTSALREDGSLTIRAWRHPHTE HVQ
21193	51561	A	21320	3	605	KKLTPVVRSRVERDPRVRRGLR PHPVLSSLRPPGQGPAPSVDEPQ NLFHLPSGEKIPFLFLLLLLFTPP PRPPVLSRPRTRPWRRP*ACFP MTLAAICGPTRSPWPSQPAPV/V AGNIKTL*DAYEFVVDVRDFSP EDIIVTTSNNHIEVRPEKLAADG TVMNTFAQQCQLPEDVDPTSV TSALREDGSLTIRARGHPHTEH

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21194	51562	A	21321	3	450	SSAAEVQEPRGAPGSPSIPSASR PGPAPRPASLPPSQMQAAALPE EIRWLLEDAEEFLAEGLRNENL SAVARDHRDHILRGFQQIKA\G GDIGQDSSDDNHSGTLGLSLTY DAPFLSDYQDEGMEDIVKGAQ ELDNVIKQGYLEKKS*DH
21195	51563	A	21322	1	399	IGQDSSDDNHSGTLGLSLTSDA PFLSDYQD/EG*VHQISDHWEK LRTWC*VYCDKGMEDIVKGAQ ELDNVIKQGYLEKKSKDHSFFG SEWQKRWCVVSRGLFYYYANE KSKQPKGTFLIKGYSVRMAPHL RRDS
21196	51564	A	21323	3	1189	RLPARPPPDQGPRPVPPLSRPAK CRLAVLPEEIRWLLEDAEEFLA EGLRNENLSAVARDHRDHILRG FQQIKARYYWDFQPQGGDIGQ DSSDDNHSGTLGLSLTSDAPFL SDYHDEGMEDIV*GAQELDNVI KQGYLEKKSKDHSFFGSEWQK RWCVVSRGLFYYYANEKSKQP KGTFLIKGYGVRMAPHLRRDS KKESCFELTSQDRRSYEFTATSP AEARDWVDQISFLLKDLSSLTIP YEEDEEEEEKEETYDDIDGFDS PSCGSQCRPTILPGSVGIKEPTEE KEEEDIYEVLPDEEHDLEEDES GTRRKGVDYASYYQG\LWDC\ YGDQPDDLSL\QRGDLILFLSKE YNMYGWWVGELNSLVG\IVPK EYLHHLPLKWKERWKPREIYFF
21197	51565	A	21324	47	225	NSHHVRGRPRCADSSSPSGDRG QPEAQPAPDSSAPEHAQEPGRA AVKRPDL*SHMTRRP

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21198	51566	A	21325	66	725	AILIILLSSEGLWSSDQHRLVGV QDSPPQGSLGCYFSAMATSEQS VCQARASVMVYDDTSKKWVPI KPG\QQGFSRINIYHNTVSNTFR VVGVKLQDQQ\VVINYSIVKGL KYNQATPTFHQWRDARQVYG\ LNFASKEEATTFSNAMLFALNI MNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEFL ERRTSATGPILPPGHPSSAASAP VSCSGPPPPPPPPVPPPPTGA\TP PPPPPL\PAGGAQGSSHDESFHV QDWPLAISWGPSLRRVPNGPED ASGGSSPSGTSKSDANRASSGG GGGGLMEEMNKLLAKRRKAA SQSDKPAEKKEDESQMEDPSTS PSPGTRAASQPPNSSK\AGRKP WERSNSRGYFCVLDSVQNPAL WPKSPES*EPPSVSSL/ISRMKPA GS\VSDMA\LDAFDLD\RMKQEI LEEVVRELHKGERKEIID\AIRQ EA*SGISRKKNLGHRAHPPTRTS FICSQRPRLM
21199	51567	A	21326	301	390	
21200	51568	A	21327	72	415	
21201	51569	A	21328	395	697	RVMSPVHVNTICSPHPHSDGDV IVPIVLSNERYHWP\VLGWVGG VDCDEFFRVVLGEARLH\LDGV AHQH*TKEGTISNLFQ\ATSVSH LVEVVPQKLSWVI
21202	51570	A	21329	36	399	VEILTSKRAGDWFKEELRLLGG LDHIVDKVKECVDHLSRDEDEE KLVASLWGAQRCLRVLQSVTV HNPENQSYLIAYKDSQLIVSSA KALQHCEELI*QYNRAVDTLCL ADCKPLPHPTVL
21203	51571	A	21330	1	177	
21204	51572	C	21331	198	350	
21205	51573	A	21332	113	228	
21206	51574	A	21333	1	466	

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21207	51575	A	21334	1	4133	ASGCWRKEVGAGSANGVEMV QGPVQTPALTIHRRKRRRRRRR RPSGGTQQALLPAPAVAASES* ARARPAALEAGREVAGPP\SCPP NRASYLPKAESLASLGSHLPAL LSRARVPRPPAGRKERE\RRKRP \VAKAPARL\RGEYETG\VKMTS RFAKTYSRKGGNGSSKFDEVFS NKRTTLSTKWGETTFMAKLGQ KRPNFKPDIQEIPKKPKVEEEST GDPFGFDSDDESLPVSSKNLAQ VKCSSYSESSEA
21208	51576	A	21335	3	221	
21209	51577	A	21336	1	580	
21210	51578	A	21337	2	1095	ARGNRPPPPPRTERGVLESRTRS RHRAPRLPPAMPAPRAPRALAA AA\PASGKAKLTHPGKAILAGG LRGG\IQICMTFPTEYVKTQLQL \DERSHPPRYRGIGDFVRQTVRS HGV\LGLYRGLSSLLYGSIPKAA V\RFGMFE\FLSNHMRDA\QGRL DSTRGLLC\SLGAGRGPRP*VV VCPMETIKVKFIHDQTSPNPKY RGFFHGVREIVREQGL\KGTYQ GLTAT\VLKQGSNQA\IRF\FVM TSLRQW\YPRGTTPNKAHEPF*I TWGSFGA\IASASQVSFGNTPLD VI\KTRMPGPWRPHK\YR\NTWD \CGL\QILKKGGGSRAF\YKGTV PPLGPGLAWDVAI\VFV\IYDEV G*SCFNKVWKNGIKA
21211	51579	A	21338	3	375	TAGDSGAEDGPASRVSQMPTLP PPMPWNLPAGVDCTTSGVLAL TALFFKMEEANLASRAKAQELI QATNQILSHRKPPSSLGMTPAP VPTSLGLPPGPSSYLLSGSPPLG GC\GSTPPTPPGLAA
21212	51580	A	21339	51	3789	GRGHPHGGGELLPASPRGSPEG DQPGQGDPEEKEGRVVPRGGA PDVPSAHALVPEPQTVLGLHQR VTAQPGRHGAH*LHGDRLHSG RPQRPTHTGWAPCLPYPTLGSG *RRHHGNPAGTPRSLLFPF\PEK ELEAPPPAPRFDIYDPFHPTDEA YSPPPAPEQKYDPFEPTGSNPSS SAGTPSPEEEEEEEEEEEEEED EEEEEGLSQSISRISETLAGIYDD NSLSQDFPGDESPRPDAQPTQP TPAPGTPPQ
21213	51581	A	21340	286	393	
21214	51582	A	21341	64	610	

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21215	51583	A	21342	1	4433	MWAQLLLGMLALSPAIAEELP NYLVTLPARLNFPSVQKVCLDL SPGYSDVKFTVTLETKDKTQKL LEYSGLKKRHLHCISFLVPPPAG GTEEVATIRVSGVGNNISFEEK KKVLIQRQGNGTFVQTDKPLYT PGQQVYFRIVTMDSNFVPVND KYSMVELQDPNSNRIAQWLEV VPEQGIVDLSFQLAPEAMLGTY TVAVAEGKTFGTFSVEEYVLSP FLLLLSSVLPKFKVEVVEPKELS TVQESFLVKGGL*\
21216	51584	A	21343	3	522	ELRTWIEGLTGLSVGPDFQKGL KDGTILCTLMNKLQPGSVPKIN RSMQNWHQLENLSNFIKAMVS YGMNPVDLFEANDLFESGNMT QVQVSLLALAGKMGTNKCASQ SGMTAYGTRRHLYDPKNIILPP MDHSTI\SLQMGTNKCASQVG MTAPGTRRHLYDTKLGTSNKCL
21217	51585	A	21344	1	1230	MHQEDLRAWYLLGLPSHQNE TTDVSVVVEPSLTDATYPKQA KQWLSPELRVSTAQPTAWRL RAPAITHQDIALIPGPTARWL SPEMAQGEVGEKILLPDPTLP LTDPRLTGSTEQKKDLAAGPVG SALRRRPPAVSSTQFNKGPSYR LLADVQNRLLPKYDSQKEAEL RSWIKGFTGLSIRPDFQKGLKD GIILCTLVNKLQPGSVPKIN\ASV *NWH*LENLSNFLKAMVSYGM /NPVDLFEANDLFESGNNMQVR VSLLALAGKAKTKGLRSGVDIR DKYSKKQNFDDTTMKASQCVI RLQITNKCASQSGMTAYGTRR HLYDPKNRILPPMDNSTISLQM GTNKYASQVGMTAPGTQRHIY DTNLGIDKCENSSMSLKMGYT QVANHSGQVFGLGRQIYEPKY
21218	51586	A	21345	2	389	

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21219	51587	A	21346	1	1113	MHQEDLRAWYLDLGLPSHQN AQPTAWKCQRAPSPYTHQDMA LIPSPTARWLSPEKEPKQGEVG EKSLLPDPTLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRLLADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIILCTLVNKLQPGSVP KIN\ASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANNLFESG NNMQVRVSLLALAGKAKTKGL RSGVDIRDKYSEKQNFDDTTM KASQCVIRLQITNKCASQSGMT AYGTRRHLYDPKNRILPPMDNS TISLQMGTNKCASQVGMTAPG TQRHIYDTKLGIDKCENSSMSL
21220	51588	A	21347	353	1260	SCWCLKLALAVSST/QFNKGPS YRLLADVQNRLLFKYDSQKEA ELRSWIKGFTGLSIRPDFQKGLK DGIILCTLVNKLQPGSVPKIN\AS V*NWHQLENLSNILKAMVSYG M/NPVDLFEANDLFESGNNMQ VRVSLLALAGKAKTKGLQSGV DIRDKYSEKQNFNDTTMKARL CVIRLQITNKCASQSGMTAYVT RRHLYDPKNRILPPMDNSTISLR MGTNKCASQVGMTAPGNQWH IYDTKLGIDKCENSSMSLKMGY TQVANHSRQVFGLGRQIYEPKY QPGGPVAHGAPSAGNCPGPGE
21221	51589	A	21348	3	530	
21222	51590	A	21349	1	853	MPESWLAAFPPYGDIKKVVGL QLKEGLHQNLTMQDSIQIFDFQ LPGLLRPSSVLWTLKPYHTAGL ASDRDSYKGILACMPCMFGSRR SPLRDIKSHQADLELEVKNSLD TIHRLESELKKQSKIQSQMKVE KAHLEEEIAELKKSQAQDKAKL LEMQESIKDLSAIRADLANKLA EEERAKKTSA*GAFGP/LIAQAN SRDEGTATIITQLELERDVHQRE LKDLTSSLQSVKTKHEQNIQEL MKHFKKEKSEAENHIRTLKVPL LNYPDDTEGIFLVAHEVNKA

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21223	51591	A	21350	1	652	NTSLINTKKKLETDISQIQGEME DIIQEARNAEEKAKKAITDAAM MAEELKKEQDTSAHLERMKKN LEQTVKDLQHRLDEAEQLALK GGKKQIQKLEARVRELEGEVES EQKRNVEAVKGLRKHERKVKE LTYQTEEDRKNILRL\QDL\VDK LQAKVKSYKRQAEEAEEQSNV NLSKFRRIQHELEEADF\RADIA ESQVNKLRVKSREVHTKIISEE
21224	51592	A	21351	21	5868	PAAMSSDSEMAIFGEAAPFLRK SERERIEAQNKPFDAKTSVFVV DPKESFVKATVQSREGGKVTA KTEAGATVTVKDDQVFPMNPP KYDKIEDMAMMTHLHEPAVLY NLKERYAAWMIYTYSGLFCVT VNPYKWLPVYNAEVVTAYRG KKRQEAPPHIFSISDNAYQFML TDRENQSILITGESGAGKTVNT KRVIQYFATIAVTGEKKKEEPA SGKMQGTLEDQIISANPLLEAF GNAKTVRNDNSSRFGKFIR
21225	51593	A	21352	54	399	
21226	51594	A	21353	441	1585	VPPMGGGPPFVGPVGFGPGDRS HLDSPEAREAMFLRRAAVAPQ RAPILRPAFVPHVLQRADSALSS AAAGPRPMALRPPHQALVGPP LPGPPGPPMMLPPMARAPGPPL GSMAALRPPLEEPAAPRELGLG LGLGLKEKEEAVVAAAAGLEE ASAAVAVGAGGAPAGLAVIGP\ SLPLALAMPLPEPEPLPLPLEVV RGLLPP\LRITELLSLRPRPRPPR\ PEPPPGLMALEVPEPLGEDKKK GKPGEIEHRCIATA/AQGASWE DPPTCWKWDAE*LSRVFCGDL G\NEVND*HLGHAASARFPIPSL KAKVIR*QSAQARPKGYG\FVS FKDP\SDYVRP\MREMNGKYVV LAPPIKLRKSMWKDRNLDVFR KKQKEKKKLGLR

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21227	51595	A	21354	1	1122	MPGGKIGFLIEKGATEQSSTGN DFDELREEGGRRSNYSELQEDI QTKGKEVENFEKNLEECVTTIS NTEKCVKELMELKTKARELRE ECRSFRSQCNQLEERVPAMKDE MNEMKREGKFREKRIKRNEQS LQEIWDYVKRPNLPLIGVPESD RENGTKLENTLRDIIQENFPSLT RRGQPFRIMENTENAPKDNLLE KEQLPRHNNCLELTQEEPAWD LQFDLLDLNDISSALKHHEEKN LISLLPQRGADYLSFRSHFQKNF VCVENCSLQERTVTGTVKVKN VSFEKKVQIRITFDSWKNYTDV DCVYMKNVYGGTDSDTFSFAI GLPPVIPTEQKIEFCISYHANG\Q IF\WDNK*WGRKYKNCVIVQW
21228	51596	A	21355	71	1124	GPPPLCLMSCTRMIQVLDPRPL TSSVMPVDVAMRLCLAHSPPV KSFLGPYDEFQRRHFVNKLKPL KSCLNIKHKAKSQNDWKCSHN QAKKRVV\FADSKGLSLTAIHV FSDLPEQPAWDLQFDLLDLNDI SS\ALKHH\EEKNLILDFP\QPST DYL\SFRSHFQK\NFVCL\ENCSL Q\ERTVTGTV\KVKNVEF*GRKF QIRYHFSDSWEKLTLDVDCVY MENVY/GVGTGSDTFSFAIDLPP VIPTEQKIEFCISYHANGQVFW DNNDGQ\NYWIVHVQWKPDG VQTQMAPQ\DCAFHQTSPKTEL ESTIFGSPRLASGLFPEWQSWG RMENLRLLCDELSNNVTGLDLS YSPMQS
21229	51597	C	21356	204	273	
21230	51598	B	21357	1	1062	
21231	51599	A	21358	1	397	QRPI*PTKPIGQRVSKGHQP\TR H\DFTQF\LAAHETISRLVGFSA GQV\QYLDLIKK\DPSKLFNEER LIDKTKVTYLKWLPESESLFLA SHASGHLYLYNVSHPCASAPPQ YSLLKQGEGFSVYAAKYNDLF

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21232	51600	A	21359	71	1736	FRTSLKDVWHTPLTPFLPPLKSI DLNKPIDKRIYKGTQPTCHDFN QFTAATETISLLFGSFSPRRTWA WCGPAV*AGPCPTAFLGTLRLI DKTKVTYLKWLPESESLFLASH ASGHLYLYNVSHPCASAPPQYS LLKQ\AWGFSFYAAKSKAPRNP LAKWAVGEGPLNEFAFSPDGR HLACVSQDGCLRVFHFDSMLL RGLMKSYFGGLLCVCWSPDGR YVVTGGEDDLVTVWSFTEGRV VARGHGHKSWVNAVAFDSLY TTRAEEAATAAGADGERSGEE EEEEPEAAGTGSAGGAPLSPLP KAGSITYRFGSAGQDTQFCLW DLTEDVLYPHPPLARTRTLPGT PGTTPPAASSSRGGEPGPGPLPR SLSRSNSLPHPAGGGKAGGPGV AAEPGTPFSIGRFATLTLQERRD RGAEKEHKRYHSLGNISRGGSG GSGSGGEKPSGPVPRSRLDPAK VLGTALCPRIHEVPLLEPLVCK KIAQERLTVLLFLEDCIITACQE GLICTWPRPGKAFTDEETEAQT GEGSWPRSPSKSVVEGISSQPG
21233	51601	A	21360	2	467	LMQ/NWDAAMEDLTRLKETID NNSVSSPLQSLQQRTWLIHWSL FVFFNHPKGRDNIIDLFLYQPH MLADKLNMTPEEAERWIVNLI RNARLDAKIDSKLGHVVMGNN AVSPYQQVIEKTKSLSFRSQML AMNIEKKLNQNSRSEAPNWAT QDSGFY
21234	51602	B	21361	1	909	
21235	51603	A	21362	3	3617	YWKERPTQKVIPRATENHGLKS YLQKTKLSIDEAAFLLPDTNLK SELLELLTHWLQVGVPMTPSLG SINLLGWLTELRETHTYICWFIV KETTRDTDEEMCRTEPALACSI SHYCDDGCIQMLNTPETLQCSA KDSKHFIPKECSIPGENRPPSDT GKTVKFLSLNIFNLQLAESTDA EQRANCILRCFLTETTLNYQKIL SVRPGTKLATASHVSGLGLQTP PFGLAQHLIRPHAFLAPKDPLTS FTERNSRSG

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21236	51604	A	21363	75	2141	GPRLGLTTMWHEARKLGRRLR GLLFDSRKRAERRREYYEKIKK DPAQFLQVHGRACKVH\LDSA VALAAESPVNMMPWQGDTNN MIDRFDVRAHL\DHIPDYTPPLA HHHFSQNQESDER\KCNYERYR GLVQNDFAGISEEQCLYQIYIDE LYGGLQRPSEDEKKKLAEKKA SIGYTYEDSTVAEVEKAAEKPE EEESAAEEESNSDEDEVIPDIDV EVDVDELNQEQVADLNKQATT YGMADGDFVRMLRKDKEEAE AIKHAKALEEEKAMYSGRRSR RQRREFREKRLRGRKISPPSYAR RDSPTYDPYKRSPSESSSESRSR SRSPTPGREEKITFITSFGGSDEE AAAAAAAAAASGVTTGKPPAP PQPGGPAPGRNASARRRSSSSSS SSSASRTSSSRSSSRSSSRSRRGG GYYRSGRHARSRSRSWSRSRSR SRRYSRSRSRGRRHSGGGSRDG HRYSRSPARRGGYGPRRRSRSR SHSGDRYRRGGRGLRHHSSSRS RSSWSLSPSRSRSLTRSRSHSPSP SQSRSRSRSRSQSPSPSPAREKL TRPAASPAVGEKLKKTEPA\AG KETGAAKV\PKLTPQEKLKLRM QKPL\NRQFKADKKAAQRKR*S QAEHERQERKDEA\RAMARKIG MKERER\REKEREEWERQYSRQ SRSPLP/RDYSREYSSSRRRSRSR SRSPHYRH
21237	51605	A	21364	1	609	
21238	51606	A	21365	1	1227	
21239	51607	A	21366	1	1626	
21240	51608	A	21367	370	4388	GFIWNRITPTEDGQTRELQNHL GLSAPVPRGRKGKKVKTQTSSF DIQKAEWLRKYNPEQLLQDEG YKKHIKHHCNKVLLRVRMLYY LKQEVIGNECQKVFDGVDASDI DVWVPEPDHSEVPAEWWDFD ADKSLLIGVFKHGYEKYNTIRA DPALCFLERVGKPDEKAVAAE QRANDYMDGDVEDPEYKPAPA IFKDDIEDDVSSPGDLVIADGDG QLMEGDKVYWPTQSALTTRLR RLITAYQRTNKNRQIQQIQ

SEQ ID NO:	SEQ ID NO: of peptide sequence.	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
21241	51609	A	21368	1	530	AEADAIIQMVREGQRARRQQQ AATSESSQSEASVRREESPMDV DQPSPSAQDTQSIASDGTPQG\E KEKEERPPELPLLSEQL\ALDEL WDMLGECLKELEESHDQHAVL ETHRTVLNQILRQSTTHLADGP FAVLVDYIRVLDFDVKRKYFR QELERLDEGLRKEDMAVHVRR DHVF
21242	51610	A	21369	1	217	
21243	51611	A	21370	274	599	PVSKESRVAPLCDFCLPFIQSES SQSEASVRREESPMDVDQPSPS AQDTQSIASDGTPQGEKEKEER PPELP/LLSEQLSLDELWDMLGE CLKELEESHDQHAVLVLQPA
21244	51612	A	21371	2	731	TPTPPTAPTPVTSAPALVAATAI STIVVAASTTVTTPTTATTTVSI SPTTKGSKSPAKVSDGGSSSTD FKMVSSGLTE^QLQLSVEVLTS HSCSEEGLEDAANVLLQLSRGD SGTRDTVLKLLLNGARHLGYT LCKQIGTLLAELREVNLEQQKR AQCETLSPDGLPEEQPQVCKQK GKMQSRF\SGLGSASSPAAVR QLEAEADAIIQMSESSQSEASVR REESPMDVDQPSPSAQDTQSIA
21245	51613	A	21372	208	423	LYVKPTAPPK*AL*SEGLE*MSP QCLWQGLQQGKAQKKLLEVP NKLTQTIN*PANVLILA*GGSSS YRPPHK

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21246	51614	A	21373	1	2002	MPQLPGISLPEGVDPSFLAALPD DIRREVLQNQLGIRPPTRTAPST NSSAPAVVGNPGVTEVSPEFLA ALPPAIQEEVLAQQTAEQQRPE LAQNASSDTLMDPVTLIQTLPS DLRRSVLEDMEDSVLAVMPPDI AAEAQALRREQEARQRQLMHE RLFGHSSTSALSAILRSPAFTSR LSGNRGVQYTRLAVQRGGTFQ MGGSSSH\NRPSGS\NVDTLLRL RGRLLLDHEALSCLLVLLFVDE PKLNTSRLHRVLRNLCYHAQT RHWVIRSLLSILQRSSESELCIET PKLTTSEEKGKKSSKSCGSSSHE NRPLDLLHKMESKSSNQLSW/L SSVSMDAALGFR\TNIFQIQRSG GRKHTEKHASGGSTVHIHPQA APVVCRHVLDTLIQLAKVFPSH FTQQRTKETNCESDRERGNKA CSPCSSQSSSSGICTDFWDLLVK LDNMNVSRKGKNSVKSVPVSA GENKVSEAQANSGSGASSTTTA TSTTSTTTTTAASTTPTPPTAPTP VTSAPALVAATAISTIVVAASTT VTTPTTATTTVSISPTTKGSKSP AKVSDGGSSSTDFKMVSSGLTE NQLQLSVEVLTSHSCSEEGLED AANVLLQLSRRPARMLAMHW PSLYNVETEKTLALPNLIALQTS PFASGVIAKSSTDRLINQCAPV WRWR
21247	51615	A	21374	1	6384	MVSPEPKTGHSIRNWLDELKDL PILHAYSNLPSSPAVDLAIHSSK EGRMDWTEGQVTGPVVRSAAT SGAGSTTSGVVSGSLGSREINYI LRVLGPAACRNPDIFTEVANCC IRIALPAPRGSGTGNGSSRIPRES APEMATAESLVEELSEDAAGG ASPGVELPALGCSELPAAEVSP TASSKNLETICEYAYCMAMLPE TGLDPYPKRGFLDLTQERIWTD IPPSPGNIPTTHPLMVRHADHSS LTLGSGSSTT
21248	51616	A	21375	1	1356	
21249	51617	A	21376	80	608	

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21250	51618	A	21377	298	1374	GRGDWPDILNLTQATASWTPR WCCLRKPVEAPSGGATEERTLS LTSLGLSMPADPCEGGARSCLV TESARGGLQNGQSVDVEETLPS EPENGALLRSERYQGPRRRACS ETLAESRTAVLQQRRAAQLPG GPAAAGEQRASPSKARLKEFLQ QCDREDLVELALPQLAQVVTV YEFLLMKVAESLGITEFLRKKEI HPDNLGPKHLSRDMDGEQLEG ASS\EKREREAAEEGLASVKRP RREALSND\TT\ESLAANSRGRE KPRPLHALAAGTIVSQEEDIVT VTD/GRGACLRMGPLEGVPLEA VESVVTVEPEPSQ*NGVRY*NS SDFIQRRSMASNVYFSNVNIAQ MNLLFIKNNVFL
21251	51619	C	21378	354	530	
21252	51620	A	21379	1	1272	MVLSEKASGSTLRGCTEERTLS LTSLGLSMPADPCEGGARSCLV TESARGGLQFLQQCDREDLVEL ALPQLAQVVTVYEFLLMKVAE SLGITEFLRKKEIHPDNLGPKHL SRDMDGEQLEGASSEKREREA AEEGLASVKRPRREALSNDTTE SLAANSRGREKPRPLHALAAES HTTTVSGGNGSVFQAGPQLQA LANLEARRGSIGAALSSRDVSG LPVYAQSGEPRRLTQAQVAAFP GENALEHSSAQDTWDSLRSPGF CSPLSSGGGAESLPPGGPGHAE AGHLGKVCDFHLNHQQPSPTS VLPTEVAAPPLEKILSVDSVAV DCAYRTVPKPGPQPGPHGSLLT EGCLRSLSGDLNRFPCGMEVHS GQRELESVVCLSAETMAF*NFP\ MGA\MSYCL\RD\RSRFLFRLPM GLSCPLQVQ
21253	51621	A	21380	90	204	
21254	51622	B	21381	13	423	

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21255	51623	A	21382	1513	2405	RRAQYRRWWRRWRRRHREPE KEKRRHSRSHSRRRRTLIF*TQS RSRSRE*LHCQSRSR**FKSPRQ RRSHSRERGRSTARHYRST\KER QQRRSRSGTRSPKKSRCPKRKL SLSPSPGKHKKKKKDKERNRY ERERSTSKKKSKDREKDQERKS ESDTDVKVTRVYDEEEQGYDT SQEIEMHADNPAAIQTVVLQRD DLQNGLLSTCRELSRATAELER AWREYDKLEYDVTVTRNQMQ EQLDHLGEVQCWCYRTEKYV MERGPEQDPKRAFLDFVQERIQ GESAVQSESKFIKTVKK
21256	51624	A	21384	1	180	
21257	51625	A	21385	3	115	
21258	51626	A	21386	3	312	LPTALLRSTMALLHSGRVLPGI AAAFHPGL/AA/AASARASSWW THVEMGPPDPILGVTEAFKRDT NSKKMNLGVGAYRDDNGKPY VLPSVRKFVTVQTISGTGAL
21259	51627	A	21387	3	395	STMALLHSGRVLPGIAAAFHPC\ LAAAASARASSWWTHVEMGPP DPILGVTEAFKRDTNSKKMNLG VGAYRDDNGKPYVLPSVRKAE AQIAAKNLDLLPLLNVVCSLSS HTVSPAAQGGTRKEDILGFACC
21260	51628	A	21388	1	303	
21261	51629	A	21389	2	425	RPE*WKEIATVVKKRNLFALFD MAYQGFASGDGDKDAWALHH FIEQGINVCLCQSYAKNMGLYG EHVGAFTVVCKDADEAKRVES QLKILISPMYSNSPLNGAQIASTI PNTPVGLKVWVMGGLHDHPQ VMSDEKETTLRA

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21262	51630	A	21390	3	1508	HEAGAGSLCVCPARPLLRPAAA HCPSYRSTMAHACTSGRVLPGI AAA\FHPGLAAAASARASSWW THVEMGPPDPILGVTEAFKRDT NSKKMNLGVGAYRDDNGKAL PCCPSVRKAEGPRLPQKIWDKE YL\PIGG\LAEFCKASAELALGE NNRSLERVGRFVTVQTHFWEL GALRI\GASFL\QRFFKFSRDVFL PKPTWGETTHPSFRDAG\MQL\ QGYR\YYDPKTCGFDFTGAVED ISKIPEQSVLL\LHACG/HNNPTG VDPRPEQWKEIATVVKKRNLF AFFDMAYQGFASGDGDKDAW AVRHFIEQGINVCLCQSYAKNM GLYGERVGAFTMVCKDA\DES KRVESQLKILIRPMYSNPPLNG ARIAAAILNTPDLRKQWLQEVK GMADRI\IGHAGLQLVSNLQGR EG\STH\NWATHSPTKLGMFCF HRG*KLEQVERLIKEFSIYMTK DGRISVAGVTSSNVGYLAHAIH QVTKYVSLVRGNGDNLSVLSL
21263	51631	A	21391	1	184	
21264	51632	A	21392	70	253	
21265	51633	A	21393	1	351	VMEFYCQSCETAMCRECTEGE HAEHPTVPLKDVVEQHKASLQ VQLDAVNKRWGTLPKPPTGCL YLRPGLMASC\QLTNQKASI/VD DIHSTFDELQKTLNVRKSVLLM ELEVNYGLKHK

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21266	51634	A	21394	208	2546	WLHCMQQQRAGSKTAGPP\CQ WSRMAS\EGTNIP\SLVVGQI\DK QFLICSICLERYKNPKVLPCLHT FCERCLQNYIP\AHSLTLSCPVC RQTSILPEKGVAALQNNFFITNL MDVLQ\RTPGSNAEESSILETVT AVAAGKP\LSCPNHDGNVMEF YCQSCETAMCRECTEGEHAEH PTVPLKDVVEQHKASLQVQLD AVNKRWGTLPKPPTGCLYLRP GLMASC\QLTNQKASIVDDIHST FDELQKTLNVRKSVLLMELEV NYGLKHKVLQSQLDT\LLQGQE SIKSCSNFTAQTLNHGTETEVLL VKKQMSEKLNELADQDFPLHP RENDQLDFIVETEGLKKSIHNL GTILTTNAVASETVATGEGLRQ TIIGQPMSVTITTKDKDGELCKT GNAYLTAELSTPDGSVADGEIL DNKNGTYEFLYTVQKEGDFTL SLSLYDQHIRGSPFKLKVIRSAD VSPPTEGVKRRVKSPGSGHVKQ KAVKRPASMYSTGKRKENPIED DLIFRVGTKGRNKGEFTNLQGV AASTNGKILIADSNNQCVQIFSN DGQFKSRFGIRGRSPGQLQRPT GVAVHPSGDIIIADYDNKWVSI FSSDGKFKTKIGSGKLMGPKGV SVDRNGHIIVVDNKACCVFIFQ PNGKIVTRFGSRGNGDRQFAGP HFAAVNSNNEIIITDFHNHSVKV FNQEGEFMLKFGSNGEGNGQF
21267	51635	A	21395	1	591	
21268	51636	A	21396	3	608	LEGDQRWINTVSQALHLLSTLY GPFPNCYGIGRCAKMAYELWR NLEEEEDGETKGRRPEIGHIFLL DRGKLCPAFLSSFSPRRHGNME GVVAKLKS*S*GCESQL*GAWV LGPMESIKAALGHAV*KAGSGR TFMVRDLCF\DVDFVTALCSQV VYEGLVDDTFRIKCGKCYGPLH LGKMDGSSALAPATWGRVCGR DPHPE
21269	51637	A	21397	268	402	
21270	51638	A	21398	139	452	

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21271	51639	A	21399	1	2497	MGPVAAPLGLSLPATDGAHSV RGNSVLVPSGLIPKDYRSLKTQ YLQSYGPEHLLTFSNLRRAGLL TEQAPGDTLTAVESKVSKLVTD KAAGKITDAFSSLAKRSNFRAIS KKLNLIPRVDGEYDLKVPRDM AYVFGGAYVPLSCRIIEQVLER RSWQGLDEVVRLLNCSDFAFT DMTKEDKASSESLRLILVVFLG GCTFSEISALRFLGREKGYRFIF LTTAVTNSARLMEAMSELPGK KDLFIETDLMSPLDRIANVSLLK QHEVDKLYKVENKPALSSNEQ LCFLVRPRIKNMRYIASLVNAD KLAGRTRKYKVIFSPQKFYACE MVLEEEGIYGDVSCDEWAFSLL PLDVDLLSMELPEFFRDYFLEG DQRWINTVAQALHLLSTLYGPL SQTCYGIGRCAK\MAYEFVEGT WEEEEDGRNPRARREGFG\HIF LL\DR\DVDFVDSTLLPKLVYEG LVDDTFRIKCGSVDFGPEVTSS DKSLKVLLNAEDKVFNEIRNEH FSNVFGFLSQKARNLQAQYDR RRGMDIKQMKNFVSQELKGLK QEHY\LLSLHIG\ACESIMKKKT KQDFQE\LIKT\EHALLEGFNIRE STSYIEEHIDRQVS\PIESLRLMC LLSITENGLIPKDYRSLKTQYLQ SYGPEHLLTFSNLRRAG\LLTEQ APGDNLTAVESKVSKL\VTDKA AGKITDALS\SLAKRSQFRAISK
21272	51640	A	21400	1	216	
21273	51641	A	21401	2	270	
21274	51642	A	21402	1	600	SGRALHASWAAGGVGAYSGRL RSDALEGESFA\LSF\SSASDAEF DAVVGYLEDIIMDDEFQLLQRN FMDKYYL\EFEDTEENKLIYTP\I FNEYISLVEKYIEEQ\LLQR\IPEF NMAAFHHNITPSVPVCRHHKD EVAW*QYSAMLAPPFTRFSWA F*RNVFGTYRGRKKEGRGL\DL SSGLV\VTSLCKSSSL\PASQNNL RH
21275	51643	A	21403	1	297	

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21276	51644	A	21404	1	1419	MGAPLLSPGWGAGAAGRRWW MLLAPLLPALLLVRPAGALVEG LYCGTRDCYEVLGVSRSAGKA EIARAYRQLARRYHPDRYRPQP GDEGPGRTPQSAEEAFLLVATA YETLKIVFPELKIVKELTTLLMP SRAVWIIWSHKMSGGGAGPEL DIGYVPVLLHMPKRIGSGMDTS RSTTVIPVEIRNKELIALLVKAQ DRQEEETNYKLRPFNGLSYEVG YLVILQDEETRKDYDYMLDHP EEYYSHYYHYYSRRLAPKVDV RVVILVSVCAISVFQFFSWWNS YNKAISYLATVPKYRIQATEIA KQQGLLKKAKAKSKNNKVQR RNS*\EEENIIKNIIKSKIDIKGGY QKPQICDLLLFQIILAPFHLCSYI VWHCRWIYNFNIKGKEYGEEE RLYIIRKSMKMSKSQFDSLEDH QKETFLKRELWIKENYEVYKQ EQEEELKKKLANDPRWKRYRR WMKNEGPGRLTFVDD
21277	51645	A	21405	1	1266	
21278	51646	A	21406	1	739	
21279	51647	A	21407	1	428	

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21280	51648	A	21408	99	2338	MPEEVHHGEEEVETFAFQAEIA QLMSLIINTFYSNKEIFLRELISN AS\DALDKIRYESLTDPSKLDSG KELKIDIIPNPQEPYPGLWVDTG IG\MTKADLINNLGTIAKSGTKA FMEALQAGADISMIGQFGDGFY S\ANLVAK\KVVVITKHP\DDEQ YAWESSAGGSFTVRADHGEPIA \RGT\QVILHLKEDQTEYLEERR V\QEVVKKH\SQFIGYPITLYLE KEREKEISDDEAEEEKGEKEEE DKDDEEKPKIEDVGSDEEDDSG KDKKKKTKKIKEKYIDQEELNK TKPIWTRNPDDIT\QEEYGEFYK SLTNDWEDHLAVKHFSVEGQL EFRALLFIPRRAPFDLFENKKKK NNIKLYVRRVFIMDSCDELVPE\ YLNFIPGVVDSEDLPLNIFRKML QQNK/ILWKVIRKNIVKKCLELF SELAEDKENYKKFYEAFSKNLK LGIHEDSTN\RRRLSELLRYHTS QSG\DEMTSLSEYVS\RMKETQ MSIYYITGESK\EQVANSAFVER VRKRGFEVVYMT\EPI\DEYCVQ QLKEFDGKKLV\SVTKEGLELP EDEEEKKKMEESKAKFENLCK LMKEILDKKVEK\VTIS\NRL\VS SPC\CIGHKHLGAGQALIERDHE KPRALRDHPPQGGIMMGKKAP *ESPPDHPHFVETRAGRKADAR QVMIRAVKD/LWWVLLV*NPP LLSSGF\SLEDPQT/HTPNRIYRI
21281	51649	A	21409	1	426	
21282	51650	A	21410	1	1305	
21283	51651	A	21411	446	3180	VAVRLGSASQFPSGARPQLPRP PSWSSSIHSPISTTGLSESTDSDS KSGLRGFSAYNPSSRIPKSTTSS NSSDGAVTASNQDTGIPWVLV TGPTPPVNSPVESLQGSAFSSGF STPRGLVKGPTLPPDSNLTSVSD YTWIFVRGPPIPNDLSQVSIQAP PTPSNTPECQYKGLPHPQCPASP GVWYQDHLYPITFPQCRHKHL LHPITSPQCQGRRLPPPQCLTLR GVQYKNLLHPVILSSCRHKDIL NLITLAE

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21284	51652	A	21412	24	667	MLPWLNCITTGVPWTPTSKRW LRNSKVCDCCDKTPSNAFSLLS VPPTTTSPASLAWWSGCARLLD LGSSSLMMSPTMASPACRPWL GQRWRLISGSWAWAIVPVT*VP VPEPSWKNRAG*PGCSSYESPH MRRPTRPSASCLEWAPRASLA MHLMATSFCVLLSSARITSEKA PLSGEGIHKVKNWNPSFPPASPP FPMGSVTTAGPRTWMTLP
21285	51653	A	21413	1	304	RAQVLPARCYPGSTVSPLGFRG LPLPRGGSEIPRCATAATRPHR MPFLFYLFLQQQHRPHHWHGG AAVPGFWTSAHPA\CDVTYHGF PSLQALAGPPWQCI
21286	51654	A	21414	1	7629	
21287	51655	A	21415	180	423	
21288	51656	A	21416	17	753	QAHTRRAGGRAQVLPARCYPG STVSPLGFRGLPLPRGGSEIPRC ATAATRPHRMPFLFYLFLQQQH RPHHWHGGAAVPGFWTSAHPA \CDVTYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGGL/RLAAAATRVLI*GGP QGPLHPAWSGHQGG*LHLPDG PRQAPGCARGCPYVAHCPT*LQ LAPYHVPGEGTEPPDQQGTGKL FPEPVGTLCWLGPSALSGHHHF YDLSRTP
21289	51657	A	21417	17	1087	QAHTRRAGGRAQVLPARCYPG STVSPLGFRGLPLPRGGSEIPRC ATAATRPHRMPFLFYLFLQQQH RPHHWHGGAAVPGFWTSAHPA \CDVTYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGGL/RLAAAATRVLI*GGP QGPLHPAWSGHQGG*LHLPDG PRQAPGCARGCPYVAHCPT*LQ LAPYHVPGEGTEPPDQQGTGKL FPEPVGTLCWLGPSGWIRCLLK NYRLLPLDLEGLLGNAFDGHQ LLRPLIFCQDHLREGPPIGRGDS QGEELEPQLPSSLSSIPYGFCDH CWTKDVDDPPLVTHPSPGSRD GHMTQAWPVKVVSPLATVIGH VMQASLLAL

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21290	51658	A	21418	3	1584	TQKNTAVRAHRLWGREKISRK EGAGPTPQESRRIGARSGALMT RKGRGMQEVEELSETGKVVKQ HRVGEALRVVVLVWAGSLG/D RRGLVLGRRGYYGAVPAVEMP ARALLPRRMGHRTLASTPALW ASIPCPRSELRLDLVLPSGQSFR WREQSPAHWSGVLADQVWTL TQTEEQLHCTVYRGDKSQASRP TPDELEAVRKYFQLDVTLAQL YHHWGSVDSHFQEVAQKFQG VRLLRQDPIECLFSFICSSNNNIA RITGMVERLCQAFGPRLIQLDD VTYHGFPSLQALAGPEVEAHLR KLGLGYRARYVSASARAILEEQ GGLAWLQQLRESSYEEAHKAL CILPGVGTKVADCICLMALDKP QAVPVDVHMWHIAQRDYSWH PTTSQAKGPSPQTNKELGNFFR SLWGPYAGWAQAGLLGNAFD GHQLLRPLIFCQDHLREGPPIGR GDSQGEELEPQLPSSLSSIPYGF CDHCWTKDVDDPPLVTHPSPG SRDGHMTQAWPVKVVSPLATV IGHVMQASLLAL

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21291	51659	A	21419	837	2785	WTRMLFAVSCNDGECQNSNVI LFCDMCNLAVHQECYGVPYIPE GQWLCRRCLQSPSRAVDCALC PNKGGAFKQTDDGRWAHVVC ALWIPEVCFANTVFLEPIDSIEHI PPARWKLTCYICKQRGSGACIQ CHKANCYTAFHVTCAQQAGLY MKMEPVRETGANGTSFSVRKT AYCDIHTPPGSARRLPALSHSE GEEDEDEEEDEGKGWSSEKVK KAKAKSRIKMKKARKILAEKR AAAPVVSVPCIPPHRLSKITNRL TIQRKSQFMQRLHSYWTLKRQ SRNGVPLLRRLQTHLQSQRNCD QVGRDSEDKNWALKEQLKSW QRLRHDLERARLLVELIRKREK LKRETIKVQQIAMEMQLTPFLIL LRKTLEQLQEKDTGNIFSEPVPL SEVPDYLDHIKKPMDFFTMKQ NLEAYRYLNFDDFEEDFNLIVS NCLKYNAKDTIFYRAAVRLRE QGGAVVRQARRQAEKMGIDFE TGMHIPHSLAGDEATHHTEDA AEEERLVLLENQKHLPVEEQLK LLLERLDEVNASKQSVGRSRRA KMIKKEMTALRRKLAHQRETG RDGPERHGPSSRGSLTPHPAAC DKDGQTDSAAEESSSQETSKGL GPNMSSTPAHEVG\GEPQFCSP KRTRRQ/HGPPKRPGRPPKNRES QMTPSHGGSPVGPP/RAPHHEFP ASAQAG*EPQFCSPKRTRRQLD
21292	51660	A	21420	1	2625	MENKITGYTTVDISQWHRKEHF EAFQSVAQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARL MNAHPEFRMAMKDGELVIWD SVHPCYTVFHEQTETFSSLWSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGFIENMFFVSANPWV SFTSFDLNVANMDNFFAPVFTM GKYYTQGDKVLMPLAIQRDSE DKNWALKEQLKSWQRLRHDL ERARLLVELIRKREKLKRETIKV QQIAMEMQLTPFLILLRK

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21293	51661	A	21421	164	1401	PPKGRGMQEVEELSETGKVVK QHRVGEALRVVVLVWAGSLG/ DRRGLVLGRRGYYGAVPAVE MPARALLPRRMGHRTLASTPA LWASIPCPRSELRLDLVLPSGQS FRWWREQSPAHWSGVLADQV WTLTQTEEQLHCTVYRGDKSQ ASRPTPDELEAVRKYFQLDVTL AQLYHHWGSVDSHFQEVAQKF QGVRLLRQDPIECLFSFICSSNN NIARITGMVERLCQAFGPRLIQL DDVTYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGGLAWLQQLRESSYEEAH KALCILPGVGTKVADCICLMAL DKPQAVPVDVHMWHIAQRDY SWHPTTSQAKGPSPQTNKELGN FFRSLWEPYAGWAQATPPSLQ VLFSADLRQSRHAQEPPAKRRK
21294	51662	A	21422	751	2107	SSEHPRELHRIPISWAMSELKDC PLQFHD\FKSVDHLKVCPRYTA VLARS\EDDGIGIEELDTLQLEL ETLLSSASRR\LRVLEAETQILT D\WQDK\KGDRRFLKLG\RDH\E FGAPPKHGKPKK\QKLE\GKAG HGPGP\CPGRPKSKNLQPK\IQE YEFTDDPIDVPRIPKNDAPNRF WASVEPYCADITSEEVRTLEEL LKPPEDEAEHYKIPPLGKHYSQ RWAQEDLLEEQKDGARAAAV ADKKKGLMGPLTELDTKDVDA LLKKSEAQHEQPEDGCPFGALT QRLLQALVEENIISPMEDSPIPD MSGKESGADGASTSPRNQNKP FSVPHTKSLESRIKEELIA\QALL *AGDLLAKDSEDEVLAELRKR QG\EL\KALSAHNRTKKA\DLLR LAKEEVSRQE\LRQR\VRRAERE GMDAFRKIHGLPGRRKRNSPPK K\EKDQAWKNS*KEREEHP
21295	51663	A	21423	107	331	

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21296	51664	A	21424	387	1071	NNPEWRTLIYVDKENGEPGTR VVAKDGLKLG\SGPSIKALDG\R SQVS\TPRFGKTFDAPTQPYLKL PRKALG\TVNR\TTEKSVKDPGD PSNKKQPKLFRPKKDGPEEGLL KAKKPLFPGLQD*CPIPEIRKIPF PFNPS*TLRSF*PCPEEHPDCGTF PL*VGV\PLMIPLTREREL*KSW FQLGPPFHLWKDGPLPPWGIPIC LQFSFQGISVRTWGV\DLPPVCC DIDI
21297	51665	A	21425	480	1270	RSVKKVGAQRPGSGGGWGGN EGWVPQATAPGWAYTHVLFLY LFVTTPISAALRADGFGDNPFY HCLVAEILPAPGKLLGKSTWPL EVHLSSRPQRSPHRLPEALLPFS LSQG/HCVVGYGIYYFIYSTWK GRTIYLEDIYVMPEY/RGYWAE AEAGVGAKHPTDPTVIPCPQSP AGVIF*SPSAQTIAIFCLFLSTTG QGIGSKIIKKVAEVALDKGCSQ FRLAVLDWNQRAMDLYKALG AQDLTEAEGWHFFCFQGEATR KLAGK
21298	51666	A	21426	182	797	LPFARPWDFGPRQRGSGWLPC GSREAKEGDCGDIL\RLIRVKTA GPELAEFEKLFGSGERSVEEAL ESRLAFGDNPFYHLFW*AEILP APGESYWG/HCVVGYGIYYFIY STWKGRTIYLEDIYVIAGNIGV QGIGSQK*SKKV\AEVALGIRGC SPNFRLARPLD\WNPEGPWDLY KAPRSPKI*RKLEGWHFFCFQG EATRKLAGK
21299	51667	A	21427	224	490	QAGFISARNITWR*ANRRSTWR SYRRKSGRTANCPPISPPACSRC SAPIFIPKNGWWRAMVAPLKW PSTGAFNRLFVPLLTWWRSPDR
21300	51668	A	21428	301	773	HGPGTQQRPRSIWRMPQ*ARPG GRSLAVGGGPRPRAAGGFP*VA SRARRCQR\AHGCHCAFSPLSP ALLSQDAGLCQSRPLLLGQRRC LSQEVWSGLGNVHFCQPPEDA ATTPSCPEALTAQGQQASVCDR VSHRFSTWSMVRCSDRTEGQR LQTLGD
21301	51669	B	21429	1	1380	

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21302	51670	A	21430	1	1660	AGVLASHPNSTDVHIINLSLTFH GQELLSDTKLELNSGRRYGLIG LNGIGKSMLLSAIGKREVPIPEH IDIYHLTREMPPSDKTPLHCVM EVDTERAMLEKEAERLAHEDA ECEKLMELYERLEELDADKAE MRASRILHGLGFTPAMQRKKL KDFSGGWRMRVALARALFIRPF MLLLDEPTNHLDLDACVWLEE ELKTFKRILVLVSHSQDFLNGV CTNIIHMHNKKLKYYTGNYDQ YVKTRLELEENQMKRFHWEQD QIAHMKNYIARFGHGSAKLAR QAQSKEKTLQKMMASGLTERV VSDKTLSFYFPPCGKIPPPVIMV QNVSFKYTKDGPCIYNNLEFGI DLDTRVALVGPNGAGKSTLLK LLTGELLPTDGMIRKHSHVKIG RYHQHLQEQLDLDLSPLEYMM KCYPEIKEKEEMRKI\IGRYGLT G\KQQVSPIRNLSDGQKCRVCL AWLAWQNPHMLFLDEPTNHL DIETIDALADAINEFEGGMMLV SHDFRLIQQVAQEIWVCEKQTI TKWPG\DIL\AYKEHLKSKLVD\

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21303	51671	A	21431	78	2022	NNSNLPLWVIIMPSDLAKKKAA KKKEAAKARQRPRKGHEENGD VVTEPQVAEKNEANGRE/TTRE VDLLTKELEDFEMKKAAARAV TGVLASHPNSTDVHIINLSLTFH GQELLSDTKLELNSGRRY\GLIG LNGIGIGKSMLLFAIGKREVPIP EHIDIYHLTREMPPSDKTPLHCV MEVDTERAMLENEAERLAHED AECEKLMELYERLEELDAD*AE MRASRI\LHGLGFTPAMQRKKL KDFSGGWRMRVALARALFIRPF MLLLDEPTNHLDLDACVWLEE ELKTFKRILVLVSHSQDFLNGV CTNIIHMHNKKLKYYTGNYDQ YVKTRLELEENQMKRFHWEQD QIAHMKNYIARFGHGSAKLAR QAQSKEKTLQKMMASGLTERV VSDKTLSFYFPPCGKIPPPVIMV QNVSFKYTKDGPCIYNNLEFGI DLDTRVALVGPNGAGKSTLLK LLTGELLPTDGMIRKHSHVKIG RYHQHLQEQLDLDLSPLEYMM KCYPEIKEKEEMRKIIGRYGLT GKQQVSPIRNLSDGQKCRVCLA WLAWQNPHMLFLDEPTNHLDI ETIDALADAINEFEGGMMLVSH DFRLIQQVAQEIWVCEKQTITK WPGDILAYKEHLKSKLVDEEPQ LTKRTHNVCTLTLASLPRP
21304	51672	A	21432	313	599	
21305	51673	A	21433	737	1006	DNPVVFVFGSVYMLDYVY*FS YVEPPLHPWDEAHLIMVDKLF DVLLDSVCQYFIEDFCINVNQG YWSKILFFCCISARLWYQDDAG
21306	51674	A	21434	1108	1260	GVNF\NLSCFLLWAFSAIHFPLH TALNVSQRFWYVVSLFSLVSK NIFISAF
21307	51675	A	21435	804	917	
21308	51676	A	21436	158	298	
21309	51677	A	21437	1	1068	
21310	51678	A	21438	1	1188	
21311	51679	A	21439	122	352	
21312	51680	A	21440	647	662	ICGVISEGSVLFH*SISLFWYQY HAVLVT/DSLVV*FEVT*HDASS FVLLA*DRRPEGSSPKSP
21313	51681	B	21441	53	692	
21314	51682	B	21442	1	925	
21315	51683	A	21443	606	900	

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21316	51684	A	21444	33	852	CWKFWARAN*AGGITLPDFKL YYKATVTKTAWKFHFTMFGV DLKETCTAPSLWKDLALNTVE LVCKLCVRQVEGARQIFQLNCT VSE
21317	51685	A	21445	3	795	
21318	51686	A	21446	475	1023	CWFSAGDGGLPGPDYGQDFAA HPAGAGALYKCRDLINDNILRT VSCQSHDDGDIRGMAFARQ*Q RPVQIDHNMARRG**AATFQPI NKTFSGIHWPHGMRTGGTNPN FENIECTNHIHTLGLPFSEVERN DCDGFNFQLHIFRQTRDLHTAP GRIGRLMLIEELLIDFVDGGKII QIGDKHGH
21319	51687	A	21447	1637	2020	PSSEEFTGGPARGFPERARAQL TGRTPGQRTQLDNDLLTKSTP WRGVMGPTLLPGLLAGPFQPL GHTGPFYPQGFRWQKTHWVRL AQAHWQF*LGQFRGPKTADGG GSKGPGLSASHGAKHHVITYV
21320	51688	A	21448	1051	1185	
21321	51689	A	21449	1290	2025	
21322	51690	B	21450	1	1410	
21323	51691	A	21451	3269	3678	SLSIRLATAPCWLRYFASSRRFQ PTRSAGSVTDSSVTASASSPG*R *NASP\CRERSHRSSRGQARRSL HLWDRSDR*TLPCDHGRCCHA NDQQVGFAGNYSTAGQT*RWT GFTAGHAGRDINKSADKLPAT AGKR
21324	51692	B	21452	2655	2825	
21325	51693	A	21453	1	896	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNHSTTWKLN NLLLSDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITTDPTE\YK LPSENTTNTSTQIN*KI*KKWIN SSTHTLSQD

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21326	51694	A	21454	23	559	TPGLRQSSLSPSAFASQNAGVS GIGGFLVSLTSRMKPWTLAMFR CVWSFFLLVGSWSCWLQE*SC RPSQ*VSQFL/NSSASGVVCCSC LELFVPPGGFVVSLASRVKLQT FTVSVTAHKGGVDPKSEQQQD LVQKAKEHSFCSVEADLSGLPL LAGAACFYSLMEPHPHPADWSI LQRAD
21327	51695	A	21455	26	323	
21328	51696	A	21456	221	734	
21329	51697	A	21457	293	2103	PCHSALSSPLPHRDCIALCFLNS GTSFVAGFAIFSILG\FMF\QEQG VPISEVAESGPGLAFIAYPRAVV MLPFSPLWACCFFFMVVLLGL DSQFVCVESLVTALVDMYPHV FRKKNRREVLILGVSVISFLVGL IMLTEGGMYVFQLFDYYAASG MCLLFVAIFESLCVAWVYGAK RFYDNIEDMIGYRPWPLIKYCW LFLTPAVCTATFLFSLIKYTPLT YNKKYTYPWWGDALGWLLAL SSMVCIPAWSLYRLGTLKGPFR EVIIPVSIRMTKVAGTAGLSGN VGPRCDLSRIEELPDGGTRCGM DSRVSGTTSNGETKPVYPVME KKEEDGTLERGHWNNKMEFVL SVAGEIIGLGNVWRFPYLCYKN GGVVGFYNSIKNIPILQRVILFV RIHNMLNKGQGVLAKCDAAK KIEEKEADAGSASVPGDVMRT KKLSFEGAWHPCLLVGLKLSD ALELRGGFISARIAGPRAAESDS VGLERELRVCIANKLPGEADAA GPGTTFWKHCSMPITDGADAV EGRNTQEAFFRQLNPEAAFLHF MEMVDTNALHVHGIHTRKNHP GQKEAAHSQHGTFPIRWTLNLL KRTFQKGNRAEPNSPAM
21330	51698	A	21458	1	419	MKLRTLAVSATALKVARLEFV PFDVRMCSEFLSSGVKLQTFAV SVTALNALRLELFVPPGGLMVS LASGVKLQIFTVSVTAHKSSVD PKTLG/CVDGTGRRGAGGGAH RGGLGRTGAHGGGGRLRHGGL QVSSPAPRKGS

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21331	51699	A	21459	24	1639	GGMDSRVSGTTSNGETKPVYP VMEKKEEDGTLERGHWNNKM EFVLSVAGEIIGLGNVWRFPYL CYKNGGGAFFIPYLVFLFTCGIP VFLLETALGQYTSQGGVTAWR KICPIFEGIGYASQMIVILLNVY YIIVLAWALFYLFSSFTIDLPWG GCYHEWNTGNWVDVVE/HGG* GEWCGNGSNTPHVCR/VTGWT W*SRWLKGMVWEWIQHTPCV QGTGWTW*STWLKG/PGNRVD VVEHVAEGNGVGMDPTHPTCA GNRVDVVEQVAEGNEHCMEF QKTNGSLNGTSENATSPVIEFW DSPPGPQFVCVECLVTASIDMF PRQLRKSGRRELLILTIAVMCY LIGLFLVTEGGMYIFQLFDYYA SSGICLLFLSLFEVVCISWVYGA DRFYDNIEDMIGYRPWPLVKIS WLFLTPGLCLATFLFSLSKYTPL KYNNVYVYPPWGY\SIGWFLA LSSMVCVPLFVVITLLKTRGPFR KVGGVGESDLLKEGTERGWT WGRTHNWGQGADTNSECGAA LQSHRILTRRTLKTSPVAFQKCS
21332	51700	A	21460	1358	4787	RRCYCGIWSRYLLKRLWKWIS GEGWAEKDSARRRGICTFWLE FE/VTCLSWNSLF/YAHINVDISG MKVPWLYVGMCFSSFCWHIED HWSYSINYLHWGEPKTWYGVP SHAAEQLEEVMRELAPELFESQ PDLLHQLVTIMNPNVLMEHGV PVYRTNQCAGEFVVTFPRAYHS GFNQGYNFAEAVNFCTADWLP IGRQCVNHYRRLRRHCVFSHEE LIFKMAADPECLDVGLAAMVC KELTLMTEEETRLRESVV
21333	51701	A	21461	1	5773	MEEKPLKVKGKDSSEKKRKRK LEKVEQLFGEGKQKSKELKKM DKPRKKKLKLGADKSKELNKL AKKLAKEEERKKKKEKAAAAK VELVKESTEKKREKKVLDIPSK YDWSGAEESDDENAVCAAQN CQRPCKDKVDWVQCDGGCDE WFHQVCVGVSPEMAENEDYICI NCAKKQGPVSPGSHKAVITVV VKAVSYLKFEEESTSELMWLL AAFSSFWVVGIKALDFVWPLA REEKEIGDNKDLERNKIGVNM

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21334	51702	A	21462	85	1333	STSRALSGAQRFGRLIDHGARV PALLLLLLPL\VHVSATTPEPR\E LDDEDFRCVCNFSEPQPDWSEA FQCVSA\VEVEIHAG\GLNL\EPF LK\RVDADADPRQYA\DTVKGF PR/VRRASQVGAAQVPA\QLLV GALR\VLA\YSRFKELTLEDLKI TG\TMPPLPLEATGLALS\SLRLR NVSW\ATGRSWL\AEL\QQWLK PG\LKVLSIAQAHSPAFSCEQVR CFPGPSPA*DLSDNPGTGANAE LMAALCPHKFPA\IQNL\ALRNT GNGRRPQGVCAALAAAGVQPH SLDVSHNSLRANRNPS\AP\RCM \WSNA\LNSPQICRFAGAGTGVP KGPAPAKL\RVLRSSACNRL\NR A\PQPWTSLPE\VDNLGQLDGNP FPGSPGTGPSPTEGSMN\SGVVP SLCNVRTCRVGVSGTLVLLQG ARGFA
21335	51703	A	21463	1640	5804	TITGSSPLAGGHHSTCRGRMDM VENADSLQAQERKDILMKYDK GHRAGLPEDKGPEPVGINSSIDR FGILHETELPPVTAREAKKIRRE MTRTSKWMEMLGEWETYKHS SKLIDRVYKGIPMNIRGPVWSV LLNIQEIKLKNPGRYQIMKERG KRSSEHIHHIDLDVRTTLRNHV FFRDRYGAKQRELFYILLAYSE YNPEVGYCRDLSHITALFLLYL PEEDAFWALVQLLASERHSLPG FHSPNGGTVQGLQD
21336	51704	A	21464	1	960	
21337	51705	A	21465	1	1317	
21338	51706	A	21466	1	3393	
21339	51707	A	21467	2745	6141	QGSKGTCHPQAQQPWDEGVW QEAPSQSEPWGQSQEPPTMPQR LPHARQHTPLPLGSADYRRVVS VRPQGPHRDPKDSRDAAKREQ GSLAPRPVPASRGGKTLCKGYR QAPPGPPAQFQRPICSASPPWAS RFSTPCPGGAVREDTYPVGTQG VPSLALAQGGPQGSWRFLEWK SMPRLPTDLDIGGPWFPHYDFE RSCWVRAISQEDQLATCWQAE HCGEVHNKDMSWPEEMSFTAN SSKIDRQKVPTEKGATGL
21340	51708	A	21468	65	320	
21341	51709	A	21469	3	505	

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21342	51710	A	21470	2	1756	CRCHSELSGSSL*/CCTRGIGGAI GAVGFRSQAASTLAGQPDGNG VCVHAGNSRIFVPLPVGLEVKG FSHSAFTFGIESHISQSNINGTLV PPSALISILQKGLQYVEAEISINK DGTVFDSRPIESLSLIVAVIPDV VQMRQQAFGEKLTQQQASAA ATEASAMAKAATMTPAAISQQ NPPKNREATVNGEENGAHEINN HSKPMEIDGDVEIPPNKATVLR GHESEVFICAWNPVSDLLASGS GDSTARIWNLNENSNGGSTQL VLRHCIREGGHDVPSNKDVTSL DWNSDGTLLAMGSYDGFARIW TENAPALDVDWQNNMTFASCS TDMCIHVCRLGCDHPVKTFQG HTFCTCIESICFWGGLRKLTTM TEGKRLRPKTFCSDGGALLPPA GRRPHLLTGPDIFFKRLSALFQN EVNAIKWDPSGMLLASCSDDM TLKIWSMKQDACVHDLQAHSK EIYTIKWSPTGPATSNPNSSIML ASASFDSTVRLWDVEQGVCTH TLMKHQEPVYSVAFSPDGKYL ASGSFDKYVHIWNTQSGSLVHS YQGTGGIFEVCWNARGDKVGA SASDGS\VCILWQLSGKQ
21343	51711	A	21471	1	1647	
21344	51712	B	21472	4	267	
21345	51713	A	21473	1	1824	
21346	51714	A	21474	33	543	TFEGANNFVGDPIVLPCNPPKG LPPLHIYWMNIELEHIEQDERV YMSQKGDLYFANVGRKRDSRN D\YCCFA\AFPRIKGLLYRKMPM /RNLTVNSSNSIKAKENPKLLLA SPLRSGSESSITILKGEILLLECF AEGLPTPQVDWNKIGGDLPKG REAKENYGKTLKIENVY
21347	51715	A	21475	197	516	TYLAAGRTPTLDPWNQERCTM PSGSIWILETTHSSFGWVTVAH LSSDPKGCQF*VGSRIGEGSATD PAFCASCSATWTIRPSRSNGA*G VNG**VCWLEPLAGPHR

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21348	51716	A	21476	1	1766	MNVALTHIDTHHAEFEMALQA ALVWNTLRTAGGKKSVHLASA LLVHEIIIDGANLTISNVTLEDQ GIYCCSAHTALDSAADITQVTV LDVPDPPENLHLSERQNRSVRL TWEAGADHNSNISEYIVEFEGN KEEPGRWEELTRVQGKKTTVIL PLAPFVRYQFRVIAVNEVGRSQ PSQPSDHHETPPAAPDRNPQNIR VQASQPKEMIIKWEPLKSMEQN GP\GLEYRVTWKPQGAPVEWE EETVTNHTLRVMTPAVYAPYD VKVQAINQLGSGPDPQSVTLYS GEDLPEQPTFLKVIKVDKDTAT LSWGLPKKLNGNLTGYLLQYQ IINDTYEIGELNDINITTPSKPSW HLSNLNATTKYKFYLRACTSQ GCGKPITEESSTLGEGSVSLEKC ENKLIRNIGTKKQGTAIRIPENV EAALELRKQQKLEECGGFRRRE NANEQQGVTEEFKQQNEKLRF LLLKIVILAVAREMTWNGEGR DLSEPSLTVVFADLSSPAYSLHT TMAQEPGPGLFLSLSTIPWPISSI PMIHASVQVSWIPLLRNSLMVH IHSSLEQRNLKVHISKEQKKLNS VDSDLTDNPPTHTVN
21349	51717	A	21477	1	1440	
21350	51718	A	21478	266	3974	RAMEPLLLGRGLIVYLMFLLLK FSKAIEIPSSVQQVPTIIKQSKVQ VAFPFDEYFQIECEAKGNPEPTF SWTKDGNPFYFTDHRIIPSNNS GTFRIPNEGHISHFQGKYRCFAS NKLGIAMSEEIEFIVPSVPKFPK EKIDPLEVEEGDPIVLPCNPPKG LPPLHIYWMNIELEHIEQDERV YMSQKGDLYFANVEEKDSRND YCCFAAFPRLRTIVQKMPMKLT VNSLKHANDSSSSTEIGSKANSI KQRKPKL

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21351	51719	A	21479	1	2421	QAGAMASGSVAECLQQETTCP VCLQYFAEPMMLDCGHNICCA CLARCWGTAETNVSCPQCRETF PQRHMRPNRHLANVTQLVKQL RTERPSGPGGEMGVCEKHREPL KLYCEEDQMPICVVCDRSREHR GHSVLPLEEAVEGFKEQIQNQL DHLKRVTRLKFTDFLAQGEQA RAELLSLTHMEREKIVWEFEQL YHSLKEHEYRLLARLEELDLAI YNSINGAITQFSCNISHLSSLIAQ LEEKHQQPTRELLQDIGDTLSK AERI\RIPEPWITPPDLQEKIHIFA PKCLFLTESLKQFTEKMQSDME KIQELREAQLYSGGSIVGGHEP GEPRGIKAGYGTCNCFPEEEKC FCEPEDIQDPLCDELCRTVIAAA VLFSFVVSVLLSAFCIHCYHKF AHKPPISSAEMTFRRPAQAFPVS YSSSGARRPSLDSMENQVSVDA FKILEDPKWEFPRKNLVLGKTL GEGEFGKVVKATAFHLKGRAG YTTVAVKMLKENASPSELRDL LSEFNVLKQVNHPHVIKLYGAC SQDGPLLLIVEYAKYGSLRGFL RESRKVGPGYLGSGGSRNSSSL DHPDERALTMGDLISFAWQISQ GMQYLAEMKLVHRDLAARNIL VAEGRKMKISDFGLSRDVYEE DPYVKRSQGRIPVKWMAIESLF DHIYTTQSDVWSFGVLLWEIVT LGGNPYPGIPPERLFNLLKTGH

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21352	51720	A	21480	79	2253	PSATLSCPTSVAASLGEPAVFPL SLRGHRRRHRPGHSKPSVRGRV WDTGPGGAALRPPGASQEQRT GESAGELGSVQSSAPGPMPVRP RRPGAMASGSVAECLQQETTC PVCLQYFAEPMMLDCGHNICC ACLARC\WGTEET\NVS\CPQCR E\TFPQRHMRPNRHLANVTQLV KQLRTERP\SGPGGEMG\VCE\K HREPLKLYCEEDQMPICVVCDR SREHRGHSVLPLEEAVEGFKEQ IQNQLDHLKRVKDLKKRRRAQ GEQARAELLSL\TQ\MEREKIVW E\FEQLYHSLKEHEYRLLARLEE LDLAIYNSINGAITQFSCNISHLS SLIAQLEEKQQQPT\RELLQDIG DTLSRAERIRIPEPWITPPDLQE KIHIF\AQK\CLFLTESLKQFTEK MQSDMEKIQELREAQLYSVDV TLDPDTAYPSLILSDNLRQVRY SYLQQDLPDNPERFNL\FPCVLG SP\CFIAGETIIWEGRGWGDKAK WTIG\VC*RLSCQEKGGVTSAP QNGFW\AVSLWYGK\EYW\ALT SPMTALPLRTPFQ\RVGIFL\DYD A\GEVSF\YN\VTERC/HTPFTFSS CLPFGGLVRPLLSSLSYSGREK VQLPLINLPP*SGIDGGFLAHVG \NHGSFPWKTFPFEGRVNSGPK GLLAVILRPGTRHLVCLANVLS KLGILNHVPRPCSGRHGCPCSLP SFFLPMQIVKCNEMYQDILEIKT
21353	51721	A	21481	1	1068	

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21354	51722	A	21482	955	2548	MSLCGARANAKMMAAYNGGT SAAAAGHHHHHHHHLPHLPPP HLHHHHHPQHHLHPGSAAAVH PVQQHTSSAAAAAAAAAAAAA MLNPGQQQPYFPSPAPGQAPGP AAAAPAQVQAAAAATVKAHH HQHSHHPQQQLDIEPDRPIGYG AFGVVWSVTDPRDGKRVALKK MPNVFQNLVSCKRVFRELKML CFFKHDNVLSALDIL*PPHIDYF EEIYVVTELMQSDLHKIIVSPQP LSSDHVKVFLYQILRGL\KYLHF RLGILH\RDIKPGNLLVNSNCVL KICDFGLARVEELDESRHMTQE VVTQYYRAPEILMGSRHYSNAI DIWSVGCIFAELLGRRILFQAQS PIQQLDLITDLLGTPSLEAMRTA CEGAKAHILRGPHKQPSLPVLY TLSSQAT\H*TGHLLFAECGFDP SKRISAKDALSHPYLDEGRLRY HTCMCKCCLSPS\TGRVNT\SDL EPVT\NPKFDDTFEKNLSPVRQV KEIIHQFILEQ\QKGNRV\PLWIN PQSAVFKSFISSTVAQPSEMPP\S PLVWE
21355	51723	A	21483	119	692	SYKSRLARKS\TGGKAP\RKQLA YKKPASQECGPLTGGVKKPHR YR\PGTVAAP*NLDGYQKSTE\L MIRK\LRFQR\LVREIAQ\DF\KT DLRFQSAVIRWLCRMAS\EAYL VWPFLKDTNLVCLSMPKRVTIY AKKTFQLSTPASRGERALRIHS WMGKHFILKKKKKKFLFFLLL VVLNVRYFFFHGVKRYLSI
21356	51724	A	21484	2	363	RFTKVEMKEK\MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAKL

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21357	51725	A	21485	1	1468	MRNLRNIQKAKATINLGISFDE GLKGFMWSRIEAAPLPNTRWC LPHGYSGPANSGGCYYITTGMS CWLSDLYPRHDGVHVGLQGK DLEHDIPVDLGSRPTSVDPVSRS APGPQGPKAPVDSGSRTTPANP GAGPSPVDPSSRPAPVASGFRLI MIDQNTKLIPVPGWPLRLRLKI YLSSRSASLDSGSRFAPVDTNFI PVPTDRGHSHAPEDPVDRLTSV DPTKEKNWMENEFDKLTEVGF RRSVITNFSELKEHVLTHRKEA KNLEKRLDEWLSRITCAEKSLN DLMELKTTVRELREAYTSFMS QFDQAEERISVIEDQINEIKLKSL QAQEDARHRNTDQRSSENRRS EPWSLEERKREQWNSLKQNAD QQDTEAMSDYK/R/YSSET*RRR *LFCLLRKVHSKEGP*KKDQRE TRNQKGLGFLRDRPQWVSGKM KQECLQLGTPWP*IIIGQWQYFP RDGMGVRTDFCRIFQRLARMR LCEGCLMNS

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21358	51726	A	21486	1	2589	MSPVTLWVRTSSRGEDRCGMC TPGRDTGFAPISGMCSKYRSCTI NEDTGLGLAFTMPMSLDTKHIP NFGKVHGYIMRHHKNEDTIPW RRNTKKEEARGTQPLEADDQN PGWEDGKPGSLENEGRRSHRG NPAPDMPQPPKEDLFILPDEYK SCLRHKRSLLRSHRNEELNVET LVVVDKKMMQNHGHENITTY VLTILNMERILKKTSFTIIHPSA MERCPVLNLQIRDSLWNHCFSL ATTVHRFHPVGRHALKKMYKL PSAYINVSITKYTQRFALTYISC VFHRNAAFVAVPGEGRCCAGV DVPAPMSLRSPGPHWPQEHGA LWISCTVRGMASCLGQLCRVS MRVRANIGKVQKPRLRISNGK GLHTQSELSGSAYLEKGWRGA APGLDSRNEKGTEGARDSGTPG RQSQTLQRGPPGPVPGSSKIAPQ TLTRQGSMTASRKLVLLLPEFC ERTGEQSGQLYPPSPLLVEWV MPAGTSSTVDPLLPELCRRWER QALSLCRLYRQRTSVSIKALCD HTETRSVALSTCQGLECNSSPA RKQNWMENEFEELTEVGFRKS VITKFSKLKEHILTHRKEAKNLE KRLDEWLTRITSVEKSLNDLME LKTTVRK\LHEAYTSFNSRFDQ VEERILVIEHQINEIKQEDKVRE KRVKRNEQSLQEIWDCVKRPN LCLIGVPESDGENGTKLENTLQ
21359	51727	A	21487	260	1292	RLCAFNKRMTFQFNFTIEDHLE NELTPIRDGALTLDSSKELSVSE SQKGEERDRKCSAEQFDLPQD HLWEHKSMENAAPSQDTDSPL SAASSSRNLEPHGKQPSLRAAK EHAMPKDLKKMLENKVIETLP GFQHVKLSVVKTILLKENFPGE NIVSKSFSSHSDLITGVYEGGLK IWECTFDLLAYFTKAKVKFAG KKVLDLGCGSGLLGITAFKGGS KEIHFQDYNSMVIDEVTLPNV VANSTLEDEENDVNEPDVKRC RKPKVTQLYKCRFFSGEWSEFC KLVLSSEKLFVKYDLI\LTSETIY NPDYYSNLHQTFLRLLSKNGRV LLASKAHVQRNSLSRL

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21360	51728	A	21488	263	1466	RLCAFNKRMTFQFNFTIEDHL\E NELTPIRDG\ALTL\DSSKEL\SVS ESQKGRKE\RDRKCSAEQF\DLP QDHLWGNISSMGKWQAPS\QG HRTSSTSVAASSSRNL\EPHGKT ALLAGAGQRSMAMPKRF*RRC LEN*SPLET\LPGFQHVKLSVVK TILLKENFPGENIVSKSFSSHSDL ITGVYEGGLKIWECTFDLLAYF TKAKVKFAGKKVLDLGCGSGL LGITAFKGASKEIHF\QDYNSMV IDEVTLPNVVA\NS\TLEDGGKM DVKWSPDVEKMPGNPKVTQ\L YKC\RFFS\GEWS*VL*ALYLSSE K\LFVKYDPHSSPSET\IYNP\DY YSNL\HQTFLRLLSKNG\RVLLA SKAHYFGVGGGVHLFQKFVEE RDVFKTRILKIIDEGLKRFIIEITF
21361	51729	A	21489	2	367	
21362	51730	A	21490	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
21363	51731	A	21491	1	690	
21364	51732	A	21492	1	714	
21365	51733	A	21493	1	1536	
21366	51734	A	21494	1	765	
21367	51735	A	21495	1	972	
21368	51736	A	21496	1	2670	
21369	51737	A	21497	2	1178	
21370	51738	A	21498	2	827	
21371	51739	A	21499	1	777	
21372	51740	A	21500	168	1057	IRLKNDHDGELRNKTICINRNL AEIKKFSENYENKETMYLNLW DVAKAVLRGQFIALNARIKKLE KSQVYNLISQLKELENQEQTNP KASRRQEITKIRAELKEVETWK TLKKINESGRGVDCSS/DASNGT KPDGE*L**VDKSR/PSEARQAN IHIQEIHGTPQR*SLRRATPRH/II VRFTKVEMKEKMLRAARKKG WVTHKGKPIRLTADLLAETLQ ARREWGPIFNILKEKNFQLRISY PAKLSFIREGEIKAFTEKQILRDF VTTRPALQELLKEALNMERND RYQPLQKHAKL

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21373	51741	A	21501	3	1263	GRTIQTKGKEV\ENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERVSAM EDEMNEMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTPQRYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRAILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQEIQRTPQR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK
21374	51742	B	21502	1	2356	
21375	51743	A	21503	2	484	
21376	51744	A	21504	2	902	ASFFSKKTSGFGGWGAGGPGD PGMGNHGGFRGGFSRGIRGWG HSRGQGPGQGRGAHRGKTKDK EWTSIPKLGHLVKDMKIKFLEEI YLFFLAIKEFEIIDFFLGASLKDE VLKIMPVQKQTHASQRTRLKG FIVIGDYNG/HVGLGVKCSKEV A/TAIRGAIILG*LSIVPMCRGY WGSKIGKPHTVPCKVTGHCGS VLVHFIPAPRGTGIVSVPMP/KK LLLMAGIYDCY/ARSCTATLGN FTKATFDAISKTYSYPTPNLWK ETVFTKSP/YEFRNSGQEFTDYL VKT/HIRVSVQRTQAPAVATT
21377	51745	A	21505	2	407	STISCGGNFPIPRGGSGVASLER AESSSTEPAKAIKPIDRKSVHQI CSGPVVPSLSTAVKELVENSLD AGATNIDLKLKDYGVDLIEVSG NGCGVEEENFEGLTLKHHTSKI QEFADL\LSDVTISTCHVSAKVG
21378	51746	A	21506	362	490	
21379	51747	A	21507	3009	3889	
21380	51748	A	21508	1	504	LDDLHKWFLSSFLLTAISIGIKF LLKIHISRGSGVLLQLLPGNPSP AAHGTEELEPKFLEQGYLRAVL PGPRVHATA*LEPTVTDQGYAR AGLPIQEVEDVLFGVLVVLLHV IGQVAEDRNQVAAQGHHQES/C PAQCWGDCTHLEIAGWRGIRRS DANPRSQRKGFG

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21381	51749	A	21509	2	1101	WTERRLGSVRGDRLRERSRPA VNRTPRMSRVPSGAPRGTPSRR WWMMKCWDHQPLG*IPAPHV GPLAG/IRKKEWSDESEEEPEKE LAPEPEETWVVEMLCGLKMKL KQQRVSPILPEHHKDFNSQLAP GVDPSPPHRSFCWKRKREWWD ESEESLEEEPRKVLAPEPEEIWV AEMLCGLKMKLKRRRVSLVLP EHHEAFNRLLEDPVIKRFLAWD KDLRVSDKYLLAMVIAYFSRA GLPSWQYQRIHFFLALYLAND MEEDDEDPKQNIFYFLYGKTRS RIPLVRNRRFQLCRCLNPRARK NRSQIALFQKLRFQFFCSMSGR AWVSREELEENTGPRGDVDFQ QELYSNANGRQQERGEEPFVQI
21382	51750	A	21510	3	918	
21383	51751	A	21511	1	792	
21384	51752	A	21512	3007	3885	
21385	51753	A	21513	615	845	GHTASPPPRSPQAQGRAPSVAP PPTTPQICPTTPSSFSSKRTYAG GWDLPQGQADC*SPCGAQGG WVTLAVASASS
21386	51754	A	21514	357	562	GSSTCGRETERVVLKKRKRSPT HFQYRNSPTAEARPQLE\PTQW GRRSHSPRPSAPLPCSCPQKSRK SV
21387	51755	A	21515	1	1335	
21388	51756	A	21516	537	1164	SSTEPAKAIKPIDRKSVHQICSG PVVLSLSTAVKELVENSLDAGA TNIDLKLKDYGVDLIEVSDNGC GVEEENFEGLISF\TLKHHTCKI QEFADLTEVETFGFQGEALSSL CALSDVTISTCHASVKVGTRLV FDHDGKIIQETPYP\HPRGTTVS VKQLFSTLPVRHKEFQRNIKK\R ACFPFAFCRDCQFPEASP\AMLP VQPAELMAV
21389	51757	A	21517	224	903	GFTWYIGMAQPKQERVARARH QRSETARHQRSETAKTPTLGNR QTPTLGNRQTPRLGIHARPRRR ATTSLLTLLRAFGKKTQS/STEP AKAIKPIDRKSVHQICSGPVVLS LSTAVKKIVGNSLDAGATNIDL KLKDYGMDLIEVSGNGCGVEE ENFEGLSWDSTGVFDHDGKIIQ KTPYPHPRGTTVSVKQLFSTLP VRHKEFQRNIKKPVGEKYMRS VDTQACSCI

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21390	51758	A	21518	2	1321	VKSRAALLGPGA/LSPLEVSRRR PWTERRLGSVRGDRLRERSRPA VNRTPRMSRVPSGAPRGTPSRR WWMMKCWDHQPLG*IPAPHV GPLAG/IRKREWSDESEEEPEKE LAPEPEETWVVEMLCGLKMKL KQQRVSSILPEHHKDFNSQLAP GVNPSPPHRSFCWKRKMEWW DQSEESLEEEPRKVLAPEPEEIW VAEMLCGLKMKLKRRRVSLVL PEHHEAFNRLLEDPVIKRFLAW DKDLRVSDKYLLAMVIAYFSR AGFPSWQYQRIHFFLALYLAND MEEDDEDSKQNIFHFLYRKNRS RIPLLRKRWFQLGHSMNPRARK NRSRIPLLRKRRFQLYRSTNPRA RKNRSRIPLLCKRRFQLYRSMN SRARKNRSQIVLFQKRRFHFFCS MSCRAWVSPEELEENTGPRGD VDFQQELYSNANGRHQAGGEE

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21391	51759	A	21519	1	2654	RSACGSPAWNFPSPRGGSGVAS ME\RAESSSTEPAKAIKPIDQKS VHQICSGQVVLSLSTAVKELVE NSLDAGATNIDLKLKDYGVDLI EVSDNGCGVEEENFEGLTLKH HTSKIHEFADLTQVETFGFRGE ALSSLCALSDVTIFTCHASAKV GTRLMFDHNGKIIQKTPYPRPR GTTVSVQQLFSTLPVRHKEFQR NIKKEYAKMVQVLHAYC\SFQ QASV*VAPISLDK/RKRQPVVCT GGSPSIKENIGSVFGQKQLQSLI PFVQLPPSDSVCEEYGLSCSDA LHNLFYISGFISQCTHGVGRSST DRQFFFINRRPCDPAKVCRLVN EVYHMYNRHQYPFVVLNISVD SECVDINVTPDKRQILLQEEKLL LAVLKTSLIGMFDSDVNKLNVS QQPLLDVEGNLIKMHAADLEK PMVEKQDQSPSLRTGEEKKDV SISRLREAFSLRHTTENKPHSPK TPEPRRSPLGQKRGMLSSSTSG AISDKGVLRPQKEAVSSSHGPS DPTDRAEVEKDSGHGSTSVDSE GFSIPDTGSHCSSEYAASSPGDR GSQEHVDSQEKAPETDDSFSDV DCHSNQEDTGCKFRVLPQPTNL ATPNTKRFKKEEILSSSDICQKL VNTQDMSASQVDVAVKINKKV VPLDFSMSSLAKRIKQLHHEAQ QSEGEQNYRKFRAKICPGENQA AEDELRKEISKTMFAEMEIIGQF
21392	51760	A	21520	238	413	
21393	51761	A	21521	288	467	
21394	51762	A	21522	1	3038	MDVGWDLGEDCWQEHLHTAF SFDCWPCSQNGDRVPSVNPVG GGAPRSYLQVASAECWAAAPA VHVGEPVHAGGLHTERGADPV IGLYLVHRGGACQTPTVGNRQ TPTLGIHARPRRRATTSLLTLLL AFGKNAVRTEPAKAIKPIDRKS VHQICSGPVVPSLSTAVKELVE NSLDAGATNIDLKLKDKESGL\I KVQANEWGVKEETSKGLLLKH HTSKIQEFADLPQVETFGFRGE ALSSLCALSDVTISTCHV
21395	51763	A	21523	34	256	ETGPPGSAPGRLEFTNIKRVVVP QERVELETLLVSYFSPRTPRRTP PPFPHPCS*EDNVITVFSSIKNGP GSSR

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21396	51764	A	21524	727	2953	HVSGYDDVPLGTLSLDIWPPAL FSVVSFAAFFFTPPIEAVLKSFSC LLVWYIGMAQPKQERVARARH QRSETARHQRSETA/KTPTLGN RQTPTLGNRQTPRLGIHARPRR RATTSLLTLLRAFGKKTQS/STE PAKAIKPIDRKSVHQICSGQVVL SLSTAVKKIVENSLDAGATNID LKLKDYGMDLIEVSGNGCGVE EENFKGLTLKHHTSKIQEFADL TRVETFGFRGEALSSLCALSDV TISTCHVSAKVGTRLVFDHDGK IIQKTPYPHPRGTTVSVKQLFST LPVRHKEFQRNIKKAQR/PQAR/ CYRCS*PNVSPGPGMAAASTLS A*PRSQSSYFISCKA/EDNAICPI AEQKAEGKFSSRYRNHDSAEN RRDGSMTRPRTDWTLKRACTE KRRPQHASSFEWRGHSLCWDR EQRDAETLKMLLDSGLSVQKK TKDRTETRFGEMGQILGKIMMS HQPQPQEEQSPQRSTSGYPLQE VVDDEVSGPSAPGVDPSPPRRS LGWKRKRECLDESDDEPEKEL APEPEETWVAETLCGLKMKAK RRRVSLVLPEYYEAFNRLLEDP VIKRLLAWDKDLRVSDKIPSEP TILGASPKTLPPASRICIRPSNTP PPRNFHMSTVTPMLSYLANDM EEDDEAPKQNIFYFLYEETRSHI PLLRELWFQLCRYMNPRARKN CSQIALFRKYRFHFFCSMRCRA

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21397	51765	A	21525	1054	2349	SCPQIIFLSSCLQVASAECWAAA PAVHVGEPVHAGGLHTERGAD PVIGLYLVHRGGACQTPT\IGSR QTPTLGIHARPRRRATTSLLTLL LAFGKNAVRCALIGPGSLTSRT RPLTEPLGEKERREVFFPPRPER VEHNVESSRWEPRRRGACGSR GGNFP\SPRGG\SGVASLERAES SSTEPAKAIKPIDRKSVHQICSG PVVPSLRPNAVKELVENSLDAG A\TNVDLKLKDYGVDLIEVSG\ NGCGVEEENFEGL/TSLSALKH HTSKIREFADLTRVETFGFRGE/ AL*ASLCALSDVTISTCHVSAK\ VGTLTGVFDHDGKIIPENPPNPH PRGTTVSVKQLFSTLPV\RHKEF QRNIKKKRA\CFPFAFCRDCQFP EASPAMLPVQPAELTPR\STP\PH PCSLEDNVITVFSS\VKNGPGSS KMICTNGSSPSS
21398	51766	A	21526	2	393	
21399	51767	A	21527	2	165	
21400	51768	A	21528	3	196	
21401	51769	A	21529	1	411	
21402	51770	A	21530	1	1727	GPQGVGRMAEGKAGGAAGLF AKQVQKKFSRAQEKVLQKLGK AVETKDERFEQSASNFYQQQA EGHKLYKDLKNFLSAVKVMHE SSKRVSETLQFIYY\SEWYGHEE LKAIVWNNDLLWEDYEEKL\A DQAVRTMEIYVAQFSEIKE\RIA KRGRKLVDYDSARHHLEAVQN AKKKDEAKTAKAEEEFNKAQT VFEDLNQELLEELPILYNSRIGC YVTIFQNISNLRDVFYREMSKL NHNLYEVMSKLEKQHSNKVFV VKGLSSSSRRSLVISPGVRTATV SSPLTSPTSPSTLSLKSESESVSA TEDLAPDAAQGEDNSEIKELLE EEEIEKEGSEAGSSEEDDPLPAC NGPAQAQPSPTTERAK\SQEEV LPSSTTPSPGGALSPSGQLSSSA TEVVLRTRTASEGSE\RPKKTAS IQRTSAPPRRPPPPRATASPRPCS GNIPSSPTASGGGSA\TSPRASL GTGTASPRTSLEI*PNPE\PPEKP VRTPEAKENENIHNQNPEELCT SPTLMTSQVASEPGEAKKMED KEKDNKLISADSSEGQDQLQVS MVPENNNLTAPEPQEEVSTSEN
21403	51771	A	21531	1	1530	

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21404	51772	A	21532	499	1587	HPRDPEAPSGPLWSASLPALYS QGHANEFDGSNSTSHAVLVLV QKHIKAVLSNKLCLSTSSLVQG VNAHLGTLIWPQPRGYLSPRSA IPWFSVPTVTSGLHFPWEVQ*LF LLSCWGKAHQSLPQRMPPLLC CQGMWVPEGSMATVGLSQQLF DSALLLLQKAGALNLDITGQLR SDDNLLNTSALGRLIPEVARQF PEPMPVVLKVRLGATPVAHGS TQTTATLRPASPFVGGSWATGP PNSAFPSPSSP/CLVVVNLRTPAS L/SSKGEALREHVCAWWMSQL TVASSNVGFIDTDQVRTLMGTV FEKPLLDHLNGSLGHGELPSLV WVNLHYVAPEIFVYEGYVVISS GTLLPEPEAKTTGRP
21405	51773	A	21533	1385	3111	IAPSEVKEHKMVLEMLNPIHYN ITSIVPEAMPAATMPVLLLTGLF LLVWNYEGTSSIPGPGYCMGIG PLISHGRFLW\MGIG\SACNYYN RVYGEFMRVWISGEETLIISKSS SMFHIMKHNHYSSRFGSKLGLQ CIGMHEKGIIF\NNNPELWKTTR PFLYERLCHAPASVRMVTVCA ESLKTHLDRL\EEVTT\ESGLCG TCLTLLRRVHGWDTSNTVFL\G IPL\EESAIVVKIQG\YFDAWQAL LIKPDIFFKISWLYKKYE\KSVK DL\KDA\IEVLIAEKRRRISTEEK LEECMDFATELILAEKRGDLTR ENVNQCILEMLIAAPDTMSVSL FFMLFLIAKHP\NVEEAIIKEI\QT VIGERDIKIDDIQKLKVMENFIY ESMRYQPVVDLVMAQSL*EG* C*SMGYPV\KKGTNIYSWNIG\R VHRL*FFPKPNEFTLENFAKNV PYRYFQPFGFGPRGCAGKY/LS AMVMMKAIL\VTLLRTDST*RT LPGTSVFESIQEGYTTCPWHPD\ ETKNML\EMDLYPKETSDRCLG TLRRKAGQYLTLGAFSPSVCSP TNHPILCPLVFILHSGTLSGPMA
21406	51774	A	21534	129	378	IVCKFSVSTHKNIRAKKPDERLP ECGTQIRKDTLKRVRRTVLHYL C\PPPSVPEIPAWR\GDCSP/VGK EGKCTPDLNPNIELRPV

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21407	51775	A	21535	1	474	MQKQIISVTEVEWYPKYNSNM KEYWSTQNHQFEQLSTHKNIR AKKPDERLPECGTQIRKDTLKR PCPLDRPLWPHITAEQGSKPST WPAPCDP/IF*ANIHLPSLHTGPC RSKVQAHSSRPGCQASSTCVPR LQDLPC*PRFRLTLVDQDARPA APVYQGSRTYPADPDSRPAPVD SGCIISGQADW
21408	51776	A	21536	2	325	
21409	51777	A	21537	2	1011	WAFSITERREFQVYYNSCPSSS WIGDARAFSPPDPTGLYPIYSQ DTQTFRLWLNYNTDFPGSPAC KWQAMELLSPQSPFRVDRGEH LPFLVKGARYTLVPAGQEGAL AAWLEALRGQLGRRGAVVSM MDAEGLERSSPDCAMGLSDGE WQLVLN\VWGKVEADIPGHG\Q EVLIRLFKGHPETL\EKFDK/FTR HLKSED\EMKASED\LKKHMCH TVLTP\LGVHILRE\KGHH*RQR FKPLGTSSHCHPSTKIPPLKVTL EFHLPGIAFIQVLAEQAIPGDFG\ AECPGAQLKQRPWELF\RKNNG LPTYKEAGAFQGARALAGFPTP THLGPPGFKKRAGV
21410	51778	A	21538	157	322	
21411	51779	B	21539	1	975	
21412	51780	A	21540	218	388	RKLPLAGLPCINRQHS*SNVNIC FLTPV*KIQN*LQSEQFLPYPTIV IITLCFFAV
21413	51781	A	21541	663	933	GCAGPCLVNQMFGKQYYLGKS HHP\SLVSLNRGAHCTVGKPQG PSGP*KLGYYFKVFPPCG*FWK YGPSWGMEERAWTGSPLGPGP PLKKV
21414	51782	A	21542	389	1033	NQGLRNLGLCRTCLVNKMFTS SILGKSHRHSLVSINQGNNALW KAAG\PLPLKAGYC\QGFSPCHS LKYG\SWDEKDLTVPQPDTLKG SVLRWISKRGKPLAVEIEEGHC L\CLPLGTECLGIK/PPIVHLFNSE IGE\NRPYGGR*DMFCSNGCLG* FL*LPLRCLG\GEKHKSGL/HVHI PVIVPPLELNYDIDSFAHMFF\V DLS\LIITLLSCYIPFC
21415	51783	A	21543	82	163	
21416	51784	B	21544	1	211	

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21417	51785	A	21545	71	1086	NMNLSLVLAAFCLGIASAVPKF DQNLDTKWYQWKATHRRLYG ANEEGWRRAVWEKNMKMIEL HNG/EKYSQGKH\GFTMAMNA FGDMTNEEFRQMMGCFRNQKF RKGKVFREPLFLDLPKSVDWR KKGYVTPVKNQKQCGSCWAFS ATGALEGQMFRKTGKLVSLSE QNLVDCSRPQGNQGCNGGFMA RAFQYVKENGGLDSEESYPYV AVDEICKYRPENSVANDTGFTV VAPGKEKALMKAVATVGPISV AMDAGHSSFQFYKSGI\YF*PDC ISKNLDQGVLVVGYVFEGANS NNSKYWLVKNSWGP\EWGS\N GYVKIAKD\KNNHCGIATAASY
21418	51786	A	21546	170	412	LWLSFLLMHWH*IPLAAVSVFT VSN/PILDFS*IQLKTPKHFGNLG NTGFLGKQLRLLLRSLVSVSRL HCLLGYRRTQMPPL
21419	51787	A	21547	1	753	
21420	51788	A	21548	125	464	TAVFLTQSLFGGLFTRTRMKFG TMTRI/RGDLPWEINPLSSCSLL HEKDPPTTSGPQTNQPKKHLTN FKSRKVERTKGLLKTHLTKLSH QLKKAWTILLPLSLLRIQACPR NAT
21421	51789	A	21549	1	753	
21422	51790	A	21550	291	671	
21423	51791	A	21551	10	453	TALLLTQSLFGGLFTRTRMKFG AMTRIG\DLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGCLPWSFTLSGKSR FPGAGASTPQPLLLHP
21424	51792	A	21552	740	1010	TAMLLKQSLFGCLFTRTRMKF GAVTRIG\DLP*ETNPLSSCSLLR DKDPPTTSSPQTHQPKKHLTNF KSGCSSPGRARSQSFLSLCSSTL
21425	51793	A	21553	134	358	TAMLLTQSLFGGLFTRTRMKFG AVIRIG\DLLWEINPLSSCSLLHE KDPPTTSGPQTDQPKKHLTNFK SSCSSPG
21426	51794	A	21554	392	645	

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21427	51795	A	21555	1	1900	MQNALESLSNRIEQVEERNSEL EDKFFELTQSNKDKEKRIRKYK QSLKEVWDYVKGPNLRIISVPE EEENSKSLENIFGEIIEENLPSLA RHLDNQIQEAQRTLWKLIAKRS LPRHIVIRLSKVKTKERILRAVR QKHQVTHLTCKESYKLKVKG WKRHFMQMDTKNEQGIKNEN HLIISIDVEKASDKIQQRFMIKTL SKIGIQGKYLNVIKAIYDKPTAN ITLNREK/LESIPSEKLKAFPLRT GTRQGCPLSPLFFNTVLEVLAR AIRQEKEIKGIQIGKEEVKLSLF ADDMIMYLENPKDSSRKLLEWI KESNKVSGYKTHVHKSVALLY TKQ*\QAENQIKNRNPFAIAAKK KKKKKKKKKRNSRIYLTKESK DLYKENYKTLLKEIIDNMNKW KHIPCSWMGRISIVKKL*\LQKA IYKLNAILIKIPPLLFTELEKTILK FIWKSNKS\RIAKVILSKKNKSG GITLPDFKLYYTIRKINSKWIKD LNLRPETIQILEDNIGKTLLEIGL GKDFMTKNPKANAKKKTKINR WDLIKLKSFCTAKGTVSRVKRT HRVGENLPHYTSIHPTIYTIYTS DKGLISRIYNEFKQIVTRTTCVF LHPPHPKAKTTSYGDQLLGGN
21428	51796	C	21556	10	339	
21429	51797	B	21557	97	1458	
21430	51798	A	21558	1	387	
21431	51799	A	21559	3	604	GSVIAYYWSEFSIPQHLVEEAE RVMAEERVFMLPPRARSLKSFV VTSVVAFRESEGQGWAWDWPP FHGVGLGPGPLQGTGTPRAQCP REKTTCWPGTSL*IIRKQE*GNG LYQEMLYSPSYSSATDSKTVQR TQDNSCSFGLHARGVELMRFTT PGFPDSPYPAHARCQWALRGD ADSVLSLTFRSFDLASCDEARS DLV

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21432	51800	A	21560	1000	2084	FRGTPVQRGGGWADLPGRCGE LGRRLRSEEQARRVHKAPS/DF GTG/LKENTGKVNGLEEGVEFL PVNNVKKVEKHGPGRWVVLA AVLIGLLLVLLGIGFLVWHLQY RDVRVQKVFNGYMRITNENFV DAYENSNSTEFVSLASKVKDAL LYSGVPFLGPYHKESAVTAFM WVWREGSVGCTPDWLGVGSG YSVWGTKREMVLEVLDWRAK EGPRCVLLEGSVIAYYWSEFSIP QHLVEEAERVMAEERVVMLPP RARSLKSFVVTSVVAFPTDSKT VQRTQDNSCSFGLHARGVELM RFTTPGFPDSPYPAHARCQWAL RGDADSVLSLTFRSFDLASCDE RGSDLVTVYNTLSPMEPHALV
21433	51801	A	21561	3	2820	TGALILQKGEIRVINQTTCENLL PQQITPRMMCVGFLSGGVDSC QVPPGQEGGRQFPLKETNNRK GRLPKRLRPHTWCCYSLECSSY SLRCTEDTWTEDQKVNGLEEG VEFLPVNNVKKVEKHGPGRWV VLAAVLIGLLLVLLGIGFLVWH LQYRDVRVQKVFNGYMRITNE NFVDAYENSNSTEFVSLASKVK DALKLLYSGVPFLGPYHKESAV TAFSEGSVIAYYWSEFSIPQHLV EEAERVMAEERVVMLP
21434	51802	A	21562	111	465	
21435	51803	A	21563	2	197	
21436	51804	A	21564	359	405	EMQSRED*RK*YL*RIVNCVPL RERLGYVCGGLGERSKEGTLWI YQGLQKSQDTGRV
21437	51805	A	21565	208	287	IVSRSEKGWVMYVEGWEREAR REHYGYIKGYKNHRIHMMQSS KALV*LEDLRKHI*IFRCVFSNP QVILML
21438	51806	C	21566	141	305	
21439	51807	A	21567	170	973	RMAACRALKAVLVDLSGTLHI EDAAVPG\AQEALKRLRGASVII RFVTNTTKESKQDLF\KRLRKL G\FDISEDEIFTSL\TAARSLL*\R KQVTPMLLVD*SGHYLIFKGIQ TSDPN\AVVMGIGTRTFSLSKF WNQAFRLLLGWSTSDSNSQSQ GFQEFKMGLALGPWTIL*LL*K YATDTKATVVGKPEKTFFLGSI AGHWLLNLEEAVMIG\DDCRG\ DVGGAQDVGMLGILVKTGKYR ASDEEKINPPPYLTCESFPHAVD

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21440	51808	A	21568	42	211	
21441	51809	A	21569	92	366	AGSEMRPGLTWACSLARLLLSP SFIKHWFLESCLLSCSRSGSGYA QWCPPHQSASAAGHCQTPAHA QAYLSSPPQMDHSSVRSLLEAC QTY*SASAAGHCQTPAHAQAY LSSPPQMDHSSVRSLLEACQTY
21442	51810	A	21570	1	834	
21443	51811	A	21571	3	835	
21444	51812	A	21572	1	1649	MPIVLVDWSDIREQKRLMVLR ASVALHGRSVTLYEKAFPLSEQ CSKKAHDQFLADLASILPSNTT PLIVSDAGFKVPWYKSVEKLG WYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKR LTKSNPISCQILLYKSRSKGRKN QRSTRTHCHHPSPKIYSASAKEP WVLATNLPVEIRTPKQLVNIYS KRMQIEETFRDLKSPAYGLGLR HSRTSSSERFDIMLLIALMLQLT CWLAGVHAQKQGWDKHFQAN TVRNRNGSLLTNWPSVPPTIKE EENSEEELAAATTSKEQEPIGTD LDAVRTPEPLEEFPKREDQEGS PPETSLPYKWVVEAANLLIPAV GSSLSEALDLIESDPDAWCDLS KFDLPEEPSAEDSINNSLVQLQA SHQQQVLPPRQPSA\LVPSVTEY RLDGHTISDLSRSSRG\ELIPISPS TEVGGSGIGTPPSVLKRQRKRR VALSPVTENSTSLSFLDSCNSLT PKSTPVKTLRFS\PSQ\FLNFWN KQDTLELESPSLTSTPVCSQKV VVTTPLHRDKTPLHQKHAA

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21445	51813	A	21573	59	2384	PRPGSRSGLCRRAGERGAVRAG GMSRRTRCEDLDELHYQDTDS DVPEQRDSKCKVKWTHEEDEQ LRALVRQFGQQDWKFLASHFP NRTDQQCQYRWLRVLNPDLVK GPWTKEEDQKVIELVKKYGTK QWTLIAKHLKGRLGKQCRERW HNHLNPEVNKSCWTEEEDRIIC EAHKVLGNRWAEIAKMLPGRT DNAGKNHWNFTIQK/RKGDTG GFLREYKD*KPPVYLPL\ELEDK DGLQSAQPTEGQRSLLTNWPSV PPTIKEEEN\SEEELAAATTSKE QEPIGTDLDAVR\TP\EPLEEFP\K REDQEGSPPETD/SLPYKWVVE AVNLLIPAVVS\SLYEALDLIGS\ DPDAWCDLSRFDLPEEPSIEDSI NNS\LVQLQAS\HQQQILPPRQP SA\LVPSVTEYRLDGHTISDLSR SSRGELIPISPSTEVGG\SGIGTPP SVLKRQRKRRVALSPVTENSTS LSFLDSCNSLTPKSTPVKTLPFS PSQFLNFWNK\QDTLELESPLA DYPPQVCSQKVVVTTPLHR\DK TPLHQKHA\AFVTPDQKYSMD NTPHT\PTPFKNALEKYGPLKPL PQTPHL\EEDLKEVLRSEAGIELI IEDDIRPEKQKRKPGLRRSPIKK VRKSLALDIVDEDVKLMMSTL PKSLSCRTTAPSN\SST\LTLSGIK EDNSL\LNQGLLAGPSPRKAAC VPEGPESHFHGQLAPYVPVPGK
21446	51814	A	21574	190	889	SLPRRLESPGRLAMAARGVIAP VGES/LCRYAEVPCSPSAKRPDA DVDQQRLVRSLIAVGQGVAAL AFAG\RYAL\RIWKPLE\QVITET AKGRFQTPRFSSY**GG/FLNII* LRREA\GLILGVSP\SAGKAKIRT \AHR\RVMILESPQIKGGSPYVA AKINEAKD\LLETTTKRLMLKD HTEGKKNEGTSKKKKSPAKYS KTWSFLIFYMGFDHSLIFRPLSC ITNKMLIVLLFIIF

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21447	51815	A	21575	2	652	EGYIC/RHFTGSSALLTRTHITY GVIANVAVVRINSPNS\RMLAA CKTLQEVTQLSQEAQRIVEKLE KSTKPIVAAINGSCLGGGLEVAI SCQYRIATKDRKTVLGTPEVLL GALPGAGGTQRLPKMVGVPAA LDMMLTGRSIRADRAKKMGLV DQLVEPLGPGLKPPEERTIEYLE EVAITFAKGLADKKISPKRDKG LVEKLTAYAMTIPFVRQQVY
21448	51816	C	21576	98	316	
21449	51817	A	21577	35	247	
21450	51818	A	21578	1	2391	LQLKMVACRAIGILSRFSAFRIL RSRGYICRNFTGSSALLTRTHIN YGVKGDVAADRINSPNSK\VNT LSKELHSEFSEVMNEIWASDQI RSAVLISSKPG\CFIAG\ADITML AACK\TLQ\EVTQLSQE\AQR\IV EKP*KSPQSLIVGCPSNGSCLGR RTLRLPISSPQYRIATK\DSKTVI *VPPE\VFLGGPLPGRQGGHTK GCPKMGGVCLPAFGHECLTGR SIR\ADRAK\KMGLVD\QLVGTP GTQGLKPPEERTIEYLEEVAI\TF AKGLADKKISPKRDKG\LVEKL TA\YAMTIPFVRQQVYKKVEEK VRKQTKGLYPAPLKIIDVVKTG IEQGSDAGYLCESQKFGELVMT KESKALMGLYHGQVLCKKNKF GAPQKDVKHLAILGAGLMGAG IAQVSVDKGLKTILKDATLTAL DRGQQQVFKGLNDKVKKKAL TSF\ERDSIFSNLTGQLDYQGF* KRPDMGELKAVF\EDP*SLSHR VLKGKVGSR*FPDHWYSLPSNT SALPISEIAAVQQKT*EG*LGMH YF\SPVDKMQLL\EIITTEKTSKD T\SASAVA\VGLKQGK\VIIV\VK DG\PGLLVTYQGVFAPMMS\EVI RILQEGS/VDPKKLGFPWTTSFG F\PVG\AATLV\DEVGCGMLAK HV\AEDLGKVFG\ERFGGGNPE L\LTQMVSKGFLG\RKSGEGLLT SSGRVVKRKILNSTMD\SI*ASL
21451	51819	A	21579	119	387	VEDSKEIFSSA*DYLSTHSKHVP ASHESYHVNPNLCNPVAPTSGA HSIV*KWPSWLGTVAHSCNPSN FGRPRRADCLSSRSSRPAWPTR
21452	51820	B	21580	73	3177	

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21453	51821	A	21581	1399	5140	SGEPERALRGAAMRPSGTAGA ALLALLAALCPASRALEEKKVC QGTSNKLT\QLGTFE\DHFPQPS QRMF\NNCEVV\LGNLEITLCER NYDLSFLKTI\QEVAGYVLIALN TVERIPLENLQIIRGNMYYENSY ALAV\LFNYDANKTGLKELPMR NLQEILHGAVRFSNNPALCNVE SIQWRDIVSSDFLSNMSMDFQN HLGSCQKCDPSCPNGS\CWGAG EENCQKLTKIICAQQCSGRCRG KSPSDCCHNQ
21454	51822	B	21582	82	305	
21455	51823	A	21583	122	219	YAKRIYDVYYVHTAYTCTFHA *KIRGMTQ*NW
21456	51824	A	21584	404	1228	GLAAFLARARGRRRKELPGSPR PLPQLPAGGPSPRWRAMRPSQR RPPTLPMAASPAHWPRESLVLY HWTQSFSSQKVRLVIAEKGLVC EERDVSLPQSEHN/EMPWFMRL NLGEEVPV\IIHRDNIIQ/CTMDQ IHLTMWERTFHRERHVGALMP EVGSRAA\PRVLQY\RELLDALP MDAYTHGCILHPELTTDSMIPK YATAEIRRHLANATTDLMKLD HEEEPQLSEPYLSKQKKLMAKI L\EHDDVSYLKKILGELAMVLD QIEGGAGRKRKLENE
21457	51825	A	21585	3	1194	KNLSVKLSENGTLKNCVVADS ETDIDVYMYTRVYVYIPRIENS WNDTIKLVTGATISAVGGDIDA QGEWAFPLLGIPSLSPGPEWKV RVVIPDKGLVCEERDVSLPQSE PKEPWFMRINLGEEVPVIIHRD NIISDYDQIIDYVERTFTGEHVV ALMPEVGSLQHARVLQYRELL DALPMDAYTHGCILHPELTTDS MIPKYATAEIR/SDI*PNATTDL MKLDHEEEPQLSEPYLSKQKKL MAKILEHDDVSYLKKILGELA MVLDQIEAELEKRKLENEGQK CELWLCGCAFTLADV\SLGATL HRLKFLGLSKKYWEDGSRP\NL QSFFERVQRRFAFRKVLGDIHT TLLSAVIPN\AFRLVKRKPPSFFR ASFLMGSLG\GMGYFALHGTSR

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21458	51826	A	21586	1	929	MDPSIYFLPSKREGHLQAYIRDS VPEDPLILIFFSASSDQRPWLKA PHLPALRGFRGGGAGGGAQSR TTEDYVAWAKGNSPTSPSPRSR GGCSAKLSGPRRPPRRPGRLFN MAASANSVSRAWRTESPEGLE SLHSTSLSAISVSRPEGGAELSD TADTMGFGDLKSPAGLQV\PTI TWRTRATSRGMCHHKQMWQY LKPCPAHRLPTCVMPYV/GYNH IKSYEKEKASLPGVKKALGKYG PADVEDTTGSGATDSKDDDDID LFGSDDEEESEEAKRLRE/DTSC TI*IKESQKTCTCCQVFHLTRCE
21459	51827	A	21587	1	2405	MALRVVRSVRAVLCSLHVACE KVGMQIPRFCYHERLSVAGNC RMCLVEIEKAPKDQSMMFGND RSRFLEGKRAVEDKNIGPLVKT IMTRCIQCTRCIRFASEIAGVDD LGTTGRGNDMQVGTYIEKMFM SELSGNIIDICPVGALTSKPYAFT ARPWETRKTESIDVMDAVGSNI VVSTRTGEVMRILPRMHEDINE EWISDKTRFAYDGLKRQRLTEP MVRNEKGLLTYTSWEDALSRV AGMPPALALQSAEIAASARPPP RLGSEEPLCLAAHRLGCEEPLC LAASLESEERLCPAAIPPGNLRY VFISSAKTDKYSKLAPVEWVTV EKVPENVEVTLELGNRQSRDR VSRIPGNAIVIWFTGFKWKKTV TTLWFLNLAIADFIFLLFLPLYIS YVAMNFHWPFGIWLCKANSFT AQLNMFASVFFLT/GDQPGPLY PLDPSCLISSASNPQELSDCHYI HLAFGFSNWRSCPVLPGHCGV Q*SYSLL*QFSEA*S*PHFDQAP CSDLGEIYHWLSLPFANNEYLL LVSHLQGEEAKHPDLQ*AFLDN SGCGCGLCGLLDSLSPV*HLGA HHSPQ*LFPPCDAGWNPPLHWF GIPQ*LLEPHPLCPN**EVPSSLP VLSC*DTQVHTVGSQLFW\QVL KEAKKPMVVLGSSALQRNDGA AILAAVSSIAQKIRMTSGVTGD WKVMNILHRIASQVAALDLGY

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21460	51828	A	21588	1	2065	MLRIPVRKALVGLSKSPKGCVR TTATAASNL\IRVFVDGQSLM\V EPGTTVLQACE\RIGMQIPRFCY HERLSVAGNCRMCLVEIEKAPK DQSMMFGNDRSRFLEGKRAVE DKNIGPLVKTIMTRCIQCTRCIR FASEIAGVDDLGTTGRGNDMQ VGTYIEKMFMSELSGNIIDICPV GALTSKPYAFTARPWETRKTES IDVMDAVGSNIVVSTRTGEVM RILPRMHEDINEEWISDKTRFA YDGLKRQRLTEPMVRNEKGLL TYTSWEDALSRVAGMLQSFQG KDVAAIAGGLVDAEALVALKD LLNRVDSDTLCTEEVFP\TAGA GTDLRSNYLLNTTIAGV\EEAD VVLLVGTNPRF\EAPLF*C*EFR KSW\LHND\LKVALIRAVPVDL\ TYTYDHLG\DSPKILQ\DIASGK/ SHPFSQVLKEAKKPMVV\LGSS ALQRNDGAAILAAVSSIAQKI\R MTSGVTGDWKVMNILHRIASQ VAVL\DLGYKPGVEAIRKNPPK VLFLLGADGGCITRQDLPKDCF IIY\QGHHGDVGAPIADVILPGA AYTEKSATYVNTEGRAQQTKV AVTPPGLAREDWKIIRALSEIAG MTLPYDTLDQVRNRLEEVSPNL VRYDDIEGANYFQQANELSKL VNQQLLADPLVPPQLTIKDFYM TGEVTEINEALAENPGLVNKSR YEDGWLIKMTLSNPS

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21461	51829	A	21589	56	2352	ATRPPRGSSWCRQFSRTASAAP GRSNMLRIPVRRALVGLSKSPK GCVRTTATAASNLIEVFVDGQS VMVEPGTTVLQACEKVGMQIP RFCYHERLSVAGNCRMCLVEIE KAPKVVAACAMPVMKGWNIL TNSEKSKKAREGVMEFLLANH PLDCPICDQGGECDLQDQSMM FGNDRSRFLEGKRAVEDKNIGP LVKTIMTRCIQCTRCIRFASEIA GVDDLGTTGRGNDMQVGTYIE KMFMSELSGNIIDICPVGALVTS KPYAFTARPWETRKTESIDVMD AVGSNIVVSTRTGEVMRILPRM HEDINEEWISDKTRFAYDGLKR QRLTEPMVRNEKGLLTYTSWE DALSRVAGMLQSFQGKDVAAI AGGLVDAEALVALKDLLNRVD SDTLCTEEVFPTAGAGTDLRSN YLLNTTIAGVEEADVVLLVGTN PRFEAPLFNAWIRKSWLHNDLK VALIGSPVDLTYTYDHLGDSPK ILQDIASGSHPFSQVLKEAKKP MVVLGSSALQRNDGAAILAAV SSIAQKIRMTSGVTGDWKVMNI LHRIASQVAALDLGYKPGVEAI RKNPPKVLFLLGADGGCITRQ\ DLPKDCFIIYQGHHGDVGAP\IA DVILPGAAYTN\KSATYVNTEG *ASASIMLAVTT\PGLSREDW\KI IRALSEIAGMT/LFPYDTL/DIQV RNQIGKKSSPNLV\RYDDIEG\A
21462	51830	A	21590	246	761	MRLQGAIFVLLPHLGPILVWLF TRDHMSGWCEGPRMLSW\CPF LQSLICLLQTAI\YSVVG*VLVS HTWPWYPMGWEQVLYI*ITYA VQLTISWTVLVLFFTVHNPGLV RHTVLSSRSNVGEGETTWLQK HILAALLLLPYLAWLTVTSALT YHLWRDSLCPVHQPQPTEKSD
21463	51831	A	21591	1	1497	
21464	51832	A	21592	1	1731	

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21465	51833	A	21593	1	6626	PRSLCFSLWAEAAVLADGGLR RRRRLLRGTMSASFVPNGASLE DCHCNLFCLADLTGIKW*KYV WGGPTSAPILFPVTEEHPILSSSS RCLTAHVLGVRRRDQRPERRE\ L*IFWWGEDP\VLLTLFTMTYQ KKKMECGRMDFPMNAVLCFS KAVHNLLERCLMNRNFVRIGK WFVKPYEKDEKPINKSEHLSCS FTFFLHGDSNVCTSVEINQHQP VYLLSEEHITLAQQSNSPFQVIL CPFGLNGTLTGQAFK
21466	51834	A	21594	1263	1906	AVRGMVRNARAVLKTGGTFLS PALEPLVAGGSGG/EFSQLGAEE RKAIARF/AIDHVDRRVPVLIGT GG/TNARETIELSQHAQQAGRT ASTIDSVAHLRSMIHTVK/GAHP HFTVLCGYDDHLF/NTLLLGGD GAISASGNFAPQVSVNLLKAW RDGDVAKAAGYHQTASIPDQLI HPYESRLFKCQHVLTRGITSF*L LCPPGSLRRQGISTYHSLLHN
21467	51835	B	21595	113	484	
21468	51836	A	21596	300	780	KSGTNETIRRKARGGKIK\MDD LRG\PRCQ*EPWKRLLMTIMPS CLHLWAQNTTVSILSFVDKDLL EPGCSVLLNHKVHAVIGVLMD DTDPLVTVMKVEKAPQETYAD IGGLDNQIQEIKESVELPLTHPE YYEEMGIKPPKGVHPFGPTWPR VKPFCPRQ
21469	51837	A	21597	2	840	AIEHCQSGDNPESRRGFLLQQW LGRNPALVPHPGRTGHSQPPVT FHRHPSDCQRSPAGRFKGGPSH RGQPPPFHKSPPMTTASHLARC ARTYHQ\DSEAAINR\QINLE\LY ASYVY\LSMSYYFDRD\DVALK NF\AKYFLHQSHEER\EHC*ENL MKACRTNEGWPNLSFQDIKET KTCDD\WESGLNA\ME\CALHFE KKC*IKSLLEL\HKL\ATDKN*PP ICVDFI*DTFTLNEQ/V*KAIKRI WGDH/V*PKLWRKMGSAPNLG FGEYLF*QSTPWGDSDNES
21470	51838	A	21598	3	390	

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21471	51839	A	21599	1	483	FQLEVTPQNITLNPGFGGPVFS WRDQAVLRQDGVVVTINKKR NLVVSVDDGGTFEVVLHRVWK GSSVHQDFLGFYVLDSHRMSA RTHGLLGQFFHPIGFEVSDIHPG SDPTKPDATMVG\LQKDYSKDP WHGAEVSCWFIHNNGAGLIDG AYTDYIVPDIF
21472	51840	A	21600	1	1521	
21473	51841	A	21601	1	837	
21474	51842	A	21602	3	310	EVRANLSSQALRMWLDYGFVT PLTSMSIRGMADQDGLKPTIDK PSEDSPPLEMLGPRRTFVLSALQ PSPTHSSSNTQRLPDRVTGVDT* V\VT*PYVLCWNLC
21475	51843	A	21603	62	462	MPLPLPSAFVLSALQPSPTHSSS NTQRLPDRVTGGFSVNGQLIGN KARSPGQ\HDGTYFGRLGIANP ATDFQLEVTPQNITLNPGFGGP VFSW\RDQAVLRQDGVVVTI\N KKRNLVVSVDDGGTFEVVLHR VWK
21476	51844	A	21604	37	2883	SMDGAMGPRGLLLCMYLVSLL ILQAMPALGSATGRSKSSEKRQ AVDTAVDGVFIRSLKVNCKVTS RFAHYVVTSQVVNTANEAREV AFDLEIPKTAFISDFAVTADGNA FIGDIKDKVTAWKQYRKAAIS* EKA\GLVRASGRTMEQFTIHLT VNPQSKVTFQLTYEEMLKRNH MQYEIVIKVKPKQLVHHFEIDV DIFEPQGISKLDAQASFLPKELA AQTIKKSFSGKKTSNGSHSRRF QGHVLFRPTVSQQQ
21477	51845	A	21605	1	1008	
21478	51846	A	21606	1	435	
21479	51847	A	21607	1	676	IRHQGAAAQEGDAETPGSVERR GRRAGAEDGMSQAPGAQPSPP TVYHERQRLELCAVHALNNVL QPAA\FSQEAADEICKRLAPDSR LNPHRSLLGTGNYDVNVIMAA LQGLGLAAVWWDRRRPLVPS WPCPKGLG*ILN\LPSPVSLGLL SLPLRRRHLRWPCARL/VTVSY YNLDSK\LRAPEGPGGLRTE/LR GLSLAAALAQGLCEVLLVVTK EVEEKGSWLRTD
21480	51848	A	21608	89	316	ELLSPLLVAPGPSDLTVTGLKSF SSPSLCSLNTLLAGTSRLMVA*L YESLGQGEDLGLLTPGPEFLSIS SYCNFM

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21481	51849	B	21609	1	1920	
21482	51850	A	21610	1	1727	LPRVLGHSGHRGGLSSRRSQGL VSRFRLRALCGAGSDMWRLPG LLGRALP\RTLGP\SLWRVTPKS SSPDGPQTTSST\LLVPVPNLDR SGPHGPGTSGGPRSHGWKDAF QWMSSRVSPNTLW\DAISWGTL AVLALQLGR\HIHFQAFLAAGP\ KRVE\HCS\WHSPL\DRFFSSP\L WHPCSSLRQHILPSPDGPAPRHT GLK/ENPRLGKE\EASAQPRNFS HNSLRGARP\QDPSEEG\PGDFG FLHASSSIESEAKPAQPQPTGEK EQDKSKTLSLEEAVTSIQQLFQL SVSIAFNFLGNQMDPAPRQEGT ENMKSGDHTAAFSYFQKAAAR GYSKAQYNAGLCHEHGRGTPR DISK/SV*KAGLYYQLAASQGH SLAQYRYARCLLRDPASSWNPE RQRAVSLLKQAADSGLREAQA FLGVLFTKEPY\LDEQRAVKYL WLAANNGDSQSRYHLGICYEK GLGVQRNLGEALRCYQQSAAL GNEAAQERLRALFSMGA\ASPG APTNLTVTGLKSFSSPSLCSLNT LLAGTSR\LPH\ASSTGNLGLLC RSGHLGASLEASSRAIPPHPYP\ LEKN\VVRLGFG
21483	51851	A	21611	1104	1680	LATPDVRYCYLSTYTSLPNPAR RFFLFSLCCKFSHSH\KTATVKK YNKSEYPWDLVKAHLQGAFTS NITFDISELQNKILDLNRHTQEF QPSLEDWTEFQEGLESLNPWTY LKYHSNILYVVLGVMLFCLCLL FIVCKIGWTANRRMRAAQPGL TFFQLIHKQGDMQGAEGPWDV TNSAFHWRLYDQTANCLS
21484	51852	A	21612	364	824	LCIILFKQLSTWRTGCAQPTKR GYTELQTEGPMLKSMFLWLGE QVQILQL\HSNCIVILTTLV/FCV TNLE*FIVCKIGWTANQKMGA AKPGLTFFLLICK\QKGDM*GA KGPWDVINSAFH*RM
21485	51853	C	21613	196	504	
21486	51854	A	21614	3	142	

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21487	51855	A	21615	1178	2285	IVWLMTTGGQCRY*LSALIKL* DR/WFQRLCIHVIQRLRPVHAH LYLQPGMEDGNSFRQMFRSTR SLHIPTRDLPLSPDTTVVLHQVY NVLLGLLSRAKLYVDAAVHGT TKLVPYFSFMTYCLISKTEKLM FSTYFMDLWNLFQPKLSEPAIA TNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNYILAD HDDQDVVLFNRGMLPAYYGIL RLCCEQSPAFTRQLASHQNIQW AFKNLTPHASQYPGAVEELFNL MQLFIAQRPDMREEELEDIKQF KKTTISCYLRCLDGRSCWTTLIS AFRILLESDEDRLLVVFNRGLIL MTEGKD\TFMIVCC*TTSFLIISS SIYYAELQSTVKNLLKH
21488	51856	A	21616	1	436	
21489	51857	A	21617	369	508	
21490	51858	A	21618	2150	3120	DLRALALLLSVHTPKQLNPALI PTLQELLSKCRTCLQQRNSLQE QEAKERKTKALALWTTIITFRV GGGSNTLGVTGLRVVCSAEPPK YKC*KQN*LPTSPPNVILMTFRE VSLLACVFTDDEGATPIKRRRV SSDEEHTVDSCISDMKTETREV LTPTSTSDNETRDSSIIDPGTEQ DLPSPENSSVKEYRMEVPSSFSE DMSNIRSQHAEEQSNNGRYDD CKEFKDLH\CSKDSTLA\EEESE\ FPSTSISAVLSDLADLRSCDGQA LPSQDPEVALSLSCGHSRGLFS HMQQHDILDTLCRTIESTIHVVT RISGKGNQAAS
21491	51859	A	21619	2	4049	EEENGREYKFDVSSELLEWIWH DNMQFLQDKNIFEHTYFGFMW QLCSCIPSTLPDPKAVSLMTAK LSTSFVLETFIHSKEKPTMLQWI ELLTKQFNNSQAACEWFLDRM ADDDWWPMQILIK\CPNQIVRQ MFQRLCIHVIQRLRPVHAHLYL QPGMEDGSDDMDTSVEDIGGR SCVTRFVRTLLLIMEHGVKPHS KHLTEYFAFLYEFAKMGEEESQ FLLSLQAISTMVHFYMGTKGPE NPQVEVLSEEEGEEE
21492	51860	A	21620	58	219	

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21493	51861	A	21621	195	1187	RVPRTWLLPSFCASRSRENEGL SEFGASQTVTPSPASSVQAWEA MEPEFLYDLLQLPKGVEPPAEE ELSKGVCKKYLPPTSRKDPKFE ELQKVQQEWINATLLPEHIVVR SLEEDMFDGLILHHLFRKWAAL KLEAEDIALTATSQKHKLTVVL EAVNRS\CSWRSGRPSGA/WEST WNKDLLSTLHLLVALAKRFQP DLSLP/D/HTNVQVEVITIEVAA NFVNQKLDRLGLSVQNLDTQV GTGVILLLLIGQLEGFFLHLKEF YLTPNSPAEMVSFVTLALELL/I GRGPAQLPC/LALKVSAT/MDA KSTLRVLYGLFCKHTQKAHRD RTPHGAPN
21494	51862	A	21622	96	1350	AAGLLPPGLVPEDPRRTRNLLP FGIQGPPFALSRPLFSCVESGWA WEAMEPEFLYDLLQLPKGVEPP AEEELSKGGKKKYLPPTSRKDP KFEELQKPA\VLMEWINATLLP EHIVVRSLEEDMFDGLILHHLF QRLAALKLEAEDIALTAT\NQK HKLHSWCWRP*TGVCSWRSGR PSGA/WESIFNKDLLSTLHLLEA LAKRFQPDLSLPTNVQVEVITIE STKSGLKSEKLEEQLTEYSTDK DEPPKDVFDELFKLAPEK\LNA VKEAIVNFVNQKLDRLGLSVQ NLDTQFADGVILLLLIGQLEGFF LHLKEFYLTPNSPAEMLHNVTL ALELL/IGRGPAQLPC/LALK/TI VNKDAKSTLRVLYGLFCKHTH KAHRDRTPPWSPELTLTASKAQ SLPVSPAGGPEAAGCPPTVPLFP
21495	51863	A	21623	1	87	
21496	51864	A	21624	45	277	
21497	51865	A	21625	171	511	GKFRYSPALHSWATRLRTSTAA GHCCMNSSQNKLSSKSWAMTR HALNVKRFTIFQSHQCSLSKKV NLSLFQQGAERLPSQELTHLLL QEVRCE*RDFPPEEATWTGLPV LPSQ
21498	51866	A	21626	276	387	
21499	51867	A	21627	1	218	

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21500	51868	A	21628	139	9009	ESSEDVSGGLPFLVDLGFRSVC VSLFHVKNPVQWDQKLPKKKK PVRSYCGSKLLQREVIQPDVME EMVVSCVIKHLNLVDALQSLIN FQYQEEHAEEYDLLCKIMGETF KKLNAMERQLQNKMKELELLC SMKEVSFDGNDLENMVLSLRE KFLQEVNSLIQKPSHPLAKTKT LVKSLMNRAELLLHVTIAAQSG LTRSISGTPAETPACKSASETKV ISHAVRQPVFLRSMSAPSDLEMI GNEDLEFTRANQRR
21501	51869	A	21629	1697	2056	
21502	51870	A	21630	237	1545	KPENKKSRTGRNRTKSTPGYRA /RPAAATARISARSTK*WKNSL AGRWARHICWTLWALIPRITLR /HVMAAGFPQRMQKDYRDAID ALCDANRFGQKKRLGFWRYKE DSKGVGLCSYLLIGFYYTDPKN GAAAMKAFVVTRVGDVFLAFA LFILYNELGTLNFREMVELAPA HFADGNNMLMWATLMLLGGA VGKSAQLPLQTWLADAMAGPT PVSALIHAATMVTAGVYLIART HGLFLMTPEVLHLVGIVGAVTL LLAGFAALVQTDIKRVLAYST MSQIWLRCSSRLACRHGCGGSL ECLQHEGIPYSRMGRPHTTSAL RRFTSEFGMGSACFTLGYFFMY KQAVILLLMLFTASVSAACTLPI AIDHGTPGPAELLTVALRYNLS SYDAAYLELALRLEIPIAKGSPN FAFRRAATGNEGIKMHFLRNK GILWI
21503	51871	B	21631	1	1440	
21504	51872	A	21632	525	716	PKTPAGPVEPMHQVPSSKRVPT RDKRTRGDSTRHSGQSKPTKRY NHAYEI*PRIKWFIPDAGC
21505	51873	A	21633	8	136	
21506	51874	A	21634	1476	1611	GCDPAPGLPAPPHT/QP/DH*NQ RQIGIG*FLTGTVPATHLRQRLA AA
21507	51875	A	21635	461	827	AALQMRDTSDPADCGEQSVCG YSEPVPEYACFHRIQDLHDTET AACFSHAGSGRTHV*SQSEHAA GSVLWSYRYRC*TGTAGYTDR FSQQRCHVRRGISPRCWPEYQS RSWCRLFPSPESAG

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21508	51876	A	21636	1	3735	MAEASVFQTVDPWRPGFATIPD FLKERYDKTTRIIIDFCFLIATGV CFLPIVLYSGALALNSLFHVGES LQISHGAAIWLLVILLGLAGILY AVIGGLRAMAVADSINGIGLVI GGLMVPVFGLIAMGKGSFMQG IEQLTTVHAEKLNSIGGPTDPLP IGAAFTGLILVNTFYWCTNQGI VQRTLASKSLAEGQKGALLTA VLKMLDPLGLKPDLLAYNTAL RALIPQRLIAFDDAVRSTLKEEE KLVNSSDWGY
21509	51877	A	21637	840	1064	WSVENYHRRGYGGHIPLPAASP AVAAQWCDAGR*VPPAARRW HRHQVYLTYLITLDRGLSRARF CIPSAHCSAY
21510	51878	A	21638	979	1409	RLVVDIFHDNRHAFPRRLVSDA AAHNACTQHRGLFRGFNVFGE FLRFAFYILIVKENADQCAGFV GMRQRDKTFVFQV*GFFTTKT GRSFNGFYCGDGGRIMF/LPLFV RPSL*RW*SSWWLQSCSVLVVP ASADVLLSSRGRR
21511	51879	A	21639	903	1397	LPTLPMMVCCTTPTSSRKHWM *NPSTLT/HAWVPYTNFSPIYEG KCGMSGARVEGKVIYETQSTH KLLAAFSQASMIHVKGDVNEE TFNEAYMMHTAASPHYGIVAS TETAAAMMKGNAGKRLINGSI ERAIKFRKEIKRLRTESDGWFF DNAAGYIDTITLGGPS
21512	51880	B	21640	1	5305	
21513	51881	A	21641	129	723	LITARGQVADRNLRDLLAPWV PDAPSRALPEMTLDSRVAAAV DLFVARIGHQADGRRYIPQAIA QGVAAIIAEAKDEATDGEIREM HGVPDIYLSQLNELLSALAGRC YHEPSDNLRLVGVTGTNGKTT TTQLLAQWSQLLGEISAVMGT VGNGLLGKKKEKAAIQYNTLC KSCTLTHPKPHNESDH/IRCRC*

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21514	51882	A	21642	1	2230	MMRTSGGTRDNESSSDDERER ENRLSDEKSNEYANLVGGERY EPDEENPMLGFRGAGRYVSDSF LRLCSSLEIVKARETVALIQGLK H\DLLADDTALRALIPQRADRFP MNAVRSTLKEEEKLVNSSDWG Y\DAQAFARWRPEYGYFAKQA GFTVKTSASLAALWQVVNQIG GKERYFFGNILWQTRALMDRAI GHKLAKGRPEREYLQTGDAVD SWKVIVVEPEKQLTLLFGMKAP GLGRLCFSLEDKGDYRTIDVRA FWHPHGNRAEREKPRFQPYSRR KSFIGQNMLLPMSIMPPVFRRVI CPLGVARLGKFRDPVYLVCVFT RQIFRYYTSGDEFLQINTTGGED IDDIDDIKLFVYEESYGISKESH WREAINAKAMGAMTLNWQEK RWQRFFNSEEPGNIEPVYMLEK VENQNHAKWEVHNFTMGYQR QVTEDTYEYLLLNVVGVPVPD NIHPMTKDEAGVWSWRTPILK GNLYEYFFNVDGVRSIDTGTA MTNPQRQVNSSMILVPGSYLDT RSVAHGDLIAITYHSNALQSER QMYVWTPPGYTGMGEPLPVLY FYHGFGDTGRSAIDQGRIPQIM DNLLAEGKIKPMLVVIPDTETD AKGIIPEDFVPQERRKVFYPLNA KAADRELMNDIIPLISKRFNVR KDADGRALAGLSQGGYQALVS GMNHLESFGWLATFSGVTTTT

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21515	51883	A	21643	1	1549	MDASGHHVRGFASGMGCCRV RRTMKRETGGGRLAGFRLVGT LGQHLGAHRSASKGHQILAAA RHVDRLAK\LQLA\NVSCHEVD LSWPDNLPALLQDIDTVYFLVH SMGEGGDFIAQE\RQVALNVRD ALREVPVKQLIFLSSLQAPPHEQ SDHLRARQATQ\EIRSEGNVP\V TELRAEIIVGAGS\AAL\EVM\RD MVYNLPVLTPPRWVRSRTTPIA LENFLHYLVALLDHPASEHRIF EA\AGPEVFSYQQQFEHFMAVS GKR\RWFDPPSPLPT\RWISVWF LNVITSVPPTTARALI\QGLKHD LLADDTALRALIPQRLIAFDDA VRSTLKEEEKLVNSSDWGYDA QAFARWRPEYGYFAKQAGFTV KTSASLAALWQVVNQIGGKER YFFGNILWQTRALMDRAIGHK LAKGRPEREYLQTGDAVDSWK MIVVEPEQQRTL\LFGMQAPGL GRL/CCFSLEDKGDY\RTID\VRA FWHPHGMPG/L*F*WLLMIPAH LFIFRGMAKQIARLAVPSTDLID
21516	51884	A	21644	201	363	SLRGSRTAASPCWAVPVHVPG HGAGEPAHHPGHQP*LPPPHPH VLLPLQPVLA
21517	51885	A	21645	3	440	PFSLPFSLGLTASLFMNTWLAIS SNCDGFIPASPACFCSFLLMSSA L*RTKAM*IMC*FSGLSGSKGV YIR*ASHSLS*NCAGLSSFP*MT SESLLTFVAF*APLINPSKRASLS RFSLCISSLSCGSNWGSVPGNW VLPYSWGF
21518	51886	A	21646	359	543	VVTPDSGSSH*KANSFCLSGAN LMLKKASFRSKQVNQLSSAGS NPSNMYGLGTVGCKVTVA
21519	51887	A	21647	2	582	
21520	51888	A	21648	3	574	
21521	51889	A	21649	1	195	LCVFFVLVSFFLSPLDSQLAVV C*FDGTGIGMYLTSAVSPPPRN GVVASVMYAVVTPMLNLFICS
21522	51890	A	21650	2	457	
21523	51891	A	21651	21	545	PPCTSLRPLHAFSGKMTHLNRG TLSLLDSQLHNLIALQMTCFKD VEIPNFFWEPSVTPSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGVGGYLGSDVSSSP RKRAVASVMYTVVTPMLNPFI YSLRNRDMKSVLRRPHSSAV

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21524	51892	A	21652	899	1039	LWTSSLTAESSPMRAA*LRETSI VSAASRAFSAALSSSALRAFSA C
21525	51893	A	21653	804	1390	QGTIILKVLRHLRWTWIPSRASL RTGYCFCLTGWTPGLTSISTGA WLTANPGGLSSAHTLGHRLAR AGLISWPGSVKKSLHSSSRGSIR VIMTPVPGNFSSKEPCSVKEIVA LSLLSKSLPNKGKGQSGMYKN* *ITLCPPIVQVWGKQKACFAET PMAPMMSIVFLDKGATEAVTT ECSALVSTRKSMSLPPTV
21526	51894	A	21654	84	730	HLSDSKSQVRYQPSADLSFLLG HYNPQSSRRVLSVLDSQLHNLI ALQVTCFKDVEIPNFFCDPSQLP HLACCDTFTNKIIMYFPAAIFGF LPISGTLFSYSRIVSSILRVSSSG GKYKAFSTCGSHLSVVC*VYGT GVGGYLSSDDVSSSPRKAAVAS VMYTVITSMLNPFIYSLRNRDIK GVLRQPHGSTVQFQYLLICSIPF VVWVKKGSKVK
21527	51895	A	21655	1049	1979	
21528	51896	A	21656	2244	2901	LRCLSLPFLEAWKRDMLLSVM A\YDRFVAICHPLYHSAIMNLCS VGFLVLLSFFFF\LSLSDSQLHN LIALQMTCFKDVEIPNFFWEPS QLSHLACCDTFTINIIMYFPTAIF GFLPISGTLFSYYKIVSSILRVSS SGGKYKAFSTCGSHLSVVC*FY GRGVGGYLSSDVSSSPRKGAV AAVMYTVVTSMLNPFIYRLGN RDIKSVLRRPTEHCLISKK
21529	51897	A	21657	1	2850	

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21530	51898	A	21658	1	1703	KKMALTSFLPAPTQLSQDQL\E AEEKARSQRSRQPSLVSSRREPP PYGY\RKAWIPRLLEDF*DRGA FPEIHVAQYP\LDMGRKKKMSN ALAIQVDSEGKIKYDAIARQGQ SKDKVIYSKYTDLVPKEVMNA\ DDP\DWQRP\DEEAIIEITEKA\R VAL\EKSVSQKVA\AAMPVRAA *QIGPLLQYIPIHTISGKGVAIQT SWS*TRRVIR\MVEMQ\KDPM\E PP\RFKINKKIPRGP\PSPPAPVM HSPSRKMTVKEQQEW\KIPPCIS *LGKMAKGY\TIPL\DKRLAAD GEEGLQDSYTLNGKFSAKLAE ALYIADRKAREAVEMRAQVER KMAQKEKEKHEEKLREMAQK ARERRAGIKTHVEKVKYFSTVH TEDGEARERDEIRHDRRKERQH DRNLSRAAPDKRSKLQRNENR DISEVIALGVPNPRTSNEVQYD QRLFNQSKGMDSGFAGGEDEI YNVYDQ\ALIGGKYMAQSIYRP SKN\LDKDMYGDD\LEARIKTN RFVPDKGVFLVQTRRQRGREGP \VQFEEDPF\GLDKF\LEESPTAM GGS\KRPSG*PAAPREHGAWKA RKRRKE
21531	51899	A	21659	2	1588	CLRRALPGSIESAPTAPPPPPSGE GSQAYISRLPATLIVLILERRQL LGVWRRARCCSLINLAHRRHC GMPTRESPCAILARRYEGRRSPS TVAQPPPPPPPIELAPSTSETPIQ ATRGAHPAQPSS/VPPA/PARPPE RPPVPEQGPSGTHPDPTP/PGPT NAPQRPSAP\PNTTN*PTRHMH QLPDAA*TPYPAYGSDYL*AR* DATASHQASCTN/SPDAA*TPYP AYAKIERA*ENPVPSAIKIIGRSS SSGRQASPWGMA/SPHWRSWR MGPNGSGKRPRRAAERISCCRN AQGRTHSQKAYIQQQPQCCVN VHLQPPD/PTPAQ/PSQTLSPPDS /PAPPLPAYPS/TQHPTAPPPTSSP MSS/RIVKPHPQHCGARPGQGK ERDETERKDAKERNRRTATPTT RHTDRLPRTAHGPPPP\PPPPPPP PPPPPPPRDSPRRPRRREKPEQQ KEGGQTGRTQRKETARRGEER ETGRKKTRGAPPPRPAAARRPH ETAETKRRPPARQHRPPRRRPS DGTERTRHQLGFIMLGLLSWN

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21532	51900	A	21660	2	192	RVDICSTNYCWWLYPMTSGPSF SYV*GP*EEDVRE*MCGRDGL* YLSIGVVCGFICQHHNRAQ
21533	51901	A	21661	783	2119	GSEMPVTVMLTLGEPGHFMSS LG\CWCGVEDEAAPSKQSIYIQ RETQVRTPMAGVSPKKAHPCE MCGPILGDILHVADHQGTHHK QKLHRCEAWVNILYDSGNFHR RQNEHIGEKPYRGSVEEALFAN RCKLHVSG\SHLSSVRV/EKDFL LRSGLLQQEATHTGKSNSKTEC VSLFHGGKSHYSCGGCMKHFS TKDILSQHERLLPTEEHFVWCE CGKSSSKYDSFSNHQGVHTREK PYTCGICGKLFSSKSHLLVHQRI HTGEKPYECEVCQKFFRHKYH LIAHQRVHTGERPYECSDCGKS FTHSSTFRVHKRVHTGQKPYEC SECGKSFAESSSLTKHRRVHTG EKPYGCSECEKKFRQISSLRHH QRVH/T/NERAYECSESSLIKYW RIHT*VRSCDCSKCGK/CFTQRS ALLGYWRVHTR\KSPYK*NKFG QFCSHTSVFLQDYS
21534	51902	A	21662	84	437	KMTSTQPVKFSLFASHSVPCGQ SFPGRRAFAPAMPRRRIPSSDHL PEPGQSHQHVNRQRWACRELI AAFLPSSYRL*LVETGGEIGQRN RASCHSPFPAGSSPGIFQTEIGKP CLLP
21535	51903	A	21663	69	446	
21536	51904	A	21664	880	1365	
21537	51905	A	21665	1705	2196	RQNQREGDDDTEDQPPRPGTQ MTELFFLIQMLCFMANALRQL VHPL/MGNVHEYFADLKMPAC AVSAFLCAMHRSITSMFE*DNG PGPADADAR\LDMRIQVFMFCA NTLPARVLQRNKNPGQDHPET AERRAESQRIIEKGLKCIQGKGI VNSISMKEGVDAFIH
21538	51906	A	21666	1	1147	
21539	51907	A	21667	254	557	AADEIGGIAVETVTEDAHLLCG CTVVAIPPRICVSAGGGAGDRK SSVRFHQNLAQVHITRGV/VWT MTNSHIITCCATAFGTTTSPSPT ESTGVPCGRRNQH

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21540	51908	A	21668	557	1031	SSRNASGAVRKISRGMPDKKW NMALT*HSR*ANFSPLPVSGLS RRKICTIPRAQRIR*PICADRLSV ASPAACGI\AYTRRYSHDGATA EKYAHLQSRFRQQCRQFHPAA YDESPHRNRRRKWRPTYRCHP APDHRTACLRSAFYGNAPGCV QTERSW
21541	51909	A	21669	572	825	QARISTSFFRESLPSRHPVPRYR PLEAFWTPCTRGYYRFFFSPAR ENAEYRTL\KHWAKFLLVRASF PGASTLCCKSPGRTISV
21542	51910	A	21670	303	899	EDNYSGSSLYCFDDVASVQMP GSNGNCRR*CAGKTSG/TWRNS LVRQWLLTAQKKTLLHAVSNL PKTWAQILFSKQRVLRSPLNRH LIW*CAAVKL*LLVLYPAIRQSI SSKSIAKSLSRRYFR\LPIGDSM* NRW*RIFTIIGMYIGTAL*SDGAI VVCRLCENLPGSFHQRHQRCD AASLAGGSEPIAFSRAGRTPGP
21543	51911	A	21671	1	1320	
21544	51912	A	21672	99	761	IDNAPPDQTTVHAFAANSENHS PPQLPYETPDDADPTHQAFSRW RHRPQAYSADALLRERLPPTHR HRGQSPDSLTSLPYWRGRRKY RAAPALT*TPPDTLFDSPP*PAV PPPVAKELPVTAQRQVHNAMS ANSFVIFHPVKIRNNIVLQPAIAI QRRNGHGVTRCAAALHSRHGS LSVARHRVHLPVCRQADDKPA PAPLRPARYCLCPNQSAAVRYL R
21545	51913	A	21673	62	680	SSRNASGAVRKISRGMPDKKW NMALT*HSR*ANFSPLPVSGLS RRKICTIPRAQRIR*PICADRLSV ASPAACGI\AYTRRYSHDGATA EKYAHLQSRFRQQCRQFHPAA YDESPHRNRRRKWRPTYRCHP APDHRTACLRSAFYGNAPGCV QTGPVRRSGAASASSPAVFLSG TSPWSFARTIALVRGRSRKSTRT RLWHISAHC
21546	51914	A	21674	411	481	

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21547	51915	A	21675	402	915	RLASKLFTTVTPRGGVGELQAT TRNAAVAGIKRKRSNRGRPAEE PELTADRGQGENEITEAATAAK ARRTMRPKTGNQNPDKHRTRG LQICHTFNANGNRARCSAANA MAATISGLSSGLSGTGWQETIR PPLAAIF*SSCASNDIHLPKSFLA LPNGTAPLNGLPSIAS
21548	51916	A	21676	1416	1832	GSAPRQRHLAGRRPVTTRPKHV SHHGPQENSAHRLSHVDNESTC IVCGTLRLQHSARYFPPSLPETL FLAPVNHSV/EYNWQAAVPK*I Y*HQTFPGRDCQHLLFHFVRKF GVRESI/AQVVAVRAATSAWRY SRSSAITL
21549	51917	A	21677	97	300	
21550	51918	A	21678	756	1179	RRRLPSPYCRAAAGSSPSYECF AHQRSVASSRGHTGTRQFYRE HWFLRCIRRLSGTRLLAYHRCF QPHLACSGKRAVSASSTRSADV AAWYRV/CAKPFSSSS*VQEDL SYLRFSAS*P*TVIL*PACRKPCR KRRGQRRWR
21551	51919	A	21679	3	1279	
21552	51920	A	21680	1	2448	
21553	51921	A	21681	317	1985	PNTPLTSKLPLLTHPLTLLTPSA SGWQKTTKLSCVF/PETEKYAH ERLAHHVAQGANQYAPMTGV QALREAIAQKTERLYGYQPDA DSDITVTAGATEALYAAITALV RNGDEVICFDPSYDSYAPAIALS GGIVKRMALQPPHFRVDWQEF AALLSERTRLVILNTPHNPSATV WQQADFAALWQAIAGHEIFVIS DEVYEHINFSQQGHASVLAHPQ LRERAVAVSSFGKT\YHMTGW KVGYCVAPAPISAEIRKVHQYL TFSVNTPAQLALADMLRAEPEH YLALPDFYRQKRDILVNALNES RLEILPCEGTYFLLVDYSALSTL DDVEFC*SLTQEHGVAAIPLSVF CADPFPHKLIRLIQTAAINLLVN HERRANAVINVDHAEIPFLRIIL PFLRQRQHHAVIIDHHPNAELL FQQIFHLHRRCPRRFRHGLRHA GHRINLTVDFQRQVDGMVRPQ FTVAMPAIFRFRTAAPSASVHQ SGVRLPYQFMALIASDNFCCW VHGGYITLAVNGNDAIGSVFNN QIVKCPRFTQCLGEVINTLTDLP HFTGQLW

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21554	51922	B	21682	160	312	
21555	51923	A	21683	80	452	
21556	51924	A	21684	158	1980	REDTAHLPAVGFLPQNPFRAIR ASGEMLLPLLLLLPMCWAVEV KRPRCV\SLTNHHFYR\ESKPFT\ CLDGSATIPFDQGQRLTYCDCK \DGS*RSQATAA\CP\NGQA:H\C HQTLGL*SPL**SPSKPGSNDGV CDCCDGTDE\YN\SGVI\CENTC KEEGPVRRRESLQQMA\EVTRE G\FRLEEDPLFEGLGKKAREEK QKKL\IELQAGK\KSLEDQ\VEM LRTVKEEAEKPEREAKEQHQK LWE\EQLAGFQGPNREQDARA ADAFKELDDDMDGTVSVTELQ THPELDTDGDGALSEAEAQALL SGDTQTDATSF\YDRVWAAIRD KYRSEALPT\DLPAPSAPDLTEP KEEQPPVPSSPTEEEEEEEEEEE EEAEEEEEEEDSEVQGEQPKEA PPPL\SPPQPASPA\EEDKMPPYD EQTQA\FIDAAQEARNKFEEAE RSLKDMEESIRN\LEQEISFDFGP NGDV/FAYLYSQ/CARDLTTNE YV/YTRLCPFQVLFFAGNPNSG VFPTSLGHLGASW/VLGPDHGQ VSVAMKF*ARHGACWQGPNPL QHP*RFWFGKET\MVTKHPQ*P SRCEYLHGS**TPAA\CPEPPAL KQPQPKD\DHDEVLSWMGARE
21557	51925	A	21685	59	359	LLRIGNDWCIPKGITPTTHIIKLP IGEIRQPNATLDLSQSVDNEYY CLLLAKELGLNVPDAEIIKAGN/ GARVSGRTF*QALEC*ANGFTS LATGGYVSDI
21558	51926	A	21686	1	213	MSIAVTTTDPTNTGVSTTSSSSL TGSNAADLQSSFLTLLVAQLKN QDPTNPMENNELTSQLAQISTV SGIEKLNTTLGSISGQIDNSQSL QASNLIGHGVMIPGTTVLAGTG SEEGAVTTTTPFGVELQQAADK VTATITDKNGAVVRTIDIGELT AGVHSFTWDGTLTDGSTAPNG SYNVAISASNGGTQLVAQPLQF ALVQGVIRGNSDITTFGVNMKL AHLGRQALMGVMAVALVAGM SVKSFADEGLLNKVKERGTLLV GLEGTYPPFSFQGDDGKLTGFE VEFAQQ*FAHGQQRRRFTKQFS DFAGGAAEKPGPDQSNGKQRA DVAIGTNQHGQRD

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21559	51927	A	21687	1	2339	MSGGQTEKQAQLIRDFQPDMI MVTPSYCLNLIEELERQLGGDA SGCSLRVGVFGAEPWTQAMRK EIERRLGITALDIYGLSEVMGPG VAMECLETTDGPTIWEDHFYPE IVNPHDGTPLADGEHGELLFTT LTKEALPVIRYRTRDLTRLLPGT ARTMRRMDRISGRSDDMLVLR RRHLCRPSACQLCRPPSLPATD RVLELFAQSGAQWLVILGDVL NHGPRNALPEGYAPAKVAERL NEVAHKVIAVRGNCDSEVDQM LLHFPITAPWQQVLLEKQRLFL THGHLFGPENLPALNQNDVLV YGHTHLPVAEQRGEIFHFNPGS VSIPKGGNPASYGMLDNDVLS VIALNDQSIIAQVAINPAPEKEG FLIMEQRRLASTEWVDIVNEEN EVIAQASREQMRAQCLRHRAT YIVVHDGMGKILVQRRTETKDF LPGICATSKVRKLLCKSAALLP VSELLLVLLTPVFVGSAVIGKL GAFAIHIDGITVKRRLVRNTVL QFCGRSRQPLEYVSAGDTGPVL RALKRMMAMRHYMRSQTVKG VTDTRAIDEVALSVAQVEEMY RYLAIANYEDRFVIPTSHREMA GDAFAERNGCGFTFGDGCHGS DSKFNLFNSSRIDAINITEILKVI GLLMEYPDELLWECKEDALALI RRDAPMLTDFTHNLLNAPLLD KQAEWCEVFDRGRTTSLLLFEH
21560	51928	A	21688	391	631	
21561	51929	A	21689	2779	3348	LMQLHNGLPVAGLRQFCQQLV IQRLYFFTTATAHQCTRHMCHR HRSLLTAHRQMALCFQYVDDL HHAFADVLINNACYPLLMGEQ GVFIYNGTQQLLHWVIIDSRQD HGFGGL*KSRIVCERRRL*SQH GQFVFRHHVPDHRIDIAFNNAL *TLVIREISSVPASVGVGIDFPGG AATWAGPVVIKPGQS

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21562	51930	A	21690	1	1239	MPNVDVVGEMVNTMSASRSY QANVEVLNTEKAMSIAVTTTDP TNTGVSTTSSSSLTGEQRRRFTK QFSDFAGGAAEKPRPDQSNGK QRADVAIGTNQHDAARILRKG TMTTLLNPYFGEFGGMYVPQIL MPALRQLEEAFVSAQKDPEFQ AQFNDLLKNYAGRPTALTKCQ NITAGTNTTLYLKREDLLHGGA HKTNQVLGQALLAKRMGKTEII AETGAGQHGVASALASALLGL KCRIYMGAKDVERQSPNVFRM RLMGAEVIPVHSGSATLKDAC NEALRDWSGSYETAHYMLGTA AGPHPYPTIVREFQRMIGEETK AQILEREGRLPDAVIACVGGGS NAIGMFADFINETN/VSVGPQH AYLNSSVRAD*VSITDDEDLQA FKTLTASYKTTPAAAKTSLHVP
21563	51931	A	21691	32	1778	WDARVFSHSGWVLYLIRQYCSI SAVSSCGSTTGSACSATSWATA TSDSVTHLRLFSYRGSDHFRMR RFNHFRLRFGNLNGGFYDTGHF FNNWRANNRFDSGGDRDLSHH RLHMYFFLFALLFNLYILRTYN WIADPDFARGQFRRRARYGQR HWRLGWITLVTIATTTLTTYAQ VTRRAARTTRHATVVTVISIVL FLLFWCSLRYDWHYCILILRSTP SVLSQYPVGNELRRRRLVHLHL LCTYSDDDSRDPRYRQESRTRN GVVPVIVNIDVHRFGQTGDQH GAMIIPVIFLLNVAMHERASGHI PNGNRTYYLSRSQPPVFALMVE LFEEDGVAVARYLDHLKMEYA FWMDGAESLIPNQAYRHVVRM PDGSLLH\RYWCDCHTSCD*SW LEDVETAKHSGRPPNEVYRDLR AGAASGWDYSSRWLRDTGRLA SIRTTQFIPIDLNAFLFKLESAIA NISALKGEKETEALFRQKASAR PMREYETGEQWDKPNGWAPL QWMAIQGFKMYGDDLLGDEIA RSWLKTVNQFYLEQHKLIEKY HIADGVPREGGGGEYPL\QDGF GWTNGVVRRLIGLYGEP

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21564	51932	A	21692	1	2514	MKTLIARHKAGEHIGICSVCSA HPLVIEAALAFDRNSTRKVLIEA TSNQVNQFGGYTGMTPADFRE FVFTIADKVGFARERIILGGDHL GPNCWQQENADAAMEKSVEL AVVIDLWSRAVIGWSMSPRMT AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK RHNLRGSMSAKGCCYDNACVE SFFHSLKVECIHGEHFISREIMR ATVFNYIECDYNRWRRHSWINS LLSQKRNTQGRIEDGRQH
21565	51933	A	21693	1	1527	
21566	51934	A	21694	792	1602	HCLSARRYELVCQPK*AFVR*L LR*IAVLR\HLNIQHLRRSHSLR HGRRHTRKGERGTINIVNGTPI HERSRNIDNRRSPSPYIRKRGAH TELRSDHPLLINQHWHHFAGM VAVTNGRIVAVIRHHDQAIIWL HRLNKPGKVTVNDLQTFGITCD VFCMTSEVGFLNVGANKRRRM GVKFVEGDIHNPLAIHQILPAH AIRIVDDICHLTHQHGWHACFI QFLWHLHFFIDAIAHMHDLETV VISARTRRIDTNKAPFFAFCGIE
21567	51935	A	21695	1	1530	LSQQTVNTLQAGHQTIHFFMG VIHGQRRPTHRRDVVIGHQWH CAVMSGTHSNAVIIEKTANIIGV VFTEIKSNNAKPVLWAIESNAA ATDGEIVFDGEILKSACEINDSD KKIEVALGHYNAEQFRNIGERS PKIPFTIPLVNCPMTGEIANILGS KPGTIFTMLRDTGGIKPHERKR AVAHLTLSEREEIRAGLSAKMS IRAIGYWR*IASPSTFSRE\VQRK GGHR\YYKAVDANIRANRMAK RPKPCLLDQNVPLRKLVLEKLE MKWSPEQISGWLRRTKPRQKT LRISPETIYKTLYFRSREALHHL NIQHLRRSHSLRHGRRHTRKGE RGTINIVNGTPIHERSRNIDNRR SLGHWEGDLVSGTKNSHIATLV DRKSRYTIIVRLRGKDSVSVNQ ALTDKFLSLPSELRKSLTWDRG MELARHLEFTVSTGVKVYFCD PQSPWQRGTNENTNGLIRQYFP KKTCLAQYTQHELDLVAAQLN NRPRKTLKFKTPKEIIERGVALT
21568	51936	A	21696	2	140	IITNSISRPGDPPMSDPHS*SPAS SSAKTETKSLFNAFLV

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21569	51937	A	21697	1817	4083	KGLLTSFHYIKTPEVPNLCVEG GTRLQIWPACSSTGSGGTCWK APPQPPRPPTSSSPS/PAPPSEAF VLSAGAMQLEAGAYSLVIIKES KNNVGVDVIKRKHFCTAGGNV NQYNHYGKHCVLSCSGPASGA QPLYRMAQPPSPPNMAAGIPPA ARISSSITSPLLKPSWLHLLAHP VLQAHLTEEGLGRSHHVQRGQ CLVSKSVFTNACWEMQNVKRF TDFIPLHKNTRGPEPLCRRRNQ APNMACMQQHWQRRN
21570	51938	A	21698	247	281	KPGKQHSMLK*SALLPSAHGPT S/CKEARCHPVQILPPELLF*MP KKICPPLCYLWTVKAWETTFH AEV
21571	51939	A	21699	531	716	PRRLRAAPPDLGGFRLLPR/LPE ASGCSP*SQRLFQKAPSPAPCS WRRSRFCVKTCVLPMGGQ
21572	51940	A	21700	202	606	ITCLHAHVTWCQILPYLMLPAP LLRPLPTPLTVAGVGQSLPEIQL SVTLPLQPGRNQGSLESRHLVS WAEPP*DPAVSALPLQPGRNQG SLESRHLVSWAEPP*DPAVSAL PLQPGRNQGSLESRHLVSWAEP
21573	51941	A	21701	444	1167	FRLHGHLERGPFYFLSPLAVQS SQSCLRRFTTRYHLP\YVLNRK NSWHVAHIFRRHAKPEEQAPIY SHIHFTSDLDEVLNDPDVKLVV VCTHADSHFEYAKRALEAGKN VLVEKPFTPTLAQAKELFALAK SKGLTVTPYQNRRFDSCFLTAK KAIESGKLGEIVEVESHFDYYRP VAETKPGLPQDGAFYGLGALFT NQQGFFKSSLLSIFADSSSSVAG RSPHNLVKKRGGIVAISAFAG
21574	51942	A	21702	1	668	

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21575	51943	A	21703	1	1308	MRVYMDGRLIVSTRQRKVLAA GPMLYAATRAPAFTMSGDNLV RSHASIYMTSCHTLLGEQAGYA VFGALLPAITLLHLNSACCIVYV SCLLADAGHRDSLQQAGDKWT TTDSYSSSCTSETLGSACVRYA HSSRNHVRFALSDLDEVLNDPD VKLVVVCTHADSHFEYAKRAL EAGKNVLVEKPFTPTLAQAKEL FALAKSKGLTVTPYQNRRFDSC FLTAKKAIESGKLGEIVEVESHF DYYRPVAETKPGLPQDGAFYG LGVHTMDQIISLFGRPDHVRL* HPGALRNKSPIWTNPFEAQL\FY G\DLKAIVKTSHLVKIDYPKFIV HGKKGSFIKYGIDQQETSLKAN IMPGEPGFAADDSVGVLEYVN DEGVTVREEMKPEMGDYGRV YDALYQTITHGAPNYVKESEVL TNLEILERGFEQASPSTVTLAK
21576	51944	A	21704	199	706	SHDVCRINADRQRDRNNRRQR RSLRVYKLGNQQQNNGIGPRIL FHHFTQYALNFRHMRTEHGFC HPCDTVHRHDGDHTGTEDFVF/ WR*TRDWFWSG*\YQRPGQQH KHLNNQYHRQRFAAEGWTQV RISTKKGDYSDCPEENPHCQPV AGRYHYSLVGRVSNATLARLIR
21577	51945	A	21705	354	569	SRAVCWQVGTRLWAIFGVS*E LQRHVLVVFAGFWIVKNSRNL FLVCRAEHKRSVVKGLLRQQG AGLLVPLS
21578	51946	A	21706	373	462	
21579	51947	A	21707	1	1293	

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21580	51948	A	21708	1	1371	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAVYGIAWMA ETMFAPACYGYYILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPFQSVKAD IATNPFKRPGGAFIRITQTFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTEGAIPFAAADPLRVIPSIM VGSVCGAVTAALVGAQCYAG WGGLIVLPVVEGKLGYIAAVA VGAVVT\LFV*TC*KVWRVKM GLRLMKKKTTWIWILKLI
21581	51949	A	21709	961	1116	
21582	51950	A	21710	228	388	RRGRNRYPALQ*TMFLPADGP ARCLSRQAAILKESVLPK*GRP DVVFSPAYPY
21583	51951	A	21711	1168	1851	LHRTGQRPAAQRTETHHPFFNH FARLQVDTVVINHHQHTVAFQ NRTFRSEI*RNNVDIFQPDVLPD ILLGPVREREDADAFAFVNLPV VVVPQLRALIFRIPAMEAVTER VNSLFSAGFLFVTARTTEGGIKT VFVQRLFQAFSFHNIGMFRAAV HEWINPHRHAFRVFMHQQFAA VGFSSTIAELIHLAEFPAGIDMQ QRERQRTWIKRLARQMQHDAG IFTDRVEH
21584	51952	A	21712	1	2653	
21585	51953	B	21713	632	709	

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21586	51954	A	21714	1	1214	MHDQQVIDAYHPDLRRTRAAS QSIIPVDTKLAAGITRFFPQFND RFEAIAVRVPTINVTAIDLSVTV KKPVKTDVGGAGTVKLNRCQI ARISRQDVITPPGCVFEKALTLL IASGRNDTLARQNNHTKESLVE KPFRKILVIKMRYHGDMLLTTP VISTLKQNYPDAKIDMLLYQDT IPILSENPEINALYGISNKGAGTF DKIKNVLSLIKTLRANNYDLVI NLTDQWMVALLVRCLPARMKI SQLYGHRQHGIWKKSFTHLAPI HGTHIVERNLSVLEPLGITDFYT DTTMSYAEDCWKKMRRELDA LGVKDHYVVIQPTARQIFKCRD NDIISKVICMIRGSPTEGRWSVF FFYPADFTFVCPTELGD/GC*PL RRTAETGRRRIRSIYRYSLHPQS
21587	51955	A	21715	25	1086	
21588	51956	A	21716	1	1113	
21589	51957	A	21717	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21590	51958	A	21718	1	2076	
21591	51959	A	21719	2742	3109	VWTEGTGNASRARR/WKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLEKRAV SATQLMAKAVKGQSSLLPVSL VKKKNHPGALIRKPPLPARWPI LLIQLARQVSRLETGQ

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21592	51960	A	21720	174	1608	TAAKRKIPSASIRSIND*KY*VC KRT*CVGQLAA\ENADGTVAEY NGYHVVFALAGSPKDADDTSI YMFYQKVGDNSIDSWKNAGR VLMNPLMILVKIIKLSLTLACH ALLDCKTLTLTELGRNLPTKAR TKHNIKRIDRLLGNRHLHKERL AVYRWHASFICSGNTMPIVLVD WSDIREQKRLMVLRASVALHG RSVTLYEKAFPLSEQCSKKAHD QFLADLASILPSNTTPLIVSDAG FKVPWYKSVEKLGWYWLSRV RGKVQYADLGAENWKPISNLH DMSSSHSKTLGYKRLTKSNPIS CQILLYKSRSKGRKNQRSTRTH CHHPSPKIYSASAKEPWVLATN LPVEIRTPKQLVNIYSKRMQIEE TFRDLKSPAYGLGLRHSRTSSS ERFDIMLLIALMLQLTCWLAGV HAQKQGWDKHFQANTVRNRN VLSTVRLGMEVLRHSGYTITRE DLLVAATLLAQNLFTHGYALG
21593	51961	A	21721	1	3285	
21594	51962	A	21722	1095	1188	
21595	51963	A	21723	568	1263	
21596	51964	A	21724	2	1688	
21597	51965	A	21725	1456	2046	SKGKVAIVSSHQEVRASPRRSP LGSEERPGPHTSRQAAGQPHPG TCSSVHCQGSWGLQTQNSEVIH DGDVEAISVGEDAAPGPRVHG ADLGQEEEAFR*VVMGGLPDR DSALAPVPEPMHRGWAVRAAE GAVQNDPVGGSERSWGAGSHS QPFSHRPAPHTRGLAQAQTEAA GEGAVPEVHRGAVLAGVRAPG WAQP
21598	51966	A	21726	335	595	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE*I L\WTGGDNESVS/MR*FFRPLER DLYNRIWHEIGLLLVSLL
21599	51967	A	21727	80	428	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNGLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21600	51968	A	21728	622	1281	

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21601	51969	A	21729	1066	1827	VPQAKGNNVVITSYMTNRGFF EDKKATFAPSFLMNIKGNKTSV VKNSILEQGQLTWLQVAKRAG LGGGQSGRTVLRERVRIEIAST HIALQHAIVTGDAVGMDDIPQE ARQYRHNQAYAYSIQGDGAED DDERIAFASHTIQECRSQGPGG YPFKIYSSRKDRIPISQSLLESHF TVHEETAPDLETTG*PGCKDHG NLCC/LSSVKLRYSMYRIKAGL WMTHPG*RTYWV
21602	51970	A	21730	1	1326	
21603	51971	A	21731	1	1971	
21604	51972	A	21732	1	1626	
21605	51973	A	21733	1	1810	
21606	51974	A	21734	305	442	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE
21607	51975	B	21735	1	1938	
21608	51976	A	21736	531	669	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21609	51977	A	21737	80	428	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
21610	51978	A	21738	10	426	
21611	51979	A	21739	314	451	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21612	51980	A	21740	1	1139	MWGIGSRTPIYNKILVYSSPEVS CEKPKYVKSQTSTHTGFESHKR YIFYLRLVGKNLHVSAMGLGK SQERRKKALKSQPQQPADSFPS LPTVEGLTTSGEVAAGFWLSGE ALSSC*LLSASVHLLLACLGMG KCSCSGFWLYF
21613	51981	A	21741	306	444	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE

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21614	51982	A	21742	189	1089	HHTAHCQ*CWL*S/DHGINPLRS WVGTG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNGSLLTNWPSVPP TIKEEENSEEELAAATTSKEQEP IGTDLDAVRTPEPLEEFPKREDQ EGSPPETSLPYKWVVEAANLLI PAVGSSLSEALDLIES
21615	51983	A	21743	1	1135	
21616	51984	A	21744	80	430	RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF
21617	51985	A	21745	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21618	51986	A	21746	773	1015	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADASF STDLYHGTLKPASLTMSGVVLL GRMLARSARNWS
21619	51987	A	21747	391	527	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21620	51988	A	21748	671	1030	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE*I LGDGW*Q*VRVER*FFRPLERD LYNRILACPLINT*PTPVVRLKP *TVWSMGPVVGTPARPIRTSGA CWWCW
21621	51989	A	21749	221	478	AEQDCTILPVLRHFTFFKSRKVS SICIRFE*ILTSCLGVRISTGKLV ARTHGSFADDQTLFFMTLAVS GELWTPSPWRPNSIRTS
21622	51990	A	21750	590	940	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21623	51991	A	21751	473	613	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADADT

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21624	51992	A	21752	342	1459	SFLWRFRLRGGSERFCLAGIPSA SGV*NIPSASIRSIND*KY*VCKR T*CVGQLAA\ENADGTVAEYN GYHVVFALAGSPKDADDTSIY MFYQKVGDNSIDSWKNAGRVF KDSDKFDANDPILKDQTQEWS GSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDTLKI NGVEDHKTIFDGDGKTYQNVQ QFIDEGNYTSGDNHTLRDPHYV EDKGHKYLVFEANTGTENGYQ GEESLFNKAYYGGGTNFFRKES QKLQQSAKKRDAELANGALGII ELNNDYTLKKVMKPLITSNTVT DEIERANVFKMNGKWYLFTDS RGSKMTIDAKSTLLESTEGSMT PPMTATEPFLRFLKGEIAQPKPH
21625	51993	A	21753	2094	2201	
21626	51994	A	21754	81	1080	HHTAHCQ*CWL*S/DHGINPLRS WVGTG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQEHPLWSL ALVRRRSPAQSPHVGTGSSGST GCSSQAPCMKSNNALIVILGTV TLDAVGIGLVMPVLPGLLRDIV HSDSIASHYGVLLALYALMQFL CAPVLGALSDRFGRRPVLLASL LGATIDYAIMATTPVLWIYPLV
21627	51995	A	21755	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21628	51996	A	21756	1	593	MGVNDLWQILEPVKQHIPLRNL GGKTIAVDLSLWVCEAHPVKK MMGSVMKKHLRDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AAYPIPDDQVQSVLISMLLIAL MLHLTCGLAGVHAQKQGWDK HFQANTVRNRNVLSTVRLGME VLRHSGYTITREDSLVAATLLT QNLFTHGYVLGKL*GDLSVLSL
21629	51997	A	21757	410	547	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE

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21630	51998	A	21758	719	814	AGLFKSRKVSSICIRFE*ILTSCL GVRIFNR
21631	51999	A	21759	1	1596	
21632	52000	A	21760	80	430	RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF
21633	52001	A	21761	1343	1480	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21634	52002	A	21762	2	151	
21635	52003	A	21763	258	396	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21636	52004	A	21764	1	3081	
21637	52005	A	21765	449	586	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21638	52006	A	21766	563	2042	
21639	52007	A	21767	1001	1093	
21640	52008	A	21768	1814	1870	
21641	52009	A	21769	2760	3723	HHTAHCQ*CWL*S/DHGINPLRS WVGTG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNVLSTVRLGMEVL RHSGYTITREDLLVAATLLAQN LFTHGLFGPSVDAPPPKRGFKR PKLPELRLQRFFGGVITPPLESY SLPSDPVHLFPPRRPPRQLTASP LRARAPYECSSCKDA
21642	52010	A	21770	860	3503	
21643	52011	A	21771	4597	6030	
21644	52012	A	21772	1513	3464	AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE
21645	52013	A	21773	1	453	

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21646	52014	A	21774	1	1526	MSSSHSKTLGYKRLTKSNPISC QILLYKSRSKGRKNQRSTRTHC HHPSPKIYSASAKEPWVLATNL PVEIRTPKQLVNIYSKRMQIEET FRDLKSPAYGLGLRHSRTSSSE RFDIMLLIALMLQLTCWLAGV HAQKQGWDKHFQANTVRNRN CKMATLKEKLIAPVAEE\EANS\ PNNKIT\VVGV\GQVGMA\CAISI LGKVSWPDEL\ALVGCFWEDK LKGGNDGSFQHGELIFFQTPKN CGQDKGLFWGPPNS*RFVSW*L AGSPVQPRRGRIRLKSWVPEK WLMVFQIPLFLKIV\KYSP*FAS* LVVSHPV\DIPTYVT\WETKVGL PKHRVIGSGCNLDSARFRYLMA EK\LGIHPS\SCHGW/IFWGEHG DSSVAWCWNGVNVAGVSLQE LNPEMGTDNDSENWKEVHKM VVESAYEVIKLKGYTNWAIGLS VADLIESMLKNLSRIHPVSTMV KGMYGIENEVFLSLPCILNARG LTSVINQKLKDDEVAQLKKSA DTLWDIQKDLKDL
21647	52015	A	21775	2	355	
21648	52016	A	21776	2	178	
21649	52017	A	21777	1	888	
21650	52018	C	21778	127	255	
21651	52019	A	21779	1	1824	
21652	52020	A	21780	330	476	
21653	52021	A	21781	452	500	

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21654	52022	A	21782	3	1584	DAWAAVSRGDEPGWGSGSWR LLQHWGVSCWSDPKRFSSALQ GYIITDWCAPFNKRIWKREQPE ETFPNTETNGEFGK\RPAEDME EEQAFKRSRNT\DEMVEL\RILL\ QSKNA\GAVIGKGGKNIKALRT DYNASVSVP\DSSVPERILCISA DIETIGEILKKIIPTLEEGLQLPSP TATSQLPLESDAVECLNYQHYK GSDFDCELRLLIHQSLGREGIIG GQRCLKSKELRGGTLQTTIKLF QECCPHSTDRVVLIGGKPDRFV\ ECIKIILDLISESPIKGR\AQPYDP NFYGWKPMDYG\GFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMQPYRRDYDDMSPRR GPPPPPPGRGGRGGSRARNLPL PPPPPPRGGDLMAYDRRGRPGD RYDGMVGFSADETWDSAIDTW SPSEWQMAYEPQGGSGYDYSY AGGRGSYGDLGGPIITTQVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGSEDRIITITGTQDQI QNAQYLLQNSVKQYSGKFF
21655	52023	A	21783	211	1635	KNMETEQPEETFPNTETNGEFG KRPAEDMEEEQAFIRSRNTDEM VELRILLQSKNA\GAVI\GKGGK NIKALRTDYNASVSVPDSSGPE RI\LSISADIETIGEILKKIIPTLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RVV\ECIKIILDLISESPIKGRAQP YDPNFYDETYDYGGFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMPPS\RRDYDDMSPRR GPPPPPPGRGG/RGLGSRARNLP LPPPPPPRGGDLMAYYKRGRP\ GDPYDGMVGFSADETWDSPID TWSP\SEWQMAYEPQGG\SG\Y DYSY/AQGGRGSYGDLGGPIITT QVTIPKDL/ALGSIYWKKGGQR\ IKQIPS*VGELSIKIDEPL\EGSED \RIITITG\TQDQIQ\NAQYLLQ\N SVKQYADVEGF
21656	52024	A	21784	860	1201	TISEPPALILLPIAVPSFSTTCRLP EDIIVVSAFPPLLIFCVPLLILVP VAMP*LLIFCVPPLIMVFVAFPA TSITPPLSIRVASALALVKTDIVP LSLIIVLFAEPYAFMSK

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21657	52025	B	21785	1	3750	
21658	52026	A	21786	1	1350	
21659	52027	A	21787	189	1939	TAMAGRMPCAEVISGSATRPD GPKALFKPIGRPHQAIRPINKPP AAPPKQAVTNGFMRGRVPPKT LTVPSESSLAPMTLVVIVVKEA LPPAKIFSTPVPYQPTRRAPDAE PLSASKTPSVYLVNFVVSPEDL RKLTVDVLPALRANTRALWQV EVSAFPSFMTQATPATQPLINAE PAVAAPTEQNPQVGPVMPGVQ GADAPVVAQNGPSRDVKLTFA PIAPPPGSMVLRGLNPNGSLEFG MRSDEVVTKAMVQLELTPWH GYGCQCPFLPVKYLYAAIGFSV MIEALNQLAIFNRRRFLSANQT LRQRTTEAVMRLLSGQKEDAE LDAETASMLVDHGNQQIFNPQ ERRMIERVLNLNQRTVSSIMTS RHDIEHIDLNAPEEEIRQLLERN QHTRLVVTDGDDAEDLLGVVH VIDLLQQSLRGEPLNLRVLIRQP LVFPETLPLLPALEQFRNARTHF AFVVDEFGSVEGIVTLSDVTETI AGNLPNEVEEIDARHDIQKNAD RSWTGN/GLLPLGDCRL*QASP TGCINRRGS\HYGYPTLYEFRKR FLTPGTVCKRCDQRGDAMRVQ VQWVFYTYILPLANE
21660	52028	A	21788	558	1563	TNNRL*K*GNN**LTNQKKSRT RWIHSRILPEAGC/GIASVGRNN CGLWRFTPAKAISWGKIHPVFQ RQILRVLSQTLFPN/MSLGRNLG YGLKMFGVPRAELKPRFKEALP MVNLEGFEDRFVDQISGGQQQ RVALARALILKPKVLLFDEPLS NLDANLRRSMRDKIRELQKQF DITSLYVTHDQSEAFAVSDTVL VMNKGHIMQIGSPQDLYRQPA SRFMASFMGDANLFPATFSDG YVDIYGYHLPRPLHFGTQGEG MVGVRPEAITLSDRGEESQRCV IRHVAYMGPQYEVTVEWHGQE ILLQVNATRLQPDVGEQYYLEI HPYGMFVLADAA
21661	52029	A	21789	201	312	CSWHDRFPDWKAGTHLLARG* QLSLPVWLCPVLKLS
21662	52030	A	21790	925	2388	
21663	52031	A	21791	1	759	

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21664	52032	A	21792	1	1086	MEKKITGYTTVDISQWHRKEHF EAFQSPAQCTKNQTVQLDITAF LKTVKKNKHKFYPAFIHILARL MNAHPEFRMAMKGVPGGDSV KNTSRVWSGNERDQKLLTENA LNDLIPSFLLTGQQTPALGRRVS GVIEIADGSRRRKAAALTESDY RVLVGELYDEQMPPLSRLGND YRPTSAHPQKRRYASRLQNEFA GNISALADAENISRVRDVNLLL EVLGVDSVEKTFRVWSGNERD QELLMEDALDDLIPSFLLTGQQ TPAFGRRVSGVIEIADGSRRRK AAALTESDYRVLVGELDDEQM AALSRLGNDYRPTSAYERGQR YASRLQNEFAGNISALADAENI SRKIIPRCINS\AKLP
21665	52033	A	21793	1	935	MLRDLLKNVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMVLKNVVRETDEVGKGQI RMRTVFEQAIDQRSSTDNEGAP VIPKHTLNTQPVEDTSLSTPAAP MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI ADGGSSRSKKRRRGCEGGRR/V RQGCPDQKHPAAFSVSGGKIHL SGRTPVEKRPRLPQPRDLGARA FAACRGSRGRPWNWLPAALRL HADLGCVRGGGGGWPGANPY PAPASSTC
21666	52034	A	21794	181	923	QHAIVTGDAVGMHHIPQEARQ YRHNQAYAYSIQGDGAEDDDE RIVRFHTRCLTEAFEKLQCGGV VNQLSRRGNNQHISSTYDINRA DTQVRRAVNNYDIIVMSNSFN\ ASRSIRCGSVGSLPSSNLPINSVS IRCRAR/SG/EE*CQAPASKWAL LHK*HRPFPQDRKAGECLLHEY EDLVPIRDTLRLFPGGRYLPRA KHVAPSEPDPEQDEQKLRFCKR HLYGQQPRSPVEIRLQHVAIAY PTHHAYD

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21667	52035	A	21795	178	798	IRLEPFKINVLEQITKHIEKLQCG GVVKQLSRRGNNQHISSTYDIN RADTQVRRAVNNYDIIVMSNSF N\ASRSIRCGSVGSLPSSNLPINS VSIRCRAR/SG/EE*CQAPASKW ALLHK*HRPFPQDRKAGECLLH EYEDLVPIRDTLRLFPGGRYLPR AKHVAPSEPDPEQDEQKLRFCK RHLYGQQPRSPVEIRLELVAIA YQTHHA
21668	52036	A	21796	499	972	
21669	52037	A	21797	3	1141	SRVKLGQSSESQVAALKTREPM NIATLEVLVLKGLRVCFVKVNH PKGPASMYPGWVPILYIHAEDP LLPFYLGEKEDVTYAIKPTCWP GLDIIPSCLALPRIETELMGKFD EGKLPTDPHLMLRLAIETVAHD YDVIVIDSAPNLGIGTINVVCAA DVLIVPTPAELFDYTSALQFFD MLRPLLKNVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMVLKNVKEFAGNISALAD AENISRKIITRCINTAKLPKSVV/ ALFSHPGELSA\GDALQKAFTD KEELLKQQASNLHEQKKAGVIF EAEEVITLLTSVLKTSSASRTSL SSRHQFAPGATVLYKGDKMVL NLDRSRVPTECIEKIEAILKELE
21670	52038	A	21798	1	617	LEPASLSIPNLLLHPRGLRAITIA VFGKQNTYIRLEPFKINVLEQIT KHIEKLQCGGVVKQLSRRGNN QHISSTYDINRADTQVRRAVNN YDIIVMSNSFN\ASRSIRCGSVGS LPSSNLPINSVSIRCRAR/SG/EE* CQAPASKWALLHK*HRPFPQD RKAGECLLHEYEDLVPIRDTLR LFPGGRYLPRAKHVAPSEPILSC
21671	52039	A	21799	181	953	QHAIVTGDAVGMDDIPQEARQ YRHNQAYAYSIQGDGAEDDDE RIVRFHTRRLTFKINVLEQITKHI EKLQCGGVVKQLSRRGNNQHI SSTYDINRADTQVRRAVNNYDI IVMSNSFN\ASRSIRCGSVGSLPS SNLPINSVSIRCRAR/SG/EE*CQ APASKWALLHK*HRPFPQDRK AGECLLHEYEDLVPIRDTLRLFP GGRYLPRAKHVAPSEPDPEQDE QKLRFCKRHLYGQQPRSPVEIR LQHVAIAYQTHHAYD
21672	52040	A	21800	1	798	
21673	52041	A	21801	1	1782	

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21674	52042	A	21802	666	1131	KGRGTYGNERDQELLT\EDALD DLIPSFLLTGQQTPAFGRRVSGV IEIADGSRRRKAAALTESDYRV LVGELDDEQMAALSRLGNDYR PTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTRQ LPKSVVGFFSHPGELSARSGDA
21675	52043	A	21803	1	3297	
21676	52044	A	21804	1	898	
21677	52045	A	21805	1	1977	
21678	52046	A	21806	1	1929	
21679	52047	A	21807	181	755	QHAIVTGDAVGMDDIPQEARQ YRHNQAYAYSIQGDGA\GMTM SALLDFIHGA***YIRCGSVGRL PSSNLPINSVSIRCRAR/SG/EE*C QAPASKWALLHK*HRPFPQDR KAGECLLHEYEDLVPIRDTLFL FPGGRYLPRAKHVAPSEPDPEQ DEQKLRFCKRHLYGQQPRSPVE IRLQHVAIAYQTHHAYD
21680	52048	A	21808	181	456	QHAIVTGDAVGMDDIPQEARQ YRHNQAYAYSIQGDGAEDDDE RIVRFHTRCLA*SRRAVNNYDII VMSNSFNGQSEHQVWIGGQFT FIKFAH
21681	52049	A	21809	1	780	
21682	52050	A	21810	1	1050	
21683	52051	A	21811	5	735	PPAAP/MGNLLMARVGVKARG KAHYLPLLRGESVRKTSRVGSG NERDQELLTEDALDDLIPSFLLT GQQTPAFGRRVSGVIEIADGSR RRKAAALTESDYRVLVGELDD EQMAALSRLGNDYRPTSAYER GQRYASRLQNEFAGNISALADA ENISRQIITRCINTAKLPKSVVAL FSHPGELSARSGDALQKAFTEK RTLKQQALTSEQKKRGI/YEAE EVSSSLSPQGRLSNRSASKDMY

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21684	52052	A	21812	1	887	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETK AVGSGNERDQELLTEEAWNDL ILSFLLTGQQTPAFGRRVSGVIEI PDGSRRRKAAALPKSDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAFTDKEELLKQQASNLHEQK KAGVIFEAEEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMVLNLDRSRVPTEC/IEKIEA ILKELEKPAP
21685	52053	A	21813	345	921	RWRLQNLSFCSSCSGSGSEGAT CFARGSAYELGQRYASRLQNA FAGKISALADAEIFSRKII\TRCIN TAKLLKSVVALFSHPVELSARS GDALQKAFTDKEELLKQQASN LHEQKKAGVIFEAEEVITLFTSV LKTSSASRTSLSSRHQFAPGAT VLYKGDKMVLNLDRSRVPTEC IEKIEAILKELEKPAP
21686	52054	A	21814	1	1989	
21687	52055	A	21815	6	311	
21688	52056	A	21816	3	848	PGGDSVKNTSRVWSGNERDQK LLTENALNDLIPSFLLTGQQTPA LGRRVSGVIEIADGSRRRKAAA LTESDYRVLVGELYDEQMPPLS RLGNDYRPTSAHPQKRRYASRL QNEFAGNISALADAENISRVRD VNLLLEVLGVDSVEKTFRVWS GNERDQELLMEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLVGEL DDEQMAALSRLGNDYRPTSAY ERGQRYASRLQNEFAGNISALA DAENISRKIIPRCINS\AKLP
21689	52057	A	21817	1	969	
21690	52058	A	21818	1	1614	

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21691	52059	A	21819	1	832	MDDIPQEARQYRHNQAYAYSI QGDGAEDDDERIVRFHTRVTV DSDTLASDAARLTCRHGLARD VKFTLEVLRGDSVEKTSRVWS GNERDQELLTEDALDDLIPFFLL TGQQTPAFGRRVSGVIEIADGS RRRKAAALTESDYRVLVGELD DEQMAALSRLGNDYRPTSAYE RGQRYASRLQNEFAGNISALAD AENISRKIITR\CINT\AQLAKSG VALFSHPGELSAPSGDAL*KAF TD*EEFL*PQGSNLY\EQKKAG\ VIFGS*KKFSLFLTSVV
21692	52060	A	21820	678	1338	TLRQTKPDNSAEIADGSRRRKA AALTE\SDYRVLVGELDDKQM AALSRLGNDYRPTSAYERGQR YASRLQNEFAGNISALADAENI SRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFTDKEE LLKQQASNLHEQKKAGVIFEAE EVITLLTSVLKTSSASRTSLSSR HQFAPGATVLYKGDKMVLNLD RSRVPTECIEKIEAILKELEKPAP
21693	52061	A	21821	1	1809	
21694	52062	A	21822	2	1010	
21695	52063	A	21823	284	2177	
21696	52064	A	21824	1	1296	
21697	52065	B	21825	1	1044	
21698	52066	A	21826	637	1073	IRLEPFKINVLEQITKHIEKLQCG GVVKQLSRRGNNQHISSTYDIN RADTQVRRAVNNYDIIVMSNSF N\ASRSIRCGSVGSLPSSNLPINS VSIRCRAR/SG/EE*CQAPASKW ALLHK*HRPFPQDRKAGECLLH EYEDLYPSVIH
21699	52067	A	21827	1	2403	

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21700	52068	A	21828	1471	3186	LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFTPVI GVAAIKTGTTVHIVSSSSLLGG DHGPSRIGGLLLVCDYGPLVSS SGISGPTRIVGLIISLGPGYHLCF RSDYRTGITDPLYIGDATIRVSL RVYSLPSRSRIEHVVANCGMIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNSIDSWKNA GRVFKDSDKFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYS GVMARGNAITLPVCGRDVKYT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFTDKEE LLMQQASNLHEQKKAGVIFEA EEVITLLTSVAKTSSASRTSLSS RHQF\APGATV\LYKGDKMVLN LDMSR\VQLECLDRLHACRSTL
21701	52069	A	21829	158	926	AGPVIQNYVNTQPV/EETSYSTP AAPMVDSLIARVGVMAPGNAI TLPVCGRDVKFTLEVLRGDSVK KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTPAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQQGGSSRV GDNSIDSWKTRGRVL
21702	52070	B	21830	1	3774	
21703	52071	B	21831	1	1495	
21704	52072	A	21832	556	1622	
21705	52073	A	21833	1	2616	

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21706	52074	A	21834	1412	3310	SVTSCLKVTSVCLTSAAASCRS VLMRSTAELQCASHTLRKRKA ARRLISLMMTARKARKITRRW RIGEAADLVGVSSQAIRDAEKA GRLPHPDMEIRGRVEQRVGYTI EQINHMRDVFGTRLRRAEDVFP PVIGVAAHKGNDPQGTASMYH GWVPDLHIHAEDTLLPFYLGEK DDVTYAIKPTCWPGLDIIPSCLA LHRIETELMGKFDEAQPNLGIG TINVVCAADVLIVPTPAELFDY TSALQFFDMLRDLLKNVDLKG FEPDVRILLTKYSNSNGSQSPW MEEQIRDAWGSMVLKNVVRET DEVGKGQIRMRTVFEQAIDQRS STDTSLSTPAAPMVDSLIARVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLLTGQQT PAFGRRVSGVIEIADGSRRRKA AALPE\SNYGVLVAELDDEQMP AYPRLGNDYRPTSAYERGQRY ATRLQNEFAG\NIS\ALADAENIS \IITRCINTAKLPKSVVALFSHPG ELSARSGDALQKAFTDKEELLK QQASNLHEQKKAGVIFEAEEVI TLLTSVLKTSSASRTSLSSRHQF APGATVLYKGDKMVLNLDRSR VPTECIEKIEAILKELEKPAP
21707	52075	A	21835	783	2371	
21708	52076	A	21836	3236	4718	
21709	52077	A	21837	1	2481	

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21710	52078	A	21838	2450	3963	LLTAPITGGIGTINVVCADDVMI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPDVRILLTKYS NSNGSQSPWMEEQIRDAWGSM VLKNVVRETDEVGKAAPMVDS LIARVGVMARGNAITLPVCGRD VKFTLEVLRGDSVEKTSRVWS GNERDQELLTEDALDDLIPSFLL TGQQTPAFGQR\VSGVKEIADGI RRRKAAALTE\SDYRVLVGELD DEQMAALSRLGNDYRPTSAYE RGQRYASRLQNEFAGNISALAD AENISRKIITRCINTAKLPKSVV ALFSHPGELSARSGDALQKAFT DK\EDLLKQQASNLHGAEKSW GCYFEAEEVITLLTSVLKTSS\A SRTSLSSRHQFAPGATVLYKGD KMVLNLDRSRVPTEYRYGVFL NVLLPATKYFQLHDPSLRNMEL NYSLASEDLVLKGLRVLLVEG NDPQGTASMYHGWVPDLHIHA EDTLLPFYLGEKDDVTYAIKPT CWPGLDIIPSCLALHRIETEYNG
21711	52079	A	21839	1573	2858	EPVFEQAIDQRSSTDTSLSTPAA PMVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISQ*ICWKYFCAG*C GKYF\RKIITRCINTAKLPKSVV ALFSHPGELSARSGDALQKAFT DKEELLKQQASNLHEQKKAGV ISPPEEVITLLTSEIKTSSASRTSL SSRHQFAPGATVLYKGDKMFIT VKIAKRSQAPCMKSNNALIVIL GTVTLDAVGIGLVMPVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPVLGALSDRFGRRPVLL ASLLGATIDYAIMATTPVLWIY PLVNSPSC
21712	52080	B	21840	63	368	
21713	52081	A	21841	189	204	SLPSGIKPQSSSKASSRIQVAPT M*SLPRQPLAWPSGHEACPQG
21714	52082	A	21842	153	370	LIAGAFRKASGGNNIFRRPKTL* LRRQPR*PQKSTPRRNKLGHYA IIKFPLTTESAVKKIEETNTLVFT VLV

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21715	52083	A	21843	842	1770	CTPEKCLPAVHRRNWLRNAEPP VWKRHLSPICRKRQGRATKPK RRPWYTTPPTRRVRDVALRPYS RH/GRQPHAKKKIRMSLTFRRP KTLRLRRQPRYPRKSTPRRNKL GHYAIIKFPLTTESAVKKIEENN TLVFTVDVKANKHQIRQAVKK LYDSDVAKHTEERRHDEQNNIL TREAKNRNDNTRNRARTETNT ETQKNSGYQALISFHSYYSDTS DNKAHLVSYQSGQCTYDRLG WNLLIRMTCRSLQHTYDIQSTQ IASCFHPVSVRVNLRLYCANYG GISAVFMPLRKELLILTRSSNSK VSQLRI
21716	52084	A	21844	353	605	EMAPKAKEAPAHPKAEAKAKA LKAKKAVLKGVRSHT/RKKKIR MSLTFRRPKTLRLRRQPRYPRK STPRRNKLGHYAIIKFPLTT
21717	52085	A	21845	301	946	PGSYLKPLSWTVALSLRPGFMS RWPCQRLTWQRRSVTQASGAS GASLCASRLPRDKTAPKAKEAP APPKAEAKAKALKPKKAVVER CPHTHAKKRIRMSPTFRRPKTL RLRRQPRYPRKSTPRRNKLGHY AIIK\FPLTTE\SAGKKNKKNNTP LVHCGC*RPTRHQI\RQAVKK\L YDSDV\AKVTTLICPDKEKKAY VRLAPDYDALDVANKIGII
21718	52086	B	21846	12	115	
21719	52087	A	21847	1397	1489	
21720	52088	A	21848	519	747	SGSVISPIAAT*YRIFAVL*SVQ* **AGPGDLSGDGELP*SVAIQPN VFIAVSSITCNWLPFGKCGSTY WMCQSM
21721	52089	A	21849	185	456	QHQPLEVASQWKVCSVSVKLL SQSSDVTRVPLEGLDRLSERSG SLSVL*SGILWALDAASQLVSL LP*LTRYHDPRVSSL/SSTYV*SP
21722	52090	A	21850	789	1086	

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21723	52091	A	21851	1	766	SGRKEANY\YGSLTQAGTVSLG LDAEGQEVFVPFSAVLPMVAP NDLVFDGWDISSLNLAEAMRR AKVLDWGLQEQLWPHMEALR P/LGLAVYIPEFIAANQSARA\D N\LIPGSRAQQLEQIRRDIRDFRS SAGLDKVIVLWTANTERFCEVI PGLNDTAENLLRTIELGLEVSP\ STLF\AVASILGGLCLSFNGSPQ NTLVPGALELAWQHRILVGGD DFKSGQTKVKSVLVDFLIGSGL KTMSIVSYNHLGNNDGEN
21724	52092	A	21852	2	2122	WKSWMVFTAMKLVKAHHRLK LRLKGYLPVTCLEGTRNQRIAA TIRHNRARGRHQITAMSEIVRE LSQLGWDDNKIGKELGMDSDE VLRLKQINGLQELFADRQYSRA WTLKLAQAFSCCQQRRFLLGK TETNQFMWEGIGAKHRQRNRR YAVLLRQPLAKLNIIQARYPNQ HRQHAGECNPHCQAGGDIVDR CPARCFTKGDSKDGSPPQATWP FHNSATMTAKRLSEASQCGSK KSILRERIIYRPSITRYPFQSTMN HPLPEQTLGCIATDYGSSPSPDR SPGPAHYYWTDHSTANIRYQV AAEENGEYTYVERVKIPLDHGT LLIMERATQADWQLEQIRRDIR DFRSSAGLDKVIVLWTANTERF CEVIPGLNDTAENLLRTI/D/RSV WEVSPSTLFAVASILEGCAFLN GSPQNTLVPGALELAWQHRVF VGGDDFKSGQTKVKSVLVDFLI GFRLQRP/SSIVSYNHLG\NNDG ENLSAPLQFRSKEV\SRSNVVD DMVA\SNP\VLYTPGEEPDHCV VIKYVPYVGDS*RAL\DEYTSEL MLGGTNTLVL\HNTC\EDSLL\A APIML\DLGAA*PSCCQRVTFLA LDIGTPSRRPFHPVLVPAQAFFF KGATLSPPGKP/VLVNAAFSAS AAAIENI\LRACVGLPPQNHMLL EHKMERPGPSLKRVWTPWLPP YPMLNKKGPGSRCQPMAAPVD
21725	52093	A	21853	1	1908	
21726	52094	B	21854	1	1833	

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21727	52095	A	21855	1	749	MFQLMKASSGGEAACMPAGL MENYKHTTVLLDEAVNGLNIR PDGIYIDGTFGRG\LGEEGRLLA IDRDPQAIAV/AKTIDDPRFSIIH GPFSALGEYVAERDLIGKIDGIL LDLGVSSPQLDDAERGFSFMRD GPLDMRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPNDPELEEIEQA LKSSLNVLAPGGGVSIISFHSLE DRIVK/RFMREHQFCVVVRSGV GLKT*SVR
21728	52096	A	21856	532	1418	CFASGFIGELRKNIVGFIEQDHT RGLVFRLTPGRTLRAESLNLVIC LPMNFQPYDSDADWVITGVPF DMATSGRAGGRHGPAAIRQVS TNLAWEHNRFPWNFDMRERLN VVDCGDLVYAFGDAREMSEKL QAHAEKLLAAGKRMLSFGGDH FVTLPLLRAHAKHFGKMALVH FDAHTDTYANGCEFDHGTMFY TAPKEGLIDPNHSVQIGIRTEFD KDNGFTVLDACQVNDRSVDDV IAQVKQIVGDMP/VYLTLYNCG GPS*QFHSLRPAQSPLDRCRAR YLAPQCVPDFRTLQR
21729	52097	B	21857	64	1842	
21730	52098	A	21858	1	503	MRWLVSPIEDTGHKALLFACL ALHRACVSGHCLSPKCVGVDG RSHEMVAPGLFLDWLLDGTGV WDGTSTNVEGAQEHAVLILLII TDGVISDMEETGMPWCRLPSCP CPSSSGRGQCGLRCHGVPGWG RRMLRSHTGEEAARDIVSSFPF ESSATMSEEVYDPRSLYERLQE QRTGSSRTARQEAVVGSKVTV SQPGHRQETTVLEHLVQY/FILL IITDGVISDMEE/TRHAVVQASK LPMSIII/VGVGNADFAAMEFLD GDA/GMLRSHTGEEAARDI/VQ FVPFREFRNNVRGGL*PSISI
21731	52099	A	21859	2223	2363	

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21732	52100	A	21860	3	693	GDDGKWMLVHRTEVIKYTLDP VWKPFTVPLVSLCDGDMEKPIQ VMCYDYDNDGGHDFIGEFQTS MSQMCEARDSVPLE\FECINPK KQRKKKNYKNSGIIILRSCKINR DYSFLDYILG\GCQLHVSPLGID F\TASNG\DPLDPSSLHYINPMG TNEYLSAIWAVGQIIQDYDSDK MFPALGFGAQLPPDWKVSHEF AINFNPTNPFCSGVDGIAQA\YS TCLPHIRFYGPT
21733	52101	A	21861	1	2231	MYSQEGNQFCNRTDCQELLPPP PAPMAHIPSGGAPAAGAAPMG PQYCVCKVELSVSGQNLLDRD VTSKSDPFCVLFTENNGRWIEY DRTETAINNLNPAFSKKFVLDY HFEEVQKLKFALFDQDKSSMR LDEHDFLGQFSCSLGTIVSSKKI TRPLLLLNDKPAGKGLITIAAQE LSDNRVITLSLACRRLDKKDLF GKSDPFLEFYKPGDDGKWMLV HRTEVVIKYTLDPVWKPFTVPL VSLCDGDMEKPIQVMCYDYDN DGGHDFIGEFQTSVF\KMCEAR DSVPLEFECINPKKQRKKKNYK NSGIIILRSCKVNQRGQARARG QVSGHTEGTDRALDLEPARPVF KSRLCHILALWPSELHLTRPQSP HLWNGDINEAEHVQGYSSLTFL CGGQGRHELTFQGLSWWENCH CELLPPTVGMQGAEDIGWGHP VLSGISVTVTPMINRDYSFLDYI LGGCQLMFTVGIDFTASNGNPL DPSSLHYINPMGTNEYLSAIWA VGQIIQDYDRPRSFLKPDPWAG TEAVTGQHVMFSVYETHVEWG RQIGLPDVANQNTRHPVKFEFQ VSHEFAINFNPTNPFCSGVDGIA QAYSACLPHIRFYGPTNFSPIVN HVARFAAQATQQRTATQYFILL IITDGVISDMEETRHAVVQASK LPMSIIIVGVGNADFAAMEFLD GDSPHAALPTRGRRQPRDIVQF
21734	52102	A	21862	694	825	QPGLSINIEAGAVPRPFARRYW GNLG*FLFLGVLRCFSSPGSPH
21735	52103	A	21863	1032	1127	FYAKAEAGDRTVA*PHKPKMF LSIHHRVAKI
21736	52104	B	21864	1	564	

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21737	52105	A	21865	43	617	PIIQKVRSHTPKRAPTACTYTVS GSFSLPSPGFFSPFPHGTGSLSVS QEYLALEEWSPHISARDCTCSG LLIELPSTGIFVYGAVTLYRAPF QTLPVTHALIQALGCSP\FARRY WGNLG*FLFLGVLRCFSSPGSP H*PMDSVNDSVSKHT/EVSPFG N\PGYNGSYHLTDAYRRLARPS SPLT\PGHPPLYG
21738	52106	A	21866	2969	3593	
21739	52107	A	21867	1219	1503	HFTDGQNNRQHGCGVRRQAG KQVVCKVEHQNQYNHRCVW* ESFQVRTHGTGEPVNKTRTSQA VSHHNQSCQVDQCVPCAVIAG NVFPRHNVQGQH
21740	52108	A	21868	193	378	
21741	52109	B	21869	1	1473	
21742	52110	A	21870	3536	3926	PKMVRWLARKCWNTVSTVRC FWMAMPTPVFAPCAAIKTASA R*MSWASSR*PNRGCVKSATLR QFS*VAAMK*PPVAQ*WW\LGR NASTAGGDSGAGRSLDDGEPTP CGMGLEQKRHGNPAGCVAPSR WS
21743	52111	A	21871	140	901	MAMSKVKSITRESWILSTFPEW GSWLNEEIEQEQVAPGTFTMW WLGCTGIWLKSEGGTNVCVNL WCGTGKQSHGNPLMKQGQQM PPMAGVKKLQPNLRTTPFVLDP FAIRQIDAVLATHDHNDHIDVN VAAAVMQNCADDVPFIGPKTC VDSWIGWGVPKERCIVVKPGD VVQVTALEIHAPDAFDRTAPIT WLADQKRRRTVKG/MDDAPL* QVSYRPSTPPRCCYWSLLSSSV YYSKRPFAHGYARLCIPFMD
21744	52112	A	21872	287	392	
21745	52113	A	21873	1	492	
21746	52114	A	21874	569	1061	SGTVLDM/SEYSRVQIRKQPYLS KGYIPVRQKTKAAWLLKAVTFI DLTTLSGDDTSSNIQRLCYKAK YPIREDLLKALNMHDKVAAGF PAGQTHLKTRLEEIRLAVEDGA TEIDVVINRSLVLTGQWEG/LYS PVVYSALPCNI*HSRLFLPSGNA LLLWLWCLHS

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21747	52115	A	21875	2	1072	ARSNIRMVTAFRSLPAGSSGAA RA\MSAHNRGTELDLSWISKIQ VNHPAVL\RRAEQIQARRT\VK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGIT\TAAVCV\YP ARV\CDAVKGTSRPAG/CVNIPV GISRAAGF\PAG\QTH\LKTRLEE I\RLAVEDGSLQKIDV\VINRSLG A*QAQWE\ALYDEIRQF\RKAC GEA\HLKTILA\TGELGTLTNVY K\ASMIAMMAGSDF\IKTSTGKE TVNATFPVAIVMLRAIRDFFWK TGNKIGFKPAGGIRSAKDSLAW LSLVKEELGDEWLKP\ELFRIGA ST\LLSDIER\QIYHSCGLGRYGS LFMDLSQCL
21748	52116	A	21876	3	221	
21749	52117	B	21877	49	342	
21750	52118	A	21878	1	828	
21751	52119	A	21879	1362	2405	RPPWRHWDGNSSVLVHFQLHF LLRPLQTLSLGLEEELLQRGIRA RLREHGISLAAYGTIVSAELKG GSRPCAVWWPSEPGAGRCPGN SFSCGNSQCVTKVNPECDDQED CSDGSDEAHCECGLQPAWRMA GRIVGGMEASPGEFPWQASLRE NKEHFCGAAIIN/DQPLRS*NHR FQDPTKWVAYVVRPTSAARRP APCGPSKKA/WISGWGYLK/EG LP*ASPRPAMVKPEVLQKA/DW ELLDQALCASLYGHSL/TDRMV CAGYLDGKVDSCSVLFLFRGTI SFFFSEDRNLIRYVLLYSIFVVN CISGKPQPGPPVLRALCQHPHQI DAGPQYRASCWVTVPKLQGIF
21752	52120	A	21880	600	904	SVSLLDEETALPFSWDELRLSA LLDT*AAFQEIELAFQDPQCVG LLTAP/YADAAFSGSTDIAMFLL VPILSARKPASPRSS*TFSHLATE PLPASIK*AAA
21753	52121	A	21881	393	572	
21754	52122	A	21882	165	432	PGMAVSYEKISKYPVEFLPAQA NIAGHNDAPEEREPFQW*LWLL LPNF*LQEKCSPTLCHFLSRRTQ SEFPSSTAAGNLSVSLLYPCKS
21755	52123	B	21883	1	1011	

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21756	52124	A	21884	783	1234	YYRRCGAASPHGRDPVQIG*TS SQPR*SAYRN/PASVIPVARHSA RAPAILRP*VVVAERSERSIPGL RATPAEIRTTSAPSSAGVASSPE KPLIFTAIDSHTGSHWSDIIHVC AKKLQNYVPKLNASLLLTPSIY VTRTTRSGPIPPARQ
21757	52125	A	21885	249	398	GYFDIFSYDTAIPGQSAEQDAR ED*AF*MPDRAYSQPCSSLVFP KGCKK
21758	52126	A	21886	309	845	CGAREERGRGCHHVHSQLRGP GPAPGQVQQPQLVPAPVVPELP GLRGLSWQARRTRARHRQGQV QDHQPDPTVHAQLRGVQLGEA PLQLHHGD*DHRAP*GYFDIFS YDTAIPGQSAEQDARED*AF*M PDRAYSQPCSSLVFPKGCPVPG RGCAAGVQAAGAAHPPLDHPA LQPLQGR
21759	52127	A	21887	1236	2100	DLLCGRGCQGRRPRHLQPQTEL EAPEVPAERPGRGPAVAARSDP RAQAEDVPGYNPLSGKPAKQQ VHEGHHPGAPGHRRPGGAAVP AGGPHRCLPAQPARPCGGAAEP RGGPAGAH*ARGSRAAGEGQP WWPSPRLGAGPPAAPVHAAPG SHLLPGHHLPTQPSALAAAQ\PL AEEPREQ/PGAGGPQPGSPTLRG VEVVPLPHAAGGAGAVPVGGA ACPTAPHPAASAPAPVLLSQLG TQHPPRRDPPHCSCAGIQDSGW AGPPALWSLLHVAKPAQARRP CALLHPGV
21760	52128	A	21888	1931	2185	AKAFSFFRYISRVSRNRTCLSRS SMRRSFDSSNADAAFSGSTDIA MFLLVPILSARKPASPRSS*TFS HLATEPLPASIK*AAA
21761	52129	A	21889	1254	1760	
21762	52130	A	21890	1	2001	SIRRPKRARPIRIKKIPEQQG/PQ PAVLPVQTVATRDRELPQMP/P VGPETLKRDPPVRAMTIPATAA VYKPYWGATPLPIA\KPSPAG*Q *SRRFSKGYFGFD
21763	52131	A	21891	195	545	HSPGSFYSRRDAQSPAPAIRAA V*AEVQ*TPLCHDRITHFPEDW RGWQRS*F*PAACRVAGSLPVP VSPQIQHPYCRSSAQYLPCGAG LPLPGFDRLCPRSLFQGLAVTG GSCGPS

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21764	52132	A	21892	825	1299	YSCRTEHPPRLATAEYRHHQRA ADAGR*RHAGVAFYPIKERYR QPEPAFSYQ/PRRWSASRNRRPS R*RMRRFPANSSTPFPPAPPLRR KRVASLIGGRMLRLTGAGIAEE RMIAPQLPECILHELTERPHPFP LGIDLILTCGERLLAIPRTTHVE
21765	52133	A	21893	1460	1810	RATHVLTWVRGTPKRAEMILG SSRSMSAAAVTVLISPATAQRW ITRAP*PSPIRSPSVSRLTATRPSS ITKARALSPMAAPALRSTVTTP PRITVEKPLLMEKIPRVPKSRAI SAL
21766	52134	A	21894	231	704	QSQKPDTRGRLFVAKAPPCVQR HKVRWLRLVMITSAHYLPLRR* *PAHPASGGCCPNRAKYTQRPA E*ISYRPD*EAVR*SRAPAKVTQ SNPASRVALRRPAPRAVHQATII PVDESTLLPAPLAVSARQKVRQ AIPLRDSPVRRPTLDVRHRATG L
21767	52135	A	21895	1291	1925	RQLLRWSNR*IAR*SLTQPARRF PAYHYAHPAAAAAPGDPLGAD LQLCARHYHRQRHCVPRHAGY PRSDGLHPQPRGRWRIRCSDCL RVPF
21768	52136	A	21896	1	445	MFISGLDDFFIDVVYWVRRIKR KLSVYRRYPRMSYRELYKPDE KPL/DDYGSGVE*NGRHRQYGR AGGDHARLRKLSYLCWHLPQR PRYSA*C*RSVRSLPECA*GSLR ASWP/HPAKPTV*TTCWTPSPN LSVAPISLLLVLFCMTPKM
21769	52137	A	21897	79	377	SRKSGISIGAVKRPTH*GS*KAR SIC*NAAYVSKKAESLSSFPEKS ESTQRVKAVLSS**ASQGCGDT AQYVLLSFKGSQQA*QVCGR* KAY**DLSRE
21770	52138	A	21898	1282	1535	GSTYEIASATPSPSAKPSNRSPSP MSRPQSNPKPNSLHSC*P*GNL RSTPESGK*ATPPPPPAYTLVLF KLANPQLPEESPWAF
21771	52139	A	21899	3775	4031	CRRTAASRTPRKRTQTAPTHAT NKPQKPQTSTDRGNRREPEKTE PS*HLRPNPQEPGRRGQTQQ\EP APRHQPPKPQGEPTTPQKQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
21772	52140	A	21900	1	2595	MESHTVTDYNFGRLLNESFAN CETDRNYLGIFKCGFWLSGTRK SAFLTKSQVTLTRPVDHTLRNE VLGSTKYQVPGYRRKTNTNLE ESNVLIGYDVAPGGGKQIDGKK AEGRELMVPVAGRPLCRSSSM ELLLLLPLHIPREQMLLADAYW NLHQSCQSKTSPDTAKCPLDRC PRVFKSQSYKASTFDGLSMDTE VIKSNGKQGWRQRRLANMKDI DKQTQAATFVLSQGMQRSGND RIILVTGASDGIGREAAMTYAR YGATVILLGRNEEKLRQVASHI NEETGRQPQWFILDLLTCTSEN CQQLAQRIAVNYPRLDGVLHN AGLLGDVCPMSEQNPQVWQD VMQLFRAGIINADPGAFFVTGF RRYCCFTLCCRSFRFGFYRRRF RHRSCRQRAMRHSGTGQGQGN EQCFNSVFHTVFSLFVNSGITLT AVKTVNKWQCSEMEKAAKAT FSCYSCNAFFCEAASGLLLFQRI ANFDFRLFTQVTHQSFKDDLGI KMETTKPSFQDVLEFVRLFRRK NKLQREIQDVEKKIRDNQKRVL LLDNLSDYIKPGMSVEAIQGIIA SMKGDYEDRVDDYIIKNAELSK ERRDISKKLKAMGEMKNGEAN RKERSSMFRDRPLKRMKSKRD DDSYDEDVEDDEGVGEVRVHR VNHAPANAQEHEAARPSPQHQ YQPPYASAQPRQPVQQPPEAQV
21773	52141	A	21901	1	96	
21774	52142	A	21902	105	430	ASIFVMLVRGAEPMEKRQQRG LFTVPGLLLAFCSHVLSCVNPLI PVDNPYYPPLSELIPAPPQPNDR AQRVSERGSGRAPNTQTASPRA LADSLMQLAR\QVSRLESGQ

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21775	52143	A	21903	843	2055	HHRMAQNLSRYGNDKRPEESQ FRVVNVKPVTLYDVAEYAGVS YQTVSRVVNQASHVS\AKTREK \VEAAMAELNYIPNRVAQQLAG KQSLLIGVATSSLALH\APSQIV AAIKSRADQLGASVVVSMVF\R SGLVACHTAPHNLL/ARKRGPA GLIINYPLDD\QDAIAVEA\ACT NVPALFLDVSDQTPI\NSIIFSHE DGTRLGVEHL\VALGH\QQI\AL LAGPLSSVS\ARLRLAG\WHNFL TGN\QIQPIA\ER\EGDWSAMSGF QQT\LQMLNEGIVPHWRLLVAQ RSRMALG\AMRRHYPESGLRV GA\DILRVGGNTTIPED\SSCYIP AL*PPIKQDFRLLGA/QTSVDR\L LQLSQGQAVKGN\QLLPVSL\V KRKTTL\APNTQTA\SPRALPRF H*MQLA\RQVSRLESGQ
21776	52144	A	21904	1	1201	
21777	52145	A	21905	1	492	
21778	52146	A	21906	646	934	
21779	52147	A	21907	1	1713	MLCTKWDKLGLEKNAGKNKN AYKWYGWPANAPDEPHIEQLV GECRVMRQLKRLISRIAPSPSSV MVVGESGTAIPVVSHAEFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDFGYLEFEGGANFSWGEM YGFFDWENFYNGRHNKPGSEQ RYTFKNTKPYLSWVDTGFSLYL HAYGTYGSANRVNFLDDM\FL AGFGFQF*PAGGW/WGSNPFFA K\RYTRSKPYYT\GDNGYV\AG WVAGYNFMLGSEKFTLTNWN EYEFDRDATYAADFLPLYDVD CQDNGNLEYDTYSQPEWKHNL FDHYLAVLYRFKDESGKEQFSG AVVKTREATPGKEIEAITRRML DFSPRLKKLADCPSPRPVFEALC ICSMLDALLLLCPLDYHASCDN YSYALLDPQGFPLPHRRLWGPY IDVDVPMLHLIQHAWAQDALL SCLYSDLLYMSSFPYPAGTLTR LMGVTSYNHKNTLLTYCITLMS TIRFAYDGDEEIAMKYTDFLKG ELSMNIRPLHDRVIVKRKEVET KSAGGIVLTGSASAKSTRGEVL AVGNGRILENGEVKPLDVKIGD IVFFNDGYRGEI
21780	52148	A	21908	2060	2404	
21781	52149	B	21909	1	1377	

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21782	52150	A	21910	52	1719	IGQVVDVDTCFTRIHLVFVNFD NDTGSIHVLNDTTTFSYRSYTG VNGNSTFHTSTNQRLISAQSRN GLTLHVRTHQCTVGVIVFQERD QGRTDGYHLLGGYVHVVNLV AAEQAGFAFATASYQVFYEVA FFIQVGVRLGDNVVAFFDSRQV VNFVSYNTVGHFTIRSLKEAVF VSLCVHGQRVDQTDVRTFRGF DWTDATVVSRVYVSNFEACTF TGQTAWAECGDTTFVRNLRQR VVLVHKLRQLAGTEELFHCCG SQDPQQPWGWNLRVNPLAQTT GHAHEAQRKQWHKGNEEADD PEPERAFTPGFVQFETERFRPPV GHPCEAAEDHAADDHVMEVR NQEQAVMQNEVRARYGQQHA SHPAHREGDDKTDGPQHRRME HDAALIHGEQPVEDLHPGRDG DNHCGDTKEGVYVRARTHRKE VVQPNDERQHGDTDGCPYQRG ITKQTFTREGCRNFGEHTENRQ DQDVNFRVAPGPNQVDVHHH VATHIVGKEMGAQIAIQGQHAT YRQNGKDL*SNRGVASGNPQC RHRAHRRATDCQTVIKQPVFFG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
21783	52151	A	21911	608	2508	YITATSCSGWMIRWCAKAAKC CA/CSRGPGGKLRRHKGAEETL CGNTRVLIAPQLPAVIIATLSGS RSQTGRREGPTPTTVMIQDHTG SSTDDECSANVQRIFNRIMLCSI VSRPRTIPFHDLAQSFRQFRNVK CLWCAFEGAQLMRIQPAIVMV KTIHRERLNSGQFRCHQEARNI PPHRQSRFLASRGLLAELMFML YGIGELPEIVTLPKEIRGNVDNS RHAVFLANSGMPELRFIRTHGS RFTSQDCTLFNWLARIITPVLQS WLNDEEQQVALRLLEKDRDHH RVLVDITNAVLSHLDLDDLIAD VAREIHHFFGLASVSMVLGDHR KNEKFSLWCSDLSASHCACLPR CMPGESVLLTQTLQTRQPTLTH RADDLFLWQRDPLLLLLASNG CESALLIPLTFGNHTPGALLLAH TSSTLFSEENCQLLQHIADRIAI AVGNADAWRSMTDLQESLQQ ENHQLSEQLLSNLGIGDIIYQSQ AMEDLLQQVDIVAKSDSTVLIC GETGTGKEVIARAIHQLSPRRD KPLVKINCAAIPASLLESELFGH DKGAFTGAINTHRGRFEIADGG TLFLDEIGDLPLELQPKLLRVLQ EREIERLGGSRTIPVNVRVIAAT NRDLWQMVEDRGVI
21784	52152	A	21912	147	2699	MTIRAICSCCPLPDA*NVLM*IY MSTFQASGNGQQLQIARIVIQNI TG
21785	52153	A	21913	432	1016	FCPSSCLAATAPAA*AGWSFLP SPAEQNRWRFPLSRFCQIPAPL/ LGTLIISLSVFCSILAASAAEIPG SVDGIYNKSPSLI\WVKIPRQLY *AAREPSAPKAPPPAAWFSASA VLSATA\MINTNQKAIERVTAFR RNFATDPVAHQDRDHYDRQQR RTRHRIRFGERQRAKQTPFLPFQ GEDRDKRQRDNQQTDK

SEQ ID NO:	SEQ ID NO: of nucleotide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
21786	52154	A	21914	1	1146	MTTSMLNAKLLPSAPSAAVVV VRVVVVVGNAPTSRKVGPEEK DWSMASSGTTSTRKRFTGAEFI VHFLEQ/PGH*DCDRHSG/S/CSI LPVYDALSQSTQIRHILARHEQ GAGFIAQGMARTDGKPAVCMA CSGPGATNLVTAIADARLDSIPL ICITGQVPASMIGTDAFQEVDT YGISIPITKHNYLVRHIEELPQV MSDAFRIAQSGRPGPVWIDIPK DEQTAVFEIETQPAMAEKAAAP AFSEESIRDAAAMINAAKRPVL YLGGGVINANARVRELAEKAQ LPTTMTLMALGMLPKAHPLSL GMLGMHGVRSTNYILQEADLLI VLELAGVQTVDTDVNASKPAS ATRHIAFQTVTIGCDRNLADSV VFPHSVDDIGKVAA
21787	52155	A	21915	1001	1037	MVGMASSCMPAFTRLELYSVIS QSTQIRH/ILARHEQGAGFIAQG MA/RTDGKPAVCMACSGPG/AT NLVTAIADARLDSIP/LICITGQV PASMIGTDA/FQEVDTYGI/STM TLMALGMLPKAH/ALSLGMLG MHGVRSTNYFCQEADLSIVLG ALFDAGQIGKTSSFCPNAKI/IH VDIDRAE/REFPCPIPKACDLLS H/YGLINAVAACVDDNAIITTD VGQHQMWTAQAYPLNRPRQW LTSGGLGTMGFGLPAAIGAALA NPDRKVLCFSGDGSLMMNIQ* MIIAIPTGVKIFNWCSPCIRPHR VPFCDAVAIGFIVTFSDVIQIASI YEIPCRDPTGVASTEYSSSSCRR RRNTTLCDPGSPAQRQSPQAGQ NPSCPAHRRSATGVGD
21788	52156	A	21916	135	449	
21789	52157	A	21917	5	214	
21790	52158	A	21918	2	337	IGIAKHAQQLLLNVMQTRAVG AEVQTVSATGSAVRQALANNL QPFAIFFQINA/W**RAGRYPDD HGISPETALYGWHTSATGTAG MR*SVRPWLQSGQGCSGWRRQ QPRWSP
21791	52159	A	21919	1	774	

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21792	52160	A	21920	2	914	RHIRTPAHLERFIVDIALNVADG HRAKLIVQSAGTFAQTVLRADS SANFRQGVGLVRQFRRFKNTPL VGELQPVRDVVVYRAFPLAVW VAARQAAVSLRFGLAFGKRLV NFNKLNFADLQRFLWRINAAQ LSCATTT/ADPAVLLHHWTSV* PAQI*WR\S*PVRQNLFTALRAG MLHMLGDKTTQMLFMDRQSV NA*DLDQFRVNAFAEIAAFIEN VSETAGHARTEVNAGFTQNAD DTTRHIFTTVVANAFYHGDSTG VTHAETFTRAACGIQTTTGRAI QAGVADNACFMAAEGGTNRR TNGD
21793	52161	A	21921	204	371	PGPAGAQSAALYRWSPGQAVS RADWFRFADC*IYPENRRNAGS AYRPRLSPAYCG
21794	52162	A	21922	2664	2970	TPDTAPAGCRSRAPDGPSLPRQ MPRRRG*FHTARYCRTPRAITA *R*TE*STCPARTGEWYAHARY APGTSRQTATMPPTMPRRRASS YSSTQPDGRRQNC
21795	52163	A	21923	318	459	
21796	52164	A	21924	577	888	TNSSNQQLAEGNRERLIGRNTA GPERITAGRR*LFSCQNRPCGW RFNKCHIGMPVVVIWRIIVMGI QHDDLVNPFGMRVNRVNMQF AKTLGQRALLLRRNSLIA
21797	52165	A	21925	3	711	AGAHSGPSHPALATTAARQSV AGNRSGISGFSGHSRNPTRMSA RCL*SS\ALERLMRRLNGGEIQI SDVTTTTPS\LSPQVYCSAMSRN LCTRATPRWQSAGHPYCRWTA SYCAIYSDRSIRGNYSTRQSFAS GRRV\PTGSWQKTESEKDCSTC CANWANDRTPLPTSTSSANCST NVQTSVVPVLRRWIWLTSLRV VLTVSLKSVCARGTSPQASCWF VKRAASSATSPVVITTC
21798	52166	A	21926	244	535	TRYPDDHGISPETALYGWHTSA TGTAGMR*SVRPWLQSGQGCS GWRRQQPRWSP**RSC**CSVY PATL*FCRLYNQTSGPGHSDLP AFPDSDRRKI

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21799	52167	A	21927	869	2923	PKKDLKIATSAMMEAAYSV*SR TLFW/SPVRDSQVTDTQWQGL MSQLRLQGFDTLVLQWTRYGD AFTQPEQRTLLFKRAAAAQQA GLKLIVGLNADPEFFMHQKQSS AALESYLNRLLAADLQQARLW SAAPGITPDGWYISAEIDDLNW RSEAARQPLLTWLNNAQRLISD VSAKPVYISSFFAGNMSPDGYR QLLEHVKATGVNVWVQDGSG VDKLTAEQRERYLQASADCHD GAAPHGK\VFKLIIA*RARR
21800	52168	B	21928	72	690	
21801	52169	A	21929	1	2241	
21802	52170	A	21930	1607	1893	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPAFFQLLIK HVD/SMCHQRLSGSRKSKHNVI AVVFSYCSVSVFSASCPTHQVL LQTQYF
21803	52171	A	21931	1	3960	
21804	52172	A	21932	1	1281	
21805	52173	A	21933	1	1491	
21806	52174	A	21934	1	1254	
21807	52175	A	21935	1	723	
21808	52176	A	21936	740	880	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPGFFPTVN
21809	52177	A	21937	1	1191	
21810	52178	A	21938	1033	1248	
21811	52179	A	21939	1	1425	
21812	52180	A	21940	1	2784	
21813	52181	A	21941	676	1467	
21814	52182	B	21942	1	3288	

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21815	52183	A	21943	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIG\LQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCLALHRIETEL MGKFDEGKLPTDPHLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK
21816	52184	A	21944	1790	2947	TDFSVRCKGCRTGPFLRLIFQDR IVGVELIAVF*NTGPRFSSCRLS WRRPFDKTCRMRWHQRLSGFP QEQNDGKQQPILC
21817	52185	A	21945	1	888	
21818	52186	A	21946	252	1863	RKNPFILH*LFR*TLRQTKPDDS AGKGVKI**HTQNQRSGRSQND F*RRLW
21819	52187	B	21947	1	1794	

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21820	52188	A	21948	138	341	PNPRGLLNTITPEHFKSKLHIPT TYRQSNGITASHYSYARN*RVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGLLELL KAAASLVFLEQHKPYEEIGTSF GSVLVSVVGEGPFVEEDLRKSF PGRWDKKHKMFDAIEEPKKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYLVFEANTGTENGYQGEE SLFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGIIELK YDYTLKKVMKAADHFQTPVTD EIERANVFKMNG
21821	52189	A	21949	761	916	NKRIFPSHVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPAFFQLSIE LSPT
21822	52190	A	21950	1	1437	
21823	52191	B	21951	50	1690	
21824	52192	B	21952	1	1032	
21825	52193	B	21953	1	1974	
21826	52194	A	21954	878	1202	SVYNKRIFPSDVKVAEPDHSCV *SFRIGSLASNLSLSLKTRPAFFQ LSIE\FRRPFDKTCRLMCHQRLS GFPHEQTQRDSTCIQLLFRQRF AAASCPTHQVLLQTQYF
21827	52195	B	21955	7	1702	
21828	52196	A	21956	527	665	NKRIFPSDVKVAEPDHSCV*SFR IGSLAFNLSLALKTPARVFSTVD
21829	52197	A	21957	469	687	
21830	52198	A	21958	2	1018	EGSDSRAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDRKTYQNGQQFIDEG NIPPATPYAERPYYFEDKGLKY LGKPTVEPSVCGGRLESPWQTA GVSPTVQKLKSLKFDVRGQEES VWEKDEAALANWTVPNHTCD NLKTCHTLHGSVMAETAVFNP KKLKNSPR\IVQSNHLI
21831	52199	B	21959	7	1113	
21832	52200	B	21960	1	1188	

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21833	52201	B	21961	1	1414	
21834	52202	B	21962	1	1515	
21835	52203	A	21963	1652	1916	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQND F*RR
21836	52204	A	21964	1	1353	
21837	52205	A	21965	1	1507	MAAQDAMVTRTSSQTDCKEPG LKWAGVVLMLLLCWLMFQVL WEACQQKTGEHKTMLQMILCN KSYQQLRLVITPMYLMLGDWL SKNCGQNSTPSLGDNPPERQTQ EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDDLHIHAEDTL LPFYLGEKDDVTYAIKPTCWPG LDIIPSCLALHRIETELMGKFDE GKLPTDPHLMLRLAIETVAH*P AEK*HQNHSSPF*PRFFAVSLRT GSSYHCILSSH
21838	52206	A	21966	729	843	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLLINM
21839	52207	B	21967	1	1416	
21840	52208	A	21968	1	1794	
21841	52209	B	21969	1	1171	
21842	52210	A	21970	1108	1250	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPGGASRVP K
21843	52211	A	21971	1	2535	
21844	52212	A	21972	743	898	NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPAFFQLSIE LSAT
21845	52213	B	21973	1	1605	
21846	52214	B	21974	1	1873	
21847	52215	B	21975	1	2946	
21848	52216	A	21976	1419	1498	
21849	52217	A	21977	1	2314	
21850	52218	A	21978	1	1215	

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21851	52219	A	21979	1	1851	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDRNRERHTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSVMAETAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVA\KYVEIF\GLPFAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAPSPS KGLYSVHINPYLIPFFIGLQN\RL TQFRLSETKEIPNPYAM/RLYTN TLCQYRKPDGSGIVSLKIDWIIE RYQLPQSYQRVWTPGINCPEPC PGVWTPGINCPGAWGIHGPHGS AENTGPLHPGQTSAQLETSLLP SLRSARELELAQLSPRRKQNRS LQNIGVTPSLRVPWPKASNVQQ FIDEGNYTSGDNHTLRDPHYVE DKGHKYLVFEANTGTENGYQG EESLFNKAYYGGGTNFFRKESQ KLQQSAKKRDAELANGALGIIE LNNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWYLFTDSR
21852	52220	A	21980	3197	5376	
21853	52221	A	21981	543	5690	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQND F*RRWSRSY
21854	52222	A	21982	2241	2614	ETLTTLKTKAINTLYSKPTREQ KTDTKAKNLYLTKRTTAAART SSVKKAISFNRALKNAMLS*RT APSVS*IRHRV*NLTMRSSSSSA PSPWML*A*AWLCRYCRASCGI SSIPTASPVTMACC
21855	52223	A	21983	31	892	
21856	52224	A	21984	548	855	
21857	52225	B	21985	1	1825	

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21858	52226	A	21986	1	3146	MEWGKFKRLVLPSQGKSKPEQ RCQYRHTVGDQATLPLRSRVE KRNGEAEGRIYRKLWDVALLC CVQEVINGERKPLRALTEVKSG FRLREDSDKFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQNVQQFIDE GNYTSGDNHTLRDPHYVEDKG HKYLVFEANTGTENGYQGEES LFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGIIELN NDYTLKKVMKPLITSNTCDN
21859	52227	A	21987	1	3107	MNEMKREEKFREKRRERNEQI LQEIRDYVKRSNLHLIGVSKSD GENGTELENTLQDIIQENFPNLA RQANIQIQEIQRMLQRYSSRRTT PRHIIVRFTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLSAET LQATKEWRPIFNILKEKNFQPRI SYPAKLSFISEGETKYFTDKQM LRDFVTTRPALKELLKEALNME RNNRLVKSLAWASQNGFRSPA LLPLSLMLCAPLQEADGTNLG WLAHCGLLCTGDH
21860	52228	B	21988	239	2825	
21861	52229	A	21989	7533	11119	
21862	52230	A	21990	1	3718	MEVIPEGYRLSELKKCSKWIVV MVARLYEYTKNQQIIHLKWVN HMLGCLLDRNDPLRDVDEAAV PVLCICSADDPVCGPPDHTLTTE LFHSNPYFFLLLSRHGGHCGFL RQEPLPAWSHEVILESFRALTEF FRTEERIKGLSRHRASFLGGRRR GGALQRREVSSSSNLEEIFNWK RSYTRLMAAAAGAAAAPGSRE PQDRPECGAGHPGPRYYRHPER WLLRPEAFLGPLRTRAPSAEDS QRERPAARSGPEM
21863	52231	A	21991	1	697	
21864	52232	A	21992	1	978	

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21865	52233	A	21993	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIG\LQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCLALHRIETEL MGKFDEGKLPTDPHLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK

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21866	52234	A	21994	1184	2229	RSSVATVALLHAVINHK/KRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THIFFDMLRDLLKNVDLKGFEP DVRILLTKYSNSNGSQSPWMEE QIRDAWGSMVLKNVVRETDEV GKDTSLSTPAAPMVDSLIARVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGAVSQ GGESFIYMPLTGAAAFLSEMPC PERRNLKKQCGYSGFAACGYQ SQERKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESFPWFIKRA HSPSRGLYSVHINPYLIPFFIGLQ NRFTQFRLSETKEITNPYAMRL YESLCQYRKPDGSGIVSLKIDWI IERYQLPQSYQRMPDFRRRFLQ DHNSSPEREQNWMENEFDELT EVGFRRWVITNSSELKEHVLTQ CKEAKNLDKRLQELLTRISNLE NIDDLMELKNTAQELHETYTSI
21867	52235	A	21995	82	325	
21868	52236	B	21996	220	1173	
21869	52237	A	21997	1	1599	
21870	52238	A	21998	188	421	
21871	52239	A	21999	1	596	MGMTDMGKSKKKSQGPPSFPP GGAPPPAIGAPAGRERPPGTGD PFNQRPCDNLKTCHTSHGSVM AETAVINHKKRKNSPRIVQSND LTEAAYSLSRDQKRMLYLFVD QIRKSDGTLQEHDGICEIHVAK YAEIFGLTSAEASKDIRQALKSF AGKEVVFYRPGEDAGHEKGYE SFPW/FIKRSPE*RRGKFPFTQM GQD
21872	52240	A	22000	1	1527	
21873	52241	A	22001	2	870	

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21874	52242	A	22002	1	4304	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPDFRRRFLQCINA GHEMTKAIAIAQFNDDSPEARK ITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPD
21875	52243	A	22003	740	1159	SLPNLDNSAICSSSSSPTRTR*SL SVSAAALRRRLPSAISMTPDTL RPNAGVC*PVSRKEGMRSSSAS SVSSSWSRSLPDHTREVFSTLSP RSTSRVNFTSRPHTGKVMALPR AITPTRAINESTIETAGEDNEVSS TG
21876	52244	A	22004	664	1844	SGNLKACHPSHGSVMAETA\VI NHKKRKNSPR\IEQ*KDGYQQA YSLSRDQKRMLYLFVDQIRKSD GTLQEHD\GI\CQIHGAQYR*QIS D*PFAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPW FIKRAHSPSRGLFSGHIPP\YLIPF FIGVKNRLTQI\RLFETKEIPHPS AL\RYYESLGQDRK\PDGSSIGS LK\IDWIIERYQLPQSYQRMPDF RRRFLQHFLAHAGCPKGTQNFT FRMKFIIFSIKKVLPPVDTILAHD PVIHTCHLRESFGSVSPSSPKSN RLPCPEVILFHYGESWNLLRAD QRLIFAKSWPRASRYQQGHQD LFILRSDLPSQVFIRDKLMERRN RRTGRTEKARIWGSDGQNGQE PGYVEAGCPPLLLTV
21877	52245	A	22005	3	272	
21878	52246	A	22006	1	528	
21879	52247	A	22007	461	831	LLNLATWRYLGTLTRGTAS\VA VAGILAALRITNNKLSNHVFVF QGAGEAAMGIAHLLVMALRRK K\GTERTTATRKIWMVDSK\GLI CQGEGSHLN/HHEKEMFAQDH PEVNSLEEVVRLVKPTAM

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21880	52248	A	22008	3	1894	EGEDRGLPRTMGAALGTGTRL APWPGRACGALPRWTPTAPAQ GCHSKPGPARPVPLKKRGYDV TRNPHLNKGMAFTLEERLQLGI HGLIPPCFLSQDVQLLRIMRYY ERQQSDLDKYIILMTLQDRNEK LFYRVLTSDVEKFMPIVYTPTV GLACQHYGLTFRRPRGLFITIHD KGHLATMLNSWPEDNIKAVVV TDGERILGLGDLGCYGMGIPVG KLALYTACGGVNPQQCLPVLL DVGTNNEELLRDPL\YIGLKHQ RVHGKAYDDLLDEFMQAVTD KFGINC\LI\QFEDFANANAFRLL NKYRNKYCMFNDDIQGTASVA VAGILAALRITNNKLSNHVFVF QGAGEAAMG\IAHLLVMALE\K EGVPKA\EATRKIW\MVDF\KGL IVKGRSHLNHEKEMFAQD\HPE SNSLDEVVRLVKPTAIIGVAAIA EA\FTEQILRNMASF\RRAPIIFA LSNPPRKAECTA\EKCYRVTEG PRGFFASGKSFLRSVDL/ESMGK TFIPGGRGNNA*RVPRGWQLG VHSPGGDPGHIP\DEIFLPDSRA KLPQEVSEQHL\SQGRLYP\PLS T\IRDVSLRIAIKVLDYAYKHNL V\SYYPEPKDKEAFCKIPGSYTP DYDSFYT/VDSYIWAQGKAMN
21881	52249	A	22009	322	567	
21882	52250	C	22010	338	603	
21883	52251	A	22011	127	417	
21884	52252	A	22012	253	424	
21885	52253	A	22013	124	1235	YLCLLPKGQGDRALSRTSQWP QMSQSQACGGSEQIPGIDIQLN RKYHTTRKLSTTKRFPTACWR KKVGAFTKIIEAMGFTGPLKYS KWEDLRLRALRIVY*LCGRKLD FEGFFSK\CS\MPDTFNSWFLINP YFHVWMCLVRMKQEGRSGKY MCRIIVHFMWEDVQQRGRVM GVNPYILKKNMILMTNHFYA\A ILGYDEGILSDDHGLAAALWK NLL\N\RKCEDPRHLELLVEYVR KQIQYLDS\MNGEDLLLTGEVS WRPLVEKNPQSILKPHSPTYND RGTFDGLGPPHGPPAGFRGTSR EEKCLVGPRTPARKWPELDLLN KHLSKYLAPICVEFPLSVPQESD LLGYRAWENPLALPGCPSSLRG

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21886	52254	A	22014	282	435	GGGASPAACSGSPDSS\HSATA GTGCRRPARPPPAPPTPTPWRS RQQGSRAS
21887	52255	A	22015	3	399	IVALPFGHHHSQTSPLPNLLQTA ACLLLHFLLLSGVETGRPGPWQ PRIRARGPPAPPGPARPAKPRRR /GCRGPAREACWYGCRRPARPP PAPPTPTHGAAGSREAERASEL/ C*GARPLRLGSAGTIMVSACVP
21888	52256	A	22016	279	872	KIPIISLSLKLGQASSKIIPTPQNP HLSPGTKRDSSFQPWSLSAFIIT GQCCSYIVRWGLWKPRLILVV KKYAALSAEMLLVKVEEPSPA ACSGSPDSSSFCNCW*PAAAGR L/ASAAQRPPTPNAHKRSRQQG SRASERAS/CKGRGRYGLGALG GRGGRALGGSRWPPPLPGETLF SGCKHRRRRRGSDAAPGEEAG
21889	52257	A	22017	106	398	NAAPFSRHAAFQGFSWAVCIFR LPAERALRLFPASCLVLPGGPS GVAP\HGWPLPTTAPPLLQGVW RVEVGEHEMAEIFSSAKKEAAG ALQRPCIPVW

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21890	52258	A	22018	1	1806	MRGNTAGGPGDEKPDSTHPPW EGTLQEAQEMKKVVRFMWTS GGPDPQHWRGSGLYGQLVAQ MLHIDVAQVYMDSWWPRCST LAWLRFIWTAGGPDAPHWLRS GLGGQLVAWMLHVGVAQVYV DSWWPSCSASMWLSFMEHKQ CLTLGYEVALFLQHFLSRAFVL VWVPRKEKAQVLRQGLSLTFR ENPGVCVMSSYRPWLITAAAD MQPSKPGGTGSYCSYWSPTDN TPRLAAACTWNLGSSHGSAPG VRTFIEAGFSPPFLAPKALALTL SDSDSRWGPNPVYAQPQP/PEP AWGPNPV*GQPQPRNRPG\PEP CVCSTPTAEPPWGPNPVSTPTA EPAWGPNPVYA/PTPTAEPPWG PNPV*GQPQP/REPAWGPNPVY GQPQPRNRPGS\PPQGNLYCSA ALGATDPSQSWHQCSQNLLPA DKGAKREAPW/PRPPSGEVDHQ VWHLHGWPLPTTAPPLLQGVW RVEQTPASHHRQPRPRQSSPST KAPPVITVNQGPASHHRQPRPR QSSPSTKAPPVITVNQGPASHH RQPRPRQSSPST/TGPASHHRQP RPRQSSPSTKAPPVITVNQGPAS HHRQPRPRQSSPSTKAPPVITVN QGPASHHRQPRPRQSSPSTKAP PVITVNQGPASHHRQPRPRQSSP STKAPPVITVNQGPASHHRQPR PRQSSTLTKAPPVITVNQSPASH

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21891	52259	A	22019	27	1367	RILAGPARAEAGSASDRSTGHL FPRGVGMDLCHPQPAELSSGET DELPRI*WHRKQLLEDIQKLKD EIADVFAQIDCFESAGDSRMAH KENELCIGRKKFNMDPRQGRW LWRARATGCGGCMGAPAW\FL SGEGLNKTAIGTYLGER*ERVE P*RGRK*RCAGVYRCVDVQAL R*VVLGQGPGPQGWHSPSGWG CRDPRYCLCNPGVFQSTGARRG VGPRAPGPLQHCQA*ISQTRPPF ERFVSMNRGINNGSDLPEDQLR VREAQPTQPGPGESRRDLSLDG WPFFNPDREGWLLKLGERPTD TRRRTHTHARAGTHRCMHTTV SRVLLGLPLPPPLPAQPTSQ/PPT SRC/LRLQDPE/CWSHWEIS*TE RGESRVVEGKHESYRISATSAE ERDQWIESIR*GVPRSGDGFPSP SRRPCFFWVLRDSWRWHWGL VTLRVPSPAAPGDP
21892	52260	A	22020	140	356	
21893	52261	A	22021	2	1147	APARGPAVASGPSPGPAAEPVQ NTETAAMTTHVTLEDALSNVD LLEELPLPDQQPCIEPPPSSIMYQ ANFDTNFEDRNAFVTGIARYIE QATVHSSMNEMLEEGHEYAV MLYTWRSCSRAIPQVKCNEQP NRVEIYEKTVEVLEPEVTKLMK FMYFQRKAIERFCSEVKRLCHA ERRKDFVSEAYLLTLGKFINMF AVLDELKNMKCSVKNDHSAY KRAAQFLRKMADPQSIQESQNL SMFLANHNRITQCLHQQLEVIP GYEELLADIVNICVDYYENKM YLTPSEKHMLLKVMGFGLYLM DGNVSNIYKLDAKKRINLSKID KFFK/HAAGGAPFRRHADRAGQ IH*DQCSL*REQVQVDVHPEQH QPPVQYLRADGSDPG

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21894	52262	A	22022	47	1581	ALVLMYLASSICMSPKRGTTCS CLERGSRCPTSEPPPPPEPPPGRS SRCRPGLGPYGGGGEKMADDP SAADRNVEIWKIKKLIKSLEAA RGNGTSMISLIIPPKDQISRVAK MLADEFGTASNIKSRVNRLSVL GAITSVQQRLKLYNKVPPNGLV VYCGTIVTEEGKEKKVNIDFEP FKPINTSLYLCDNKFHTEALTA LLSDDRQVWDFIVIGG/SVGALF GHTPKGNTRGGPWHKFTVGIFP K\KHG*EGGQ\SALRFARLRME KRHNYVRKVAETAVQLFISGD KVNVAGLVLAGSADFKTELSQ SDMFDQRLQSKVLKLVDISYG GENGFNQAIELSTEVLSNVKFIQ EKKLIGRYFDEISQ/DLTGKYCF GVEDTLKALEMGAVEN\LIVYE NL\DIMRYVLHCQGT\KEEKILY LTPEQEK\DKSPFH\DKETGQE\L ELIESMPLLEWFANNYKKFGA\ TLEMFTDKSQKGSPV**KDLGG IGG\ILRYQSRFPGEWNTKKET MNFLTLMTTR
21895	52263	A	22023	1	296	VEDERVCAGPAWERQAGQERP ARKVQGKAPEAEGKHGCLLDI LVCTYLAEKGLSGSCGLTEALV AFGEGSSLGRKNCRDPWGSLR QEPHWSDP/WSGPPERCKGKPQ RRRGSTDAFWTSWSART*PRRG SLAAVG*QRHWWPLGRAAV*E ERTAETPGAPSGRSLTGQTLGS LHV
21896	52264	A	22024	5	309	LPDADLFCPACGAAAGRARSA GMRPVFAVSVARTPSPR/PPPAE PQFPRLPCGSIGSPFFRDIDTIQK FPDMLSSFFFRDIDTIQKFPDML VFNCCCLLNQSR
21897	52265	A	22025	1	258	RGRSRIARSASGPRPALVRPPAR PPAP*TPRSWSCWSSC*PRSASA TGSPSA*ATDAHADSSKAMLPE PTSSISKFSTLQTVPFRL
21898	52266	A	22026	119	692	PSSHSVRTATYSSLRQSAVSTRT STTTTLAFMARAGGRAGGRAR VGGRTPSGQCGCPACGAAAGR ARSAGMRPVFAVSVARTPSPR/ PPPAEPQFPRRPQR\GAPAPSGG GASLPAPRALASSIPAQLMKPG RAKGSAGNLHPG\EGRPGARRS DPAGAARSLACP*IWPKQTPSP LASSSSFFLSETPECAH

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21899	52267	A	22027	2	246	
21900	52268	A	22028	1	927	
21901	52269	A	22029	251	1077	VTMGKVLAVSSLPAGPPPPPVP ALVGLPPPPP*HPGFRLPPLGGG LGARTSVGRGLERTPGAATASA AGGAEDGACRCLPNPCTFEECH RKCKEL*MEGVKFTENKAL/SS KMAIQTQQSKFVKWQVDGEYR GSDFTVDVTLWNPDVLMGSGI LVAHYLKSITPCLALGSELVYH RRPGEEGTVMSVAGKYTLNNW LATVDVEFEASTRMQDTNVSF GYQLDLPKANLLFKGSVDSNW IVGATLEKKLPPLPLTLALGAFL NHRKNKLRSGFGLTIS
21902	52270	A	22030	1	1171	GGGSGFGCAWRTGWERSPGRE QAPPPATMGNVLAASSPPAGPP PPPAPALVGLPPPPPSPPGFTLPP LGGSLGAGTSTSRSSERTPGAA TASASGAAEDGACGCLPNPGTF EECHRKCKELFPIQMEGVKLTV NKGLSNHFQVNHTVALSTIGES NYHFGVTYVGTKQLSPTEAFPV LVGDMDNSGSLNAQVIHQLGP GLRSKMAIQTQQSKFVNWQVD GEYRGSDFTAAVTLGNPDVLV GSGILVAHYLQSITPCLALGGEL VYHRRPGEEGTVMSLAGKYTL NNWLATVTLGQAGMHATYYH KASDQLQVGVEFE\ASTRMQDT SVSFGYQLDLPKANLLFKGSVD SNWIVGATLEKKLPPLPLTLAL GAFLNHRKNKFQCGFGLTIG
21903	52271	A	22031	14	434	CYCQGILSPPPCPPFLLGSAQTS AICSWVRGVPAESSTSSFPKAP* VALESRGEAPTLHLPVTSRFLQ CVSSEQECVPWKP/HSSPRPRFL DISPSPTCVRL*APGPVPFDPHQ KTWRSPLGTRAQGVGPRDRDS CRIVPG

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21904	52272	A	22032	989	1859	VYGDSRWSLALSPRLECSGA\IS AH*NLCLPGSSDSPASRITGISG ARHHAQLI/L/YVFLVEMRFHH VGQAGLKLLTSGNP/HHLGLPK CWDYSRKPPPRPPRPII\FSFFFL RWSLALVAQAGMQWDDLSSL QPLPPGFK*FSCLSLLRSWDYG CPPPRLANFVCVCVCVLV/VDG GFTMLARLGLELLTSGDLPPFG LPKCLGFTGMSHCARPIFFF\FE MESCFATQAGVQWCDLSSLQP LPPRFK*FSCLSLLSSWDYRHM PPCLANF/CFGIFSRDRVSSCWP GRSQTPDLK
21905	52273	A	22033	157	376	SHQDFMRTAANLLQTGWCTGS NTGAGARWGLCRASLSRCRCA APSAPCSGSRCS*RSWKGTHPS LPPRCRGRS
21906	52274	A	22034	298	399	
21907	52275	A	22035	1	185	
21908	52276	A	22036	311	516	WKAERRTRHLLQTGWCTGSNT GAGARWGLCRASLSRCRCAAP SAPRSGSRCS*RLWKGTHPSLPP RCR
21909	52277	A	22037	1	1487	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAKSQGCSRN ARHQKARSMPLQDQHLALAIL LELAVQRGTLSQMLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLLQTFQSIICSKDTPPSEGN MHLLSGPLSPSESFLRESFFTVQ NCRNNEEVTLICKADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFCVGQYLEVR LYALSDAEDGRGHPLMASVIHL LWRLQTSQIHYSYNEEKDEDH CSSQWAHLPANRDCSHRWALG DHSQAFLQAIADNNIQDHNVKT HQEQGRSYKEVCTPVIERLRFL SNELRPAVGNDLSIISEFKLLSSL PRWRRIAQKIIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIAIKSPKTITSENP LG/REPGEHPASPLPPDDAQHA HPAAQRKQPRPPAQFRHAGPHS DGTAPDWPQL

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21910	52278	A	22038	263	375	AGPRRMRRISAWAVSTPLTDSP SPGHQPA/GEVAGAGSF**HPP/P PCPSRYCPQMTPPPPPPAPPPAL PPPPPPAPASPPLPPAPSPPPHAP PQALPPPPALPPPPPASPPLLPPA LSPPLPAPP/PPSAPPASPPPAPPP PPAPPPSPPPAPPPSAPSSPAPLPP APASPP\SPAPPPPAPPPAPHPPSP PAPPCPPLPRPRGPSVPQEKVHQ V*IPVP\PAGEGGPAPGRIWPQG WRRAGKPPTWEEALAAFPPWT ALPPASAVPAQPPRAH*VAPAL *WALHRRSDSDSDSSNLSPRIPG TGGQRRQPR*DS*APACSEVAG AGSF
21911	52279	A	22039	1	2001	
21912	52280	A	22040	1846	7725	PEPFCHRAAHWSNQYCPFQFQ DTDSPRQTLTVLIKDNGEPSLST TATLTVSVTEDSPEARAEFPSGS APREQKKNLTFYLLLSLILASV GFVVTAFGVIIFKVYKWKQSRD LYRAPVSSLYRTPGPSLHADAV RGGLMSPHLYHQVYLTTDSRR SDPLLKKPGAASPLASRQNTLR SCDPVFYRQVLGAESAPPGQIR YPVPEESQEGTFVGNVAQDFLL DTDSLSARRLQVAGEVNQRHF RVDLDSGALLIKNP
21913	52281	A	22041	108	340	PQPSQVMSFHGDSGSCRRWAT AGT*ATSPPCSSSIFLRRMHSGH WCSCWPVRGTPCRDFTAQMAG PSRGSKTNRSMW
21914	52282	A	22042	275	752	EKTHKTCRCGRGCGKRGTL*H CWWECNLLQPLWKMVW\KWL KELKVELLCDLAVPL/LGINPEE KKSLYEKDTCT/R/LFMAAQLAI AKKWNQPKCPSINKWLQKLW YIYMMEYYSAIKRN\LTAFAAT WMRLETIILSQGDPLESTCSRSQ ANRQEITSVPKA
21915	52283	A	22043	25	202	DAEAWAMELADVGA*ASSQG APQPEEPAASLGVNEKGGAGG RSGRRPLGRDRPRPTRLL

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21916	52284	A	22044	1	2290	MEKLGVEPEEEGGGDDEEDAE AWAMELADVGAAASSQGAPQ PEEPAASLGVNEKGVHDQVLPT PNASSRVIVHVDLDCFYAQVE MISNPELKDKPLGVQQKYLVV TCNYEARKLGVKKLMNVRDA KEKCPQLVLVNGEDLTRYREM SYKVTELLEEFSPVVERLGFDE NFVDLTEMVEKRLQQLQSDEL SAVTVSGHVYNNQSINLLDVLH IRLLVGSQIAAEMREAMYNQL GLTGCAGVASNKLLAKLVSGV FKPNQQTVLLPESCQHLIHSLN HIKEIPGIGYKTAKCLEALGINS VRDLQTFSPKILEKELGISVAQR IQKLSFGEDNSPVILSGPPQSFSE EDSFKKCSSEVEAKNKIEELLAS LLNRVCQDGRKPHTVRLIIRRY SSEKHYGRESRQCHIPSHVIQKL GTGNYDVMPPMVDILMKLFRN MVNVKMPFRLTLLSMCFCSLK AVNTATTRLIDYYLMPTISITSR SGKHSFKMKDTHMEDFPKDKE TNRDFLPSGRIESTRTRESPLDT TNFSKEKDINEFPLCSLPEGVDQ EVFKQLPVDIQEEILSGKSREKF QGKGSVSCPLHASRGVLSFFSK KQMQDIPINPRDHLSSSKQVSS VSPCEPGTSGFNSSSSSYMSSQK DYSYYLDNRLKDERISQGPKEP QGFHFT\NSNPA\VSAFHS\FPNL QSEQLFSRNHTTDSHKQTV\AT
21917	52285	A	22045	2	141	
21918	52286	C	22046	278	489	
21919	52287	A	22047	130	426	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
21920	52288	A	22048	357	1579	QRRPRPFPSQGISMTECFLPPTSS PSEHRRVEHGSGLTRTPSSEEIS PTKFPGLYRTGEPSPPHDILHEP S*SNGLMDEKDHGKKKGNFKK KEKRTEGYAAFQEDSSGDEAE KLMPRFEEAYGRTTETEKVQEF QRLLKELPEGNYLLISLFVVHM DHVITKELEAKMNIQNIYIVVSP TVQISNLVLYVFFTHVQELFGN VVLKQVTKTRRWSNVATMPTL PETQAGFKEEIRIQELLLNCLHQ DLQGGIKDLSEEERLWEEKEIL TKQEELLGMEQFLRRQIASEKE EIECLRAETAEIQSHQQQGLSET EEYSSESESEDEEELQIILEDLQR QNEELEIKNNHLNQAIHEESEA VIEPRMQPWLLQLQPDRAKQQ AQEDEEPEWRGGAMQTPKNGI
21921	52289	A	22049	182	2212	VTEKTSSLPSQGISMTECFLPPT SSPSEHRR\VEHG/SAGLTPGPPA SEEIQPLPKFPGLY\RTGEPPHPP P*HPSHEPSLM*CPDDEKDHGK KKGKFKKKEKRTEGYAAFQED SSGDEAESPSKMKR\SKGIHVFK KPSFSKK\REKDFKIKEKPKEEK HKEEKHKEEKHKEKKSKDLT\A ADVVKQWKEKKKKKKPIQEPE VPQIDVPNLKPIFGIPLADAVER TMMYDGIRLPAVFRECIDYVEK YGMKCEGIYRVSGIKSKVDELK AAYDREESTNLEDYEPNTVASL LKQYLRDLPENLLTKELMPRFE EACGRTTETEKVQEFQRLLKEL PECNYLLISWLIVHMDHVIAKE LETKMNIQNISIVLSPTVQISNR VLYVFFTHVQELFGNVVLKQV MKPLRWSNMATMPTLPETQAG IKEEIRRQEFLLNCLHRDLQGGI KDLSKEERLWEVQRILTALKRK LREAKRQECETKIAQEIASLSKE DVSKEEMNENEEVINILLAQEN EILTEQEELLAMEQFLRRQIASE KEEIERLRAEIAEIQSRQQHGRS ETEEYSSESESESEDEEELQIILE DLQRQNEELEIKNNHLNQAIHE EREAIIELRVQLRLLQMQRAKA EQQAQEDEEPEWRGGAVQPPR DGVLEPKAAKEQPKAGKEPAK
21922	52290	B	22050	34	322	

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21923	52291	A	22051	137	1546	QMLGGRPPPRWLQLAKARALA RRRPPPSLHLTLPTALSLKS/RTP VPKSIPISETPNIPPVSVQPPASIG PPLGVPP/PEPSHGDDQPRPG\PL PIFMEQQIMQQIRPPFIRGPP\PM PPTPTAPCPTPCFPASGPRPVAP ETWAPLPAPCTGPCY\PPHPPPE/ PPPP/SPGNPPGLLPPPPPGAPLPS LPFPPVSMMPNGPMPVPQMMN FGLPSLAPLVPPPTLLVPYPVIV PLPVPIPIPIPIP\PSATPSPPTGSP ATGRTSFRTPLATPRRRAASQA DTPCPPGTPSRARPSPRTRPPAA RARP*AWRPRPPSMAGARWWT *RGAPA\PPGPPGRGRPARLPRR AAGPAGRRHRPDRGPPSPAAQR DPPRAA/PRTSRRSASRAPRSAG PAAAAGTATAARPPPATQARA PRRAPRRPRPATSS*TARAAPPP/ SGAKSAEPPPEQPPPPPPPAPPK KLLSPEEPAVMRARVGQGE
21924	52292	A	22052	762	2049	RSSFSMGADLLACST/SGLGNM PY\DLLRGMEPTLGCSFEDLAL A*PGGITQE\KINEMRVAPEQQ MI\ADIHFMIAAGQDLDWIDAQ GATLLHIAGANGYLRAAELLLD HGVRVDVKDWDGWEPLHAAA FWGQMQMAELLVSHGAN\LNA RTSMDEMPIDLCEEEEFKVLLL ELK\HKHDVIMKSQLRHKSSLS RRTSHRQAS/SVGKVVRRTQPV GTGPNL\YRKEYE/GEEAILWQR SA\AEDQRTSTYNGDIRET\RTD QENKDPNPRLEK\PVLLSEFPTK IPRGELDMPVENGLRAPVSAYQ YALANGDVWK\VHEVPDYSMA YGNPGVADATPPWSSYKEQSP QTLLELKRQRAAAKLLSHPFLS THLGSSMARTGESSSEGKAPLI GGRTSPYSSNGTSVYYTVTSGD PPLLKFKAPIEEMEEKVHGCCRI
21925	52293	A	22053	2	306	SKEAFAIGLGGGSASGKTTVAR MIIEALDVPWVVLLSMDSFYK/ NAFDFDLIISTLKKLKQGKSVK APIYDFTTLSRKMDWKTLYGA NVIIFEGIMAFADKTL
21926	52294	A	22054	2	379	

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21927	52295	A	22055	352	1227	GDVSPQLSPRQKSGPLCTSCCA WPVCSPHSDAQPSCGEGGLWE KTPFLSVPHRFVPRAALASAHQ CHPLPRTLSVLKSTPQVRGMHT IIRDKETSRDEFIFYSKRLMRLLI EHALSFLPFQDCVVQTPQGQD\ *RITGVSILRAGETMEPALRAVC KDVRIGTILIQTNQLTGEPELHY LRLPKDISDDHVILMDCTVSTG AAAMMAVRVLLDHDVPEDKIF LL\SLLMAEMGVH\SVAYAFPR VKKSSPRRWDKAGQLTFFRIIP GIGNFGDRYFGTDAVPDGSDEE EVAYTG
21928	52296	A	22056	72	2746	FLVETGLHHVGQAGLKLLTSN DPPASASQSTGITGMSHHAQPR QSSYVPPMSLPASAMPVEGVG GDALWAGHASGYLGGGQLWA TSEYIPLCSSNAESLDRLLPPVG TGRSPRKRTTRQCKSEPPLLRTS KRTIYTAGRPPWYNEHGTQSKE AFAIVPVEQEKEAGQPQAAAA GWAPLGPICAGSLPVPHRGSPL PPAGLGGGSASGKTTVARMIIE ALDVPWGGSSLSMDSFYKVLT EQQQEQAAHNNCNFDHPDAFD FDLIISTLKKLKHGKSVKVPIYD FTTHSRKKDWKTLYGANVIIFE GIMAFADKTLLEGPGPAPCTGP EDSIIRHIAAPSLHKASSRANYC VLSMGTDPKLATSPIPQCVGAS YPKQRCPGEVALARPTDQAAS VQGLVPVSPCPLLASGHSLARC LHQLLDMKIFVDTDSDIRLVRR LRRDISERGRDIEGVIKQYNKFV KPSFDQYIQPTMRLADIVVPRG SGNTVGHRP*LLQHVHSQLEEV SGVPRPHGLAPSPSTHFSAATTP SWPVHLIPLRSLSPASS\SSQPAQ LCQQELGNCSKKLGLGRGRIPL SLPKGRHAGGAALASAHQCHP LPRTLSVLKST\PQVRGMHTIIR DKETSRDEFIFYSKRLMRLLIEH ALSFLPFQDCVVQTPQGQDYA GKCYAGKQITGVSILRAGETME PALRAVCKDVRIGTILIQTNQLT
21929	52297	A	22057	61	341	
21930	52298	A	22058	1	1086	
21931	52299	A	22059	1	498	
21932	52300	A	22060	104	3395	
21933	52301	A	22061	1	1653	

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21934	52302	A	22062	1	1717	
21935	52303	A	22063	172	13375	EDLFKCIMAHAASQLKKNRDL EINAEEEPEKKRKHRKRSRDRK KKSDANASYLRAARAGHLEKA LDYIKNGVDINICNQNGLNALH LASKEGHVEVVSELLQREANV DAATKKGNTALHIASLAGQAE VVKVLVTNGANVNAQSQNGFT PLYMAAQENHLEVVKFLLDNG ASQSLATEDGFTPLAVALQQGH DQVVSLLLENDTKGKVRLPAL HIAARKDDTKAAALLLQNDNN ADVESKSGFTPLHIAAHYGNI
21936	52304	A	22064	1	360	
21937	52305	A	22065	1	2577	
21938	52306	B	22066	323	3154	
21939	52307	A	22067	93	791	IRMSYAEKPDEITKDEWMEKL NNLHVQRADMNRLIMNYLVTE GFKEAAEKFRMESGIEPSVDLE TLDERIKIREIDT*KGQIQEAIRL *FNSLHPEL/LWDTNRYLYFHF ASNSILIPS*FRQ\GKTRGRRWG VAQTQLAD\RGEESRECLTEME RTLALLAFDSPEESPFGDLLHT MQRQKVWSEVNQAVLDYENR ESTPKL\AKLLKLLLWAQNELD QKKVKYPKMTDLSKGGD
21940	52308	A	22068	171	426	
21941	52309	A	22069	5	655	LLQPSVQLPNGTANTSLSFAAV SAVSPPPCRTSTATTLPPPMPSF FCVFPSPSMSPSPSEFLSCIASVS RVHSLSSSSSGSSSTASSLNFSAI MGSSSATASWVLSTTSTPPCPS ALPSSPAQES*SLAASSSAWLSE HPSFSSFTLSWASGAFCDEVSLS FSGSKLSFLSSKGDCGIPFI*TSA CPSSLDFSPCFSSSTSKSSSYSEI GKSPQPI

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21942	52310	A	22070	87	1180	NQASLEVLPSPVDSPDSIPSLPP/ SDNPNRNFSAAPVSCLPSPLPVA ASWPSDPSSCSCPSPEVFRSRAP GVPTPASVVYVTVISSAAGTSSP LRANSSTTTFPAAAVFPTNSSC WCQVSSSATSEKEEALFAIVFSS AVSEPANTSLSSAAVSAVSPPPC RTSTATTLPPPMPSFFCVFPSPS MSPSPSEFLSCIASVSRVHSLSSS SSGSSSTASSLNFSAIMGSSSAT ASWVLSTTSTPPCPSALPSSPAQ ES*SLAASSSAWPVAGISPSGAC TFPAGSASGAAKAPSPSWRCPS FRALFSLLDSSSLSLCSVSLASL SLSPPPSFLRAVMFPATFKSRRC FKYGNHCLFSDLLWLEVCAL
21943	52311	A	22071	841	1052	IGEVLLDNVLKSVF*LGSVLPIT SLKLLP/SGSKRDPAKMSHSHP AG*VTTGAFPRCGRWRLQPAA PPPPS
21944	52312	A	22072	817	866	HANPVSPPTSWPKE*SWP*CSG **RTFQSVSFAGGRRRGSWLKP PPATAWKSSSCHLPSGVRMAHF CRIPFGPRGRDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLES GQ
21945	52313	A	22073	2	3238	TTFPAAAVFPTNSSCWCQVSSS ATSEKEEALFAIVFSSAVSEPAN TSLSSAAVSAVSPPPCRTSTATT LPPPMPSFFCVFPSPSMSPSPSEF LSCIASVSRVHSLSSSSSGSSSTA SSLNFSAIMGSSSATASWVLSTT STPPCPSALPSSPAQES*SLAASS SAWPVAGISPSGACTFPAGSAS GAAKAPSPSWRCPSFRALFSLL DSSSLSLCSVSLASLSLSPPPSFL RAVMFSSDFSNPGVASNMGTT VSF
21946	52314	C	22074	88	4374	
21947	52315	A	22075	73	616	VKESLTQKSKRFQNKLINRRG WERPRSGASWTQRRALGGRGC VDRWLGII/WPHRIPGARLRGFP ALNPTPQTAPSPSPDPRPRPP/CP SDPGPRTEAQCSL\PPPP\PSPRH LDPGPEPPTPLTQQGQKGTRAP RPRCPRSQK*ATSGPAVRRREA RGSASLRTRAPSRDSTHAGIQG NVALQP

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21948	52316	A	22076	1	421	GTVVMGLPKYFISLSTKFPLSFS LSADELHIASLFLWPRSKPFGVI QRSCASQLNALPEVLKNPGDPD KMLRFAESPRNLPAGVL/GDIW TDGKGSVSLQEQVYHFPLIRPT PGS*ARASFLSCG*EEFRRHGLT FSSTRE
21949	52317	B	22077	211	2041	
21950	52318	A	22078	200	1525	IMASAHLATSAFCTRSSSSGRSG SCKRGSWDSEQALIRAWTTLPS SLHAADGSFAGGRGIPSKRWS WRAGQQSSLCLIMQTSSNCGNS FQLVSEGASWRGLPHCSCAELQ DSLNFSYHPSGLSLSVRPSSPGN SPKEQPFSQVLRPEPPDPEKLPV PPAPPSKRHCRSLSVPVDLSRW QPVWRPAPSKLWTPIKHRGSGG GGGPQVPHQSPPKRVSSLRFLT SSQCLFSMCPSSQTLQPSFLQPG PGP\SSSRPCAASPQSGSWESDA ESLSPCPPQRRFSLSPSLGPQAS RFLPSARSSPASSPELPLAT*G/L SATFPESRSQPCDLDARKTGVK RRHEEDPRRLRPSLDFDKMNQ KPYSGGLCLQETAREGSSISPP WFMACSPPPLSASCSPTGGSSQ VLSESEKEEEGAVRWGRQALS KRTLCQRDFGDLDLNLIEEN
21951	52319	A	22079	1	117	
21952	52320	A	22080	3	632	
21953	52321	A	22081	1	448	MQSETETVHLFIPALSVGAIIGK QGQHIKQLSRFAGASIKIAPAEA PDAKVRMVIITGPPEAQFKAQG RIYGKIKEENFVSPKEEVKLEA HIRVPSFAAGRVIGKGGKTAST\ *QNLCSGMKGKALKAKPSTYN CVGCGWSPRPRCSLN

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21954	52322	A	22082	233	2096	RREDEGNKTSWIHPSPWVVLIF RFFSLFFFKQPLFTMNKLYIGNL SENAAPS\DL\KSIFKDAKIPVSG PFLVKTGYAFVDCP\DESWA\LR AIKAFSGKIELHGKPIEVEHSVP KRQRIRKLQIRNIPPHLQWEVL DSLLVQYGVVESCEQVNTDSET AVVNVTYSSKDQARQALDK/L LDKLNGFQLENFTLKVAYIPDE MATQQNPFLQPRGRRGLGQRG S\SRQGSPGSVSKQKPCDSPLRL LVPTQFVGAIIGKEGATIRNITK QTQSKIDVHRKENAGAAEKSIT IPSTPEGTSAACKSILEIMHKEA QDIKFTEEIPLKILAHNNFVGRLI GKEGRNLKKIEQDTDTKITISPL QELTLYNPERTITVKGNVETCA KAEEEIMKKIRESYENDIASMN LQAHLIPGLNLNALGLFPPTSG MPPPTSGPPSAMTPPSPQSEQSE SETVHLFIPALSVRALISKQGQH IKQLSRFAGASSKIAPVEAPDAK VRMVMIAGSPEARFKAQGRIY GKIKEENFVSPKEEVKLEAHIR VPSFAAGRVIGKGGKTV\NELQ NLSSAEVVVPRDQTPDENDQV VVKITGHFYACQ\VAQRKI*EFL TQVRQHQQQKALQSGPPQSRR

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21955	52323	A	22083	8	1675	TASCRLAMALHVPKAPGFAQM LKEGAKHFSGLEEAVYRNIQAC KELAQTTRTAYGPKGMNKMVI NHLEKLFVTNDAATILRELEVQ HPAAKMIVMASHMQEQEVGD GTNFVLVFAGALLELAEELLRI GLSVSEVIEGYEIACRKAHEILP NLVCCSAKNLRDIDEVSSLLRT SIMSKQYGNEVFLAKLIAQAC\ YLFFLIPAISMLITSEFVK/FLGS GISSSSVLHGMVFKKETEGDVT SVKDAKIAVYSCPFDGMITETK GTVLIKTAEELMNFSKGEENLM DAQVKAIADTGANVVVTGGKV ADMALHYANKYNIMLVRLNSK WDLRRLCKTVGATALPRLTPP VLEEMGHCDSVYLSEVGDTQV VVFKHEKEDGAISTIVLRGSTD NLMDDIERAVDDGVNTFKVLT RDKRLVPGGGATEIELAKQITS YGETCPGLEQYAIKKFAEAFEA IPRALAENSGVKANEVISKLYA VHQEGNKNVGLDIEAEVPAVK DMLEAGILDTYLGKYWAIKLA TNAAVTVLRVDQIIMAKPAGGP KPPSGK*NWLNFYCR
21956	52324	A	22084	175	278	

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21957	52325	A	22085	208	1976	GPSPLKEHFSGLEETAYM\NILT CMELAQTTRTAYGPNGMNKM VINHLEKLLVTNDAATILRELE VQHPAAKMIVMASHMQEQEV\ GDGTNF\VLVFAGSFPVNYLKN L\WRIGLSVSEVIEGYEIACRKA HEILPNLVC\CSAKNLRDIDEVS SLLRTS\IMSKQYGLMKVF\LAK PYLLQACRIYFSWIPAISMLITSE FVK/FLGSGIRSS*VLAGMVFK KET\EGDVTSVKDAK\IAVYS\C PFDGHG*QET*GEQCLDKRTAL KDLDGIFR*GEQENLHG/AATSP KAIADTGANVVVTGGKVADM ALHYANKYNIMLVRLNSKM/W DLRRLCKT\VGATALPR\LTPSL SLKEMGHCD\SVYLSEVGDTQ\ VVVFKHEKEDGAISTIVL\RGST DN/L*LDDIER\AVDDG\VNTFQ GSLQRDKRLVP\GGGSNRNLN* PKQITS\YGET\CPGLEQYA/ILK KFA*GHLKAIPPAHWQKYSGE NSGVKAQWK*SPKLYAVHQEG \NKNV\GLDIEAEVP/SLVKDML EAGIPRYLTLGKYWAIPLATNA AVTVLRVDQHTLV*FFFMQIIM AKPAG/GGPKPPKWGRKTWGD DQNGLKIGFNFYCR
21958	52326	A	22086	1	346	PF*CTPSCLWAF*TARSAQTWS APSTRSWCSEWPKSLPSPTWLR *FRKVSSYSWSQSWSSPTASTD SSRPPHSLGASCHPGHQRSLMP PSR*RATSTAYASLSSSHRPNTQ PSPS
21959	52327	A	22087	3	484	RSSQPRVGLCGKSLQP/SSEGSC HLQGWCSFPRSVSSIMAEA*RT *PRVSSSMHGRGPTQNREATKK ASSSETSV/QVTAQEAQAEPGA AGVAG/SPASAPQDSAGACWPA QVL*GGSDRSCRGSHPGNTEPP SVLRTGTAPGA*G/SSPFSPTTQS GSCCFPFSS
21960	52328	B	22088	181	359	

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21961	52329	A	22089	290	2014	STCTPLPTASSQSRPHPPPTPTPP APWRSSNGQVPTLT*PGSTLPP G/SGKSPP/VASGGPARAKPHRA VHVSPAPSGGSPGDVAELPAAV AVRA*QAGSGQRLPAPVCVGE MGTLCPGEPADVHQVVCGLSE PRAPHRPGQPQARAHGVPSGQS LCPAQPG*DDS/AKVSSYSWSQ SWSSPTASTDSSRPPHSLGASCH PGHQRSLMPPSR*RATSTAWRA RTASTPRCLGPRPAPWSCASLSS SHRPNTQPSPSPTSVRRARLATP SSHGWALAPWTPMAPTQPTTW TRWGKTVSGRQMNTWRRPWS TCARYSGSAKRSSGSSHSPWAP PRMRMEKSNSPTASWVRTDSS LRPWGGTRSSMGCEGLKLSTR GTRSCSPSGAMRSPAWSAHSLG CRLPSTTDLQDRWRLCVPGMT SSAASVATTSQNLGWPAGTC*A LWGGGRWPATPAA\QAQPALP GQLPTRWSRCCWPSSWPLCSAS GPSHARCCSPWAMSSTPLP*HC *PSGGSCTSPEGVSCLQSRLEGF ATQPHPWAERTWEAPPGGNTV ILGLLERGSCSRRGIWRKRNQE RKAGRAPAKE
21962	52330	A	22090	363	487	
21963	52331	A	22091	234	282	
21964	52332	A	22092	742	990	
21965	52333	A	22093	1	206	LFPAFSDSRECKLMKKLLEA\H EEQNVD\SYTEA\VKEYDSIFPG WTQWLTTL\LLRIKKTIQG\DEK DLR
21966	52334	A	22094	128	1062	KPFEAAMYNSGKEAEAMALLA EAER\KV\KNSQSFFSGLFGGSS KIEEACE\IYARAANMFKMAKN WSAAGNAFCQAAQLHLQLQSK HDAATCFV\DAGNAF\KKADPQ GGPFNCFDCVAFEIY\TDMGR\F TIAAKHHISIC*DLLRQKLVDIE KAIA\HYRALADYYQGEESNS\S ANKCLLKVAGYA\ALLEQYQK\ AIDIYEQGWGPNAHWTSPPPSK Y\SAKDYFF\KAALCHFCMDML QA\KLAF\QKYEELFPVFSDSRE CKLMKK\LLKA\HGEQNVD\SY TE\SVKGITDSISRL\DQWL\TTH CLR\KKTIRGD
21967	52335	A	22095	1	1038	

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21968	52336	A	22096	20	2482	RVCSSSASTASQAVMADAWEE IRRLAADFQRAQFAEATQRLSE RNCIEIVNRLIAQKQLEVVHTL DGKEYITPAQISKEMRDELHVR GGRVNIVDLQQVINVDLIHIEN RIGDIIKSEKHVQLVLGQL\IDEN YL\DRVGQEVNDKLQESGQVTI SELCKTYDLPGNFLTQALTQRL AIIIIGHIDLDNRGVIFTEAFVAR HRARIRGLFSAITRPTAVNSLIS KYGFQEQLLYSVLDELVNSGRL RGTVVGGRQDKAVFVPDIYSR TQSTWVDSFFRQNGYLEFDALS RLGIPDAVSYIKKRYKTTQLLFL KAACVGQGLVDQVEASVEEAI SSGTWVDIAPLLPTSLSVEDAAI LLQQVMRAFSKQASTVVFSDT VVVSEKF\INDCTELFRELMHQ KAEKEMKNNPVHLITEEDLKQI STLESVSTSKKDKKDERRRKAT EGSGSMRGGGGGNAREYKIKK VKKKGRKDDDSDDESQSSHTG KKKPEISFMFQDEIEDFLRKHIQ DAPEEFISELAEYLIKPLNKTYL EVVRSVFMSSTTSASGTGRKRT IKDLQE\EVSNLYNNIRLFGKRG WKFF\ADDTQGWLLPKHLLEV QCVLISLNLI\FNF\LGFGILMDG Q*DDPGRPFTS\ELRKE\LSKLS EETKVALTKLHNSLNEKSIEDFI FC\LDSAAEACDIMVKRGDKKR ERQILFQHRQALAEQLKVTEDP
21969	52337	A	22097	1	711	VLSLFDGIATGYLVLKELGIKV GKYVASEVCEESIAVGTVKHEG NIKYVNDVRNITKKNIEEWGPF DLVIGGSPCNDLSNVNPARKGL YEGTGRLFFEFYHLLNYSRPKE GDDRPFFWMFENVVAMKVGD KRDISRFLECNPVMIDAIKVSAA HRARYFWGNLPGMNRPVIASK NDKLELQDCLEYNRIA\RIFGFP VHYTDVSNMGRGARQKLLGRS WSVPVIRHLFAPLKDYFAC

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21970	52338	A	22098	406	2885	GRGILVNGACSDQSSDSPPILEA IRTPEIRGGWAVGTGVVSGADI VSGHCRQWSLLSLFQGSGTLSL AFITWAFRETRTRSESPAVSSHT SSQSTCGQHST*HT*HARGRQG RNHVDESPVEFPATRVGSPDAQ TPARSL*LGDMPHSLTIDLTDDT EDTHGTPQSSSTPYARLAQDSQ QGGMESPQVEADSGDGDSSEY Q\DGREGLLPRV/I*GP*TRGKTS YAMVVSWKATSKRQAMSGMR WVQWFGDGKFSEVSPGKGKGF CRPEAVPACLPLNKLVSYRKA MYHALEVTWDEGMRAKP*EQ G*SKRPTELEDQLKPMLEWAH GGFKPTGIEGLKPNNTQPGGNE SPWQHPLPLLVGPLLGRVRLKT NCYNNGKDRGDEDQSRGDCW VPGIMGQMGGGRCRSGIDVIPL TPWLGL*ACLVCQTCRVSPPTT ALDLPPLASSNSPLLPCEGRELL LCSNTSCCR*ALGPVGWMWVG PQGSYVPAV*EPWSCYMCLPQ RCHGVLRRRKDWNVRLQAFFT SDTGLEYVSHRLPPLPPQIPGAQ GVGKLWFDGIATGEFGEHLETL LSCHNRVARESEESIAVGTVKH EGNIKYVNDVRNITKKNVRAV CTLRASSLPVFFPSPPHPNPARK GLYGEHPSLWQSLESLCHLTTG PGAGNK/RGLGWRFQMNPALS SFLST\GVQRDISRFLEVRESGD
21971	52339	A	22099	729	896	

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21972	52340	A	22100	1	2672	MAYKQGFLKVMVHFRKAEVT GKNHTSVHEGYTLISPAAQVLT ISCKKSILLQEQVSFKDVCVDFT QEEWYLLDPAQKILYRDVILEN YSNLVSVGYCITKP\EVIFKI/ES KGEEPW\VLEKGIPQAQCPPQK RKWKV/EMNVVREQPRKMKM TIFGEPPIPTTNKTVSVENGDRG SKTFNLGTDPVSLIKLSL*NM*L \SEMNLKNISGLIITKKNCSRKK PDEFNVCEKLLLDIRHEKIPIGE KSYKYDQKRNAINYHQDLSQP SFGQSFEYSKNGQGFHDEAAFF TNKRSQIGETVCKYNECGRTFI ESLKLNISQRPHLEMEPYGCSIC GKSFCMNLRFGHQRALTKDNP YEYNEYGEIFCDNSAFIIHQGAY TRKILREYKVSDKTWEKSALLK HQIVHMGGKSYDYNENGSNFS KKSHLTQLRRAHTGEKTFECGE CGKTFWEKSNLTQHQRTHTGE KP\L*CTEC\GKAFCQKPHLTNH QRTHTGEKPYECKQCGKTFCV KSNLTEHQRTHTGEKPYECNA CGKSFCHRSALTVHQRTHTGE KPFICNECGKSFCVKSNLIVHQR THTGEKPYKCNECGKTFCEKSA LTKHQRTHTGEKPYECNACGK TFSQRSVLTKYQF\IHTRVKAL* TS*MLEAFIHL/SKLVIQFQKRRS EKAKECQKFVE\KTSCLNM*KL SRKIKTFH*KICKLTVKNKGNK
21973	52341	A	22101	1	2817	

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21974	52342	A	22102	474	2766	NQTALYNQAQLLHGSRFANMS AEGYQYRALYDYKKEREEDID LHLGDILTVNKGSLVALGFSDG QEARPEEIGWLNGYNETTGERG DFPGTYVEYIGRKKISPPTPKPR PPRPLPVAPGSSKTEADVEQQA LTLPDLAEQFAPPDIAPPLLIKL VEAIEKKGLECSTLYRTQSSSNL AELRQLLDCDTPSVDLEMIDVH VLADAFKRYLLDLPNPVIPAAV YSEMISLAPEVQSSEEYIQLLKK LIRSPSIPHQYWLTLQYLLKHFF KLSQTSSKNLLNARVLSEIFSPM LFRFSAASSDNTENLIKVIEILIS TEWNERQPAPALPPKPPKPTTV ANNGMNNNMSLQNAEWYWG DISREEVNEKLRDS\ADGT\FLV RDASTKMHGDYTLTLRKGGNN KLI\KIFHRDGKYGFSDPLTFSSV VELINHYRNESLAQYNPKLDVK LLYPVSKYQQDQVVKEDNIEA VGKKLHEYNTQFQEKS\REYDR LY\EEYTRTSQEIQMKRPAIEAF NETIKIFE\EQCQTQERYSKGNY HLEKFKP*RAMEKEIQRIMHNY DKLKSRISEIIDSRRRLE\EDLKK Q\AAEYREIDKRMNSIKPDLIQL RKTRDQYLMWLTQKGVRQKK LNEWL\GNENTEDHYSLV\EDD EDLPHHDE\KTWECLGSS/RTRN QSLKNLFARGSRDGTFLVRESS KQGCYACSVVVDGEVKHCVI\
21975	52343	A	22103	3	392	
21976	52344	A	22104	168	404	

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21977	52345	A	22105	49	1760	YQSPAWQSHWHQKLQVRKEN MAKRVAIVGAGVSGLASIKCCL EEGLEPTCFERSDDLGGLWRFT EHVEEGRASLYKSVVSNSCKE MSCYSDFPFPEDYPNYVPNSQF LEYLKMYANHFDLLKHIQFKT KVCSVTKCSDSAVSGQWEVVT MHEEKQESAIFDAVMVCTGFL TNPYLPLDSFPGINAFKGQYFHS RQYKHPDIFKDKRVLVIGMGNS GTDIAVEASHLAEKVFLSTTGG GWVISRIFDSGYPWDMVFMTR FQNMLRNSLPTPIVTWLMERKI NNWLNHANYGLIPEDRTQLKE FVLNDELPGRIITGKVFIRPSIKE VKENSVIFNNTSKEEPIDIIVFAT GYTFAFPFLDESVVKVEDGQA\ SLYKYIFP\AHLQKPTL\AIIGLH/ IKPLGLP*LPTGETQVRWAVSG S*KVLTRLPPPSVMIEEINARKE NKPSWFGLCYCKALQSDYITYI DELLTYINTKPNL/FSLWLLTDP TSGLWTVFFGP\C\SPYQFRLTG P\GKMGKGAQEIALHGPQW\DP NISRVHSKVRSCYKEFSIFPFGK FFLKVFSFPGFGLWLFFLIFPYK
21978	52346	A	22106	262	969	EWSSVRRSLVEKRALRRPHPQC LCFRMKTIL\SNQTVDIPE\NVDI TLKGRTGIREGPPEGTLR\RDFN\ HIN\VELSLLWKEKKRGSRVDK\ WWGNQKRNWPTRSD*FVSHV QN\MIKGWLHWGFRLQG*GPV YAHFPHQPLLSRKNGVSWLKIR KFLWGEKYI\RRVSG*RPGCLL VSVSQGPRKDEINPLKG\NDIEL VSK/SSAGF*FQQATTS*KTRNI RKFL\DGIFCLLEKGLFRQA
21979	52347	B	22107	211	457	
21980	52348	A	22108	1	159	KEAENQCLDISSPGMSGHRQGH DSLEHDELREIFNDLSSSSEDED ETQHQDEK*LDISSPGMSGHRQ GHDSLEHDELREIFNDLSSSSED EDETQHQDEK
21981	52349	C	22109	167	367	

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21982	52350	A	22110	754	1950	VKGKDDAPHELGE/SQFILRLPP \EYASTVRRAVQSGHVNLKDRL T\IELHPDGRHGI\VRVDRVPLAS KLVD\LP\CVMEEPENPLLKKPF SKTAIIGQMLVSTVDGDLFPPV EEPSCLALDPKAS\KKKDKDKE KK\FIW\NHGITLPLKNVRKRRF RKTAKKEIYLNLPDV*KKELKR \LLEVPDA\EAVSTRWGIICPKV ETKG\AENQG\LDISSPGMSG\H R\QGH\DSLEHDELREIFNDLSSS SEDEDETQHQDEEDINIIDTEED LERQLQDKLNESDEQHQENEG TNQLVMGIQKQIDNMKGKL\QE TQDRAK\RQEDLIM\KVGNLGS PRTDFQAVLGMSFNQREDREK EQL\SSLQEELESLLREVKKNLM FNFQSFRLVQHLGKFFGLLLLL GYLRPCSS
21983	52351	B	22111	227	355	
21984	52352	A	22112	121	486	WGPALCIGGYLASFLASVHLMP LR*GEMLSP*GLSFSFRFPGFKE VRLVPGRHDIAFVEFDNEVQAG AARDALQGFKITLSPLKVSPPL GAFLEPCVSEWSPHSIVPRVCPQ TLHLALLGRN
21985	52353	B	22113	8	165	
21986	52354	A	22114	1	218	
21987	52355	A	22115	566	1412	TLHSMAVPETRPNHTIYIN\NLN EKIKKDELKKSLLRPSFF/SSLG QILGYSWGIHGRP*RMEGARPF SIFKEVSSGTNALR\SMQGFPFY\ DKPMRIPVLPRTRLQDIHLPRIE RAPFIGSRDPKAGERGRPKSQG DPGPPKEGLCKGGGSHPRGGG LSRGPGPGHCPPMT\KAPRI\MH HMPG\QPPLTAAPLDMIPPPG\L APGQIPPG\AMPP\QQLMPGQMP P\AQ\PLWRNPP\NHILF\LTNLP\ EET\NELMLSHAFSNQVPPGFKE GPVWVPRAGNEHRPSVEV

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21988	52356	A	22116	2	1176	FGELSTFDAVRGPPRRCPPDAD PRAPGLALPGRLLVSNSRRTHS RESRAPPAPHLLGARAGMAPPQ VLA\FGLLLAAATATFAAAQEE CVCENYK\LAVNCFCE*INRQC Q\CTSVGAQNTVICSKLGCQMF W*MKAEMNGSKLGRRAKPEG GLQ\NNDGLYDPDCDESGLFKA KQCNG\TSTC\WCVNT\AGVRRT HKDTEVTCSERVRTYWIIIELKH KAREKPY\DSKS\LRT*LQKEITT RYTLGSKFLSRVFWYENNVITI\ DLFQNFFSKKLRNDVDIADVAY YF\EKDVK\GESLFH\SKKMDLT VNGEQLDLDLLIPGQTL\IYNVD EKAP*/DFSMQGLK\AGVIAVIV VVVITSCCWKLLVLVISQKGRE WQKYEKAEIKGDGCRCHRELQ
21989	52357	A	22117	3	257	AKALQWPLGRGGGGTPRGSRP PGPH*SERGAVQPRSLPRQAA* RVPSGPADGQ*DGHGAADPGS RQRCKPWSEAADLHSECYSS
21990	52358	A	22118	1467	1748	SEYNCCEIGCPQPSWGPWGRG\ TDVRQGQVGEEEVHG/ECGGG SQG*RPG**AGSPAP*PGTWTGT AQQGPAAVLDPLRV*GGGIERH PLHSVGL
21991	52359	B	22119	1	1461	
21992	52360	A	22120	29	417	

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21993	52361	A	22121	616	1671	TATCKPWSMRTTISSSQPQKLT NSVKLPPSAKCISVSRIGGFLVS LTSRMKLRTLLICSKLLPSGGV RGLAGSGVKLQTFTVSVTALK AACLELFTSPGGFMVLLASEVK LQTFSAGDSDCLGQGRRAQRRP GPGVSAVGASGQQRAPESNERP AEEPTPAPMPSSAPRGPTEPALR RPSSADRPLAPGAGRAPGAMAS PSGSSKATGKPRGRDGRPRREE DDVTPEEKRLRLLLEEGSAQPD DGEDAPRPGRKETGTQTGGDG RGAARAALLAVGGIRAPLPSLG VAPGC\PMSKPPRRHPGATPR/P GQGGSDAAHGEEGCPCCSSAV ATCLGAGLLP\PGRGASSPSSGC ALPSSSNSRSLFSSGVTSSSSLLG RPSLPRGLPVALELPEGLAMAP GALPAPGASGLSAELGRLSAGS VGPRGA\G*ASGRAWAPPRAAR CSLAPSAG\PRAHRGHAGPWPA LSSP/GPGPSSRCPLPRRSAASLL KPAR/AINPPGEVNNSRHAALR AVTLTVKVCSFTPEPARPRTPPE GRSFEHIRRVRSFILEVSETKNP PILDTLIHLALGGSFTLFVNFCG WDELIVVLIDQGLHVAV
21994	52362	A	22122	892	1931	CTWNENQRMEIVWEVLFLLQA NFIVCISAQQNSPKIHEGWWAY KEVVQG\NFVPVPSFWGLVNSA WNLCSVGKRQSPVNIETSHMIF DPFLTPLRINTGGRKVSGTMYN TGRHVSLRLDKEHLVNISGGPM TYSHRLEEIRLHFGSEDSQGSEH LLNGQAFSGEVQLIHYNHELYT NVTEAAKSPNGLVVVSIFIKVS DSSNPFLNRML\NRDTF\TRN*H FKNDGIFYYRGL*YRGELLFQG TSSFITYDGVDGLFPTPGY/SRT ASWIIMNKPV*YNPGCKMHSLR LL\SQEPAISRSFLSMSDNFRPV QPLNNRCIRTNINFSLQGKDCP NNRAQKLQYRVNEWLLK
21995	52363	A	22123	17	417	
21996	52364	A	22124	63	449	CHPALLGPTGHGAWPRHRAPD TLRASAGGRDP*GRRSAPA*ER QP*PPVYCAGISQYD*TALSSCL RRSVRTSTDFRSLLDKSNYSVF LCFLQLAGRRYFAMWTRPEFFL ARDPRSLSWGLEWRPLSL
21997	52365	B	22125	1	1131	

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21998	52366	A	22126	359	548	
21999	52367	A	22127	755	1031	TRGVLEHMALGKGTLKDPSGP AP*NHPE\VSHAASTQEAAGPP AGRPGHGSGCLALPASSTSLEP GLRQDHDLLLQLLWREQEVFH DVIQLL
22000	52368	A	22128	1	277	
22001	52369	A	22129	1	933	
22002	52370	A	22130	339	863	PSPVPARPVCPSSAPISMRPPCP WREAEAADLRPEAPGHRDGED VGFLSSGQLSGLCSKRKLQPTR AALTLTPSAVNKIK\HFLKNNPE HVGVKVGVRTRGCNGLSYTLE YTKTKGDSDEEVIQDGVRVFIE K\KAQLTLL*TEMDYVEDKLSK GVGV\ITPNIKGTCGCGESFNI
22003	52371	A	22131	16	419	QIQHRPWP/SRSYTNVLGRKVV YLPSFFTYAKYIVQVDGKIGLF RGLSPLMMSNALYTATRCFMK KDLPPDEIEQVSNKDDMTTSLN KVANDTSYEMMMHCVSRMLP HPLHVISMRCMDQIVGREAKYS GVLSSIG
22004	52372	A	22132	3	441	RSYTKFVMGIAVSMLTYPFLLV GDLMAVNNCGLQAGLPPYSPV FKSWIHCWKYLSVQ\GASTGRR RPFLFFATSFS*NGFVDASLHAK GQLFRGSS\CFSAGCHQDHALP WSNLNHLKNTVSTWPPWVRPD HLGTPARRLQPNNNQM
22005	52373	A	22133	1	1232	MAGAGAGAGARGGAAAGVEA RARDPPPAHRAHPRHPRPAAQP SARRMDGGSGGLGSGDNAPTT EALFVALGAGVTALSHPLLYV KLLIQVGHEPMPPTLGTNVLGR KVLYLPSFFTYAKYIGQRDG\RE GLVPRLSPRLMSNALSTVTRGS MKKVFPPDEIEQVSNKDDYEDF P*RKLLKETSYEMMMQCVSRM L\AHPLHVISMRCMVQFVGREA KYSGVLSSIGKIFKEEGLLGFFV GLIPHLLGDVVFLWGCNLLAHF INAYLVDDSVSDTPGGIGKRPE SRFP\FSQALALRSYTKFVMGIA VSMLTYPFLLVGDLMAVNNCG LQAGVPP\YSPVFKSWIHCWKY LSVQGQ\LFRGSS\CFSAGCHQD HALPW\SNLNHLKNTV\STWPP WV\RPDHLGTTARRFQPNNNQ

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22006	52374	A	22134	3	1156	PRHPRPAAQPSARRMDGGSGG LGSGDNAPTTEALFVALGAGV TALSHPLLYVKLLIQVGHEPMP PTLGTNVLGRKVLYLPSFFTYA KYIVQVDGKIGLFRGLSPRLMS NALSTVTRGSMKKVFPPDEIEQ VSNKDDMKTSLKKVVKETSYE MMMQCVSRMLAHPLHVISMR CMVQFVGREAKYSGVLSSIGKI FKE\EGLLGFFVGL\IPHLLG\DV VFLWG\C\NLLAHF\INAYLVDD SFS\QAL\AIRSYTKFVMGIAVS MLTYPFLLVGDLMAVNNCGAA SWGSPPYSPVFKSW\IHCWKYL SVQGQLFRGSS\CFSAGC\HQDH GFALGVN*NHLKNT\VSTWPPW VRPDHLGTPARRLQPNNNQMC SSPAG\FQFHICHVSV\QMWG
22007	52375	A	22135	2	425	
22008	52376	A	22136	2	430	
22009	52377	A	22137	2	406	
22010	52378	A	22138	1	297	
22011	52379	A	22139	1	111	
22012	52380	A	22140	1	398	
22013	52381	A	22141	1	409	
22014	52382	A	22142	500	1234	GPNCRPPSCSAVEGAWPRPQGA GARAAIALSQKLELGGVGLVQ VQCPSLAPSSTSSILFLCLLPHPP PHRCLQENTTCLLGVEGVLLLQ SPFPLLKTDHSSLPALAPTQSQA ALWGFADFGFMFESSPGGNLG WEPDIKLTDEMVMIMGGKMEA TPFKWFMEMCVRGYLAVRPY MDVVVSLVTIMLDTGLPCFRG/ QIKFLKHRFSPNMTEREA*NFIM KVIQSCFLSNRSRTYNMIQYYQ NDIPY
22015	52383	A	22143	2	6378	SAGPAGPLQVQKLLCMCPVDF HGIFQLDERRRDAVIALGIFLIES DLQHKDCVGPYLLRLLKGLPK VYWVEESTARKGRGALPVAES FSFCLVTLLSDVAYRDPSLRDEI LEVLLQVLHVLLGMCQALEIQ DKEYLCKYAIPCLIGISRAFGRY SNMEESLLSKLFPKIPPHSLRVL EELEGVRRRSFNDFRSILPSNLL TVCQEGTLKRKTSSVSSISQVSP ERGMPPPSSPGGSAFHYFEASC LPDGTALEPE

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22016	52384	A	22144	3	398	IHKAASGVPQQPDAGCPGTGEQ QGGQRCGQ*AGP/AQAPC*SRA GTR/PTCFFVLTSLRSWYRVDSP NKLMNPLVAGFFG/CHCGSGQC LRKCSSARDRAPDARPGLDLAQ GRCCHCNKACLHASETGVGTT SVL
22017	52385	A	22145	344	498	
22018	52386	A	22146	344	406	FLADQEDPLDPRAGCR*ETTAP RIPSKGPSSTEPLHASTAVPPCQ GELGCSRASPASEKI/DLAGRLIS PCNSDTVSPGLGGFMTCAQSLI SRRPGGPIGPPGWLQGPHLG
22019	52387	A	22147	3	2058	LSGSGAPPPGVGAQAAAAAEE EEREVVRVRVKVRLAVSRPSRR GKFRSFAVDPQITSLDVLQHILI RAFDLSG*VGRCWGLLGRDRL GQEVYLSLLSDWDLSTAFATAS KPYLQLRVDIRPSEDSEYSVPPG AISPKDVIGSDVLLAEKRSSLTT AALPFTQSILTQVFSGTLGTQQ VLSWSYGEDVKPFKPPLSDAEF HTYLNHEGQLSRPEELRLRIYH GGVEPSLRKVSILSHLLVYPDG LTGRERMDYMKRKSREYEQLK SEWAQRANPEDLEFIRSTVLKD VLRTDRAHPYYAGPEDGPHLR ALHDLLTTYAVTHPQVSYCQG MSDLASPILAVMDHEGHAFVC FCGIMKRLAANFHPDGRAMAT KFAHLKLLLRHA\DPDFYQYLQ EAGADDLFFCYRWLLLELKREF AFDDALRMLEVTWSSLPPDPPE HEVELVGPPSQVADTGFGDHR G\WPVRQRHMLRPAGGGGSTF EDAVDHLATASQGPGGGGRLL RQASLDGLQQLRDNMGSRRDP LVQLPHPAALISSK\GLSEPLLN YPDPLLSSFSHPDSPSSSSPPSTQ EASPTGDMAVGSPLMQEVGSP KDPGKSLPPVPPMGLPPPQEFG RGNPFMLFLCLAILLEHRDHIM RNGLDYNELAMHFDRLVRKHH LGRVLRRARALFADYLQSEVW
22020	52388	A	22148	130	387	
22021	52389	A	22149	1	279	

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22022	52390	A	22150	105	499	DMSDTSESGAGLTRFQAEASEK DSSSMMQTLLTV/TPEAREAPA TQASSTTQLTDTQVLAAENKSL AADTKKQNADPQAVTMPATET KKVSHVADTKVNTKAQETEAA PSQAPADEPEPESAAAQSQENQ DTR
22023	52391	A	22151	285	984	TSLSCYFSRTKDSPKLGLLMVL LSIIFMNGNRSSEAVIWEVLRKL GLRPGYDWALSALAVRVVLW QERTVLGLHQSGGLVERVGCW TG*RAQGSDLGG*WVNGPELS APSLSVSWASMELPSCAGNLFS ILEMPLPTSGKCHSLE*IYLFIYF SFSSLRIHHSLFGDVKKLITDEF VKQKYLDYARVPNSNPPEYEFF WGLRSYYETSKMKVLKFGCKV QK\KDPKEWAAQYRE
22024	52392	A	22152	259	578	
22025	52393	A	22153	296	2242	NMSDTSESG\AGLTRFQA\EASE KDSSSMMQTLLTVTQNVEVPE TPKASKAL\EVSEDVKVSKASG VSKATEVSKTPEAREAPATQAS SYLLSLTD\TQVLAA\ENKSLAA *HQGNRMVDPQAC*QLPAT\ET KKVSHVADYGRFNYKGFRRLR LAPS\QAPADEPEPESAAAQFSG RFRVFGPKVKAKKARKVKHLD GEKDGSSDQSQASGTTGG\RRV SKALMASMARRASRGPIAFWA RRASRTRLAA\WARRAFALPLEI TLKPRRAKGLRR\RVAKFQ\SSQ EPEAPPPRG\LALLQGRAN\DLV KYLLAKDQTKIPIKRSDMLKDII KEYTDVYPEII\ERAGYSLE\KVF GIQLKEIDKNDHLYILLSTLEPT DAGILGTTKDSPKLGLLMVLLS IIF\MNGNRS\SEAVIWE\VLRKL\ GLRP\GIHHS\LLGDVK\KLITDE F\VKQKYLGLCQKVPNSNPP\EY EFLLGACALY**EPAKMKSPQS FACK/VYQKEGSPRNWGSSVPP REGKGRMEADFEGCKLRLTLE AKAKGPRLEAPNGPLGLGSGE MLAGP\CNWDEA\DIGNPWAK ARIPRREQKLKAKAPKRSGSA\S TGA\STST\NNSAS\ASA\STSGGF \SAAASL\TATLHIWGSSAGLWL ELGCQHQSARSGAC\GVSYK

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22026	52394	A	22154	1	487	EFRQPSFRRSIWP/YFLLTQA/VR TGNPAKFNQVLDQFGEKFQAD GTYTLIIRLRHNVIKTGVRMISL SYSRISLADIAQKLQLDSPEDAE FIVAKAIRDGVIEASINHEKGYV QSKEMIDIYSTREPQLAFHQEG KDSSVYSFREWGTRTGMSWLV CFLKLRL
22027	52395	A	22155	2	429	
22028	52396	A	22156	1	328	GTRFQADGTYTLIIRLRHNVIKT GV/RSGSEGLLEEQKPGQGKPS GYPWASEGSVSTLPTPSLLPLPG VRMISLSYSRISLADIAQKLQLD SPEDADFIVAKVGLVQEPQ
22029	52397	A	22157	138	2206	AVTPGAMKQEGSARRRGADK AKPPPGGGEQEPP\PAPAPQDVE MKEEAATGGGSTGEADG\KTA AAAA*SNFPAKSWDYSHLWKD IKEHRETS*RKAVSGKEPRFVLR ALRMLPSTSRRLNHYVLYKAV/ QGAFFTSNNAT\RDFLLPFLERA HGTQEADLLFRPRTGKAAGT\P LLPEVEAYLQLLVVIFMMNSKR YKEAQKISDDLMQKISTQNRRA L\DLV\AAKCYYYHARVYEFL\D KL\DVVRISLHG\RLRTATLRHD ADGQAT\LLNLLLRNYL\HYKL VPTSLRSLVSKSVFP/EEQAQQP NEWGQVTSYLHQGRIKAIQ\LE YSEARRTMTNALRKAP\QHTAV GFKQTVHKLLIVVELLLGEIPDR LQFRQPSLKRSLMPYFLLTQAV RTGN\LPRFTQVLDQFGEKFQA DGTYTLIIRLRHNVIKTGVRMIS LSYSRI\SLADIAQKL\QLDSPE\D AEFI\VAKAIR\DGVIEASIN\HEK AYVQ\SKEMIDIYST\RDPQLAL H\QRISFCLDIHNMVWSRPMRV PSPKSYKQGSWSLQRNGRERR NKQDLE\FPKEMA\EDDDDSFPL KLGGWGGVRGKWGTRQLCPP WGYPLPQGTCPPFSPHTAHML AFRGRGWGCWEPATPDLPPGL LPSRVTLLVQPGRRVGRQPPRG RVLASSVADRRGRISLCTPFRE WGTRTWDVYGLLCFLKLRL
22030	52398	A	22158	86	348	

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22031	52399	A	22159	3	356	LPLSMDVRAPPAVMAAVDQAL KEFGRIDILINCSSSSCGLPFCR\ AAGNFLCPAGALSFNAFKTVM DIDTSGTFNVSRVLYEKFFRDH GGVIINITATLGNRGQALQVHA G\SAKAAVD
22032	52400	A	22160	3	255	GPWSCHAGA*GPGATQVSEDQ GLREPHGSRDLCSLG*KH*GAPI CAWPMSWDGPPAAHKVRPSVS APPVCINTLCYNLASAFS
22033	52401	A	22161	3	360	
22034	52402	A	22162	240	1356	AGNPSGIPGTRVHRGQRGGFAS TWSGRGAGSTPLQNSPPRQPHR EKEFLRQVLEGGSHTGVFRPSA ARLVPNPHSLVSPDLL*LVSRA T\PHIFLAARKLAGATGRRCLPL SMDVRAPPAVMAAVDQALKEF GRIDILINCESVLSEVGGFSQAP AAPAVSHSAGAAGNFLCPAGA LSFNAFKTVMDIDTSGTFNVSR VLYEKFFRDHGGVIVNITATLG NRGQALQVHAGSAKAAVDAM TRHLAVEWGPQNIRVNSLAPGP ISGTEGLRRLDASQGMSWGRG EGAGSWGSRGLSLLLPS\GGPQ ASLSTKVTASPLQRLGNKTEIA HSVLYLASPLASYVTGAVLVA DGGAWLTFPNGVKGLPDFASF
22035	52403	B	22163	214	1647	

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22036	52404	A	22164	1765	1910	LSHPHSRTPPNRTPRRTRIPQRP AVMYSPLCLTQDEFHPFIEALLP HVRAFAYTWFNLRARKRKYFK KHEKRMSKEEERAVKDELLSE KPEVKQKWASRLLAKLRKDIR PEYREDFVLTVTGKKPPCCVLS NPDQKGKMRRIDCLRQADKV WRLDLVMVILFKGIP\LESTDGE RLVKSPQCSNPGLCVQPHHIGV SVKELDLYL\AYFVHAGRISSQS ESP\SQ\PSDADIKDQPENGTFGA SRDSFVT\SGVF\SVT*A*LRVSQ TPI\AAG\TGPNFSLSDLESSSYY SMSPGAMRRSLPSTSSTSSTKRL KSVEDEMDSPG\EEPFYTGQAR SPGKWTVSPSGLSVSWSQGMPS PTTLKKSEKSGFQQPLPFHRPPS LGNGFHTAFTDLFIYQGPQSKF HIATPSIL\HFPRHSPFFQQPGPY FSHPAIRYHPQETLKEFVQLVCP DAGQQAGQPNGSSQGKVHNPF LPTPMLPPPPPPPMARPVPLPVP DTKPPTTSTEGGAASPTSPTTRS /PGRTRPQQPFL/SYGPP*PHFLR AGIHHL
22037	52405	A	22165	63	250	
22038	52406	A	22166	1	817	SRLGHPRKDMDDDTKATLISY MSLSFRHGYCFSEDPCVHTELG IQSGRGGRGDPDPPGNALE*LA HLGP/SSHLGP*AQDGLVDAAG RASPLAGTEGAGRFSHLQPI/GP RGPPE*GAAGERFPSGVAG/GPR GAHGLPCPEQLQLQPPPPS*MP KTGSTFVAHFPSPLAQGHSPPG GGAGWCSGCSPDRPPLLGVGS HGELLNPNSPAYEVGAG/RPAT GSSGTRAGPPSPSHSAPGRTPSV SLCD/RHQCLRASPTGSIGSLPA HWREGLAGPLMD

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22039	52407	A	22167	240	1790	TAKNSYLESCPLHMENSIHQWP RQPFPPVRRQGADAACGAGSQ ALVPSHSDTDGVLPGAEWLGD GGPARVP/GAAGGRGPAPTS*A GP*LSL*APLCF\SGLSGNGKQL LGAAGRSSSHAQMHELHPAQ* HE*ATDHTGGQGPP/G*KQQNG PP/GPDNDLPAPESTPPTWNEDF LPDAIPLAHPVPRQRRPTGPAGP PGQTGPPGPAGPPGSKGDRGQT GEKGPAGPPGLLGPPGPRGLPG EMGRPGPPGPPGPAGNPGPSPN SPQGALYSLQPPTDKDNG\TQG WPLPSWTQCW/SGVPGPRGPPG PPGPPGPRGPPGPPGTPGSQGLA GERGTVGPSG/AGGAAAERGPE DPGRASPHPGAHDWDPRSPGLP RGRFWPGCCPESQPQDEEGWH PTRWGPCCPAWARPWTEERG/S RPAAGS/RGVSDISETPGRPIYPD DKSQSAVSVLCARSRLRAQLRP GAEQMNDCKGITGTRQDIHAV SFASEHNIQNWVSKHLQLSPPV TPATQAPLKVRVPQASTLVL
22040	52408	A	22168	104	271	PSCTNPYGGGRRCDSVVPNQCF TKHMQSRLLG*GEKALEGGGG RGVKSLVTKRDF
22041	52409	A	22169	494	1074	KGTTLCQKHWGGGYLHWG\HF EMMRLTIN\RSMDPKNMFAIWR VPSPFQ\PITRKSVGHRM\GGGK\ GAI*HYLTP\VKAGRLV\VEMG GRCEFARSAKVSLTQVALRSCP FASKRL*ACGTPREGCEQDQEE RERQQPRTPWTI*AE*PTAQHG WAYGKVPEPHMTLTPQGEILG ARFYMPKTCVVSVGDILYIGY
22042	52410	A	22170	61	329	NQRSGKKSQPW*STITPPSLIWL SNSSTTLSSSKMGQSYSSS*PSY NCSVSRMFGSNMVPAATASGA SLTCPLLWLSMTHFRRKVGGW A
22043	52411	A	22171	21	444	STAQSISRSDLHYFLALLVYYW AADARFLPGRIPWLIHKELEKS HTEYCLVGSSQYTPLVQVFRSN TLVSVLSTKTI*NQRSGKKSQP W*STITPPSLIWLSNSSTTLSSSK MGQSYSSS*PSYNCSSRAKSPTL TVFQS

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22044	52412	A	22172	163	1056	LEKSDHRISWSPGKTA\SPKSMP ERWHR*WAQILKD\MGIT\EYEP R\VIN\QMLEF\AF\RYVTTIL\DD AKIYSSHAK\KATVD\ADDVPIG QSRC\RAGSSLFTSPPPKRF/LLL RYLARQKKSNPFCPLIKPY\SGP RLPPDRYC\LTAP\NYRLKSFTE KGHSTSAGKELTVP\RLSVGFRL LSRTKVLPTLGAHPTPQ\TMSVF NLK*GTPHVPSPGQRFTSTRCPT S\QS\PAVKSFQFPGNLSQFQNV L\INPIH*IGSQKHSYYPLNMMS S\QNTA\NESSNALKRKREDDD DG\DDDDDDYDNL
22045	52413	A	22173	215	344	
22046	52414	A	22174	302	1330	ACEQKRGGEGGNKNRERRKGE KAGRRQGTRQPCSRCMRRTKQ VEKNDDDQKIEQDGIKPEDKA HKAATKIQASFRGHITRKKLKG EKKDDVQA\AEAEA\NKKDEAP /VFADGVEKKGEG\TTTARSSPQ PLAPKP\DEPGKAGETS\SEEKM GEG*LLATEQGSPPRLLAS\SEE KAGSAETESATKASTDNSPSSK AEDAPAK\EEPKQADVPA/AFG VFPNPLGALLLAATTPAAEDAA AKATAQPPTETGESSQAEENIE AVDE\TKPKESARQDEGKEEEP EA\DQEHAWNSGEMGFPHPHPP GCLACLSLPSSQLHSEVPSCPAH VCESVLSHPLALFLSVWANI

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22047	52415	A	22175	2	1577	HGFRLPHPQPALRRLLDQRRPK TEDRCGHWDQILDLSIIKHLFS MSFIPVAEDSDFPIHNLPYGVFS TRGDPRPRIGVAIGDQILDLSIIK HLFTGPVLSKHQDVFNQPTLNS FMS\LGHAAWKEARVFLQNLL/ SL*SQARLRDDTELRKCAFISQA SATMHLPATIGDYTDFYSSRQH ATNVGIMFRDKENALMPNWLH LPVG\YHGRASSVVVSGTPIRRP MGQMKPDDSKPPVYGACKLLD MELEMAFFVGPGNRLGEPIPISK AHEHIFGMVLMNDWSARDIQK WEYVPLGPFLGEEFWGPLSLP WGGCPWDAL\MPF\AVPNPKAV PQAPCRYLCHDEPYTFDINLSV N\LKG\EGM\SQAAT\ICKVQILK YMYWT\MLQQAHSPTLSNGC\N LRPGGPPGLSGTHQAGPEP/EKN FGSMVE\LSWKGTKPI\DLG\NG QT\RKFLLD\GDEVIITAMATRD FKWYC\QGDG\YRIGFGQ\CAGK VLPALLPIMRFSLLFWKQRAQS TPFQPCDWGSSPRAVGLVPPFQ
22048	52416	A	22176	3	623	DSRNSSILPRRGALLKVNQELA GYTGGDVSFIKEDFELQLNKQL IFDSVFSASFWGGMLVPIGDKP SSIADRFYLGGPTSIRGFSMHSI GPQSEGDYLGGEAYWAGGLHL YTPLPFRPGQGGFGELFRTHFFL NAGNLCNLNYGEGPKAHYIVK LAECIRWSYGAGIV\LRLGNIAR L\ELNYCVPMGVQTGDRICDGV QFGAGIRFL

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22049	52417	A	22177	352	2397	GPMSEGIASQGARRRRGIMGLR GLWASRADGRRGETEPEAKQEI LENKDVSFLLKVLIELLVETFTS IHH*GDDVFKAKNLIEVGVVST WCAFPVSSEELVNVPM*NIDTC QGTYCGVVSL*FPFCPSEKSCFY GQNNTMVGNNEGSMVCYRLF TFLYWNLELGTFTL*LHSKETS YGLSFFKPRPGNFERK*EAQQII EYTGLIEKLK*VAYL*KSAEYS VS\AFQSFPLGLGENRVAFSLIP KGSYLIQ*VSNGCWHLHCQPLL WGSYHRILAELRVLIESTWPFE G*LCNGTSQAFSCGPCTPSRSSA RHGHSVCGQLLVADVPGVKG MLGENNHLFLKY*SMNG*FA/L YFPLDLFSCFL*ESFPLTAPSLEG SRLTLETMYLLCQGGFGELFRT HFFLNAGNLCNLNYGKTCAIQE TIVVQLFSCLKAQYTKIRLGNIA RLELNYCVPMGVQTGDRYVLG IIFHNHIPLSSNFILFWTWFASGD TAGAARLLRLPTDDRAFRDGG GCSHNRQLPFPSTPLLFSTQSPS WKGCSHAGCMHVCLGAQLPG LGAQLGHGSESQVERLLACGG RWGARRQGCCWHDLPKAPHA GCFLAGEKKVGDDQEPCTKTA AVREGESVGCTAEGGCLGLSG GCQGWLAPGLVELRSAAARQE GSRRRRKRRRHLLRVHPQKVV
22050	52418	A	22178	1	1017	
22051	52419	A	22179	1	435	
22052	52420	A	22180	1	1353	
22053	52421	A	22181	1	834	
22054	52422	A	22182	2	2675	

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22055	52423	A	22183	72	1339	AMRGANAWAPLCLLLAAATQ LSRQQSPERPVFTCGGILTGESG FIGSEGFPGV\WPPESKCTWKIT VPEGKVVVLNFRFIDLESDNLC RYDFVDVYNGHANGQRIGRFC GTFRPGALVSSGNKMMVQMIS DANTAGNGFMAMFSAAEPNER GDQYCGGLLDRPSGSFKTPN\W PDR\DYPAGVTCVWHIVAPKNQ LIELKFEKFDVERDNYCRYDYV AVFNGGEVNDARRIGKYCGDS PPAPIVSERNELLIQFLSDLSLTA DGFIGHYIFRPKKL\PTT\TEQPV\ TTTFPVTTGLKPTVALCQQKCR RTGTLEGNYCSSDF\VLAGTVIT TITRDGSLHATVSIINIYKEGNL AIQQAGKNMSARLTVVCKQCP LLR\RGLNYIIMGPSRVKDGAR QNSWPNSFIMMFQT\RNQKLLG CP*KISQC
22056	52424	A	22184	49	170	HTVGDGRLLRRP*REFGASFL* CFLEARFGLKNWGHCWRH
22057	52425	B	22185	597	651	
22058	52426	A	22186	1	791	
22059	52427	A	22187	2	943	TGACAEPRVGLLFRLKGRCRG GRNMELGSCL\YGFREAAEEEG EPEVKKRRLLCVEFASVASCDA AV\AQCFLAENDWEMERALNS YFEPPAEES\ALERRPETISEPKT YVDLTNEETTDSTTSKISPSEDT QQENG\SMFSL\ITWEYLMGL\D LKQSVQRRARGVCSYLAL*VLS LLFNSNVSYVYTERMNQLKMV LKKMQEAPESATVIFAGDTNLR DREVSDKVSLMFEDRLLLWRLI *VPFCQYTWDTQMNSNLGITA ACKLRFDRIFFRAAAEEGHIIPR SLDLLGLEKLDCGRFPSDHWGL LCNLDIIL
22060	52428	A	22188	277	534	

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22061	52429	A	22189	29	1305	VGVVLRVECPLCPGPAPMSVPA FIDI\SEEDQAAELRAYLKSKGA\ EISEENSEGGLHVDLAQIIEACD VCLKEDDKD\VESVMNSVGIPY SWIL\EPDKQ\EAFDLKALCEKA GSKFPRR*TAPSLETCSFLSNLF H\GMG*GILPVKIHSVICSL\IKV\ AASCG\AIQYHPQLEPGIKFRK WDFLNWN\LTTGKKSTPLLKTT FMKALVE\CKKSDAASKGM\VE LLGSYP\EGNASQ\ARVDAHR\C IV\RALKDPN\AFLFD\HLLT\LKP VKFFGKASLFHCSFLTKF\VSA* MGHHMSRFYPD*LRTFH*IPLG PVTMDPGIWPKMRLLF/TFMGN GQ*KNKEISF*PQCQQEPSRLGA D\DVESHLVIDA\VRN*KWVYC QNWSRPRRKVVVSHSTHR\TFG K\QQWQTTVLTHLNAW\KQNL NK\VKNSLLSLF
22062	52430	A	22190	194	413	
22063	52431	A	22191	3	160	EVKFQWVLSLG*SFSLPKSSFQ RCGAGGAVHWSTALFLLGAAS ASSYHQRPG
22064	52432	A	22192	268	473	
22065	52433	C	22193	93	500	
22066	52434	A	22194	2	398	FFLRRSLALSPRPDCGLQWRNL GSLQAPLPGFTPFSCLSLPSSWD YRRPPPRPANFLYF**RRGFTLL ARMVSIS*PHDPPASASQSAGIT GVSHRARPETYNFCSFIIISSLPV EPEARKMTKNSDIGEIW
22067	52435	A	22195	972	2180	PRHCCASASSAPAPSRPASSSSP PAACPW*GSLLGPAATPATWR R
22068	52436	A	22196	2271	3074	RDPSTPTVVRSLGVPLLSRRRFK MAPSVAATKLAERNETMVQTC WTETQSSSDGSTPRRVRISLAL WRPSLFFSMADTSLVLNFPRVS SSGVIRPSNKRPSLAILTRISRTS SPKYMPLTIFSNSCFPGLRDPRSI SLSNSVRMSSNDPSSPKAPHS/G IDTHPPLVSFHQINVPQFLHVAS IGASADDQADFTVLVVIATGHH GAHCVIHHSYDVGIIVPSLFDGF VKQFDHICSFHSARFKSLCPGD QDGLIYFGLLARKRKRESHR

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22069	52437	A	22197	1956	2747	FAFSPK*HSCLRCPCI*FSSGLLH EVL*LLPLCWP*THGWDPGSRE ANKSPKLHAIRCVWVLEEENL WLSSNSQSLQTVKN*ESHIN*SC RSNLI/HH*FWNQVK*K*LLNIS GNCFFFLRWSL/DSVAQAGVY WRDLGSLQPPPPGFKRFSCLSLP SSWDYWHLPPCLAKFCIFSRDG /GFTIWARLVLNS*SCDLPASGS QSAGITGVSHHTW\LQVTYFLK EMRSCYFSQVGWPQTPGLKQC SHLKLLSSWDYRHMSPHLAISG
22070	52438	C	22198	85	228	
22071	52439	A	22199	2	434	
22072	52440	A	22200	1	1356	
22073	52441	A	22201	146	1909	ILHSLEISALLSLMMLTIGDVIK QLIEAHEQGKDIDLNKVKTKTA AKYGLSAQPRLVDIIA\SVPPQY RKVLMPKLKAEPIK\TA\SGIVV VAVMCKPHRCPHISFTGNICVY CP/GVGPDSDFEYSTQSYTG\YE PTSMRS/IFRARYDPFLQTKDRI EQ*RQLGHSVDKVEFIVMGGTF MALPEEYRDYFIRNLHDALSGH TSNNIYEAVKYSERSLTKCIGITI ETRPDYCMKRHLSDMLTYGCT RLEIGVQSVYEDVARDTNRGH TVKAVCESFHLAKDSGFKVVA HMMPDLPNVGLERDIEQ\FTEFF ENPAF\RPDGLK\IYPTLVIRGTG LYELWKS\GRYKSYFS**PGLN WVARFLALVPPWTRVYRVQRD IPMPLVSSGVEHGNLRELALAR NEDLRIQCRDVRTREVGIQEIH HKVRPYQVELVRRDYVANGG WETFLSYEDPDQDIL\IGLLR\LR KCSEETFRFELGGGVSIVRELH VYGSVVPVSSRDPTKFQHQGFG MLL\MEEAERIS*RRNMGLGKI AVISGVGTR\NYY\GKIGYRLPR PRTMVKMLEIMGHTQSHSFCSI LPWHEHRRIRISLNTQQRGL
22074	52442	A	22202	1	457	
22075	52443	A	22203	2	297	CVMYRDYPLELFMAQCY/GNIS DLGKGRQMPVHYG/CKERHFV TISSPLATQ/IPQAARGPGYGIM/ SIRVDGNDVFAVYNATK/EARR RAVAENQPFLIEARPT

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22076	52444	A	22204	3	1446	DWLLAKMAEAIAAAR\VWRLN RGLSHAALLLLRQLGGSGD*AR SHPPRQQQQCSALDDKP\QFPG ASAGVIDKLEFIQ\PNVISGIPIYR VM\DPQGQIHQPQARDPHLAEG ERWLKL\YKS\MTLL*HPWDRIL **VFSGQGRILLLT*TNYWLRR GTHVG\SARRLGQTRTLVFGQY RE\AGVLMYRDYPLELFMAQC YGNISDLGKGRQMPVNYG\CKE RHFVTISSPL\ATQDPSGRWGAA YAATGGANANRVR/VICYFRAR GAAS*GGDAHA\GF\NFRCHNL SCPIIFFCRNNGYAISTPTSEQYR GDGIAARGPG\YGIMSIRVDGN DVFAVYNATKEARRRAVAENQ PFSHQAHDSRVQAPSP\SDAS*T YRSVDEVN\YWENKGPPILPGF GHYLFSQ\GWWDEEQQKAWR KQSRRKDPGPVQPS\VMEAFEQ AERK\PKPNP\NLL\FSDVYQNM PAPVRQPPES\LARHFKTYGNH YPWDHFDK
22077	52445	A	22205	2	292	

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22078	52446	A	22206	1	1894	QSLADLLQSQPSITLTSQIWPSP A*GFWSWGNLSVTTPSK\PATP TRTIAATPIQTLPQSQTAPKRID TPSLEEPSDLEELEQFAKTFKQR RIILGFT\QGDAGLAMVKLYGN DFSPTTIFRFEALNLSFKNMCKL KPLLEKWLNDAENLSSDSSLSS PSALNSPGIEGLSRRRKKRTSIE TNIRVALEKSFLENQKPTSEEIT MIADQLNMEKEVIRVWFCNRR QKEKRINPPSSGGTSSSPIKAIFP SPTSLVATTPSLVTSSAATTLTV SPVLPLTSAAVTNLSVTASTSEA SSASETSTTQTTSTPLSSPLGTSQ VMVTASGLQTAAAAALQGAA QLPANASLAAMAAAAGLNPSL MAPSQFAAGGALLSLNPGTLSG ALSPALMSNSTLATIQALASGG SLPITSLDATGNLVFANAGGAP NIVTAPLFLNPQNLSLLTSNPPG GFTIEISNNNSTMVMTGMRIQIG TQAIERAPSYIEIFGRTMQLNLS RSRWFDFPFTREEALQADKKLN LFTVRKFQNIRHTLFKCENKNT FQQCLLLEQDSSCGTGFCSMTT YPVMLLSSEQPVQSLSVRQCVI LLDAAAVISGGMGAVCLLLTH LCPLCYAGLLSEITDPESFVKDL LYSVP

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22079	52447	A	22207	1	2417	MRVRTSSLPSTMLRVQNYARA KAGPEYAFVDSTECSPQWMVS PLKRGTQTNGLDFQKQPVPVG GAISTAQAQAFLGHLHQVQLA GTSLQAAAQSLNVQSKSNEESG DSQQPSQPSQQPSVQAAIPQTQ LMLAGGQITGLTLTPAQQQLLL QQAQAQAQLLAAAVQQHSAS QQHSAAGATISASAATPMTQIP LSQPIQIAQDLQQLQQLQQQNL NLQQFVLVHPTTNLQPA\QFIIS QTPQGQQGLLQA\QNLLTQLPR QSQANLLQSQPRI\TLTSQPATP TCTIAATPIQTLPQSQSTPKRIDT PSLEEP\SDLEELEQFAKTFKQR RIKLGFTQGDVGLAMGKLYGN DFSQTTISRFEALNLSFKNMCK LKPLLEKWLNDAENLSSDSSLS SPSALNSPGIEGLSRRRKKRTSI EA\NIRVALEKSFLEN\QKPTSEE ITMIADQLNMEKGVIRVWFCN RRQKEKRINPPSSGG\TSSSPIKA IFPSPTSLVATTPSPVTSSATTTL TVSPVLPLTSAAVTNLSVTGTS DTTSNNTATVISTAPPASSAVTS PSLSPSPSASASTSEASSASE\TS TTQ\TTSTPLSSPLGTSQVMVTA SGLQTA/AQLLPFKGAAQLPAN\ ASLA\AMAAAAGLNPSLMAPS QFAAGGALLSLNPGTLSGALSP ALMSK\STLA\TIQTLASGGSLS K*TSLECKLGTLVICPMREEPPD
22080	52448	A	22208	3	114	
22081	52449	A	22209	1	505	NLGVDLLPGYQDPYSGRTLTK GEVGCFLSHYSIWEEVVARGLA RVLVFEDDVRFESNFRGRLERL MEDVEAEKLSW\YSYWTLAYA LRLAGARKLLASQPLRRMLPV DEFLPIMFDQHPNEQYKAHFWP RDLVAFSAQPLLAAPTHYAGD AEWLSDTETSSPWDDDSGR
22082	52450	A	22210	3	626	RAARAAPLLHLLLLLGPWLEA AGVAESPLPAEVLAILARNAEH SLPHYLGALERLDYPRARMAL WCATDHNVDNTTEMLQEWLA AEGDDYAAVVWRPEGEPRFYP DEEGPKHWTKERHQFLMELKQ EALTFARNWGADYI/LGATLGL WQDHSVNSLGGCSPGRAGACD VPSSKFADTDNILTNNQTLRLL MGQGLPVVAPMLDSQTNV

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22083	52451	A	22211	1	2004	MRAARAAPLLQLLLLLGPWLE AAGVAESPLPAVVLAILARNAE HSLPHYLGALERLDYPRARMA LCLQGPAQPQWDLWLAGFEEE QTGTSEVHWGPTWQGSTTLEA SGHRCATDHNVDNTTEMLQE WLAAVGDDYAAAVWRPEGEP RFYPDEEGPKHWTKERHQFLM ELKQEALTFARNWGADYILFA DTDNILTNNQTLRLLMGQGLPE VAPMLDSQTYYSNFWCGITPQ GYYRRTAEYFPTKNRQRRGCL RVPMVHSTFLASLR\AEGADQL AFYPPHPNYTWPFDDIIVFAYA CQAAGVSVHVCNEHRYGYMN VPVKSHQG\LEDERVNFIH\LILE ALVDGPRMQASAHVTRPS\KRP SKIGF\DEVFVISLG\RRPDRRER MLASLWEMEISGRVVDAVDG WMLQQQVPFRNLRP*DLLPGL/ YKDPYFGPHS*PRAEVGLLSSD HYSIW\EEVVSQGAWPR\VLVV *RNDVAPLRTNFQGGGLERL\M E\DVEGKRNLSWEKPPFRILPLG R\KQVEPLRRET\AVEGLPG\LV VAG*LPNW\TLA\YALRLAGGP ASLLALQPFAPHCCPVERISLPI HCFDQ\HPNEASTKAHFWPRD\ LVAFSAQ\PLLAAPTHYAG\DAE WILLSRRHHSPWDDDSGRLISW SGSQKTLRSPRLDLTGSSGHSL
22084	52452	A	22212	1	468	ELSHNAKAKVMVASHNEDT/V LFALRRMEELGLHPADHQVYF GQLLGMCDQI\SFPLGQAGYPIL TQIHLFSPHTCRAAGGEVRCLP ALPRVWALRCGPNLIPAWDSH WKLLGTLLELCAQGPHLCDPH VLGPRGLSTFCQGQPTQPEPLG EQWPGWG
22085	52453	A	22213	1	1893	

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22086	52454	A	22214	390	2005	INRDVETACTYILRNTEDVMLE FVMREWKKSRKLLGQRLFNKL MKMTFYGHFVAGEDQESIQPL LRHYRAFGVSAILDYGVEEDLS PEEAEHKEMESCSSAAERDGSG TNKRDKQYQAHRAFGDRRNG VISARTYFYANEAKCDSHMETF LRCIEASGRVSDDGFIAIKLTAL GRPQFLLQFSEVLAKWRCFFHQ MAVEQGQAGLAAMDTKLEVA VLQESVAKLGIASRAEIEDWFT AETLGVSGTMDLLDWSSLIDSR TKLSKHF/V*VPNAQTGQLEPLL SRFTEEEELQMTRMLQRMDVL AKKATEMGVRLMVDAEQTYF QPAISRLTLEMQRKFNVEKPLIF NTYQCYLKDAHDNV\TLD\VDL SPREGWCFGAKPVRGAYLAQE RACAAEIGYEDPINPMYEATNT MYHRCLDYVLEELKHNAKAK VMVASHNEDTVRFALRRMEEL GLHPADHQVYFGQLLGMCDQI SFPLG\QAGYPVYKYVPYGPVM EVLPYLS\RRALE\NSSLMKGTH \RER\QLLWLELLRRLRTGNLFH
22087	52455	A	22215	3	303	
22088	52456	A	22216	798	2250	VPRAPQGML*GPRKDAGTPER RAGPPGGRGTADGGGCGALAG SGS/DDPRLCIWTFLVTDQLLLP TGPGRPRGSVAAAATGPGVGA LRAPARAQPRGAVDGRPLLPQ VLPHRRLEVSLGKSPKECVLW/ RHLLSESEKRPFVEEAERLRVQ HKKDHPDYKYQPRRRKSAKAG HSDSDSGAELGPHPGGGAVYK AEAGLGDGHHHGDHTGQTHGP PTPLTTPKTELQQAGAKPELKL EGRRPVDSGRQNIDFSNVDISEL SSEVMGTMDAFDVHEFDQYLP LGGPAPPEPGQAYGGAYFHAG ASPVWAHKSAPSASASPTETGP PRPHIKTEQPSPGHYGDQPRGSP DYGSCSGQSSATPAAPAGPFAG SQGDYGDLQASSYYGAYPGYA PGLYQYPCFHSPRRPYASPLLN GLALPPAHSPTSHWDQPRRNGS TAQGPKEGVAGALQGAVRSKA GLGAEKPLHSRPHSLDNGCTGC PGSGVSVRRLG

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22089	52457	A	22217	299	1631	LLEPHCGGKCFKRHWFPCSCEA SC\PSAAPQRW*HTG/SPEVPAA PGAQGREPSM/RDGEGAVRGGS CMEAGPMGLQCVDKKHQGVH N/RGEARVFLQSQVGAILPRPW PNPAPSEP/VQSPLASSTGP*VFP SRPGQQASGPA/RRHPGAEPGQ RGDAVQLLPRPQTSPHGPQDA ALSSAPHPWRQL/MASPGLQEA PLHPFCGHRSPCPVPWQLSPTD PIQSRPPARGWAPANQGRPSHP RCRGGGGAFCGHGF/SYTQPLT FRLASMVLSIHPKPPKETLRFRP NMVVAAEPGVPAMSQRRPRGC TRFSHTDKAPLDTCTDMNAYT CARRHSSTYSDHITLQGAFACT HTWAQSCTCQPPPTPAAKCLDR GQSSGMLHAGCVGWGGGTHV RVDLSSQLNRRVRPHLCMLRC WSSCHRASVSCTHPSLHTTGPV LISARTGADHTWYTAGTY
22090	52458	A	22218	383	762	RHQGNQKRKELSLK/CQKSRQE SPRAEENPKWREGKKETSESSV QKAGRAAAAQAGAAASRVPG LSGSNLAPCNKGRLSAREDVSN SKLKILSSGRKHTEHVIMLKAW GLGRQSLRCRLFDLIPSHKV
22091	52459	A	22219	325	945	QPSPLAPKADLSAREGRFQLKV RCRLQQYQQQR\RKF\AAAFLA FHFSLLGSCGILAEAG\KKEKPE KK\VKKSDCGRIGSWSVCVAPP SGDCGLGHHGRATRT*\AECKQ \TMKTQRCKIPCNWEGRQFGRG SAKLPSFQAWGECDLDT\ALKT\ KTGSLKRALHKSPNAQKTVTIS/ KSPCGKLTKPQNLQAES\KKKK KEGKKPEGRLRD

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22092	52460	A	22220	1	1908	MKYIQDFQREKQEFERNLARFR EDHPDLIQNAKKSDIPEKPKTPQ QLWYTHEKKVYLKVRPDATTK EVKDSLGKQWSQLSDKKRLK WIHKALEQRKEYEEIMRDYIQK HPELNISEEGITKSTLTKAERQL KDKFDGRPTKPPPNSYSLYCAE LMANMKDVPSTERMVLCSQQ WKLLSQKEKDAYHKKCDQKK KDYEVELLRFLESLPEEEQQRV LGEEKMLNINKKQATSPASKKP AQEGGKGGSEKPKRPVSAMFIF SEEKRRQLQEERPELSESELTRL LARMWNDLSEKKKAKYKARE AALKAQSERKPGGEREERGKLP ESPKRAEEIWQQSVIGDYLARF KNDRVKALKAMEMTWNNME KKEKLMWIKKAAEDQKRYERE LSEMRAPPAATNSSKKMKFQG EPKKPPMNGYQKFSQELLSNGE LNHLPLKERMVEIGSRWQRISQ SQKEHYKKLAEEQQKQYKVHL DLWVKSLSPQDRAAYKEYISN KRKSMTKLRGPNPKSSRTTLQS KSESEEDDEEDEDDEDEDEEEE DDENGDSSEDGGDSSESSSEDE SEDGD/EGGADRAQWEGRGVL PGGPPGDSTSFLTPQNEEDDED EDDDEDDDEDEDNESEGSSSSS SSSGDSSDSDSN
22093	52461	A	22221	129	2365	
22094	52462	A	22222	5	2730	PSLRFAISGFVWRLAAPASAAA ELRLDCSARRAPRCPRPALPSTR SAEGAVLCAFRREEQQAAATA AAAAAAATAAAAAAPAPPPRP EEEPLPPREGAAAVPGRAGEGA ATQSQGGSRWSGKPGGRAAPA RPRRWLDSWRMNGEADCPTDL EMAAPKGQDRWSQEDMLTLLE CMKNNLPSNDSSKFKTTESHM DWEKVAFKDFSGDMCKLKWV EISNEVRKFRTLTELILDAQ*HF KNPYKG\KKLKKHPDFPK
22095	52463	A	22223	1	446	RPSPPTSSM/PGLWGYSRPCSSG VPASALQA*SPAFSPASQRPPTT SWWEVP*EEGRA\PVWEGRIRA VGPAPAS*PSDLPAWSCRSWRE TRG\SPAEDAMLLRAVEPLEGC QRPLLDSEPP/SPARTSAPAASA SPPAPGGPPCLARPLPR

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22096	52464	A	22224	582	1175	THTHVPAGTHPHTQTTSHSHLI GRALTVPESPKCPCLLPSAC*PR PGRAQPAGPAWSKKEASNPGS E/PPQHSL*RRMAPPE\PVPARA VHTCRCLSSAPPGARLPLDPER RAPQSPRSPPPSAQPPPPPPPPPP PPPGRRGPSQQSWRPSPPPPRTR SRSPRRSRVRGPRAPALAAPPPP GARPGPCAAACGSPTGCS
22097	52465	A	22225	609	5241	GPQTTWCGRPTMCQHCGPAVS SWKQPSHDPCCRGGENRRQPG TPARATQGRLRRRPEGARVPSA RRGRPRARWRDKERNNTCVA ML*QVTNSTAN\APQNNPEVDS IMAELKVEAPASVDWQKRCLT LETQLFRFRLQASKIRELLADK GHGTYISPFSLAKQMQELEQRL LEAEQRAENAETQVGVMEEKV KLSNLKNVDSEGSLHRKYQELL KAIKGKDELISQLEAQLEKQKQ MRAEEAKTVQEKAAKIKEW
22098	52466	A	22226	2	205	
22099	52467	A	22227	1	6186	
22100	52468	A	22228	96	1584	DLGSGITASPPRPEPEHPVFPPA PHTPSKMGKEKTHINIVV\IGHV \DSGKSTTTGHLIYKCGGIDKRT IEKFEKEAAEMGKGSFKYAWV LDKLKAEREPG\ITIDISLW\KFE\ TTKYYITIID\APGHRDFIKNMIT G\TSQADCAVLIVAAGVGEFEA GISKNGQTREHALLAYTLGVK QLIVGVNKMDSTEPAYSEKRY DEIVKEVSAYIKKIGYNPATVPF VPISGWHGANMLEPSPNMPWF KGWKVERKEGNASGVSLLEA\ LDTILPPTRPTDKPLRLPLQD\V YKI\GGIGTVPVGRVETGILRPG MVVTFAPVNITTEVKSVEMHH EALSEALPGDNVGFNVKNVSV KDIRRGNVCGDSKSDPPQEAAQ FTSQVIILNHPGQISAGYSPVIDC HTAHIACKFAELKEKIDRRSTK KLEDNPKSLKSGDAAIVEMVPG KPMCVESFS\Q*PVIG/RTPVRD MRQTAA\VGVIKNVQKKSVGA GKVTKSAQKAQKAGK
22101	52469	A	22229	1	1023	
22102	52470	A	22230	1	396	
22103	52471	A	22231	2	1259	
22104	52472	A	22232	1	2514	

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22105	52473	A	22233	3	2027	EESDCLTEYEEDAGPDCSRDEG GSPEGASPSTASEMDVSLHFVL WGCLHVYQRMIDKAEDVCLFV AQPGELVGQLAVLTGEPLIFTL RAQRDCTFLRISKSDFYEYDSP KLECGWHSEDPNPWTSPSTGL NPLFLELCRHMVFQRLGQGDY VFRPGQPDASIYVVQDGLLELC LPGPDGKECVVKEVVPGDSVN SLLSILDVITGHQHPQRTVSARA ARDSTVLRLPVEAFSAVFTKSA RTITGCVWRYVRASASYCPYLP PLCDPKDGHLLVDGCYVNNVP GSLWRYVRASMT\RRATCPRCA TPRTGTYSWMAATSTICQASGR PHHPHTQAPPAPHTRTRRTSPA AWVPKRSSPLTWGARMRRTSA PTGTACPAGGCCGSG*IPGLTR* RFQTWLKSSPAWPTCPVCGS*R LSSPAPTASTCARPSTASRPWTL GSSTRSILRTTRRMSTAVTTTAT PAPIITPST*GTNGTGCAPQIRPA EPSPGARTSWNPSLSATFAPEEF VASP*LDVPICRMGQCCSLPGG ATLP*GPCGPQCMPGNVVPPER TAARYRQTTAYQTPACPTPPRG QRPT/CVPTVSSLQAGLQGGPRS DFDMAYERGRISVSLQEEASGG SLAAPAREPREQPAGACEYSYC EDESATGGCPFGPYQGRQTSSIF EAAKQELAKLMRIE

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22106	52474	A	22234	281	1832	NDSGLPDRPSSWNQPMEAPLQ TGMVLGVMIGAGVAVVVTAV LILLVVRRLRVPKTPAPDGPRY RFRKRDKVLFYGRKIMRKVSQS TSSLVDTSVSATSRPRMRKKLK MLNIAKKILRIQKETPTLQRKEP PPAVLEADLTEGDLANSHLPSE VLYMLKNVRVLG\HFEKPLFLE LCRHMVFQRLG/QGDYVFRPG QPDASIYVVQDGLLELCLPGPD GKECVVKEVVPGDSVNSLLSIL DVITGHQHPQRTVSARAARDST VLRLPVEAFSAVFTKYPESLVR VVQPGPPSGPAPYPAPSYGHAP RALQIIMVRLQRVTFLALHNYL GLTNELFSHEIQPLRLFPSPGLPT RTSPVRGSKRMVSTSATDEPRE TPGRPPDPTGAPLPGPTGLQGG PRSDFDMAYERGRISVSLQEEA SGGSLAAPAREPREQPAGACEY SYCEDESATGGCPFGPYQGRQT SSIFEAAKQELAKLMRIEDPSLL NSRVLLHHAKAGTIIARQGDQ MEEVKVPAFAVIVD
22107	52475	A	22235	50	4287	PGRKSPGAEDRALWGPACRLL TDSGLPDRPSSWNQPMEAPLQT GMVLGVMIGAGVAVVVTAVLI LLVVRRLRVPKTPAPDGPRYRF RKRDKVLFYGRKIMRKVSQSTS SLVDTSVSATSRPRMRKKLKM LNIAKKILRIQKETPTLQRKEPP PAVLEADLTEGDLANSHLPSEV LYMLKNVRVLGHFEKPLFLELC RHMVFQRLGQGDYVFRPGQPD A\SIYVVQDGLLELCLPGPDGKE CVVKEVVPGD\SVNS
22108	52476	A	22236	283	403	TCLSLVSGCGHCEKMNSEENW *IPIQWASSNPGRRRKNIR
22109	52477	A	22237	33	222	NGPM\CFVKQLEIPQYGYRNNV PTTTPRSNLAKELEKYSKTSFEY TINDNHTYGGLGCMRPRLV
22110	52478	B	22238	1	1860	
22111	52479	A	22239	303	672	GITACVFFSMAEGRTRAERSCD SK*AIGAPAEE*GGASPGKSPEL WQGAGYSPLGACGHKARLWIP WRRSWSGEKGARGCRGTGKK LGHQGWRWETPGRPGGAGPA GFPDPVVMGCEKEASRV
22112	52480	A	22240	1	1377	

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22113	52481	A	22241	1	2232	MQDTEKDDNNNDEYDNYDEL VAKSLLNLGKIAEDAAYRARTE SEMNSNTSNSLEDDSDKNENLG RKSELSLDLDSDVVRETVDSLK LLAQGHGVVLSENMNDRNYA DSMSQQDSRNMNYVMLGKPM NNGLMEKMVEESDEEVCLSSL ECLRNQCFDLARKLSETNPQER NPQQNMNIRQHVRPEEDFPGRT PDRNYSDMLNLMRLEEQLSPRS RVFASCAKEDGCHERDDDTTS VNSDRSEEVFDMTKGNLTLLE KAIALETERAKAMREKMAMEA GRRDNMRSYEDQSPRQLPGED RKPKSSDSHVKKPYYGKDPSRT EKKESKCPTPGCDGTGHVTGL YPHHRSLSGCPHKDRVPPEILA MHESVLKCPTPGCTGRGHVNS NRNSHRRDIQVFNLQKQEMIDR LESLSGCPIAAAEKLAKAQEKH QSCDVSKSSQASDRVLRPMCFV KQLEIPQYGYRNNVPTTTPRSN LAKELEKYSKTSFEYNSYDNHT YGKRAIAPKVQTRDISPKGYDD ANGYCKDPSPSSSSTSSYAPSSS SNLSCGGGSSASSTCSKSSFDYT HDMEAAHMAATAILNLSTRCR EMPQNLSTKPQDLCATRNPDM EVDENGTLDLSMNKQRPRDSC CPILTPLEPMSPQQQAVMNNRC FQLGEGDCWDLPVDYTKMKPR \RIDEDESKDITPEDLDPFQEALE
22114	52482	A	22242	727	4372	LWACVLPGVTLPPFLGEKTSCK MEVDTEEKRHRTRSKGVRVPV EPAIQELFSCPTPGCDGSGHVSG KYARHRSVYGCPLAKKRKTQD KQPQEPAPKRKPFAVKADSSSV DECDDSDGTEDMDEKEEDEGE EYSEDNDEPGDEDEEDEEGDRE EEEEIEEEDEDDDEDGEDVEDE EEEEEEEEEEEEEEENEDHQMN CHNTRIMQDTD\LDDNNNDEY DNYDELVAKSLLNLGKIAEDA AYRARTESEMNSNTSNS

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22115	52483	A	22243	34	1558	PASEEFNSLHGRTPRRDLECRN QQSTTEERRRHDCVQQASEHN EGKWDFAFSAQSQPKP*KPFDV PC*DSRPACP*EHTAGTSGSTSS ETCFFQSSEWPYGELGAYNIFT GPKSTLSSLVTGVSNSSSLS*LP SPKNTITNWFHTRDHSSYSEIHS KACANP*APSQPSR*ASW\IATG SFRRAGLAT*PCCTGSKLLPAW VLANHRWDRTRDGIQKQGNSE *PSSPGTRAFEGNSSSPAPAASIT SMLSPSFTPTSVIRKMYESKEKS KEEPASGKAALGDSKEDTQKA SEENLLSSSSVPSADRDYFSHY KFQTVRHYRGSSCS\PHLSQGQP FTPKEQDYSDLKGNWGRKNTH FGHSPVSLQHFFFRPVPPSSPLSP MVPNG*GLLTKLHPGFGTEDA GPGSTSTASSKFAPNWCASSWD GLESFTGNIWPHPGSALLPFN*S LVHPLLNPRPGNTSASGNGATA ANSAQ\SCILQALVSHGSSCSAF QDNPSETCPAGQACPHALP
22116	52484	A	22244	1502	2657	EGKVPLAFIVLTSLLNAVMSPSF FSCRLLVTALKVSSRCSAMKGV EFFTCWSTFKPFRPASTSSTEST TPECELSLSFSLFAERLERRGFK STLAFCSISKISTLFSAWSSNGIG AK*FPEFCPGDRMACSRPASLSS SSCG/S*PKTAGSAS*SARVREPP TEPTGRD*PFSQ\TSSIIEAKHGT LSRLKNSLKSKSPGDCSGKTAS LGTS*SAAGSCARMTSTSSSSAT PPLHSTIPSFTEAVRRLVLFLPL* SSSSILSSKPVSSMVSD*LVGPA ENHSGSSSV*ESFLLRSPKTRLL SPNSLLKRLSLKSLSRSLSLKSR RSLSL\SGDPSQRSGQRLSSHCQ SYVHQADEAHHYLSLMDFLSA GS*QRLSRGSPLQSSVSEG
22117	52485	A	22245	324	391	
22118	52486	A	22246	42	274	

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22119	52487	A	22247	1	835	MCAGNLCSWEERWAVDEKEA TDKKPHVGGFGQGAPAPAAPA AAMSGRSVRAVTRSRF*DDIKK VMAAIEKVRKWEKKWVTVGD TSLRIFKWVPVTDSKEKEKSKS NSSAAREPNGFPSDASANSSLL LEFQDENS\NQS\SVSDVYQLKV DSSTNSSPKPPKQSESLSPAHTS DFRTD\DSQPPTLGQGDPGRSPP LP\SSEVADEPPTLTKGRTSFHL ETQVVEE\EEDSGAPPLKRFCV\ DQPTVPQTGSEKLAPSRPSAFW ALPLFIAFWFWPRRVCWG
22120	52488	A	22248	3	244	
22121	52489	B	22249	271	711	
22122	52490	B	22250	73	200	
22123	52491	A	22251	885	975	GSTWWPAD*AQL*LHLPTRCM AECWEIPA
22124	52492	A	22252	102	909	PGGRHGRQNDFAAPGGRLEARI HGTVSAPLYHRVLCRLLGSRPA SAAGPAARGGDLAPGEHSFCE DGNYARVESVDRSAINRAMQN PRKSTASVCWTFTASDLPAQGV \PRTSSTRTLREDPFPPSAEKWL RAVLHHFVNEKLQQIFIELTLKP SRRSMSGRHPLDSNPVLQQQGR CDLIENKLSPPGIMSVLDDVCPP CTPRAGEQTRHCCRTAGGCGD PRAFQQLERRFVIHHYAGKTHR PLPGLTPTGNSTNARNIVMDTQ QRTGNN
22125	52493	A	22253	48	112	
22126	52494	A	22254	1243	1615	YSPSSWFSNLYQPSTGALSSSET PKDMAPMKSLREVRSQSHTSTL SRRSTSPGFRLNTKVSFHTGFSV AFTVRVFCFVRFRGSGMSFSFT* GSERPLGSIGIRLRASPTVTWISS AVGARISSC

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22127	52495	A	22255	468	1431	SVSTTRSFSVDSSAKTAAMPVT VTRTTHHNHPDVIFGAWGPP*S WGPLWALTQPLGLL\RLLQL\V STCVAFSLVASVGAWTGSMGN WSMFTWCFCFSVTLIILIVELCG APGPFPPWSWR\NFPI\TFACYA ALFCLSASIIYPTTYVQFLSHGR\ SRDHAIAATFFSCIACGC\YATE VAWTRARPGEITGYMATVPGL LKVLETFVACIIFAFISDPNLYQ H\QPALEWCVAVYAICFILAAIA ILLNLGECTNVLPIPFPSFLSALA \FCLSSSMPPPLFSGPSTSSMRSM AASLGAREM*AAAAGMPTTW VPGTADWLRPS
22128	52496	A	22256	98	414	CTRVSVAEKTSVCLFGLYWESL SISSSCESSAKWPFSTIRSASSTT RHLSCRRFLK**CFSLINSHSRP GVATTISGRRFSILCCFCVDIPPT KIAVLIPVNLAT
22129	52497	A	22257	2	224	
22130	52498	A	22258	2	115	
22131	52499	A	22259	2	118	
22132	52500	A	22260	472	648	GPGGRSFTVWWNW*RRMAQC P\PAEGVQRPECLGPHRAVPAP AHVGLHQEPSRLLPALH
22133	52501	A	22261	540	1893	GRCATPRPRWRGHQCDPPPGD VCVAWREMQLRNKKRRR\DLG NLIK\RFLTAPNSLPD/AVVLTTE EAVIFWCNVLAQQIFGL/PLEM MNEQPLEGAVREKALHTMREQ TQRMEGLVKQL/LTLSKIEAAPT HLLNEKVDVPM/MLRVVEREA QTLVYNAVNHTPEGTHITVRW QRVPHGAEFSVEE*SEGWPVPV PKPHRAVVGANAHISFCPPQEL SKRFTAIRKTKGDGNCFYRALG YSYLESLLPDAFQPLLPPQAWV SPGESQGAGIRDPLWPVPVPKP HRAVVGANAHISFCPPQELSKR FTAIRKTKGDGNCFYRALGYSY LESLLPDAFQPLLPPQAWVSPG ESQGAGTRDPLWLWLFRLWLL RLLCLLLLLLGETAQSRLALTW GRHKQGRLARLSGILGFLALRK QWLGQQVAQLLLQNLHLLLLR WAGLGVIVFQVSNQPAWERTG
22134	52502	A	22262	1	1772	
22135	52503	A	22263	107	294	LHLLSFGYLTHQLLCLHLKWDS HTLHHSHHTIAR*AGCSEATWS PPRRLRAPRSRALCSGFR

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22136	52504	A	22264	1	474	
22137	52505	A	22265	1	148	VKYHEFTCSFKKQITVPEDARL LK*DVRGRPSRLFLADPPPPHT VNREY
22138	52506	A	22266	509	2755	YQSQSFDEDEMNQVTDWVDPS FDDFLECSGVSTITVATSLGVNN SSHRRKNGPSTL\ESSRFPARK\R GNLSSLEQIYGLENSKEYLSENE PWVDKYKP\ETQHELAVHKKKI E\EVETWLKAQVLGRQPKQGG SILLITGPPGCGKTTTLKILSKEH GIQVQEWINPVLPDFQKDDFKG MFNTESSFHMFPYQSQIAVFKE FLLRATKYNKLQMLGDDLRTD KKIILVEDLPNQFYRDSHTLHE VLRKYVRIGRCPLIFIISDSLSGD NNQRLLVPKEIQEEWSISNIRFN PWAPTIMMKFLNRIVTIEANKN GGKITVPDKTSLELLCQGCSGDI RSAINSLQFSSSKGENNLRPRKK GMSLKSDAVLSKSKRRKKPDR VFENQEVQAIGGKDVSLFLFRA LGKILYCKRASLTELDSPRLPSH LSEYERDTLLVEPEEVVEMSHM PGDLFNLYLHQNYIDFFMEIDDI VRASEFLSFADILSGDWNTRSL LREYSTSIATRGVMHSNKARGY AHCQGGGSSFRPLHKPQWFLIN KKYRENCLAAKALFPDFCLPAL CRQTQLLPYLALLTIPMRKSSFR FSFYSKDIGEGLPSGRRTLWGRI GKWEGPGLDRGTWDD*TPDSG DEA\QLNG\GHSAEESLGEPTQA TVPETWSLPLSQNSASELPASQP QPFSAQGDMEENIII\EDYESDG DIEASLLIRLLLHSFHFCFHFSGT
22139	52507	A	22267	2	161	
22140	52508	A	22268	1	599	VTRLFFQPGYGTLQPQRLLMPK KNR\IAIYE\LLFK\EGVMVPKK\ DVPIPKHPELA\DRNVPNLHVM KPMQ\SLKS\RGYVK\EQFAW\R HFYWYLTK*GYQGVSISSRDYL \HLPP\EIVPCHPYGRSPSRRLAR PSG*KVLEG*ANLRGLHKNGEA DKRLPTRRECLCHPGA\DKKAE AG/ALGSSNPNFQFRGGFGRGR GQ\PPQ

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22141	52509	A	22269	1	345	KHPELADKNVPNLHVMKAMQ SLKSRGYVKE\DYLHLPPEIVPA TLRRSRPETG/RPRPKGLEGERP ARLTRGEADRDTYRRSAVPPG ADKKAEAGAGSATEFQFRGGF GRGRGQPPQ
22142	52510	A	22270	2	161	
22143	52511	A	22271	2	641	RRPQHRACSFFFSPGTGPCSRRR CLMPKKNR\IAIYE\LLFKEG\VM VAKKDVHMP\KHPE\LAD\KNG APTFHVMKGHAGLSKSPRATV KGTSFAWGDIFYW\YL\TN*GY QGVSISSRDYLSSCPREICCLAT ATARSPSKRLGKAFGLKRSWE GLRRPGEDFTRGGKFDRGYLT GRIAVATLVADKKAEAG/ALGS SNPNFQFRGGFGRGRGQ\PPQ
22144	52512	A	22272	1	1693	MFNSVPVQNEDGSFNFEGVKA EFRPGTQTQEYIKGMEDSASEV TVNREVTTDNPYTISVTNKTLS AIRIKMFMPR\AYELKVTVIKM AFELSTRCSKRLM/DGSFETVLT DVIEGKTMSGYDRSRRVNLPNF NNQVIFRVVRKTPDSNDSNVV DAIQVRSYAEVIDAKFRYPLTG LLFVEFDSKMFPNQLPTISIRKR WKIVNVPSNYDPESRTYNGNW DGTFKKAWTNNPAWVLYDLM INQRYGLDQKELGISVDKWAL YEAAQYCDQMV\LTAKAARNL ATFVT/CIIQSQTDAPREPAYIFT NDNVVNGDFSYT\SQARRACTR RAT*CLMMSKTCINRTLSQYSI/ V/EGHSTVR\NNVTSITAIG\AHV EA/KANRRGRWILKTNLRSTTV NFATGLEGMIPTIGDVVAISDNF WSSNLTMNLSGRLLEVSGSQIF LPFRVDARAGDFIIVNKPDGKP VKRTISSVSADGKTIEINIGFGFP VKPNTVFAIDRTDLALQQYVVT KIDKGDDDEEFT\SKSRRWSTIL ISTMKLITGLTSTTDRQASLSQI R/CPKPENVK\CPQSRESSRG

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22145	52513	A	22273	1	1843	MEDNLISINKIKILLSVSDGEIDE TFSLKQLMFNSVPVQNEDGSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRIKMFMPR\AYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTVLLFVEFDSKMFPNQLPTIS IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKAWTNNPAWVLY DLMINQRYGLDQKELGISVDK WALYEAAQYCDQMV\LTAKA ARNLATFVT/CIIQSQTDAYKVV RDICSIFRGMSFWNGPREPAYIF TNDNVVNGDFSYT\SQARRACT RRAT*CLMMSKTCINRTLSQYS I/V/EGHSTVR\NNVTSITAIG\AH VEA/KANRRGRWILKTNLRSTT VNFATGLEGMIPTIGDVVAISD NFWSSNLTMNLSGRLLEVSGSQ IFLPFRVDARAGDFIIVNKPDGK PVKRTISSVSADGKTIEINIGFGF PVKPNTVFAIDRTDLALQQYVV TKIDKGDDDEEFT\SKSRRWSTI LISTMKLITGLTSTTDRQASLSQ IR/CPKPENVK\CPQSRESSRG
22146	52514	B	22274	1	1452	

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22147	52515	A	22275	1	1902	MIQKVISGSKGGSQKPHNPVEM EDNLISFNKIKILLAVSDGEIDET FSLKQLMFNSVPVQNEDGSFNF EGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRIKMFMPR\AYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS IRKRWKNVNAPSNYDPESRTY NGNWDGTFKKAWTNNPAWVL YDLMINQRYGLDQKELGFSVD KWALYEAAQYCDQMV\LTAK AARNLATFVT/CIIQSQTDAPRE PAYIFTNDNVVNGDFSYT\SQA RRACTRRAT*CLMMSKTCINRT LSQYSI/V/EGHSTVR\NNVTSIT AIG\AHVEA/KANRRGRWILKT NLRSTTVNFATGLEGMIPTIGD VVAISDNFWSSNLTMNLSGRLL EVSGSQIFLPFRVDARAGDFIIV NKPDGKPVKRTISSVSADGKTI EINIGFGFPVKPNTVFAIDRTDL ALQQYVVTKIDKGDDDEEFT\S KSRRWSTILISTMKLITGLTSTT DRQASEVKPVNFTSSRHQAQPE VGLIPPPLWPQGKGIIAQTSKSS
22148	52516	A	22276	1	675	
22149	52517	A	22277	155	700	SGVLVGHALTARQPSSGRRLV VDHSANRRGRWILKTNLCSTT VNFATGLEGMIPTIGD/GDFIIVN KPDGKPVKRTISSVSADGKTIEI NIGFGFPVKPNTVFAIDRTDLAL QQYVVTKIDKGDDDEEFT\SKS RRWSTILISTMKLITGLTSTTDR QASLSQIR/CPKPENVK\CPQSRE SSRG

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22150	52518	A	22278	1	1871	MEDNLISINKIKILLAVSDGEIDE TFSLKQLMFNSVPVQNEDGSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRIKMFMPR\AYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS\ IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKAWTNNPAWVLY DLMINQRYGLDQKELGISVDK WALYEAAQYCDQMV\LTAKA ARNLATFVT/CIIQSQTDAYKVV \RDICSIFRGMSFWNGESISVIID RPREPAYIFTNDNVVNGDFSYT\ SQARRACTRRAT*CLMMSKTCI NRTLSQYSI/V/EGHSTVR\NNVT SITAIG\AHVEARPTDCGRWILK TNLRSTTVNFATGLEGMIPTIGD VVAISDNFWSSNLTMNLSGRLQ EVSGSQIFLPFRVDARAGDFNIV NKPDAKPVKRTISSVSADGKTI EINIGFGFPVKPNTVFAIDRTDL ALQQYVVTKIDKGDDDEEFT\S KSRRWSTILISTMKLITGLTSTT DRQASLSQIR/CPKPENVK\CPQS RESSRG

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22151	52519	A	22279	3307	5305	CRSSQNTQETSPDRALLVNLRP SQGPLLALWVPAEGVGGKGHC LPPRSFFRMDNQLVPAVSDGEI DETFSLKQLMFNSVPVQNEDGS FNFEGVKAEFRPGTQTQEYIKG MEDSSSEVTVNREVTTDNPYTI SVTNKTLSAIRIKMFMPR\AYEL KVTVIKMAFELSTRCSKRLM/D GSFETVLTDVIEGKTMSGYDRS RRVNLPNFNNQVIFRVVRKTPD SNDSNVVDAIQVRSYAEVIDAK FRYPLTGLLFVEFDSKMFPNQL PTISIRKRWKIVNVPSNYDPESR TYNGNWDGTFKKAWTNNPAW VLYDLMINQRYGLDQKELGISV DKWALYEAAQYCDQMV\LTA KAARNLATFVT/CIIQSQTDAYK VVRDICSIFRGMSFWNGESISVII DRPREPAYIFTNDNVVNGDFSY T\SQARRACTRRAT*CLMMSKT CINRTLSQYSI/V/EGHSTVR\NN VTSITAIG\AHVEA/KANRRGRW ILKTNLRSTTVNFATGLEGMIPT IGDVVAISDNFWSSNLTMNLSG RLLEVSGSQIFLPFRVDARAGD FIIVNKPDGKPVKRTISSVSADG KTIEINIGFGFPVKPNTVFAIDRT DLALQQYVVTKIDKGDDDEEF T\SKSRRWSTILISTMKLITGLTS TTDRQASLSQIR/CPKPENVK\CP QSRESSRG
22152	52520	A	22280	3	412	PAAVA*VKTEPETPGPSCLSQE GQTA\VKTEESSELGNYVIKIDH LETIQQLLTAVVKKIPLITAK\W QRAMTMRKVLQEILEKNPRFH HLTPLKTKHIAHWCRCHGYTPP DPESLRNDGDSIEDVLTQIDSEP
22153	52521	A	22281	2	513	IFACWGKQAWPACCNSLRGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LE/QRAKREPENEEEVDILSLSE PVKINIKKEQEEKQEEVKFYLPP TPGSEFIGDVTQKRLEEVDSTFG DDLVQGFSGGISRRYGEKPGVQ DLEVEPDSVTEMLQFYD

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22154	52522	A	22282	1	1197	MAWPCISRLCCLARRWNQLDR SDVAVPLTLHGYSDLDSEEPGT GGAASRRGQPPAGARDSGRDV PLTQYQRDFGLWTTPAGPKDPP PGRGPGAGGRRGKSSAQSSAPP APGARGVYVLPIGDADAAAAV TTSYRYGLGRDRNESPPCGGRT RRPGARGMGWAAERRRLEPGS HATSELPAASEVTPVWSVGTA GGAFAAPCPETVLEHPRAGSAP LPSQPPSWGQPSEWPAFSRVGT GLPLTPTAGPSRARGARRPCPP ALPGHCLLDRTYTGLQTLGAET LLAVVNSAAMNVGVQVVDVE LHRHSLGEDCIYPQSSESDISDA PPSLPLTIPAPVKASSPIKQSHEP VPDTSVEKGS\PGSCPFHL*GPL SHLGSSPGFLLWRPPGLLSSVA
22155	52523	A	22283	131	677	PSSLS/CDIFLRSPISTPSPSPLPRT PTSTPVHVKQGTAGSVINNPYV IMDKQPGQVIGATTPSTGSPTN KISTASQISQGTGSPVPKIHGSSF VTSTVKVIIKQEPGEAPHVPAT GAASQSPLPQYVTVKGGHMIA VSPQKQVITPGEGIAQSAKVQP SKVL/GQIG*CLPTLARADLLYS
22156	52524	A	22284	3	5128	LLKIHSSQSSPQQAVLTIPSQLK PLSVNTSGGVQTILMPVNKVVQ SFSTSKPPAILPVAAPTPVVPSS APAAVAKGEDASCFSAKSVEQ YYGWNIGKRRAAEWQRAMTM RKVLQEILEKNPRFHHLTPLKT KHIAHWCRCHGYTPPDPESLRN DGDSIEDVLTQIDSEPDHGSLG DGKSSSVGPTAVVTLLACHLEC PSSFSSADNLCRKLEDLQQFQK REPENEEEVDILSLSEPVKINIKK EQEEKQEEVKFY
22157	52525	A	22285	112	651	GGLCTMARTKADWPANRTGG KAP\RKQLAYKKPASQECGPLT GGVKKPHRYR\PGTVGGSVKFR R\YQKST\ELLIRKLPFQ/RRLVR EIAQGL*NKILRFQSAAIG\ALQE GKWRPNLVWPFLKDTNLVC*S MAKRVTIIAKKTFQLAPPHTVE NRALRIHSWMGKHFISQKKKK NFSSSCYW
22158	52526	A	22286	1	339	

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22159	52527	A	22287	2	1369	EPAPPARRSLSAAAAASGTTVD TASHSLVFSQQ\LNMQREIGFRV NCTVAM*DVYFKAHRAVLAAF SNYFKMIFIHQTSECIKIQPTDIQ PDIFSYLLHIMYTGKGPKQIVD HSRLEEGIRFLHADYLSHIATE MNQVFSPETVQSSNLYGIQISTT QKTVVKQGLEVKEAPSSNSGN RAAVQGDLPQLQLSLAIGLDDG TADQQRACPATQALEEHQKPP VSIKQERCDPESVISQSHPSPSSE VTGPTFTENSVKIHLCHYCGER FDSRSNLRQHLHTHVSGSLPFG VPASILESNDLGEVHPLNENSE ALECRRLSSFIVKENEQQPDHT NRGTTEPLQISQVSLISKDTEPV ELNCNFSFSRKRKMSCTICGHK FPRKSQLLEHMYTHKGKSYRY NRCQRFGNALAQRFQPYCDSW SDVSLKSSRLSQEHLDLPCALES ELTQENVDTILVE
22160	52528	A	22288	363	947	STARRGKSRSRPAVALQRQPSA ASRSPSSSRRRRGVSKEVSVPLA RTKQTARKSTN\GK\APRKQLA YKKPARKSA\PSTGGVKKPHRY RPGYCGRSVKFRR\YQKSH*DF* FRKLPFQAVWVRENLLKDF*K QILRF\QSRSYRVALQGGQVEA LSGVGLF*KTTNLLC*SMPKRV NNYCQKDIPAKHARIPWRTVL
22161	52529	A	22289	1	92	
22162	52530	C	22290	10	198	
22163	52531	B	22291	74	205	

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22164	52532	A	22292	2	1914	RGHCEPSRAAPSRADRHPASAL ARDPGRRRGPAGQAAPQPMEP ENIVANTVLLKAREGGGGNRK GKSKKWRQMLQFPHISQCEEL RLSLERDYHSLCERQPIGRL\LF* EFCATRPELSRCIAFQDGMAEY EATPDEKRKACGRRLMQNFL\S HTGPDLIPEVP\RQLVTNCTQRL EQGPCKELSQELTRVTHEYLSV APFADYLDSIYFNRFL\QGKGLE REAI\TKNTLRQYRVLGKGGFG EVCACQVRATGKMYACKKLE KKRIKKRKGEA\MSLNEKQILE KVN\SRFVVSLAYG\YETKD\AL CLVLTLMNGGDLKFHIYHMGQ AGFPEARAVFYAAEICCGL\EDL HRERIVYRDLKPENILLDDHGHI RISDLG\LAVHVPEGQTIKGRVG \TVGYMAPECLKNERYTFSPDW WALGCLLYEMIAGQSPFQQRK KKIKRE\EVERLVKEVPEEYSER FSPQARSLCSQLLCKDPAERLG CRGGSAREVKEHPLFKKLNFKR LGAGMLEPPF\KPDPQAIYCKD VLDIEQFSTVKGVELEPTDQTF YQKFAT\GSVPIPGKNEQMVET ECFQELNVFGLDGSVPPDLDW KGQPPAPPKKGLLQRLFSSPKD CCGN\CSDSEEELPYPPLAPSPRP
22165	52533	A	22293	102	403	
22166	52534	A	22294	1086	1436	
22167	52535	A	22295	965	1231	
22168	52536	A	22296	1434	2215	TPSFSLRTGVNKEHWVLLGFST EDGRW\MFTRGGE\DCTARIWD LRSRNLQCQRIFQVNAPINCVC LHPN\QAELIVGDQSGAIHIWDL KTDHNEQLIPEPEVSITSAHIDP DASLHGQLFNSTGNCYVWD\LT GG\IGDEVTQFIPKTKIPAHTRY ALQCRFSPDSTLLATCSA*LRR/ CKIWRTSNFSLMTEL\SIKSGNP GE\SSRG\WMWGCALIGGTPSNI VTASSNNLARLWCVKTGEIKRE YGGHQKAVVCLPFNDSVLG
22169	52537	B	22297	158	385	

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22170	52538	A	22298	145	1232	LPVRAEPTRAAAMSGDEMIFDP TMSK/NMKKKKKKPFMLDEEG DTQTEETQPSETKEVEPEPTED KDLEADEEDTRKKDASDDLDD LNFFNQKKKKKK\TKKIFDIDEA \EKGVKDL\KI*SDVQEPTEPED DLDIMLGHKKKKKKNVKFPDE DEILEKDEALEDEDNKKDDGIS FSNQTGPAWAG\SERDYTYEEL LNR\VFNIMREK\NPGYWLPGG RKRKFGPWKPPQV\VRVGTKKT FFCPLLQDICKLLHRSAQSISFA FLLG*IGVPSGSIDG**PNL*SKG RF\QQKQIENVLRRYI\KEYVTC\ HTC\RSPDT\IL\QKDTRLLFPYS AETC\HS\RCFCWPVFKTGLPQA VHGQSRGTAPVPKA
22171	52539	B	22299	50	319	
22172	52540	A	22300	3	235	LLLYPLRSLPENPLRLVQQIYSF LKGSSEK*NDLPRVPLLELGVG LLPPNQYSCSRAKPCLTCGLTM SLDGAQQGFW
22173	52541	A	22301	3	2849	WAKPVARASPAAVPGRQCQIR GAWSWGEGRGQPGPAPSPAGS PATSEESLAPMAWRCPRMGRV PLAWCLALCGWACMAPKGTQ\ AEESPFVGNP\GNITGARGLTGT LRCQLQVQGEPPEVHWLRDGQ ILELADSTQTQVPLGEDEQDDW IVVSQLRITSLQLSDTGQYQCLV FLGHQTFVSQPGYVGLEGLPYF LEEPEDRTVAANTPFNLSCQAQ GPPEPVDLLWLQDAVPLATAP GHGPQRSLHVPGLNKTS
22174	52542	A	22302	3364	3899	LVFLFDDLGIVELVLPGNIVHGI MSVRPRVAAGLRVRLQPGRRW LRGPLQLGAPLGLDLLVDVPGS PRFVVGVELPLVV/EAPRPPTPP AAAQQARS*GLECPGRGAAAP REV\LHLQTAHIHGPGPRGGPR ARPGLPGLCPP*T/FSCQEAKGE RGGAHSNGGSGSKWPPPPPPPS

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22175	52543	A	22303	1660	4652	PNPNTCLCNHVESGPCCPSTHT YTLTDLQPLFGVRVPTRPSGRG TQAEESPFVGNPGNITGARGLT GTLRCQLQVQGEPPEVHWLRD GQILELADSTQTQVPLGEDEQD DWIVVSQLRITSLQLSDTGQYQ CLVFLGHQTFVSQPGYVGLEGL PYFLEEPEDRTVAANTPFNLSC QAQGPPEPVDLLWLQDAVPLA TAPGHGPQRSLHVPGAAVGAW EGGSRLWLRAPEAGRKRWGGE VPPVTHAGAGMLRSERD
22176	52544	A	22304	54	288	SEAGQAQPAAAVGFVWTGRRA WETGEGYYSNSLSMELQL*RQ CI*DCFFSSSWRCSVPVYFKEEK YKGNLVCLLFFK
22177	52545	B	22305	243	2641	
22178	52546	A	22306	35	204	
22179	52547	A	22307	244	424	PSLFKNIMTFYPNLHFLWCRGR LYLDVWRQ/VR*FVRNTNYQLP LVLHNLLSRFNTFDELV
22180	52548	A	22308	1	477	
22181	52549	A	22309	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDYFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTMEYYAVTRRNKIVSFA ET*MELEVIIVSKLTQEQKTKHC MFSLTSGS
22182	52550	A	22310	30	199	
22183	52551	A	22311	547	682	LVFLTNQRLVSTHQGTW\WE*K *CQPVIPSL*FYFLRKFSVIVIW* *LLILP*HPMALKI/C/CCQAACS GHFTAGTGEITRPCSISSKVLKR LSRL*STSGS**LVFLTNQRLVS THQGTWMKLEAIILSKVTQEQK TKHHMLSLRSGS
22184	52552	A	22312	2	194	CPSMIDWLKKMWHRYTMEYY AA\IKKNEIMS\FAGTWMKLEAI ILSKLTQEQKN\KHCMFSLITGS
22185	52553	C	22313	1	1845	

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22186	52554	A	22314	1	1384	MRFQDRTWQVPYPSQCSWGSS RQGYVPQARGIVLDSQEAYPSP GGTTLCMHDPDKQAPG/PVRRP APGN\PNRLVVSVALQFLTFHES GITSALRVRPLPQSV\SFQGPGC TEA*RRASICRRRVS*HSTKLDL GAVAAQQQAWVAG\PRSPQRR CHQYS*AGPAWLGLQRGRGSH RPDTSPWHWFWALAGREEQVL PPESLL/RARTPGTHLAPGPGA* TRVQSGPGSWLTWAG*GTPQVI SS/PGAGAVGAPETTAVPTVSIA PRRSVEMWPETKEHLVAVARR KWVSAQEKRLSLRGCGSEKMG VSPGETRVYFPALTS\RCRRRCG RVSEPSPTASWAPAPSLGWAYQ LAGGRLVLRVGLSAGWRAACP QGGPISWLEGGLSSGVGLSAG WRAACPQGGPISWLEGGLSSST MRQPRAPQSSLPAPAPWGAPDP LAMLAAWIEARPGVWPTQPGP WQVSWVCV
22187	52555	A	22315	11	431	RHLLAAPPPAPPAAAAAAALSH CLRSSGRLAPHTSRRLPRVVKR RVNALKNLQVKCAQIEAKFYE EVHDLERKYAVLYQPLFDKRF EIINAIYEPTEEECEWKPDEEDEI SEELKEKAKIVDEKK\DEEKEDP KGIPEFW
22188	52556	A	22316	64	467	PAAWLPILVAARQLTVQMMQN PQILAALQERLDGLVETPTGYIE SLPRVVKRRVNALKNLQVKCA QIEAKFY\EEVHDLQRKYAVLY QPLFDKRFEIINAIYEPTEEECE WKPDEEDEISEELKEKAKIEDE
22189	52557	A	22317	2	177	
22190	52558	B	22318	228	377	
22191	52559	A	22319	630	767	WRVKFKNTVKIQANF*KSRFIH LTVVPVTILSQVTLQLTMSPKT

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22192	52560	A	22320	80	1362	VTACAAPAAWLPILVADIWSSY NMADIDNKEQSELDQDLDDVE EVEEEETGEETKLKARSA*LFR MM\QNPQILA\ALQERLDG/LW VETPT\GYIESLP\RVVKRR\VNA LKNLQVKCAQKETQ\FYE\EVH DLERKYAVLYQPLFDKRFEIIN AIYEPTEEECEWKPDEEDEISEE LK\EKGQIEDEKKDEEKEDPKGI P*IW\LTVFK\NVDLLSDMVQEH DEPILKHLKDIKVKFSDAGQPM SFVLEFHFEPNE\YFTN\EVLTKT YRMRLEPEPDDSDHFSFDGQEI MGCTGCQIDWKKGKNVTLKTI RK*/RRNHKGRGT\VRTGH*NQ FPNDSFSNFFCPLLKSPESGDLD ED\AEAILAADFEIG\HFL\RERII PRSVLYFTGEAIEDDDDDYDEE GEEADEEGEEEGDEENDPDY\D PKK\DQNPAECKQQ
22193	52561	A	22321	3	425	GCGCGGAAARGSPAPGRPAAS PPDCPLWLQGCYPPPSCDALSA TEADGCD*IYPPDTSRDGPHQA SLPGESSSFPGQPNDSYLPERGS ERSRQASYATPAAETQDPDEGL PQPGPEALPGGLQVPKSAAPFC GAQHAAGQ
22194	52562	A	22322	2	285	SRFEPRVRPTGGDRPHQASPPG DSSSFPGQPNDSRLPECGSECRG QASYATPAAETQDPE*RSSPTRS *SP\PGGFQVPKSAAPFCGAQHA AGQ
22195	52563	A	22323	85	473	FTMPAVALVPKELYLSSSLKDL NKKTEVKPEKISTK/QDYVHSIL GTANIKKAIEEAERLSESLKLRY KEAEVRK*LEEKDRQKEAQQL QQKRQETGRE\DGGTLAKVSLE NVLDYQDKTQKSNGEKSEKM

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22196	52564	A	22324	1	1449	MMRAHMFVYKELKQIYKKKT HPHQKVGKGYKQTLLRGRHLR GQETYEKKLTHVYETTDFKQQ QYYFHSILGPANIKKATGETER LSESLKLRYEEVEIWKKLEEKD RQGEAQWLQQKRQETGREDGS MLAKGSLEIVLDSKDKTQKSN GEKNEKCETKEKGAITAKELYT MMMDKNISLIIMDAQRMQDYQ DSCILHSLSVPEKAISPGVTASW IEAHLPDDSIDTWKKRGNVEY MVLLDWFSSAKDLQIGTTLWH LKDALFKWEKGGYKNWFLCY SQYTTNAKVTPPPQHQNEELSIS LDFTYPSLEESIPSKPAAEMPPP PIKVDEDIELISDQISDNDQNER TGPLNISIPVESVAASKSDVSPII QPVPSIKNVPQIDHTKKLAVKL PEEHIIKSESTNHEQQSPQNEKV IPDCSTKPVVSSPTLMLTDEEKA HIHAETALLMEKNKQEKELQE RQQGKQ/K/EKLRREEHEQKAK
22197	52565	A	22325	185	2983	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECRLDRDEERAYVLYM KYVTVYNLIKKRPDFKQQQAD CAYFLGQTVHILFQHRALLEKK YRAVGAITAKELYTMMTDKNI SLIIMDARRMQDYQDSCILHSL SVPEEAISPGVTASWIEAHLPDD SKDTWKKRGNVEYVVLLDWF SSAKDLQIGTTLRSLKDALFKW ESKTVLRNEPLVLEGGYENWL LCYPQYTTNAKVTPPPR
22198	52566	A	22326	313	3720	FIMPAVASVPKELYLSSSLKDL NKK\TEVKPEKISTKSYVHS/AP RKIFKTAEECRLDRDEERAYVL YMKYVTVYNLIKKRPDFKQQQ DYFHSILGPGNIKKAVEEAERLS ESLKLRYEEAEVRKKLEEKDRQ EEAQRLQQKRQETGREDGGTL AKGSLENVLDSKDKTQKSNGE KNEKCETKEKGAITAKELYTM MTDKNISLIIMDARRMQDYQDS CILHSLSVPEEAISPGVTASWIE AHLPDDSKDTWKKR

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22199	52567	A	22327	46	562	LLQGPGFCGDSMPVEARPSAA WRGGRAPGWTPFSPPDRETWK PQ/RASQGESGQRRFGPCPRSGG RPPGPGSAAHSSRSQRWRKASR AWPAAPRKGLLPPAQAWPPTP AAGL*GFLAACKR/PPVGGRGP APAPCRPASSRCFLICDSGPPCL CSASRAAWMGSAASSRVLFIEG
22200	52568	B	22328	51	445	
22201	52569	A	22329	51	366	CQWNTQTQVCYKQDVQSITAL GSAAQCTCLSSPR*SGKFKLLFS PGLPGTLVPSTIPATSAPRA/SHR AGEAWVGEPGRALAALQNSS\P DWAGYQGLPCKPSIRAA
22202	52570	A	22330	257	916	SPSGSNLETHLRAPDLGGPCPP GPRWWA*TPQPGHPQTRPSPAA QPCPFPPQCQQLIHCPC/SPAPGT VAAPPAP\PTPASQCLLCPWTSA PVCSPAPTFPCPMAPVMAFMLP SYSFP/PGTPNLPQAFFPSQPQFP SHPTLTSEMASASQP\GSPAGPR SPDSHVLVQPPGPPHHRPWVGP PHRSFSPAAARPCSSTCCSWRK PLRVALEPWGPQGPQRQQL
22203	52571	A	22331	151	1232	GRLGDARGPQGPEAPGGEEAA RADSTRACRSCGLLLGGRRGCR PSLKNAELLELTVRRVQCVLRG RARAREQLQAEARRALRCRLHP VACTKVHTFVSTCQAIDATVA AELLNHLLESMPLREGSSFQDL LGDALAGPPRAPGRSGWPAGG APGSPIPSPPGPGDDLCSDLEEA PEAELSQA/PC*GARLGARSPGQ PDHSPNCPGVSGGLGDQCQPES CRGGARPSLGSPPLLPGVQMW WG*GPGSLPGSSLPPLMDGLQG QPLVTSPAQRPSPVS*KNF*GPC SSGSGWREGATGRRKNFVELP ALSQVSPSPAFNPRLCGLWGQR WQKLVLGTSVPGSPGLNKSLN LPLQRGDERQVH
22204	52572	A	22332	1	1524	

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22205	52573	A	22333	3	8875	EDGSLLQEVGIICLARGPGCGPE TPLYSPATGLALQLQGPAAMG ALWSWWILWAGATLLW\GKSG EDWISGPTTVFSQPGLTQEASV DLKNTGREEFLTAFLQNYQLA YSKAYPRLLISSLSESPASVSILS QADNTSKKVTVRPGESVMVNI SAKAEMIGSKIFQHAVVIHSDY AISVQALNAKPDTAELTLLRPIQ ALGTEYFVLTPPGTSARNVKEF AVVAGAAGASVSVTLKGSVTF NGKFYPAGDVLRVT
22206	52574	A	22334	2	2214	ISATDGPLAPCHGLVPPAQYFQ GCLLDACQVQGHPGGLCPAVA TYVAACQAAGAQLGEWRRPDF CPLQCPAHSHYELCGDSCPVSC PSLSAPEGCESACREGCVCDAG FVLSGDTCVPVGQCGCLHDGR YYPLGEVFYPGPECERRCECGP GGHVTCQEGAACGPHEECRLE DGVQACHATGCGRCLANGGIH YITLDGRVYDLHGSCSYVLAQ VCHPKPGDEDFSIVLEKNAAGD LQRLLVTVAGQVVSLAQGQQV TVDGEAVALPVAVGRVRVTAE GRNMVLQTTKGLRLLFDGDAH LLMSIPSPFRGRLCGLCGNFNG NWSDDFVLPNGSAASSVETFG AAWRAPGSSKGCGEGCGPQGC PVCLAEETAPYESNEACGQLRN PQGPFATCQAVLSPSEYFRQCV YDLCAQKGDKAFLCRSLAAYT AACQAAGVAVKPWRTDSFCPL HCPAHSHYSICTRTCQGSCAAL SGLTGCTTRCFEGCECDDRFLL SQGVCIPVQDCGCTHNGRYLPV NSSLLTSDCSERCSCSSSSGLTC Q\AAGCP\PG\RVCEVKAEAR\N CW\ATRGL\CVLSVG\ANL\TTF DGARGATTSPGVYELSSRCPGL QNTIPWYRVVAEVQICHGKTE AVGQVHIFFQDGMVTLTPNKG VWVNGLRVDLPAEKLASVSVS RTPDGSLLVRQKAGVQVWLGA

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22207	52575	A	22335	3	7639	ITCPENSHYEVCGPPCPASCPSP APLTTPAVCEGPCVEGCQCDA GFVLSADRCVPLNNGCGCWAN GTYHEAGSEFWADGTCSQWCR CGPGGGSLVCTPASCGLGEVCG LLPSGQHGCQPVSTAECQAWG DPHYVTLDGHRFDFQGTCEYL LSAPCHGPPLGAENFTVTVANE HRGSQAVSYTRSVTLQIYNHSL TLSARWPRKLQVDGVFVTLPF QLDSLLHAHLSGADVVVTTTS GLSLAFDGDSFVRLRVPAA
22208	52576	A	22336	2	224	HCYMVVQLWKPRSLRRKSDQL WSSWNQLNTSELSSFISAEMQT EAFDCGSMAGRM*GQGRYLLA ALWDSSVPLS*PQAEPWSGVGP AHLTE/LLSPSRFVSISDLLAPKD LGTESQVSMEV*KDMGRFHWE DIPP*A*VFVIFVFQIFISRTY\DA TTHFETTCDDIKNLL*R*QGRYL LAALWDSSVPLS
22209	52577	A	22337	2	206	LSSSYLDQPCYETINRIKLYSES LARYGKSPYLYPLYGLGELPQG FAR*EPVFKTSVIQNLIFNIMCI
22210	52578	A	22338	2	457	
22211	52579	A	22339	2	1556	FVFPSEVAVGLALSPASIFLSFSS PFLRAQERLPSLLWWARSPCAF SLLGSCVRACPAMNEEYDVIV\ LGTG\LTECILSGIMSVNGKKVL HM\DRNPYYGGESASITALEDL YKRFKIPGSPPRVKWGEERDW NVDL\IPKFLKANG\QLVKMLL YTEVTRYLDFKVTEGSFVYKG GKIYKVPSTEAEALASSLMGLF EK\RRFKEFLVYVANFD\EKDPR TF\EGIDPKKTTMRDVYKKFDL GQDVIDFTGHALA\LYRTDDYL\ DQPCYETINRIKLYSESLARYG KSPYLYPLYGLGELPQGFARLR CYLWEGTYMLNKPIE\EIIVQE WGKVIGCKI*REEIARCMQLIC DPSYVKDRVEKVGQVITVICIP QPPPSKNTNDANSC\QIIIPQNQ\ VNRKSDIYVC\MISFA\HNVAAQ GKSIAIVSTTVET\KEPEKEIRPA L\ELL\EPIGTEILVSISDLL\VPKD LG\TESQIFIS\RTYDATTHFETTS D\DIKNIYKR\MTGSEFDFEEMK
22212	52580	A	22340	66	420	
22213	52581	A	22341	64	140	
22214	52582	A	22342	2	254	

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22215	52583	A	22343	82	3530	HLIVAMPEPTKKEENEVPAPAP PPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQNANSQLSILFIE KPQGGTVKVGEDITFIAKVKAE DLSEKPTI/KWF/K/GKWMDLAS KAGKHLQLKETFERHSRVYTFE MQIIKAKDNFAGNYRCEVTYK DKFDSCSFDLEVHESTGTTPNID IRSAFKRSGEGQEDAGELDFSG LLKRREVKQQEEEPQVDVWEL LKNTKPSEYEKIAFQY/GITDL\R GMLKRLKRSI
22216	52584	A	22344	66	358	TWVRGNPKPKITWMKNKVAIV DDPRYRMFSNQGVCTLEIRKPS PYDGGTYCCKAVNDLGTVEIE CKL\EVKVIYQGVNTPGQPVFL EGQQQSLHNKDF
22217	52585	A	22345	67	3515	HLIVAMPEPTKKEENEVPAPAP PPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQNANSQLSILFIE KPQGGTVKVGEDITFIAKVKAE DLLRKPTIKWFKGKWMDLASK AGKHLQLKETFERHSRVYTFE MQIIKAKDNFAGNYRCEVTYK DKFDSCSFDLEVHESTGTTPNID IRSAFKRSGEGQEDAGELDFSG LLKRREVKQQEEEPQVDVW\EL LKNAKPSEYEKIAFQYGITDLR GMLKRLKRMRREEK
22218	52586	A	22346	2	39	FQFCVSLFVYIQLNSDVLPE*PR HKKKPPTLSHWFLK*NLHL*N* NTKALKYRKLV*LTSQKH*QM TYPFCNYLKTN*VTTNTKVK*T EGY*TAKTQKLYPDKVVMATN KPLKTRSPK\PAKYGSPHDTAT WTGSGLGLEAS*HSA
22219	52587	A	22347	1	113	
22220	52588	C	22348	47	337	
22221	52589	A	22349	1	2292	
22222	52590	A	22350	2	441	LRHAKWFQARANGLKSCVIVIR VLRDL\VTRVPTWGPLRGWPLE LLCEKSIGTANRPMGAGEALRR VLECLASGIVMP/QHALRLAAF GQLHKVLGMDPLPSKMPKKPK NENPVDYTVQIPPSTTYAITPM KRPMEEDGEEKSPSKKK

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22223	52591	A	22351	45	402	HALAALEKLFPDTPLALDANK KKRAP\VPVRGGPKFAAKPHNP GFGMGGPMHNEVPPPPNLRGR GRGGSIRGRGRGRGFGGANHG GYMNAGAGYGSYGYGGNSAT QGYK*LFHKTAYGYS
22224	52592	A	22352	243	3113	FPDTTEEVKMRPMRIFVNDDRH VMAKHSSVYPTQEELEAVQNM VSHTERALKAVSDWIDEQEKG SSEQAESDNMDVPPEDDSKEG AGEQKTEHMTRTLRG\VMR\VG LVAK\CLLLKGDL\DL\ELVLLC\ KEKPTT\ALL\DKVADNLAI\QL AAVTEDKFEILQSVDDAAIVIK\ NTKEPPLS\LTIHLTSPVVREE\M EKVLAGETLS\VNGPPGNVLDR SRIAFAAFRGSLPETQRWFQ\AR ANGLK\SCV
22225	52593	A	22353	139	245	
22226	52594	A	22354	875	2019	NPNSQMPKMTRSTKQLTNKSG QIDGCPGCRVVPTWCRLGHLSH YWAVWASILRFWEVWKYWLG NMGRKSSEFPILKLNG\RTMGD *VLPFHMYV\QPVV\HPQLYPHS VTELTGDYFKPWWDGQPSLQQ VL\ERVDEWM\AKEGLL\DPNV QVQFLFTLWEDWGLKKSVLPG\ QCQ*LGAWPVGGFTSKQWD*S *KKAYSF\AMGCWPKNGLLDM NKGLSLQHIGRPHSGIDDCKNI ANIMKTLAYGGFIFKQTSKPVLI GRGQDGAGQGSLVGPPQNPPL PHQRGKRESGHKLCCPKVVPSA SLWGSMPLGRGLCCPLQGALA TWPFLEARHFCAPPSPTPQSQPS ISPSHCGPGLRGTPGTHRLLPW YNRLLWGHQDPRCAPSHP
22227	52595	A	22355	507	916	RKKNEKEGTKPPRNMGICEKT KPTFDWCT*K*RGEWNQVGKY TSGYYTGELPQSSKTGQHSNSG NTENTTKILLEKSNPKTHNW*I HQG*NEGKTVKGSQREK*GYP QREAHQTNSRSLCRNPTRQKRV GVNIKHS
22228	52596	B	22356	72	359	

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22229	52597	A	22357	1236	1987	GNSSPPGLPCKSSSSPPPPPSLTG APARRAAAAPPRPASRPRPPLA\ GGGVPQLFATRPP/PGPTRARRP TWR*GPRGSPEETPRRRREWTR RPEPGCRAQGSRRPARPPSGSS AVRSASPASSPAPAASAPLGPRS RWS*RPPSRPRR/SPPPPPPGRSR SDRER/GRRKEASPPLTLAEAPA Y/RQDQAPPPGSPHLGFQSAAG PSRTASSAP/RSGIGGRGANTPA PAAIFPPSLRPPRAGPVGDLRAS GVDAAA
22230	52598	A	22358	287	2082	LKTETSEEKARRYKDRPSQLNA VFQEQKKMIQAQESITLEDVAV DFTWEEWQLLGAAQKDLYRD VMLENYSNLVAVGYQASKPDA LFKLEQGEQLWTIEDGIHSGAC SDIWKVDHVLERLQSESLVNRR KPCHEHDAFENIVHCSKSQFLL GQNHDIFDLRGKSLKSNLTLVN QSKGYEIKNSVEFTGNGDSFLH ANHERLHTAIKFPASQKLISTKS QFISPKHQKTRKLEKHHVCSEC GKAFIKKSWLTDHQVMHTGEK PHRCSLCEKAFSRKFMLTEHQR THTGEKPYECPECGKAFLKKSR LNIHQKTHTGEKPYICSECGKG FIQKGNLIVHQRIHTGEKPYICN ECGKGFIQKTCLIAHQRFHTGK TPFVCSECGKSCSQKSGLIKHQ RIHTGEKPFECSECGKAFSTKQ KLIVHQRTHTGERPYGCNECGK AFAYMSCLVKHKRIHTREKQE/ CSQGGKSSCREAQLITHQ*CHA GEKLC*RGDYTSAFCGPSDIIKH QRP/HSQNRN/CSPCGTASGQM CSLRR*QWICTGQKPCECSECG CAFRDQLCLILCYRKPIGRK\PD LCGKGLSKNL*FIMWPKSIHCE
22231	52599	C	22359	90	344	
22232	52600	A	22360	2	543	
22233	52601	A	22361	373	490	
22234	52602	A	22362	111	396	GAPPGIWCLSLWACRALSPLSS AAQHRKRPSALSPATPAGSRPL RRCAPGFAATKTQRVQRRPPRR *GAAAGAGGS*RPLCGVVIHSV LHNTPE

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22235	52603	A	22363	1902	3474	VPQRSTGSGRARSARRPLRAPD PCAAAPRVSPQPRPSECSGGRR GGSKTWAKRNAGKELTDRNW DQEDEAEEVGTFSMASEEVLK NRAIKKAKR\RNVGFESDTGGA FKGFKRFGGYPSEEERFSGFG\S GAGGKPLEGL\SNGNNIT\SAPP FASAKAAADP\KVAFGK*LPSPS RLLVDKNVSNPKTNGDSQQPSS SGLASSKACVGNAYHKQLAAL DCSVRDWMVKHANTNSLCDL TPIFK\DYEK\YLANIETANTGN\ SGRNSESESNKVAAETQSPSLF GSTKLQQESTFLFHGNKTEDTP DKKMEVASEKKTDPSSLGATS ASFNFGKKVDSSVLGSLSSVPL TGFSFSPGNSSLFGKDTTQSKPV SSPFPTKPLEGQAEGDSGECKG GDEEENDEPPKVVVTEVKEED AFYSKKCKLFYKKDNEFKEKGI GTLHLKPTANQKTQLLVRADT\ NLGNILLNVLIPP\NMPCTRTGK NNVLIVCVPNPPIDEKNA\TMP\ VTMLI\RVKTSEDADELHKILLE
22236	52604	C	22364	65	283	
22237	52605	A	22365	3	419	
22238	52606	A	22366	1	512	CGRPPWKTGQRSQPSCPPGSSG SGRGIP\PAAWHEGEGPEAVLQ GHRAGRGDPACRGLCCLPSQL GGPTSPTSAASRACGSRGAATL VVKVKWFYHP/CRRPSWARGS ATARMRCTSPATRMRTTCRPSP TSARSWRASSMSRWPGAASAR TGRTSTTGGHLRPHHRAPGDG
22239	52607	A	22367	1	2940	MRRRRKVAAIHAGPRPRSAAA SSEQRGRGPGAARRAGGAEAA ASGVTGGGGGGAGQHAGGLG FSAGGRAPSQRPLCGSMPARLF SKQEVDYCGLPAPPASSLRSRG HRQRIYSLNQLLQEALRTGRAR PGEGPGWLVTDKGGLGWGSSH SQAQGPDSQAAWGRAPPAHGS SPAFLQVLDVRPQSSRYLPPGT RVCAYWSQKSRCLYPGNVVRA PPPCFGRLLGVPAASSGVPSTG ASGDEDEDLDSVVVEFDDGD
22240	52608	B	22368	215	356	
22241	52609	A	22369	282	499	YLLHCLPSDPPSFTNSPDGRGRR RRRQRRRRSDPPGRGRTKSSTR VPGSNRFV*FHQR*GRLKEWM ANQDTN

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22242	52610	A	22370	105	619	ACQASSHSGPVWGPGERTTPG A*ASARREPSRNQHPNLWVTE Q/I*IASPRTVANPLVPARTPTGP RTNKPKHLIKQGRGQPRQPLSG STGGAGESPASGCAGGQPAHR VWIAPAARGCGQHTPWKAPAG NGQSPRPASATRMIGPSPSLSPP APPAVVGVAALGSRNRCIL
22243	52611	A	22371	1	441	
22244	52612	A	22372	10	621	LRQLERGLAKGQPSTPVDRPLG PDPSAPGTLAGAALPPLEPPAPC LCQDPQEDSVEDEEPPGSLGLP PPQAGVQPAAAAVSGTTQPLG TGPRVSLSPHSPLLSPKVASMD AKDLALQILPPCQVPPPSGPQSP AGPQGLSAPEQQEDEDSLEEDS PRALGSGQHSDSHGESSAELDE QDILAPQTVQCPAQAPAGGSEE T*LRQLERGLAKGQPSTPVDRP LGPDPSAPGTLAGAALPPLEPP APCLCQDPQEDSVEDEEPPGSL GLPPPQAGVQPAAAAVSGTTQP LGTGPRVSLSPHSPLLSPKVAS MDAKDLALQILPPCQVPPPSGP QSPAGPQGLSAPEQQEDEDSLE EDSPRALGSGQHSDSHGESSAE LDEQDILAPQTVQCPAQAPAGG SEETIAKA

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22245	52613	A	22373	1	2271	MPGELLAPSCCCRGGPTRDRTD LSCDAAAATTILGGDRREPCAL TPGPSHLALTFLPSKPGARPQPE GASWDAGPG\LSTEAPLPATLE PRIVMGEETCQALLSPRAARTA LRDQEGWGL/SPQGSMVDEREL HPAGTPEPPSSESSLSADSSSSW GQEGHFFDLDFLANDPMIPAAL LPFQGSLIFQVEAVEVTPLSPEE EEEEAVADPDPDSASYAEADDE RLYSGEPHAQATLLQDSVQKTE EESGGLRYDTASAPTRHRSLVS PKACSCSHDCAP\AG*RGPHLTP GLRYDTASAPTRHRSLISPKAC GCSHDCVPAG*RGPHLTPGLRY DTASAPTRHRSLVSPKACSCSH ACVPAG*RGPHLTPGLRYDSTS ASARHRPHLRSRASGCGHPSNL AGRSRLCPRDRACGHHGSAGS/ SAWTGSMSGSA\RHR*WG*A*L TPKGDPGG*EPAGRRPEG\TGT GTWTQPQGGLHGCQRPGLADL AALPSASSLWAPEPSWPS/SALS PRAARG*GQPGGRLASGPGLGP AFG*PRGVISRAGRAGHLGSSD RAVSSPGAQSREEGPSRRQ*GD HRQSQAESQ*EEGPKGNVKAG LAADSGSHQDHHPEVQEHPLC HRQA*CLQGDPASAHLCG\FWR GQ\T*GP\CPASAQSRS*EV*GAL R\DLSLGP*VST\QGPG*A*VQG KGKG\GGGKGGPGGAGTA*HL
22246	52614	A	22374	2	211	
22247	52615	A	22375	43	241	
22248	52616	A	22376	184	332	
22249	52617	A	22377	1292	1923	KAGARGNQEGTMASSSG\TQK VLTIPRGCYQ*K*SKETLP*CSG WPNDAR\EAVVNC\CTEFI\HLIS SEANEICNKSEKKTISPEHVIQA LESLGFGSYISEVKEVLQECKT VALK\RRKASSRFGKPLGIPEEE\ LFGDQANKELFGKSLDQQQAE\ LAQQ\EW\LQMQQAA\HQA\QL AAASAKCI*SRRGSFSGMEEDG GWISEIPPAEFLFLL
22250	52618	B	22378	1	1701	
22251	52619	A	22379	1	147	

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22252	52620	A	22380	1	484	IRHEGRGQRGKMELVQ\VLKRG LQQITGHGG/LFRGYLRVFF\RT NDAKVGTLVGEDKYGNKYYE DNKQFFGRHRWVVYTTEMNG KNTFWDVDGSMVPPEWHRWL HSMTDDPPTTKPLTA\RKFHLG RNH*ISTWTGAPQEQYVPYSTT RK\KIQEWIPPSTPYK
22253	52621	A	22381	3	258	DMAAQIAEGMAFIEERNYIHRD LRAANILVSDTLSCKIADFGLA RLIED\FTIKSDVWSFGILLTEIV THGRIPYPGMTNPEVIQN
22254	52622	A	22382	1	738	
22255	52623	A	22383	233	1898	GAGPTGYLRRLPGWAGTMGC GCSSHPEDDWMENIDVCENCH YPIVPLDGKGTLLIRNGSEVRDP LVTYEGSNPPASPLQDNLVI\AL HSYEPSHDGDLGFEKGEQLRIL EQSV\EWWKAQSLTTGQEGFIP FNFVAKANSLEPEPWFFKNLSR KDAERQLLAPGNTHGSFLIRES ESTAGSFSLSVRDFDQNQGEVV KHYKIRNLDNGGFYISPRITFPG LHELASAITPIASDGLCTR\LSRP CQTQKPQKPQKPWWEDEWEV PRETLKLVERLGAGQFG\RCGW GTTTGTTKVAVKSLKQGSMSA GRLP\AEANLMKQLQ\HQRL\VR LYAVVT\QEPIYIITEYMENGSL VDFLKTPSGIKLTINKLLDMAA QIAEGMAFIEERNYIHRDLRAA NILVSDTLSCKIADFGLARLIED NEYTAREGAKFPIKWTAPEAI*S RGNSPPRSDVWSF\GDLLPEIFT\ HGRIP/YPQGIPNPELIQKLERGY RMVRP\SNCPEKLYQL\MRLCW KERPED\RPTFDYLRSVLEDFFK RHRRASNQPQALREPLRKPLCF
22256	52624	A	22384	3	203	
22257	52625	A	22385	2	467	
22258	52626	A	22386	1	468	
22259	52627	A	22387	1	645	

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22260	52628	A	22388	821	2637	AAASAWRATHSTTAAGRRTAL FRSPEPGNTRDTRRRRRATAPD CCRPATSPRALDWTSLHTRRHP VQNYLQWSYWQVLVSRWIAF AGLAMADYLISGGTGYVPEDG LTAQQLFASADDLTYNDFLILP GFIDFIADEVDLTSALTRKITLK TPLISSPMDTVTEADMAIAMAL MGGIGFIHHNCTPEFQANEVRK VKNFEQGFITDPVVLSPSHTVG\ DVLEGKMRHGFSG\IPITETGTM GSKLVGIVTSRDIDFLAEKDHT TLLSEVMTPRIELVVAPAGVTL KEANEILQRSKKGKLPIVNDCD ELVAIIARTDLKKSRDYPLASK DSQPQLLCGAAVDTREEDKYR LDLLTQAGVDVIVLDSSQGNSV YQY\ARVLYFKQKYPHLQV\LG GNVVTAAQAKNLIDAGVDGLR VGMGCGSICITQ\EVMACGRPQ GTCCVTR*AEYARRFGVPIIAD GGIQTVGHVVKALALGASTVM MGSLLAATTEAPGEYFFSDGVR LKKYRGMGSLDAMEKSSSSQK RYFSEGDKVKIAQGVSGSIQDK GSIQKFVPYLIAGIQHGCQDIGA RSLSVLRSMMYSGELKFEKRT MSPQIEGGVHGLHSYEKRLY
22261	52629	A	22389	2	332	
22262	52630	A	22390	3	608	MTAVHAGHLNLKWDPKSLEIR TLAAERLVTQVTTLVNTNSKGP SDKKRGHSKKVHVLAASVEQA AENFLEKEDKIVKESQF\L*E*LL AAVEYVRKQ/GKECLRPSLEEH LEGIISGAALMGDSSCKHDDHR ERIAAECNTVLQ\ACRTCF/SEY MGNAGCKERSNSLNSAIDKMT KKTRDLRRQLHKAVMDHVSDS FLETNVPLL
22263	52631	A	22391	2	2864	

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22264	52632	A	22392	14	2897	PDWRETKQRPSASGLWNLALA QLAAEMTAVHAGHLNLKWDP KSLEIRT\LAVERLLEPLVTQVT TLVNTNSKGPSDKKRGHSKKV HVLAASVEQAAENFLEKEDKIV KESQF\L*E*LLAAVEDVRKQG DLMKAAARRRSHDDPCSSVEQ GNMVQAA*TLLSAVTCLLILA\ DMGNVYKLLVQLKVVEDGILK LRNAGNEQDLGIQYKALKPEV DKLNIMAAKRQQELKDVGHRD QMAAARGILQKNVPILYTAS
22265	52633	A	22393	1	1584	
22266	52634	A	22394	1	3519	
22267	52635	A	22395	3	673	
22268	52636	A	22396	1	1574	DVPRDLEVVAATPTSLLISWDA PAVTVRYYRITYGETGGNSPVQ EFTVPGSKSTATISGLKPGVDYT ITVYAVTGRGDSPASSKPISINY RTEIDKPSQMQVTDVQDNSISV KWLPSSSPVTGYRVTTTPKNGP GPTKTKTAGPDQTEMTIEGLQP TVEYVVSVYAQ\NPSGESQPLV Q\VAVPTIPAPTDLKFTQVTPTS LSAQWALPNVQLTGYRVRVTP KERTGPMKEINLAPDSSSVVVS GLMVATKYEVSVYALKDTLTS GPAQGVVTTLENVSPPRRARVT DATETTITISWRTKTETITGFQV DAVPANGQT\PIQRTIKPDVRSY TITGLQPGTDYKIYLYTLNDNA RSSPVVIDASTAIDAPSNLRFLA TTPNSLLVSWQPPRARITGYIIK YEKPGSPPREVVPRPRPGVTEA TITGLEPGTEYTIYVIALKNNQK SEPLIGRKKTVQKTPFVTHPGY DTGNGIQLPGTSGQQPSVGQQ MIFEEHGFRRTTPPTTATPIRHR PRPYPPNVGQEALS

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22269	52637	A	22397	3	2382	QTEMTIEGLQPTVEYVVSVYAQ NPSGESQPLVQTAVTNIDRPKG LAFTDVDVDSIKIAWESPQGQV SRYRVTYSSPEDGIHELFPAPDG EEDTAELQGLRPGSEYTVSVVA LHDDMESQPLIGTQSTAIPAPTD LKFTQVTPTSLSAQWTPPNVQL TGYRVRVTPKEKTGPMKEINLA PDSSSVVVSGLMVATKYEVSV YALKDTLTSRPAQGVVTTLEN VSPPRRARVTDATETTITISWRT KTETITGFQVDAVPANGQTPIQ RTIKPDVRSYTITGLQPGTDYKI YLYTLNDNARSSPVVIDASTAI DAPSNLRFLATTPNSLLVSWQP PRARITGYIIKYEKPGSPPREVV PRPRPGVTEATITGLEPGTEYTI YVIALKNNQKSEPLIGRKKTDE LPQLVTLPHPNLHGPEILDVPST VQKTPFVTHPGYDTGNGIQLPG TSGQQPSVGQQMIFEEHGFRRT TPPTTATPIRHRPRPYPPNVGEEI QIGHIPREDVDYHLYPHGPGLN PNASTGQEALSQTTISWAPFQD TSEYIISCHPVGTDEEPLQFRVP GTS\TSATLTGLTRGATYNIIVE ALKDQQRHKVREEVVTVGNSV NEGLNQPTDDSCFDPYTVSHYA VGDEWERMSESGFKLLCQCLG FGSGHFRCDSSRWCHDNGVNY KIGEKWDRQGENGQMMSCTCL GNGKGEFKCDPHEATCYDDGK
22270	52638	A	22398	48	7500	GATMACCAAQGEERVTPCASG KRGPAATTSLVLWIPSVPPPVPF PTLWPPPSWRRQPPGGIRRDFS RRLRREANLVATCLPVRASLPH RLNMLKGPGPGLLLLAVLCLG TAVPSTGASKSKRQAQQMVQP QSPVAVSQSKPGCYDNGKHYQ INQQWERTYLGNVLVCTCYGG SRGFNCESKPEAEETCFDKYTG NTYRVGDTYERPKDSMIWDCT CIGAGRGRISCTIANRCHEGGQS YKIGDTWRRPHETGGYM
22271	52639	A	22399	1	403	NSTNKRRGFCFITFKE\EMEKKY HNVGLSKCEIKVAMSKEQYQQ QQQWGSRGGFAGRARGRGGG PSQNWNQGYSNYWNQGYGNY GYNSQGYGGYGGYDYTGYNN YYGYGDYSNQQSGYGKVSRRG GHQNSYKPY

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22272	52640	C	22400	36	214	
22273	52641	A	22401	3	182	
22274	52642	A	22402	223	452	LESMTIFPYSDDKRAQYIFIQKD LLKKPVRHYYIMTLSHWAFNT RLALQYWGKGHKTQIDSEA*Q LRNKTMKANFF
22275	52643	A	22403	1	1037	MSEEQFGGDGAAAAATAAVG GSAGEQEGAMVAATQGAAAA AGSGAGTGGGTASGGTEGGSA ESEGAKIDASKNEEDEGHSNSS PRHSEAATAQREEWKMFIGGLS WDTTKKDLKDYFSKFGEVVDC TLKLDPITGRSRGFGFVLFKESE SVDKVMDQKEHKLNGKVIDPK RAKAMKTKEPVKKIFVGGLSP DTPEEKIREYFGGFGEVESIELP MDNKTNKRRGFCFITFKEEEPV KKIMEKKYHNVGLSKCELK\VA \MSKEQYQQ\Q\QQWDSRGGCA GRA\RGRGGDQAE\GYGKGIQA RWAIKNSYKPYLNYSICQPYPP TAGTSLQALCRADFRFSQARSM
22276	52644	A	22404	299	1508	HYVGGSSSGGDGAAARAT/AR AVGGSAGEQ\EGA\MVAATHG ARGGVWEADAATGGGTASGG T\EGGSAE\SEG\AKIYASKNEED EGHSNSSPRHSEAATAQRGRM\ KMVIGGLSWDT\TKKDLKDYFS KFGEVVDCTLKLDPITG\QSRGF GFV\LFKESESV\DKVMDQKEH K\LNG\KVNDPKRAKAM\KTKE PVKKIFVGGLSPDTPE\EKIREYF GGFGE\VESIELPMD\NKTN*RG RGF\CF\ITFKEEEPVKKI\MEKK YHNVGLSKCEIKVVLLNEQYQ QQQQW*SIGGFAGIALVIGGGP SQNWNQGYSNYWNQGYGNYG YSS\QGYG\GYGGYDYTGY\NN Y\YGYGDYSNQQSGYGKVS\RR GGHQ\NSYKPHTKFIPICNLFPN RWLKQYFPNLKIQFERGSCHLL
22277	52645	A	22405	3	189	EESEPERKRARTDEVL\PEEAAP RRKMRTTRTTCPVSRY\AAP\QL LLQKLLQRRRKGSCSRG
22278	52646	B	22406	1	1356	
22279	52647	C	22407	135	260	
22280	52648	A	22408	1	1740	
22281	52649	B	22409	80	371	

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22282	52650	A	22410	257	1200	ISWCCMEQKKRLP\FSKREG\PY EFIICPSEDSSPLLRCAFCIGGMS VKEQMETIRHPLQTTRGPGPGP LFTDGPDPIPEAFLHGLLSIREM VSTEKVKPVGQESEPRVKPLEL DDSASGGVHMMVATPGRLMD LLQKKMVSLNICRYLALDEAD RMIDMGFEGDIRTIFSYFKHTSA AAIGLQLALDGGTGSGQKGKC EEFPSSMSAVSTGLEASACCLS VTMDPLETLSRMASSTSSMSSL ARAWLSPEPGDSPGMVGGLPR ELPGMAPLECGEFQRPESLCAD RNELGSQSPEFPGQEEEDEDED DEEEDEDE
22283	52651	A	22411	107	2069	GGVSPWRACVQQRMEESEPER KRARTDEV\LPEEAAPRRKMRT TRTTCPMCRYGSAGSLLLQKLL QR\RRKGAAEEEQQDSGSEPRG DEDDIPLGPQ\SNVSLLDQHQHL \KEKAESAAKESCQGRKQLEGK KEKILGRIVCRRAE\LDVK*KAD WLKGITVLIDPIKTQLGLPPR/Y MFLSMSEERHERVRKKYHILVE GDGIPPPIKSFKEMKFPAAILRG LKKKGIHHPTPIQIQGIPTILSCR DMIGIAFTGSGKTLVFTLPVIMF CLEQEKRLPFSKREGPYGLIICP SRELARQTHGILEYYCRLLQED SSPLLRC\ALCIGGMSVK\EQ\ME TIRQGVHMMVATPG/RALMDL LQKKMVSLDICRYLALDEADR MIDMGFEGDIRTIFSYFKGQRQ TLLFSATMPKKIQNFA\KSALVK PVTINVGRAGAASLDVIQEVEY VKEEAKMVYLLECLQKTPPPV LIFAEKKADVDAIHEYLLLKGV EAVAIHGGKDQEERTKA\IEAFR EGKKDVLVAT\DVASKGLVFPA IQHVINYDMPEEIENYVHRIGRT GR\SGNTGIATTFINKACDESFLI D\LKALLVRKPKQKVPPVL\QV L\HCGGWSPMLDIGRSSRGCAF CGG\LGH\RITDCPKL\EA\MQTK QVSNIGRKDYLAHSSMDF
22284	52652	A	22412	435	1428	

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22285	52653	A	22413	3	597	HKMAPYSPLVTRLQKALGVRQ YHVASVLCQRAKMAMSHFEPN EYIHYDLLEKNINIVCKRLNWP LTLLEKIVYGHLDDPASQEIEQ GK/S/YLWLWPDHVAMLQFISKI GATTSVFPYNHRMRRYLSK/TG RTDIANLADEFQDHLVPDPGCH YDQLIEINLSELKPHINGPFTPD QAHPVAEVGKVAEKEGWPLDI RVGLT
22286	52654	A	22414	29	512	
22287	52655	A	22415	1	543	
22288	52656	B	22416	271	719	
22289	52657	A	22417	1	2438	SVHKMAPYSLLVTRL*KALGV RQYHVGSVLCQRAR\VAMSHF EPNEYIHYDLLEKSINIVRKRLN RPLTLSEKIVYGHLDDPASQEIE RGKSYLRLRPDRVAMQDA\TA QMAMLQFISSGLSKVAVPSTIH CDHLIEAQVGGEE\DL\RRAKDI NQEVYNFLATAGAKYGVGFW KPGSGIIHQIILENYCVPWLSF*L GPDFHTPNGGG\LGGI\CIGSCG WPNAWEWNGLGIPWELKCPK VIGVKLTGSLSGWPSPKDVILK VAGILTVKGGTGAIVEYQGPGV DSISCTGMATICNMGAEIGATT SVFPYNHRMKKYLSKTGREDIA NLADEFKDHLVPDPGCHYDQLI EINLSELKPHINGPFTPDLAHPV AEVGKVAEKEGWPLDIR\VGL\I GSCTNFKLWKIWGRSAAVAKQ ALAHG\LKCKSQF\TITPGFPRQI\ RATFE\RDGYAQILRDLGG\IVL ANACGPCIGQWDRKDIKKGEK NTIVTSYNRNFTG\RNDANPET HAFVTSPEIVTALAIAGTLKF\N PETDYLTGHGWARSFRLGGSRI AD*VFPKGEF*PRGRDTYQHPP K\DSSGAACWDLSPTSQRLQLL EPFDKWDGKDLEDLQILIKVKG KCTTDHISAAGPWLKFRGHLD NISNNLLIGAINIENGKANSVG\ NPVTQEFGPAPD\LARYYKKHG I\RWVVIGDENYGEG\SSREHAA
22290	52658	A	22418	14	260	RLCIGDAGVSPVCGP/CSAGGGP R*LNLEGGEESSSVPRGG/CCSP VTATTAPGPCFPK*SDGSGCAE APDSGE/CS*ALGPHCGD

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22291	52659	A	22419	160	460	RLCIGDAGVSPVCGPLSAGGGP R*LNL*GGEESSSVPRGG/CCSP VTATTAPGPCFPK*SDGSGCAE APDSGNCGAFCALRSPHRHPGP KPARERLLLTGL
22292	52660	A	22420	43	418	SLGCAEQN/FPAIAIQPGMAQEE RLSRYQQFKDFQRRILVATNLF GRGMDIERVNIVFNYDMPEDS DTYLHRVARAGRFGTKGLAITF VSDENDAKILNDVQDRFEVNV AELPEEIDISTYIEQSR
22293	52661	A	22421	1	592	RFSKYMPSVKVSVFSRGLSIKK DEEVLKKNCPHVVVRTRARILA LVRNRSFSLQNVKHFVLDECD KMLEQLDMRRDVQEIFRLTPHE KQCMMF/ERLSRYQQFKDFQRR ILVATNLFGRGMDIERVNIVFN YDMPEDSDTYLHRVARAGRFG TKGLAITFVSDENDAKILNDVQ DRFEVNVAELPEEIDISTYIEQS
22294	52662	A	22422	2	575	
22295	52663	B	22423	100	412	
22296	52664	A	22424	2	441	
22297	52665	A	22425	682	1032	
22298	52666	A	22426	1	1324	MAEQDVENDLLDYDEEEEPQA PQESTPAPPKKDIKGSYVSIHSS GFRDFLLKPELLRAIVDCGFEHP SEVQHECIPQAILGMDVLCQAK SGMGKTAVFVLATLQQIEPVN GQSGQVHIFGLHIGARALVISEH ILKDEGAVEGCGVVQCLMARV TVLVMCHTRELAFQISKEYERF SKYMPSVKVSVFFGGLSIKKDE EVLKKNCPHVVVGTPGRILALV RNRSFSLKNVKHFVLDECDKM LEQLDMRR\DVQEIFRLDTTPR KQCMMFSATL\SKDI\RPV\CRK FMQDPMEVF\VDDETKLTLHG\ LQQYYVKLKTSEKNRSLFDLL\ DV\LEFNQV\IIFVKSVQRCMAL AQLL\VEQNFPAI\AIHRGMAQE ERLSRYQQFKDFQRRILVATNL FGRGMDIERVNIVFNYDMPEDS DTYLHRVARAGRFGTKGLAITF

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22299	52667	A	22427	9	1535	EAQQLVSERPAENRSWKCLLA ARGEERGASIMAEQDVENDLL DYDEEEEPQAPQESTPAPP\KKD IKGSY\VSIHSSGFRDF/LCLKPE LLRAIGGLVAFEHPSEVQHE\CI PQGHPGAWDVLLPGQSPGMGK TAVFRCWPPLQQI\EPVNGQVT\ VLVM\CHTRELAFQISKEYERFS KYMPSVKVSVFFGGLSIKKD\E EVMKKNCPHVVVGTPGRILAL VRNRSFSLKNVKHFVLDECDK MLEQLDMRRDVQEIFRLTPHEK QCMMFSATLSKDIRPVCRKFM QDPMEVFVDDETKLTLHGLQQ YYVKLKDSE\KTRKVFDLWD\V LEFNQVDILRQGQCKRCMAL\A QLL\VEQNFPAQWPI\HRGNGPQ KERPVNAYQASSKDFPSGRDPL VATQILFG\RGMDIEAKSNI\VFN Y\DMP*GLGTPYL\HRV\ARRGR FGTKRP*PFTFVSDG\NDA\KILN DV\QDRF*S*MWAEL\PEEIDIST YIEQSRLNHQLARAGPPGAAPH AASPPLSRRHC
22300	52668	A	22428	3	290	
22301	52669	A	22429	1	690	MNQTSEKEIISKEQGNVKAAGA SDVVLYKIDVPANRYDLLCLEG LVRGLQVFKERNFFLTVLEVEK SKTKVEQIQCLCSQEDIADKLG VDISATKAVHISNPKTAEFQVA RTTLLPGLLKTIAANRKMPLPL KLFEISDIVIKDSNTDVGAKNYR HLCAVYYNKNPGFEIIHGLLDRI MQLLDVPPGEDKGGYV/IQSVG KLGVLHPDVITKFELTMPCSSL EINIGPFL

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22302	52670	A	22430	2	1834	GTRPTVSVKRDLLFQALGRTYT DEEFDE\LCFEFGLELDEITSEKE IISKEQGNVKAAGASDVVLYKI DVLATRYDLLCLEGLVRGLQV FKERIKAPVYKRVMPDGKIQKL IITEETAKIRPFAGAAVLRNIKFT KD\RYDSFIELQEKLHQNICRKR ALVAIGTHDLDTLSGPFTYTAK RPSDIKFKPLNKTKEYTACELM NIYKTDNHLKHYLHIIENKPLYP VIYDSNG\VVLSMPPIINGDHSRI TVNTRNIFIECTGTDFTKAKIVL DIIVTMFSEYCENQFTVEAAEV VFPNGKSHTFPELAYRKEMVR ADLINKKVGIRETPENLAKLLT RMYLKSEVIGDGNQIEIEIPPTR ADIIHACDIV\EDAAIAYG\YNNI \QMHSPENFTP*ANQFPLNK\LT ELLRHDMA\AAGFH*STLPLAL CSQGRYWLDKLGVGYLWQQR AVHISN\PKTAEFQVARTTLLPG PP*RP*AANRKV\PLPL\KLFEIS\ DIVIK\DSNT\DVGAKKTTRQSL VAGLLPTKNPG\FEINSWGCWD RIMAVCSDV\PPGGRQGGDM*F KASEGPAFFPGAMCRDSFARGQ SL\GKLG\VLHPDVIHQIWS*PLP CSSLEI\NIGPFL
22303	52671	A	22431	1	304	
22304	52672	A	22432	1	642	
22305	52673	B	22433	1	423	
22306	52674	A	22434	1	525	LHEHPVTESPMNCSVTLQLSLY MKSVA/GIGQTGKIEPVVLPLL WFAESGAMEGETLHTFYTQLV LMPKVMHYAQYVLLALGCVL LLVPVICQIRSQ/DRCWPEGSPG *QPFAFPPA*TDIILWTEPATLM AEVSACCAPELPPPPHRVPQIIG AQAEVNEPGGPAFRALLDPGA
22307	52675	A	22435	3	483	VRGSGNSHGEVSKGRMCLAGA LPLPGACAALVLLLVILPEPLRC PLHTLYGGRDPVDSIRLWRQA GEFRHKSNITFNNNDTVSFLEY RTF\QFQPSKSHGSESDYIVMPN ILVLNKPRSTWISVCFVHGCIPA SRTGPRTESMHSKSLWKAWLA APGLPLL

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22308	52676	A	22436	1	1623	RRRPRLLPGAEPCEPRVGPRRA DMGCSAKARWAAGALGVAGL LCAVLGAVMIVMVPSLIKQQV LKNVRIDPSSLSFNMWKEIPIPF YLSVYFFDVMNPSEILKGEKPQ VRERGPYVYK/ESSRHKSNITFN NNDTVSFLEYRTFQFQPSKSHG SESDYIVMPNILVLGV\AVMME NKPMTLKLIMTL\AFTTLG\ERA FHGTALWGEV\MWGYKDPLVN LINKYFPGMFPFKGGFGVFAEL NNSDSGLFTVFTGVQNISRIHLV DKWNGLSKVDFWHSDQCNMI NGTSGQMWPPFMTPESSLEFYS PEACRSMKLMYK\ESGVFEGIP TYRFVAPKTLFANGSIYPPNEGF CPCLESGIQNVSTCRFSAPLFLS HPHFLNADPVLAEAVTGLHPN QEAHSLFLDIHPVTIIPMNCSVK LQLSLYMKSVAGIGQTGKIEPV VLPLLWFAESGAMEGETLHTF\ YTQLVL\MPKVMH\YAQYVPS WALG\CVLLLVPV/LSCQIRSQE KCYLFWSSSKKGSKDKEAIQA GSE*SLMTSAPKGS\VLQEAKL
22309	52677	A	22437	198	1062	STCVEMPRNLLYSLLSSHLSPHF STSVTSAKVAVNGVQLHYQ\HF GEGDHAV\LLLPGMLGSGETDF GPQLKNLNKKLFTVVAWDP\R GYGHSRPPDRDFPADFFERDAK DAVDLMKALKFKKVSLLGWS DGGITALIAAAKYPSYIHKM\VI WG\ANAYVT\DERPAG*YEGHP RMVSQMGVEGKKESL*EALYG YDYFARTCEKWVDGIR\QFKHL PDGNICRHLLP\RVQ\CPPPLIVH G\EKDPLVPRFHADFIHKHVKG SRLHLMPEGKHNLHLRFADEF NKLA\EDFLQ
22310	52678	A	22438	223	393	AQASPPLLPP**ERSNVPCPIS

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22311	52679	A	22439	524	1516	FILEDITGYVMAPIDGLLCREPR RGLYLEGTKPMTLFQIQFLNSV GDLLDLIPSLSPTKNGSLKVFKR WDMGHCSALIKVLPGFENILFA HSSWYTYAAMLRIYKHWDFNII DKDTSSSRLSFSSYPGFLESLDD FYILSSGLILLQTTNSVFNKTLL KQVIPETLLSWQRVRVANMMA DSGKRWADIFSKYNSGTYNNQ YMVLGPEESKAEPQSLTKGT/P VTLWEQIPTY/VRNISGTNLMFL RGKGFWA\SYNVPFHEKIYNWS GLSHC*FRKLGLGPTPYDFRPH EPKIFRRDPR/DK*LIRHPMKYI MRYN\NYKE\DPYSRGDPPVNT
22312	52680	A	22440	1	306	
22313	52681	A	22441	698	1613	FQFFQIFPEYKNNDFYVTGESY AGKYVPAIAHLIHSLNPVREVKI NLNGIAIGDGYSDPESIIGGYAE FLYQIGLLDEKQKK\YFQKQCH ECIEHIRKQNWFEAFEIL\DKLL\ DGDLTSDPFLTSQNVTGCS\NY YNFLRCTEPEDQLYYVKFLSLP EVRPAHPTLGN\QTFN\DGPIV* KVPCGEDTSTSPVKPW\LTEI\M NNYRVLIY\NG\QLGHPSVAAAP DQSAPLMG\MDWKGSP\EYKK AEKK\VWKIFKS\DSEVA\GYI\R QVGDF\HQVIIRGGGHILPYDQP LRAFDMINRFIYGKGWDPYVG
22314	52682	A	22442	1	258	
22315	52683	A	22443	366	848	
22316	52684	A	22444	1	585	ECLCVSTAVRIRHELKTMLTEL LRGGSFEFKDMRVPSALVTLH MLLCSIPLSGRLDSDEQKIQNDI IDILLTFTQGVNEKLTISEETLA NNTWSLMLKEVLSSILKVPEGF FSGLILLSELLPLPLPMQTTQVS LPYNMHLINDCSNTF*KASDSV KKQKPSSPFLPKRHKITG*GGD KTETSWSLRKYGGKNFK

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22317	52685	A	22445	625	2700	YIRGHSTPRKLWSMHLHVQAK LLQEIVRSFSGTTCQPIQHMLRR ICVQLCDLASPTALLIMRTVLD LIVEDLQSTSEDKEKQYTSQTT RLLALLDALASHKACKLAILHL INGTIKGDERYAEIFQDLLALVR SPGDSVIRQQCVEYVTSILQSLC DQDIALILPSSSEGSISELEQLSN SLPNKELMTSICDCLLATLANS ESSYNCLLTCVRTMMFLAEHD YGLFHLKSSLRKNSSALHKLLK RVVSTFSKDTGELASSFLEFMR QILNSDTIG\CCG\DDNG\LMGSR RGAHTSRTMSINAAELNQLLQS TEESPEDLFLELEKLDLEHSKD DDNLYSLLD**RGLKQMLESSG DPLPLSDQDVEPVLSAPESLQN LFNNRTAYVLADVM\DDQLKS MWFTPFQAE\EIGTDLDLVKVD LIELSEKCCSDFDLHSE\LERSFL SEPSSPGRTKTTKGFKLGKHKH ETFITSSGKSEYIEPAKKEFMLC PPPRGRGRGGFGQGIRPHDIFR\ QRKQNTSRPP\SMHVDDF\VAA E\SKEVVPQDGI/PSHPNRPLKVS QRISSRVGFSGNRGGRGAFHSQ NRFFTPPASKGNYSRREGTRGS SWSAQNTPRGNYNESRGGQSN FNRGPLPQL\RPLKFPTG*PAPK SLGTRAS*MVRGG\LGTFPGLS AKLAASGGSRGKFVSGG\SGRG
22318	52686	A	22446	2487	3161	TWWLHISIIIPGGKKSYSPRLGR GKRFATFVLLVGGELCLTSYAP PSIHPILRSEAECLNYSIFSKFLA PAGEFALPRSFDNCPRVRLRAL RLALLILLTFILCWTPYYLLGM WYWFSPH\MLTEVPPSLSHILFL LGLLNAPLDPSPSYGAFTLGCR RGHQELSIDSSKEGSGRMLQEEI HAFRQLEVQKTVTSRRAGETK GISITSI*S*QSM*EQNSKSLVP
22319	52687	A	22447	232	337	
22320	52688	A	22448	1	1449	
22321	52689	A	22449	1	2004	

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22322	52690	A	22450	3	1558	APARDRAGGGRRALPRLPAAS ARARGLTRALSRAMACRQEPQ PQGPPPAAGAVASYDYLVIGGG SGGLASARRAAELGARAAVVE SHKLGGTCVNVGCVPKKVMW NTAVHSEFMHDHADYGFPSCE GKFNWRVIKEKRDAYVSRLNA IYQNNLTKSHIEIIRGHAFF\TSD PKPTIEVSGKKYTAPHILIATGG/ MVPSTPH*EPRSRGASL*ITSDG FFQLEEIVPAAASLVGARLPLSV EMAGIL\SALGSKTSLMIRHD\K VLRSFDSMISTNCTEELENAGV EVLKFSQVKEVKKAL\SGLEAS MVTAVPGRLPVMPMIPDVDCL LWAIGGVPNTKDLSLNKLGIQT DDKGHIIVDEFQNTNVKGIYAV GDVCGKALLTPVAIAAGRKLA HRLFEYKEDSKLDYNNIPTVVF SHPPIGTVGLTEDEAIHKYGIEN VKTYSTSFTPMYHAVTKRKTK CVMKMVCANKEEKVVGIHMQ GLGCDEMLQGFAVAVKMGAT KADFDNTVAIHPTSSEELVTLR
22323	52691	A	22451	51	464	
22324	52692	B	22452	103	1184	
22325	52693	A	22453	52	148	
22326	52694	A	22454	1	3282	
22327	52695	A	22455	145	436	
22328	52696	A	22456	1	3622	MPGYRAGPFEEAFDREDERQIE CQGRGVDRKITGEHTTFSGRSG PDHELTLDSGKGCTRSMVPASA ASEDRRKLPIIVEDEGGPTRSRA CSSPARGSRPPPSAIGCSPVAQA SDSAAGPARRTALQSLSSWLGY QIDRHSVPVYVFKSPLFSVIMAP KHKSSDAGNLDRPKRSRKVLPL SEKVKVLDLIRKDKKSYAEVA KIYGKNESSIREIVKKEKEIRASF AVSPPTAKVTATVRDKCLVKM EQALHLWVEE
22329	52697	A	22457	3	422	VVELRCQDKEGNPAPEYTWFK DGIRLLENPRLGSQSTNSSYTM NTKTGTLQFNTVSKLDTGEYSC EARNSVGY/PQVPGKRMQVDD LNISGIIAAVCGLGVCYAQRKG YFSKETSFQKSNSSSKATTMSE NDFKHTKSFII
22330	52698	A	22458	1	208	
22331	52699	A	22459	122	321	

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22332	52700	A	22460	2	1169	HTPKTEQTPIPGLEDPPLGSQLR RRPGEGETDIPSRAVPPLPPLPT LCSFPAPEVQGPPASCAPAAGT LDLLRAAGCRPGKMARRSRHR LLLLLLRYLVVALGYHKAYGF SAPKDQQVVTAVEYQEAILAC KTPKKTVSSRLEWKKLGRSVSF VYYQQTLQGDFKNRAEMIDFNI RIKNVTRSDAGKYRCEVSAPSE QGQKPG\EDTVTLEVLGDVHVL APAVPSCEVPSSALSGTVVELR CQDKEGNPAPEYTWFKDGIRLL ENPRLGSQSTNSSYTMNTKTGT LQFNTVSKLDTGEYSCEA\RNS VG*SEGPCETNASR*SQHKVGII GSRS*LWALVDFPFVGLVYSYG SEGKATFSKETSFQKSNSSSKAT TMSENDFKHTKSFII
22333	52701	B	22461	57	168	
22334	52702	A	22462	1	682	
22335	52703	A	22463	398	1465	GTFPPSGLITGKKRKALLGACD CTQIVKPSGVHLKLVLRFSDFG KAMFKPMRQQRDEETPVDFFY FIDFQRHNAEIAAFHLDRILDFR RVPPTVGRIVNVTKEILEVTKN EILQSVFFVSPASNVCFFAKCPY MCKTEYAVCGKPHLLEGSLSA FLPSLNLAPRLSVPNPWIRSYTL AGKEEWEVNPLYCDTVKQIYP YNNSQRLLNVIDMAIFDFLIGN MDRHHYEMFTKFGDDGFLIHL DNA\RGFGRHSH\DEIPILSLLSQ CGMIKKNTLLHLQ\LLAQADYR LS\DVMRESLLEDQL\SPVLTEP HLLAL\DRRLQTILRTV\EGCIV\ AHG\QQSVH*FDGPSGNSSGPR
22336	52704	A	22464	2	424	GRVGVSAVIVRAWITHKYSGR DWNVKWEENLLHAVAKNYTL LQTIPPFERPFKDHQVCLEWNM GYIWNLRANRIPQCPLEN/DFRE DFHYNDTAGYFIIGGSRYVAGI EGFFGPLKYYRLRSLHPAQIFNP LLEKQLAEQIS
22337	52705	A	22465	23	323	
22338	52706	A	22466	3	287	LSVQMYAQAALDGDSQGFFNL ALLIEEGT\YERCWSHSNEESFS PCSLAWLYLHLRLLWGAILHSA LIYFLGTFLLSILIAWTVQYFQS VSGKDL
22339	52707	A	22467	1	348	
22340	52708	A	22468	1	738	

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22341	52709	A	22469	1	507	
22342	52710	A	22470	187	3682	SILCLLSPCVVQFGKPVVSILSS RSRHSPCTKKGWEGMRKHLHT RQGHK*VHV\KFP\SIMGLQGM DYFHPDISIFCNLAVIVRAW\ITH KYRGRDWNVKWEENLLHAVA K\NYTLLQTIPPFERPFKDHQVC LEWNMGYIWNLRANRIPQCPL ENDVVALLGFPYASSGENTGIV KKFPRFRNRELEATRRQRMDYP VFTVSLWLYLLHYCKANLCGIL YFVDSNEMYGTPSVFLTEEGYL HIQMHLVKGEDLA
22343	52711	A	22471	3	153	
22344	52712	A	22472	1	408	TEPEFPGRRFRPRMAVMAP\RT LVLLLSGALALTQTWAGSHSM RYFSTSVSRPGRGEPRFIAVGYV DDTQFVRFDSDAASQRMEPRA PWIEQEGPEYWDEETGKVKAH SQTDRENLRIALRYYNQSEAGS HTLFPR
22345	52713	A	22473	1	823	MAVVAPRTLLLLLSGALALTQT WAGSHSMRYFSTSVSRPGSGEP RFSAVGYVDDTQFVRFDSDAA SQRMEPRAPWMEQEEPEYWDR QTEISKTNAQIDLESLRIALRYY NQSED/GPPPKTHMTHHPISDHE ATLRCWALSFYPAEITLTWQRD GEDQTQDTELVETRPAGDGTF QKWASVVVPSGQEQRYTCHVQ HEGLPKPLTLRWEPSSQPTIPIV GILAGLVLFGAVIAGAVVAAV MWRRKSSDRKGGSYSQAASSD SAQGSDVSLTACKV

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22346	52714	A	22474	1	1162	NSRVDDFVAVMAPRTL\LLLLS GALALTQTWAGSHSMRD\FFTS VSRPG\R*EPRFIAVGYVDDTQF VRF\DSDAASQRMEPRAPWIEQ EGPEYWDQETRNMKA\HSQTD RENLRIALPLTYNQSEAGS\HTL QMMFGCERGGSDGALSFRGLP PVTAY\DGKGFTFALNE\DLRS WT\AADMAAQITQRKWETPPM WRS/EQEEAYLEG\QCV\DGLRR YL\ENGKEDAAAQRTPPKTHMT HHPIS*P*RPL*RCW\AL\AFYPC GDHT*PWQRDG\EDQTQ\DTEL V\ETRPAGDGTF\HKWAAVVVP SGEESEITPANVQQ*RVLPKPLT LKM/WEPSSPAHPSPIVGHHLLA LVL/LLGAFDHLKLWVAAVML KEGTAQVGKG*KIEKGGSYSSR LPSQ
22347	52715	A	22475	9	316	IPAMGLETEKADVQLFMDDDS YSHHSGLEYADPEKFADSDQD RDPHRLNSHLK\ILMPFVKTCL MVLPSVQTIWKSVTDVIIAPLCT SVGRCFSSVSLQLSQD
22348	52716	A	22476	3	606	RPRTKAAMGLETEKADVQLFM DDDSYSHHSGLEYADPEKFADS DQDRDPHRLNSHLKLGFE\DVI AEPVTT\HSFDKVW\ICSHALFEI \SKYRM\YRSLT\VFLGHSPWAFI CGEFSFATL\SCLAHLGF*WPFV \KTCLM/VFLPSVQTIWEEC*QM V/ISLAPLC\TSVG\RCFLFLFSLA TEPRNGILGPQVWRLGYCNTSF VIIT
22349	52717	A	22477	101	432	ATRDQLKAKPENLLGSISRDSG RTQEGIPARVPYPPPP/PTREPPQ ST*PGRNGLLGCLGGGAPRPG WLDSEAGGAPAFHCPG*CPRRH RRGGTRLKQLPPPPTTVHDQPL
22350	52718	A	22478	794	1209	VKVDEVTVKHLGCQRCQWSRC PPSCSGTCLCCGAEAPCAAQPA WPPPPAAPPPTPPAPPSD\NSSCT Q*PTPRCGT*DKDKGIFTLPKGH P*V*SLEHGFLKLGSCP\PPPPHA LVRPPQVRFNTPHGAEPQRDQL PQST

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22351	52719	A	22479	3	1041	GSNCPLRQADPGPPRHTLFMDF VAGAIGGVCGVAVGYPLDTVK VRIQTEPKYTGIWHCVRDTYHR ERVWGFYRGLSLPVCTVSLVSS VSFGTYRHCLAHICRLRYGNPD AKPTKADITLLGCGLRTRPRVP DVAH*GGQSPLADADTGFLSSS GGFRLSALLAAPPMCPVPPACP EPKYRGPLHCLATVAQ\EEGLC GLYKGSLALVLRDGHSFATYFL SYAVLCEWLSPAGHFRPDVPG VLVAGGCAGVLAWAVATPM\D GIKSRLEANGQGQ\NGYRGLLH CMVTSVREEGPRVLFKGLVLN CCRAFPVNMVVFVAYEAVLRL RPGSAHHSRSPTPRGATHQQLV
22352	52720	A	22480	38	453	
22353	52721	A	22481	287	413	DMDYRRGGWTVIHRKIGGRID FQRVR*DYLHGYADLLREFWL
22354	52722	A	22482	1	393	MPKLLKWNYEGGACWGNLW KLPNVERLCFSEATVFRSAAQC LVVGLGLLLVSRACSHEDAIEW RGDSSVVNIVEDGSNAKDESKS NDTVCKEDCEESCDVKTKITRE EKHFMCIFHNVQSLGTVCGEK GIDVN*NYTRRKTFHVYLPQCS VTGNSLRGERH
22355	52723	A	22483	505	854	
22356	52724	A	22484	584	1009	FTQKDLFIPFEVMCDMDYRGG GWTVIQKRIDGIIDFQRLWCDY LDGFGDLLGDAFL\FL*KEDNQ NAMPFSTSDVDNDGCRPACLV NGQSVKSCSHLHNKTGWWFN KCGLANLNGIHHFSGKLLATGI QWGTGNQKQLTWQE
22357	52725	A	22485	1	3123	MSHRARPCPAPFLFWMLGVKT EPAGQDRRKKARSRCCIFRVHA SGLWGLRFPSVEWGKPSRDKA QLSESPPQSVYLFAETALSAIVP GDGVAGGGGTGDGGPGAPYPG AVADMEELTIWEQHTATLSKD PRRGFGIAISGGRDRPGGSMVV SDVVPGGPAEGRLQTGDHIVM VNGVSMENATSAFAIQILKTCT KMANITVKRPRRIHLPATKASP SSPGRQDSDEDDGPQRVEEVD QGRGYDGDSSSGSGRSWD
22358	52726	A	22486	191	267	

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22359	52727	A	22487	2	609	PPPRSSEDPAKMAEVEHEEGSG PFRKFTLPAAVDL\DQ\RLDISY DQLEQPMQAVPVARPAAGGLN PGACGRKQ\HSPA*KRLLQGPS KGGAAPCHKPEAGEDATLRD\ MII\LPEMWGS\MVGVYH\GKTF \NQVEDQGVCGRPCRLGWAGV A*CRRDQLTPSFALGLPQPEMI GHYLGEFSITYKPVKHGRPGIG ATHSSRFIPLK
22360	52728	A	22488	3	461	STISLYCGLKTCPKLTCAFPVSV PDSCCRVCRGDGELSWEHSDG DFFRQPATREASHSCHRSHYDP PPSRQAGGLSRFPGARSHRGAL MDSQQASGTIVRFVLNNKHKH GQVCVSNGRTYSHGESWHPNL RAFGIVECVLCTPTPID\WPQGD *GKCRHGCPTLHYVD*LPLEKQ VILATALTMILHQADRLEVCPA FLGPEVTGELLWIPSKHQEPLC DLSSITNTSMDKCVFPMEGPIL MASPGTQTSGLLALWSVCYVL PPPSIVPQGD
22361	52729	A	22489	656	1495	TGDGELSWEHSDGDIFRQPANR EARHSYHRSHYDPPPSRQAGGL SRFPGARSHRGALMDSQQASG TIVQIVINNKHKHGQVCVSNGK TYSHGESWHPNLRAFGIVECVL CTCNVTKQECKKIHCPNRYPCK YPQKIDGKC*QNSTCFLIPEELP GQSFDNKGYFCGEETMPVYES VFMEDGETTRKIALETERPPQVI CSTFCLA\QGILQHFHIEKISKR MFEELPHGHFAFVCLLGQWKIF TEGEAQISQMCSSRVCRTELED LVKVLYLERSEKGHC
22362	52730	A	22490	1	477	
22363	52731	A	22491	1	294	
22364	52732	A	22492	56	4042	VFFTSMGEHLQKLIPASPACLA* IPQACQP*PPTPPAWQCRNLR/L AASRHQEPRGEVGGPLGHGAE RILAVPVRTDAQGRLVSHVVSA ATSRAGVRARRAAPVRTPSFPG GNEEEPGSHLFYNVTVFGRDLH LRLRPNARLVAPGATMEWQGE KGTTRVEPLLGSCLYVGDVAG LAEASSVALSNCDGLAGLIRME EEEFFIEPLEKGLAAQEAEQGR VHVVYRRPPTSPPLGGPQALDT GASLDSLDSLSRAL

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22365	52733	A	22493	173	1148	QALGLPSLLAVLALSTTDRASF SAVISRSPQRTVSSTRKEQRPLV FAFSALRLGTNACKMDGFCSTF LGAPGIRLKLLTPAGTHKSERD RTATPTRHHEKRLFCSSLSIGRQ AEEAWRADHPLPESRLFGLVPL GGAAWCRLAGSFCVCSLRLPRP IELVRAASGALLGAVRRRNHGP PHCFSTATLLCKAYRGGHLTIR LALG\GAPNRPFYRIVAAQNKC PRDGPFP*SKLGPPYDP/LLPPNS HGEKTPCPLN\LDRI\RHWIG\CG APPLLSPMEKLLGLAGFFP\LHP\ MMITNAERLRRKRAREVLLAS QKTDAEATDTEATET
22366	52734	A	22494	2	4985	AGATTALELPGQPSVTGVPELP GLPSATRALELSGQPVATGALE LPGPLMAAGALEFSGQSGAAG ALELLGQPLATGVLELPGQPGA PELPGQPVATVALEISVQSVVT TSELSTMTVSQSLEVPSTTALES YN/DERSMMSSYERSMMSYER SMMSPMAERSMMSAYERSMM SAYERSMMSPMAERSMMSAYE RSMMSAYERSMMSPMADRSM MSMGADRSMMSSYSAADRSM MSSYSAADRSMMSSYTADRSM
22367	52735	A	22495	18	174	ALIKKHFIF*IAAAKPTPPKSQV TLTKEFPVSSGSQHRKKEADSV YGEWVL
22368	52736	A	22496	3	595	IKKHFIF*IAAAKPTPPKSQVTLT KEFPVS\SGPQHRKKEADSVYG EWVPVEKNGEENKDDDNVFSS NLPSEVSRRNIMYFSFFIPESAH FIVMLCLIWDSVSLFLRAGVKR QGRV*DGQM\KQPAASH\LTVT RM/CNSLCG\TKATKWKRLRFA ENSVI\TSLPNIGPSLHLWEGSP WYSIPFSFPSLLLLKVGEVEFKR

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22369	52737	A	22497	3	5618	SSELPGPSVTPVPQLSQELPGLP APSMGLEPPQEVPEPPVMAQEL PGLPLVTAAVELPEQPAVTVA MELTEQPVTTTELEQPVGMTTV EHPGHPEVTTATGLLGQPEATM VLELPGQPVATTALELPGQPSV TGVPELPGLPSATRALELSGQP VATGALELPGPLMAAGALEFS GQSGAAGALELLGQPLATGVL ELPGQPGAPELPGQPVATVALE ISVQSVVTTSELSTMTVSQSLEV PSTTALESYNTVAQ
22370	52738	A	22498	1	4685	MAPESHILASNTMETHILASNT MDSQMLASNTMDSQMLASNT MDSQMLASSTMDSQMLATSSM DSQMLASNTMDSQMLASNTM DSQMLASSTMDSQMLATSSMD SQMLATSSMDSQMLATSTMDS QMLATSSMDSQMLATSSMDSQ MLATSSMDSQMLATSSMDSQM LATSTMDSQMLATSTMDSQML ATSSMDSQMLASGTMDSQMLA SGTMDAQMLASGTMDAQMLA SSTQDSAMLGSKSPDPYRLAQD PYRL
22371	52739	A	22499	291	7655	KRAPEKVDAYLYKQILLMKLP TKKSKKHKKHKNKKKKKKKE KEKKYKRQPEESESKTKSHDD GNIDLESDSFLKFDSEPSAVALE LPTRAFGPSETNESPAVVLEPPV VSMEVSEPHILETLKPATKTAE LSVVSTSVISEQSEQSVAVMPEP SMTKILDSFAAAPVPTTTLVLK SSEPVVTMSVEYQMKSVLKSV ESTSPEPSKIMLVEPPVAKVLEP SETLVVSSETPTEVYPEPSTSTT MDFPESSAIEALR

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22372	52740	A	22500	90	2166	SQHFGRLRRVDYLRTSKMQTSS SRSVHLSEWQKNYFAITSGICT GPKADAYRAQILRIQYAWANS EISQVCATKLFKKYAEKYSAIID SDNVESGLNNYAENILTLAGSQ QTDSDKWQSGLSINNVFKMSS VQKMMQAGKKFKDSLLEPALA SVVIHKEATVFDLPKFSVCGSS QESDSLPNSAHDRDRTQDFPES NRLKLLQNAQPPMVTNTARTC PTFSAPVGESATAKFHVTPLFG NVKKENHSSAKENIGLNVFLSN QSCFPAACENPQRKSFYGSGTI DALSNPILNKACSKTEDNGPKE DSSLPTFKTAKEQLWVDQQKK YHQPQRASGSSYGGVKKSLGA SRSRGILGKFVPPIPKQDGGEQN GGMQCKPYGAGPTEPAHPVDE RLKNLEPKMIELIMNEIMDHGP PVNWEDIAGVEFAKATIKEIVV WPMLRPDIFTGLRGPPKGILLFG PPGTGKTLIGKCIASQSGATFFSI SASSLTSKWVGEGEKMVRALF AVARCQQPAVIFIDEIDSLLSQR GDGEHESSRRIKTEFLVQLDGA TTSSEDRILVVGATNRPQEIDEA ARRRLVKRLYIPLPEASARKQI VINLMSKEQCCLSEEEIEQIVQQ SDAFSGADMTQLCREASLGPIS AV/SQTADIATITPDQVRPIAYID FENAFITVRPIVSPKDL*LYENW
22373	52741	A	22501	3	523	FFFFFPAFKMSKRG\RGWVPSG CRKFPDFPLGLP\VGTL*SNWCL TNT\GAQKTLYI\ISREGGIKGTG LTRLPRLPGVG\DMVMAHSSRK ANPELQKKGYIPA\VVIRQRKVI TVGKRWRCFFIFED\NAGVIGD\ NKG\EMKGFAITG\PRAKECAD LWPRDCIQMLGSIAWFSQYIL

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22374	52742	A	22502	3	946	GPSASVSFWLWSQQHSPRIRHP RPGERRRLLHGIPHPTAEKQPA PLRPERRGGRRRRPAGRRGCA* /GGARPCSSRSS*PASTPAPRAA PPCRSPCSARPRTGPRTGAGRPR AP/HDGPPCATPDPRDQAS\PLPP RGPRPRVAPGSP\PEGHPRELPS EGSPGPRAPGQRHVRPPRAVLR PRGLRGGGCPGPAHPAPRLQRR RAPGEAAAPGPRWPGRPGRGR AQALVPAARSRCFWKLWEAVF CLPVAAAPTRRFGARQRPQLW LHGHKGGQVGEVSSHSAGEEH LVPHAAPKRAREPHGRSGSPGG IASSWQDGS
22375	52743	A	22503	34	823	
22376	52744	A	22504	424	2339	LLRGTLQSYAWTSVIPDIATELR DAPEKTLACMGLAIHQVTICLM HTFV*TFLMFAHTCTPCLTMVN VPHIHAR*GI*CIKVLLRMGH*R PFKNENAHRGTVVRVSNIKPLC TKMAFLCAACGEIQSFPLPDGK YSLPTKVIRSLTASLFILVKKAN QNTENISRQSIK*AIRLLHKRQA LDVTLLRKSIILLHDLVDSCVPG DTVTITGIVKVSNAEEGRVQLF SLFVSQ**FINVHLF*DAPPHILV VGDPGLGKSQMLQVDNQSFSV CSFACKMR**FTSEFSPLSKDSS SGDFALEAGALVLGDQGERPK GIISDSGTF*KAFSFSVNFLSISL AKAGVVCSLPARTSIIAAANPV GGHYNKAKTVSENLK*VSSNIY TFNVLNHFNSIRKRNSSHLLSEH VIAIRAGKQRTISSATVARMNS QDSNTSVLEVVSEKPLSERLKV *MFLLLIQFGSV*MSKFSVWLIV DVYPRLSTEAARVLQDFYLELR KQSQRLNSSPITTRQLESLIRLTE VCFFLWSCFFWLKGEGCALTSL LKYR*DKNFKLF*MKYQLSSHL KLGNRPNRSTAKRFISALNNVA ERTYNNIFQFHQLRQIAKELNIQ VADFENFIGSLND\QGYLLKKG PKVY\QLQTM
22377	52745	A	22505	73	214	
22378	52746	A	22506	1	503	

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22379	52747	A	22507	3	1000	ESKLEGKAAQDIKDEEPGDLGR PKPECEGYDPNALYCICRQPHN NRFMICCDRCEEWFHGDCVGIS EARGRLLERNGEDYICPNCTIL QVQDETHSETADQQEAKWRPG DADGTDCTSIGTIEQKSSEDQGI KGRIEKAANPSGKKKLKIFQPG PGPVPTQLPVLWQVLEIAVSRSI SAFTLLHCISCKVIEAPGASKCI GPG\CCHVAQP\DSVYC\SNDCIL KHAA\ATMKFLSSGKEQKPKPK EKMKMKPEKPSLPKCGAQAGI KISSVHKRPAPEKKETTVKKAV VVPARSEALGKEAACESSTP\S WAS\DHNYNA\VKPEKTAAPSP VTVV
22380	52748	A	22508	1	2330	MAAAEGKERAGGRASGRGRSE PPRPGARASDAGPGGLREVEGT GEHSVVAAGTVPRVGVGAAAR GEERRAGLGECGPGLGGCVAG LISGKSVQAFSVGAGRWPLLRV FGGNVTFCSVVSWSLCAYTLPL GMDDKGDPSNEEAPKAIKPTSK EFRKTWGFRRTTIAKREGAGD AEADPLEPPPPQQQLGLSLRRS GRQPKRTERVEQFLTIARRRGR RSMPVSLEDSGEPTSCPATDAE TASEGSVESASETRSGPQSASTA VKERPASSEKVKGGDDHDDTS DSDSDGLTLKELQNRLRRKREQ EPTERPLKGIQSRLRKKRREEGP AETVGSEASDTVEGVLPSKQEP ENDQGVVSQAGKDDRESKLEG KAAQDIKDEEPGD\LGRPKPEC EGYDPNALYCICRQPHNNRFMI CCDRCEEWFHGDCVGISEARG RLLERNGEDYICPNCTILQVQD ETHSETADQQEA*MGDLGDA\D GTDF\TSIGNIRSRSLSRRPKGLK GRIEKAANPSGKKELKIF\QPVL EIAVSRSISAFTLLHCISCKVIEA PGASKCIGPGCCHVAQPDSVYC SNDCILKHAAATMKFLSSGKEQ KPKPKEKMKMKPEKPSLPKCG AQPVQWLLLLSSWQLGTSSGL QVTLCQPPFTEHKWLKFSVLHG ETAGPPRAHRIRKLNKYWGAC HHCMPLRPLPCLPGWPRSSPSL

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22381	52749	A	22509	149	2001	IQPPDPRNMTLAAYKEKMKELP LVSLFCSCFLADPLNKSSYKYE\ AGVGDSVGGRMKASGKTVLT GRERRAQADTV\DLNWCVISD MEVIELNKCTSGQSFEVILKPPS FDGVPEFNASLPRRRDPSLEEIQ KKLEAAEERRKRGPDLVIYEIH SPASLPFHSSDASVLGDIPPTTY SNISNSNQELLLMGGSPAPEQP HYEANILERSETTSYDNGSDAA QSFKVDGRCVFYINIPIPSNEGK VLWKAPEIATAKEPTWSPLGST GPRPCQILVVKSPVVHGKGPVL SGCGLDLLEQPTFALCFLVAGA VTITFLSCSGEEAREESAPKAMS ERQARRGGAEKQGAEGRGLQA VTTPELPYRMGLGAAFLLKERS GVLPGSFICEDFTAALKQDEEIG TMKGKIREAYFKSFVPTPVAFS GGVMLPTGGTLEMCGNNFGGH KEQAGTVLPAFAIALRVTPSAS LVLRPLNLDQAMLQGSLGLQL ADGLFWDLASIMDWTASRIQPS VSSSMKICQAFPGRPLAILLAQC AYVYGTWMKLEAIILTKLTQE QKTKHHLFSLPCCMPADISYRQ RCLGEPPHCTVWNRHLESLVM MSNSTTSPCSELLIFEVPPVAPE
22382	52750	A	22510	373	990	IQPPDPRNMTLAAYKEKMKELP LVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVIFRHWKVIE\LN KCT/SGANSFEVILKPPSFDGVP EFNASLPRRARPIPWEEIPVRKL GRRLRERREVTREADP*KQLAE KR\EHEERGDSKRAFRETTTFIK MAK/EKNLAQKMESNRENREA HLAAMLERLQEK\DKHAEEVR KNKELKEEASR
22383	52751	A	22511	524	1107	LCSPKVLGLNASCQKNFLKQK KSIKTLSTSQ/YSVSGYSLARSE NAHPEFRMAMKDGELVIWDSV HPCYTVFHEQTETFSSLWSEYH DDFRQFLHIYSQDVACYGENLA YFPKGFIENMFFVSANPWVSFT SFDLNVANMDNFFAPVFTMGK YYTQGDKVLMPLAIQVHHAVC DGFHVGRMLNELQQYCDEWQ
22384	52752	A	22512	1	1413	
22385	52753	B	22513	1	2787	
22386	52754	A	22514	1	1638	

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22387	52755	A	22515	71	2421	YTVCYFLQAAEEDETQNQHDD SSSDSGTPSGPDFNYILNMSLW SLTKEKVEELIKQRDAKGRE\V NDLKRK\SPSDLW\KEDLAGIC WRDWDKV/ENSPRNEEDVLAG MSGKSNLKGKVGKP\KVKKLQ LEETMPSPYGRRIIPEITAMKAD ASKKLLKKK/KGVDLDTAAVK\ VEFDEEFSGAP\VEGAGEEGIDS HQFPINK\GPKP\RREKKEPGS\R VRKTPTSSGKPSAKKVKKRNP WSDDESKSESDLEETEPVVIPR DSLLRRAADIHRLGGEGFDAGL TVFAPLFASPFPPRGAPYLKAA CQTPRSGIGATAISGEALKGAV SSGVDPRWASHLRVKLLEKSFS LQEIQSTEKVLSQQAKTLSLLG EPKLSKQLTGTCIYRKTNLALC RGPAAAKSLFQGAVRNDRNKK KKETSKQECTESYEMTAELDDL TEKIRKAHQETFPSLCQLGKYT TSLQKGMQRCQILDLSSVRPIV DVRPPELQDSKLVLVQAAKCA PLADHCSKPVLLKEGPEDQKD QHDVGDCWNPECQTLFDQNN AAKKEESETANKNDSSKKLSVE RVYHIKTQLEHILLRPDTYIGSV EPLSKVAEEGPAAVGGWKGWF GTESRKDPKPTGTEEVERGVW LSGREGRLLSPSVVTTMVLAEN SAIRFVGGKPSSDTVPKPKRAP KQKKVVEAVNSDSDSEFGIPKK
22388	52756	A	22516	1424	4860	GRDRYGVFPLRGKILNVREASH KQIMENAEINNIIKIVGLQYKKS YDDAESLKTLRYGKIMIMTDQ DQDGSHIKGLLINFIHHNWPSLL KHGFLEEFITPIVKASKNKQELS FYSIPEFDEWKKHIENQKAWKI KYYKGLG\TSTAKEAKEYFA\D MERHRILFRYAGPEDDAAITLA FSKKKIDDRKEWLTNFMEDRR QRRLHGLPEQFLYGTATKHLTY NDFINKELILFSNSDNERSIPSLV DGFKPGQRKV
22389	52757	A	22517	87	292	
22390	52758	A	22518	1	903	
22391	52759	A	22519	3	311	

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22392	52760	A	22520	1	1087	MPSAAWKRPVEGPATLRRPLGI AAASQCPSSPQPGCLIGAVNLK SSNRTPVVQEFESVELSCIITDS QTSDPRIEWKKIQDEQTTYVFF DNKIQGDLAGRAEILGKTSLKI WNVTRRDSALYRCEVVARNDR KEIDEIAIEVTVQVKPVTPVCR VPKAVPVGKMATLHCQGE*GP PPA\HYSWYRNDVPLPTDSRAN PRFRNSSFHLNSETGTLVFTAV HKDDSGQYYCIASNDAGSARC EEQEMEVCHTDKRGGFPWSW AAPHLWFLQDTALLPAALTGW CSVSVAFPGAQCKLSVDLSFWG LEDGGPLLTAPLGSTPVGTLCR GSDPTFPFCTALADDLYESPTPA ANFCLDIQAFSYIL
22393	52761	A	22521	628	1117	FFISVINGQVSSVQRLSGVGPAC LSCGSANPGPPPGTSPGAGAQR R*\PRADGSGSPQWPRGARVGG GRLGTGGRGRPGWRQVPRRLS PGFGR*GGTGPGPVGTSGKRGP SRRRAPANDKAACWPRFPGQP AS*TGFRGERGVKGFSSWGSG WRAWEDGGTVH
22394	52762	A	22522	2	238	
22395	52763	A	22523	131	2891	
22396	52764	A	22524	131	3103	LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDPIVASEE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTTSTIIT TTVITTEQAP

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22397	52765	A	22525	474	2527	SASPLGPYLLPSGAPERGSPGKE HPEERVVTAPPSSSQSAEVLGE LVLDGTAPSAHHDIPALSPLLPE EARPKHALPPKKKLPSLKQVNS ARKQLRPKATSAATVQRAGSQ PASQGLDLLSSSTEKPGPPGDPD PIVASEEASEVPLWLDRKESAV PTTPAPLQISPFTSQPYVAHTLP QRPEPGEPGPDMAQEAPQEDTS PMALMDKGENELTGSASEESQ ETTTSTIITTTVITTEQAPGMQPP TPMGEGPPIVKHTWILDKCNVA TLQST*ALGPNEGYIDSSDYPLL PLNNFLECTYNVTVYTGYGVE LQVTPGEYPDGELLSIRGVDGP TLTVLANQTLLVEGQVIRSPTN TISVYFRTFQDDGLGTFQLHYQ GRVRPRLFPRRPDSGDVTVMDL HSGGVAHFHCHLGYELQGAK MLTCINASKPHWSSQEPICSGM LQPQPHNATIGRVLSPSYPENT NGSQFCIWTIEAPEGQKLHLHF ERLLLHDKDR*SSEGPQTNKSA LLYDSLQTESVPFEGLLSEGNTI RIEFTSDQARAASTFNIRFEGEG PWELYEPYIQNGNFTTSDPTYNI GTIVEFTCDPGHSLEQGPAIIECI NVRDPYWNDTEPLCRGERIHN ASAVAGVVLSPNWPEPYVEGE DCIWKIHVGEEKRIFLDIQ/FVS V*NGSVFSQEKVRPTPEWW
22398	52766	A	22526	131	3125	LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDPIVASEE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTTSTIIT TTVITTEQAP
22399	52767	C	22527	161	352	
22400	52768	A	22528	2	368	LGSTHASVRINILSVDVLYFIFY RRDDNKDIDSEKEAAMEAEIKA ARERAIVPLEARMKQFKDMLL ERGVRKQSLGEIFLFCISNINMS C*KVKSKVSAFSTWEKELHKIV FDPRYLLLNLI

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22401	52769	A	22529	2	614	KDHRWESGSLLEREEKEKLFNE HIEALTKKKREHFRQLLDETSAI TLTSTWKEVKKIIKEDPRCIKFS SSDRKKQREFEEYIRDKYITAK ADFRTLLKETKFITYS*FSERCE SESL*KMLGLAAPQTEVLCSST E\RSKKLIQESDQHLKDVEKILQ NDKRYLVLDCVPEERRKLIVAY VDDLDRRGPPPPPTASEPTRRST
22402	52770	B	22530	201	296	
22403	52771	B	22531	1	1290	
22404	52772	A	22532	3	3369	SSSVMAERGGVGGESERFNPGE \LRMAQQQALRFRGPAPPP\NA AMRGPPPLMRPPPPFGMMRGPP PPPRPPFGRPPFDPNMPPMPPPG GIPPPMGPPHLQRPPFMPPPMSS MPPPPGMMFPPGMPPVTAPGTP ALPPTEEIWVENKTPDGKVYYY NARTRESAWTKPDGVKVIQQS ELTPMLAAQAQVQAQAQAQA QAQAQAQAQAQAQAQAQAQA QAQAQAQAQAQAQAQAQAQA QAQAQAQAQAQVQAQVQA
22405	52773	A	22533	43	347	
22406	52774	A	22534	1	1776	
22407	52775	A	22535	3	433	PLAPNHLGGGAVVLGAESHAS KDVAIDMMDSRTSQQLQLIDE QDSYIQSRADTMQNIESTIVELG SIFQQLAHMVKEQEETIQR*DR VNSAHPWDPVHLLPSTQQVFIE HLFM
22408	52776	A	22536	304	1403	SRGNATGLRTRIRVSTWVSQRH RSCPLQLLAVAAATSSPLPPPVT LVPPPPDTMSCRDRTQEFLSAC KFAARPVKNGI\QTN*GQLLRW LVRQRSEIHPSLAKRHLGKDLS NTFAKLEKLTILAKR\KPLFDDK AGEIEELTYIIKQDINSLIKQIAQ LQ\DFVRAKG\SQSGRHLQTHS NTIV\VSLQSKL\ASMSNDFKSV L\EVRDRGTLKQ\QREPEERQFS RAPV\SALPLSPTHRAGGA\VVL GAESHASKDV\AIDMM\DSRTS QQLQLIDEQDSYIQSRADTMQN IESTIV\ELGSIFQQLAHMVKEQ/ ERETIQRIDENVLGAQLDVE\AA HSEILKYFQSVTSNRWLMDKIF LILIVFFIIFVVFLA
22409	52777	B	22537	147	506	

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22410	52778	A	22538	2	1397	AAPGNGLSPSSWRSELACEFQH ECTAEVRFGAVVCRGARSHSFY LEREILQ/PPGMSL/PENPVTPML RHLMYKIKSTGPITVAEYMKEV LTNPAKGYYVYRDMLGEKGDF ITSPEISQIFGELLGIWFISEWMA TGKSTAFQLVELGPGRGTLVGD ILRVFTQLGSVLKNCDISVHLVE VSQKLSEIQALTLTKEKVPLER NAGSPVYMKGVTKSGIPISW*S RICTD\VPKGYSFYLAHEF\LDV LPVHKFQKTPQGWREVFVDIDP QVSDKLRFVLAPSATPAEAFIQ HDETRDHVEVCPDAGVIIEELS QRIALTGGAALVADYGHDGTK TDTFRGFCDHKLHDVLIAPG\T ADLTADVDFSYLRRMAQGKVA SLGPIKQHTFLKNMGIDVR/L*R FF*INQMRPSVRQQLLQGYDML MNPKKMGERFNFFALLPHQRL QGGRYQRNARQSKPFASVVAG FSELAWQ
22411	52779	A	22539	2	377	
22412	52780	A	22540	2	1427	
22413	52781	A	22541	2	568	CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVVPNPYTL LSQIPEEAESFTVLDLKDAFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPQGFRDSPHLFGQAQAQ DLVHFSSPGTLVVQYMDDLLL ATSSEASCQQATLDLLNFLANQ GCKRVGIALGVLTQTHGTTPQP VAYLSKETDVAAK

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22414	52782	A	22542	1	1230	GPRGTGPKGKARSEKGCSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIIYMNMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAEWFP VLDLKDAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGLILARGTRTL GKERIQPILAYPHPKTLKQLWG FLQIT/GFCQLWIPR*SKI
22415	52783	A	22543	1	211	
22416	52784	A	22544	1	472	
22417	52785	A	22545	1	393	
22418	52786	A	22546	59	411	SWPSDKQTLVVQRGQKMEQA NHPDPTDHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLALLNFLANQGYK/LSRSK AQLCLQQVKYLCL
22419	52787	A	22547	43	236	TSSLLRKEDSAPSQGKSVVFTL TSQG*VPLWRTLQLQGPFFTPSS RK*LELSSANSQQHLGCPV
22420	52788	A	22548	1	1446	
22421	52789	A	22549	1	1521	
22422	52790	A	22550	2	689	
22423	52791	A	22551	1	64	
22424	52792	A	22552	636	1586	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKDAFFCIPLHSDSQFLF AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQAQDLGHFSSPG

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22425	52793	A	22553	292	1493	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKDAFFCIPLHSDSQFLF AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQAQDLGHFSSPG TLVLQYSEIAKTLYTLIKEMER ANTHLVEWEPEAETAFETLKQ ALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTTPQPVAY
22426	52794	A	22554	2	307	
22427	52795	A	22555	3	400	
22428	52796	A	22556	2	78	
22429	52797	A	22557	395	1336	SNNRTEGASSCH\PLTEPQVCLT IEGQEIDFLLDTGTAFSVLISCPA WGTGQDSVSKKNEKKRKEKA KGNHQANAEAKIAARWNPSLE IPTEGPLVWNNPLQEIKPQYSLT ETEWGLSQGHSFLPLGWLMTE EVKVLIPEASQWKILKTLHQTF QMGIENTQQMAKSLFTGPNLL WTIRHVVKACEVCQRNNPLVH HKAPLGEQRIGHYPGEDWQLD FTHMPKSKGFQYLLVCVDTFT NWIEAFPCKIEKAQEVNKVLIH ETIPRFGLPQSLQSDNDPAFKA MITQGIFQGAKDTISPSLCLEATI LREGREGN
22430	52798	A	22558	244	638	GPLNPTFLGPPCGLGGKLVFLL LRQ*VQLFRSAGSRDRCGFLDR ERNKTNQNCGKQAKKSPKDHK NPRAVGYVPFNL*QEGNLAQP GYMSPSPSLI*SRSRQTWGSFQ MILIGTKRNRPKRKSEIRERLQP
22431	52799	A	22559	210	600	RGKRTWRERRNGWSRGFCPLP LTGSWLISRESPRLACLGEGLG VPGM*DLPHAWPTTLMCPELV GSWSH*LQE*SHGPSQ*VLQLL RWCVWSLFLLMFGCVWSFFLL VSSWSRWLRSEATDLCGECYSS

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22432	52800	A	22560	2746	5211	ETSCPLVRVHYAEAITGRCTAP EDEGSLGQKPPARRSNNRTEGA WGKRQLMSSP/STEPRVCLTIEG QEIDFLLDTGAAFSVLISCPGRL SSTSVTIQGILGQPVTRYFSHLL SCNWETLLFSHAFLLMPERPTG LLGRDILAKAGAIIYMNMGNKL PICCP\LLVEGINPEVWALEGQF GRAKNARPLQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAEWSWAL TFKDAFFCIPLHSDSQFLFAFED PTDHTSQLTGTVLPQGFRDSPH LFGQALAQDLGHFSNPGTLVLQ YVDDLLLATSSEASCEQATPDL LNFLTNQGYKVSRLKAQLCLQ EVKYLGLILARGTRALSKE*IQP ILAYPHPKTLKQLRGFLEITGFC *LWIPGYSKIARPLYTLIKETQR ANTHLVEWEPEAETTFKTLKQ ALVQAPALSLPTGQNFSLYVRE RARIALGVLTQTHGTTPQPVAY LSKEIDVVAKGWPHCLRVVAA VAVLASEAIKIIQGKDLTV*TTY DVNGILGAKGSLWLSDNCLLR YQALLLEGPVLQICTCMALNPA TFLPEDGEPIKHDCQQIIVQTYA ARDDLLEVPLTNPDLNLYTDGS SFVENGI/RKVSDVTILESKPLPP GTSAQLAELVALTWALELGKG
22433	52801	A	22561	903	4440	DHPGHIHSSPCHERPNNVSTLPF LPGEQHPILLPPRNCPGDKILEE NFRYNNYKRTMMSFKERLENT VERCAHINGNRPRQSRGFGELL STAKQDLVLEEQSPSSSNSLENS LVKDYIHYNGDFNAKSVNGCV PSPSDAKSISSEDDLRNPDSPSS NELIHYRPRTFNVGDLVWGQIK GLTSWPGKLVREDDVHNSCQQ SPEEGKVEPEKLKTLTEGLEAY SRVRKRNRNGIKVPPRSPRSTIG SPRPSMPSSPS
22434	52802	A	22562	1	501	

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22435	52803	A	22563	1688	2038	SATHGLSDSCYWLVVSRAIGRN NLSPASPASIIHALVFLAEPQLF QPRILGLIDEESGHEGGRPAAKT RKLSGPWSRPAAFMSTLLINQP QYAWLKELGLREENEGVYNGS WGGRGEVITTYCPANNEPIARV RQA\SVADYEETVKKAREAWKI WADIP\APKPKEKLVRQIG\DAL REEDSKLLRKPWCPLEDWGKIL LEGVGEVQEYVDICDYAVGLS RMIGGPILPSERSGHALIEQWNP VGLVGIITAFNFPVAVYGWNN AIAMICGNVCLWKGAPTTSLIS VAVTKIIAKVLE\DNK\LPGAICS LTCGGADIGTAMAKDERVNLL SFTGSTQVGKQVGLMVQERFG\ RHYQNWRSLLELGGNNAIIAFE DADLSLVVPSALFACCGEQLGQ RCTT/SRGRLFYYMESIHDEVFK QTLKRAYGTRSRVG\NPW\DPN VLYGAISHQGRQLSMFLGAVEE AKKERLAQWVYGGKVMDRPG N\YVEPTNVTS\LDHDASIAHTE TFAP\ILYVFK\FKNEEEVFAWE* WK*NRGLSS*HSLPKDLGAESF RW\LGP\KGTQTCG\IVKCQPFPT KWGLRLGGA\FGGEKAHLVVA RESGQ*C/WGKQYMRKVYLVL FNYS\KDLPSGPQG\IKFQ
22436	52804	B	22564	1	1434	
22437	52805	B	22565	1	1185	

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22438	52806	A	22566	1	2450	GQACHASSSPLKGSRGSPPNFEI LYGPIFEDSLAPD*PKVIAGQ\IT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLFDFALYFFHNYQA LLAKGSGPYFYLPKTQSWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDEILHALR DHIVGLNCGRWDYIFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTCHKRGAFAMGGM AAFIPSKDEEHNNQVLNKVKA DKSLEANNGHDGTWIAHPGLA DTAMAVFNDILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKGQSQNLWKFA VYSGLRHGELAALAWEDVDLE KGIVNVRRNLTILDMFGPPKTN AGIRTVTLLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFIA SQMGHETAQMVYEIYGMWID DMSDEQIAMLNARVMVYDVA SGNALFISELGPLPENVTWLSPE GEFQKWNGTAWVKDTEAEKL FRIREAEETKNNLMQVASEHIA PLQDAADLEIATEEEISLLEAW KKYRSIPLCSKVVTMMFDDRP GCPVGFPMWGRGGFDRMPPG WGGRPMPPSRRDMSPHRGPPPP
22439	52807	A	22567	1	941	MIPNVQGPMRGLEGPNYIFIKIS KNRRYTMAVTSVGLASSLCRV VRPCRAPAGVVSRGSPDDEWL FCPQARIQQQQDID/NGTLPDFIS ETASIRDA/DWKIRGIPADLEDR RV/EITGPVERKMVINALNAI\F MADFEDSLAPDW/NKVIDGQIN LRDAVNG/TISYTNEAGKIYQL KPN/PAVLICRVRGLHLPEKH/V TWRGEAIPGSLFDLA/LYFFHNY QALLAKGSGP/YFYLPKTQSWQ EAAWWS/EVFSYAEDRFNLPRG T/IKATLLD*TLAGGFQMVDPSA LGG*TGPWDHLRYIKVENIPKV GEEGDAETTGGTAV
22440	52808	A	22568	2	393	
22441	52809	A	22569	1066	1824	
22442	52810	A	22570	2	165	
22443	52811	A	22571	3	902	

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22444	52812	A	22572	1	2034	
22445	52813	A	22573	176	873	RLFGEMSKLN/HNLSEVMSKLE KQHSSKVFVVKRLSSSSRRSLVI SPPVRTSTVSSPLTSPTSPSTLSS KSKSESVSATEDLAPDAAQGED NSEIKELLEDEEIGKEGSEASSS EEEEPLLTCNGPSQAQPSPIIESA RSQEEVPPSSPALSPGGALSPSG HPLSSAAEVVLRTRTAVPQAKG NNVVITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QGQLTVN
22446	52814	A	22574	1	1890	
22447	52815	A	22575	2	1279	LSVFPRVRNFTTQAECH/KLFK VLKNFLIAGGGVHESSKRAS*T LQFIYY\SEWYGHEELKAIVWN NDLLWEDYEEKLADQAVRTM EIYVAQFSEIKERIAKRGRKLVD YDSARHHLEAVQNATKKDEAK TAKAEEEFNKAQTVFEDLNQEL LEELPILYNSRIGCYVTIFQNISN LRDVFYREMSKLNHNLYEVMS KLEKQHSNKVFVVKGLSSPSTL SLKSESESVSATEDLAPDAAQG EDNSEIKELLEEEEIEKEGSEASS SEEDEPLPACNGPAQAQPSPTT ERAKSQEEVLPSSTTPSPGGALS PSGQPSSSATEVVLRTRTASEGS EQPKKRASIQRTSAPPKPPEKPV RTPEAKENENIHNQNPEELCTSP TLMTSQVASEPGEAKKMEDKE KDNKLISANSSEKYIFQRPSVLI

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22448	52816	A	22576	1	1791	MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEKAL*KLG KAVETKDERFEQSASNFYQQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSETLQEIYSSEWDGHE ELKAIVWNNDLLWEDYEEKL\ ADQAVRTMEIYVAQFSEIKE\RI AKRGRKLVDYDSARHHLEAVQ NAKKKDEAKTAKAEEEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMSKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPTSPSTLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEEDEPLPA CNGPAQAQPSPTTERAK\SQEE VLPSSTTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPPRRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSPRAS LGTGTASPRTSLEI*PNPE\PPEK PVRTPEAKENENIHNQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE
22449	52817	A	22577	2216	2568	RPSLGLGM/C/TIWQ/TSLA/GKH RRTIETHTDDYRISLEQGTPGLE PPLNALTAISKKIGCNGFFPFQIR PGKNETDGRMFSPAIGIVEDPV TGNANGPMGAWLVHHNVLPH DGNVLRVKGH
22450	52818	A	22578	108	532	WGSKGNLLYSHQTHSVSHQFS LVACCLELEYSPFSFPYACLLSS LMRLEKHQELNLWPAHQRSMR HPQDTLVVFS/HHGRVLL*DKT SRGTIRQQHSRFTKICCSAATAA VTQANRVWSGPLANSNRPAAE GPVLAAFMGWL
22451	52819	A	22579	1	1125	

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22452	52820	A	22580	1	985	MCARGSLWGCYSGLERKCEAA LPDRVVSSKSACGAVSQDLLQ AQGRRAGPPSWLYADPVHTGT IECGGHWCLNAALLDFQSPQRL LTYLHCGLQRPMESDPPELAPM VHHQEGIYLNIRKAMYDKPTA NKLNWDKSNVSSLITGTRQEET TANGTTFATIHLQFFIQIPAVPR KTLLNRADYYFPEHNPSLTLVI NRRITKFSEPNWEAPPSRGRLTP HTAGYSSETKIPEERSDSSIRGS RKSAVLQPLLLDSQANRVWSG PLANSNRPAAEGPVC*LWWVT LHGPLKATMQVCQQPLW
22453	52821	A	22581	294	934	YPPSPAELTVCRLRQLQLRDVL YCIAYPSGPGVKPFRGNSA/G/V VFPADNLSEAQMQLI/ARELGH SETAFLLHSD/DSDVRI/RFTPTV EVPI/CGHATVAAHYVRAKVL/ GLGNCTIWQTSLAGKHR/VTIE KHNDDYRISLNALTAIS/KKIGC NGFFPFQIRPG/KNETDGRMFSP AIGIVE/DPVTGNANGPMGAWL VH/HNVLPHDGNVLRVRQ*GPR
22454	52822	B	22582	1163	5585	
22455	52823	A	22583	2	429	AACAAAMSLVIPEKFQHILRVL NTNIDGRRKIAFAITASSSSSSS SSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSVNLLSNGLYL/VKG VGRRYAHVVLRKADIDLTKRA GELTEDEVERVITIMQNPRQYKI PDWFL
22456	52824	A	22584	84	424	GVHAASDKPCWITTSQTPDVQ HRW/WLLISSML*TAPNRRSDK AFTPHPTNHAGSQLRKHPTCSI DGVIDIFHAVNTFVQHHMEETL KAFHVTGHHILIARHGLGVGKE NTEHAANVVNDQRNSGFFCRF QQTFCQTCCQLIQRFVNARLRD FISC
22457	52825	A	22585	88	381	IQVLANGLDNKLREDLERLKKI RAHRGLRHFWG*VGGLISLPTS TQHSSYSLFFFPNLLFLLCMTCD SSLFTCSLRVRGQHTKTTGRRG RTVGVSKKK
22458	52826	A	22586	355	699	FIDTTEAGSHFLYALVRFAATIT TITDDGARRLRTLFQRQQADLV SVSKSGFFTADCTHTNALIDVV RTIFNNAVF*NPGFVIARLKIEIA IIKATFGQLTEDREQVLMFQAV RR

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22459	52827	A	22587	1389	1532	SVLPGRPDARQYRQTRQSW*R WSLRLRGSYPVAGRSLSRRHRQ TERF
22460	52828	A	22588	1	427	LVHQQWIQTKKKSLIYPFCHSP SQRVVEVAALDQWLAMLYPR VEHQAVLAVVVVVVGPLVVRP YHTRRDAVRLLRQPAVFIVAV DIVRILRDAVIRPHCECTVRV\R SGSGSRLPAGSVAYGMRMSRS GARVRTLSILPVAL
22461	52829	A	22589	1	915	
22462	52830	A	22590	1166	1321	
22463	52831	A	22591	813	977	
22464	52832	A	22592	3485	4237	
22465	52833	A	22593	1	499	ARAAACAAAMSLVIPEKFQHIL R\VLNTNIDGRRKIAFAITAIKG VGRRYAHVVLRKADIDLTKRA GELTEDEVERVITIMQNPT\QYK IPDWFLNRQKDVKDGK\FQPGS *ANGLSTTKL\RENLKPLKEDSG PIKGLRQLP/WGLRVRGQHTKT TGRRGRTVGVSKKK
22466	52834	A	22594	1	1197	
22467	52835	A	22595	1	1905	
22468	52836	A	22596	37	514	WTWWLRCYENRHRHCHLLQQ LPTSPHQHAVATPTTVAVPTAP AATPPVVVAVVVAPVVVVVVP VVPVVASVPFVEPGSDVIVCAE MDEQWGYVGAKSRQRWLFYA YDSLRKTVVAHVFGERTFDVVI WMTDGWP\LYESRPAFTGRDC VDDAFFAVAGV
22469	52837	A	22597	1	471	
22470	52838	A	22598	2	323	SRIQPGSDVIVCAEMDEQWGY VGAKSRQRWLFYAYDSLRKTV VAHV/FGERTIRTLTRRLFRCLR SSHDLVSSPVSHRRRRAGSRQR HRRARGGENVEYQWGALRHG
22471	52839	A	22599	2033	2310	ARYVGNAGCTGGALFGRSQTI REAVG/ERRLAESRDVAALDTP CDPEIKMAEWMQTLKETGSTS GHIVTRRISVRISHVTPGPASQD GPDVQQR
22472	52840	B	22600	1	4891	
22473	52841	B	22601	7	1233	
22474	52842	A	22602	193	492	
22475	52843	A	22603	1	486	

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22476	52844	A	22604	62	443	RSDRLLIHGFSFPAMGFRLRKT VVAHVFGERTMATLGRLMSLL SPFDVVIWMTDGWPLYESRLK GKLHVISKRY\TQRIERHNLNLR QHLARLGRKSLSFSKSGTACCG HCLTRDIPMLHHQGNQLF
22477	52845	A	22605	971	1444	SMGSGDMRSSPSRAAALRQLPR PFRQLAVRMEMISRFRSAKEQT KSLRKWRKAKSIF*SVAQTGFN VLVCTTIIETGIDSRQPTLLSLNA RITSVCAAAPVTRSRRTFASSGY AWLLTPHPKAMTTDAKNVLKQ LPRWKISGQVRAGTARSGDSRR W
22478	52846	A	22606	1	1047	
22479	52847	A	22607	318	598	LTGFRRLCDLRFGGGAVRSVLA RSREFILQH*FRRIVTGSMGRSL VPSAPLR/PSIVLVLFRKAW*LV KTQRKMHVVSIVQKKASCWYP LLGCL
22480	52848	A	22608	1	2652	
22481	52849	A	22609	1	852	
22482	52850	A	22610	1	807	
22483	52851	A	22611	1	1740	
22484	52852	A	22612	1	3144	

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22485	52853	A	22613	173	1983	PVQNGSSPLGALPGAPLIFGPSV PAISRPGSCSPEWPTLDTSGYSA PR/WLFTAYAGSEAVFAHVFGD ALGDAGLLMSLLSPFDVVIWM TDGWPLYESRLKGKLHVISKRY TQRIERHNLNLRQHLARLGRKS LSFSKSVEQHDKLESLPGQIDKS LDEASLSLRAGSLRTITHILLPLL RPAILSALIYSFVRAITTVSAIVF LVTPDTRVATAYILNRVEDGEY GVAIAYGSILIVVMLAIIFIFDWL IGESLLSRFEKTVDDHSQSRLPA EGSILSQDISGVKLFSLLTPARG YVPIRAPCPFLCASYRFFCVARQ QGLDAALIDAPLAVDALTPLSE LLSHVGQAPCSVPVVDEDQQY VGIISKGMLLRALDREGGVRVP VDYILNGFHPLLLGMPAPLAIIV FALIACRFPGSNGRIRRSRRIRH LHKMPDATLSASYQAYVRHQT NVTALVLRSSHRFRKDRHCWG FVFLQQPILRATGQFEIQTFRYL SVFSVQRHKTNGKTALMSGNV ADKAVNRATGPTACVWLFSLR NSSMVTTRFCGLCEWADQQGA RPARISENGKRGYSYLYDVHM GAQSGETRGRQGEYASKPPSRE
22486	52854	B	22614	1	2149	
22487	52855	A	22615	1	1815	
22488	52856	A	22616	2014	3411	
22489	52857	A	22617	1	922	MVICQPINGGWQWPPSTGTDP APYFRIFNPTTQGEKFDHEGEFI RQWLPELRDVPGKVVHEPWK WAQKAAAPPQTRLHSTPTTIPH RVPGHTPNLKPIWEVDLPKFSH KATSHATDKPSDTTQNDQIVIA YMEPPEIVHETTTSSTHPSLYIIL KRQTRELRPQSVTSRIQPGSDVI VCAEMDEQWGYVGAKSRQRW LFYAYDSLRKTVVAHVFGERT MATLGRLMSLLSPFDVVIWMT DGWPLYESRLKGKLHVISKRYT QRIERHNLNLRQHLARLGRKSL SFSKSVELHDKVIGHYLNIKHY

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22490	52858	A	22618	1458	2185	YGHEWRWMPGNRPH\YGRWP QHDFPPFKKLRPQSVTSRIQPGS DVIVCAEMDEQWGYVGAKSR QHWLFYAYDRLRKTVVAHVF\ GERTMATLGRLMSLLSPFDVVI WMTDGWPLYESRLKGKLHVIS KRYTQRIERHNLNLRQHLARLG RKSLSFSKSVEKITSGPTTNATP GTQKTATDKRGGKKLPIQIPIGP ISRIASGAAINTISIGLRKFLVTA GVMLSTQRSIYDRHQVITSAGIT
22491	52859	A	22619	493	1518	
22492	52860	A	22620	963	1597	
22493	52861	A	22621	1	3052	MATDSVGLNCTPAPHARDVLL WRPSSLPVSTSCVFPLGRIGDVS DESDDKTEAPTPHRLEKAREEG QIPRSRELTSLLILLVGVSVIWF GGVSLARRLSGMLSAGLHFDH SIINDPNLILGQIILLIREAMLAL LPLISGVVLVALISPVMLGGLVF SGKSLQPKFSKLNPLPGIKRMFS AQTGAELLKAILKTILVGSVTG FFLWHHWPQMMRLMAESPITA MGNAMDLVGLCALLVVLGVIP MVGFDVFFQIF
22494	52862	A	22622	1	1233	MANDLPHSNSGDGQKPSSPDLF TAPLLADPTVGFLPNDAEELFIF LTEITEITIPCRVTDPQLVVTLHE KKGDVALPVPYDHQRGFSGIFE DRSYICKTTIGDREVDSDAYYV YRLQAVPPVQLLTGWCVTAKA PPDISAISALTAVKHGNCSSLTP LLNPPGSDVIVCAEMDEQWGY VGAKSRQRWLFYAY\DSLRAR RVVAHVFG*RTMATLGRLMSL LSPFDVVIWMTDGWPLYESRL KGKLHVISKRYTQRI\ERHNLNL RQHLARLGRKSLSFSKSVELHD KPSPQHREGVKDVMRFNEPMY PLESRPRLYVCHLRNGAQASGR RCQLPMGCACHPVSQRNDRPN RRPERHATRKTTTRQRQQNSRQ HKQTQKKAKPNKRRATERGKG PQQKAERPKRHTHCFLKLQ

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22495	52863	A	22623	3	1386	HEASSPLAMASLTVKAYLLGK EDAAREIRRFSFCCSPEPEAEAE AAAGPGPCERLLSRVAALFPAL RPGGFQAHYRDEDGDLVAFSS DEELTMAMSYVKDDIFRI*IKE KKECRRDHRPP\CAQEAPRNMV HPNVICDGCNGPVVGTRYKCS VCPYY\DLCSVCEGKGLHRGHT KLAFP\SPFGHL\SEGF\SHSRWL\ RKV\KHGHF\GWPGW\EMGPPG\ NWEPTFLPRAG\EARPGP\TAES ASGPSEDPSVNFLK\NVGESVA\ AAFSPL\NFEVDIDVEHGGKRSR LTPVSPESSSTEEKS\SSQPSSCC SDPSKPGGNVEGATQSLAEQM RKIALESEGRPEEQMESDNCSG GDDDWTHLSSKEVDPSTGELQ SLQMPESEGPSSLDPSQGGNPQ GWKEAALYPHLP\PEVEPAA*F ESLSQMVVPWGFS*LKGGWVH QGSCRPRNYDI\GAAL\DTIPVIQ
22496	52864	A	22624	1032	1127	FYAKAEAGDRTVA*PHKPKMF LSIHHRVAKI
22497	52865	A	22625	121	561	VFPGPLGSLVDICGPSRVPFPWV VPAVLPVQFVQRLPRFFRCPPV LVTSVIRSISTLIQALGSSPFARR YWGNLG*FLFLGVLRCFSSTGS PH*PMNSVNDSVSKHT/EVTPF GN\PGNNGSYHLTDAYRRLARP SSPLT\PGHPPLYG
22498	52866	A	22626	243	454	ATAGCPSCSATEGVVRNGKST AGHQRYLCSPCRKTWQLQFTY TASQP/GARIMGVGLNTVLRHL KNSGRSR
22499	52867	A	22627	3	640	
22500	52868	A	22628	236	410	
22501	52869	A	22629	116	359	

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22502	52870	A	22630	276	1905	LFLYSSHGQYGCPSCSATDGVV RNGKSTAGHQRYLCSHCRKTW QLQFTYTASQPAGQ*RTAIATVI CCNNCQRRHTNSRCHTDNCRR ADSASSHATSGSSSRGCAGSGR CGASSTRRCLGPVCCFRGSKRS WRRQHEGHKDCRKLVFHNFSFI HRMDNTAVPPVQLLTGWCVTA KAPPDISAISALTAVKHGNCSSL TPLLNPPGSDVIVCAEMDEQW GYVGAKSRQRWLFYAYDSLRK TVVAHVFGERTMATLGRLMSL LSPFDVVIWMTDGWPLYESRL KGKLHVISKRYTQRIERHNLNL RQHLARLGRKSLSFSKSVELHD KQQGLDAALIDAPLAVDAQTP LSELLSHVGQAPCAVPVVDED QQYVGIISKGMLLRALDREGGV RVPVIYPKRFRTTDVCMPLSLG TCIREIEAEFPDPIFRRSVVYICE HNTNGAMGIIVNKPLENLKIEGI LEKLKITPEPRDESIRLDKPVML GGPLAEDRGFILHTPASNFASSI RISDNTVMTTSRDVLETLGTDK QPSDVLVALGYASWEKGQLEQ EILDNAWLTAPADLNILFKTPIA DRWREAAKLIGVDILTMPAQD GTPDWNIIERLLKEWQPDEIIVG LPLNMDGTEQPLTARARKFAN RIHGRFGVEVKLHDERLSTVEA RSGLFEQGGYRALNKGKVDSA SAVIILESYFEQGY

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22503	52871	A	22631	399	2337	PEVQGLQQAGAAARRPGVGLA APRVVCEGRLRGSGLQSRLCPG ASV*ATDGVVRNGKSTAGHQR YLCSHCRKTWQLQFTYTASQP AGQ*REKEEKEEVEEEEEEEKK KRRREGEKEEKEEKEKEKKKK FKKKKKKKKKKKKKKKKKKK KKKKKKKQLSLVTVMSQQCQL WRNEARTTGACLPSPTVSAAAP PIVSTTVTAFAAATLAKGDLRS RASSKQVPLLVVLVWVWPHPG WFVKAGSVALGSSPGCVLELL CKLLTGWCVTAKAPPDISAISA LTAVKHGNCSSLTPLLNPPGSD VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSLRKTVVAHVFGE RTMATLGRLMSLLSPFDVVIW MTDGWPLYESRLKGKLHTQER KARSKQQKDADTAPPIQVGTQ TPQTVHAARDTRQASPRASKIS QHRQADGDKRQTRHAEAQAT RTHTGRRKTIKETATQQAYADE QTRRTARTHRRTARHTAAHTH RTRVAARQTTEKDNEQSDTQPP TQKTPSATATAHTPRRTETTTNI VQARHTSARERNHTRQHQATR RETTTNAHTNTPHYHAEHTQSR SQQQTTSTERPTTDSSTTINNNN HTPRTVRDERRMTQHKHPSRA STTTNRTTTTGAYQHTQRDTRD TRRDTHEDTTTQQPHTTTPTAN EAAYTAHTTKTDDHRHTADDT
22504	52872	A	22632	103	313	ATAGCPSCSATEGVVRNGKST AGHQRYLCSPCRKTWQLQFTY TASQP/GARIMGVGLNTVLRHL KNSGRSR
22505	52873	A	22633	620	832	

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22506	52874	A	22634	453	1047	AADDRGHLRPTDGLLRNGKST AGHQRYLCSHCRKTWQLQFTY TASQPAGQ*RVTGTSERREQIIQ RLRQQGSVQVNDLSALYGVST VTIRNDLAFLEKQGIAVRAYGG ALICDSTTPSVEPSVEDKSALNT AMKRSVAKAAVELIQPGHRVIL DSGTTTFEIARLMRKHTDVIAM TNGMNVANALLEAEGVELLMT AGICALLTGCCVTAKAPPDISAI SALTAVKHGNCSSLTPLLNPPG SDVPVCAEMDEQWGYVGAKS RQRWLFYAYDSLRKTVVAHVF GERTMATLGRLMSLLSPFDVVI WMTDGWPLYESRLKGKLHVIS KRYTQRIERHNLNLRQHLARLG RKSLSFSKSVELHDKVIGHYLN GDFLQSTLREAPLIPHTREHP
22507	52875	A	22635	1089	1686	TSPGYWRANSTDPDGRYCRTG TSGGVCHALSSLRCPSCSATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQPAGQ*RFLSK QEKTLLINQLASEEQQKVTSRL SDALRNGRVWQLAIIYLTIQVA VYGLIFFLPTQVAALLGTKVGF TASVVTAIPWVAALFGTWLIPR YSDKTGERRNVAALTLLAAGIG IGLSGLLSPVMAIVALCVAAIGF IAVQPVFWTMPTQLLSGTALAA GIGFVNLFGAVGGFIAPILRVKA ETLFASDAAGLLTLAAVAVIDR RGTSLNRLRNTMIALLSNPFKE RLRKGEVQIGLWLSSTTAYMA EIAATSGYDWLLIDGEHAPNTI QDLYHQLQAVAPYASQPVIRPV EGSKPLIKQVLDIGAQTLLIPMV DTAEQARQVVSATRYPPYAVH PVQLLTGWCVTAKAPPDISAIS ALTAVKHGNCSSLTPLLNPPGS DVIVCAEMDEQWGYVGAKSR QRWLFYAYDSLRKTVVAHVFG ERTMATLGRLMSLLSPFDVVIW MTDGWPLYESRLKGKLHVISK RYTQRIERHNLNLRQHTGTGW DGSRCRSQKSGGAA
22508	52876	A	22636	91	200	SGIIAFQYLLMTLKVLPVASVSI SCPS\CSATDGVVRNGKSTAGH QRYLCSHCRKTWQLQFTYTAS QPAGQ*RGGA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
22509	52877	A	22637	2649	3270	GAPVASVSISCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAGQ*RTIGRAML KNKHMTITEFVAQRMRDAQQK GEISPDINTAMTSRLLLDLTYGV LADIEAEDLARKRRLLRITRDD WRYLNRILILSLFRRAGDNCAR VSYQTPTREIKKLDGLWAFSLD RENCGIDQRWWESALQESRAIA VPGSFNDQFADADIRNYAGNV WYQREVFIPKGWAGQRIVLRF DAVTHYGKVWVNNQEV
22510	52878	A	22638	1	2470	MNADTDYSIAEAAFNKGETAM TINGPWAWSNIDTSKVNYGVT VLPTFKGQPSKPFVGVLSAGIN AASPNKELAKEFLENYLLTDEG LEAVNKDKPLGAVALKSYEEE LAKDPRIAATMENAQKGEIMP NIPQMSAFWYAVRTAVINAAS GRQTVDEALKDAQTRITNCCRI RRESLIRPGMRKNPMDVIKKKH WWQSDALKWSVLGLLGLLVG YLVVLMYAQGEYLFAITTLILS SAGLYIFANRKAYAWRYVYPG MAGMGLFVLFPLVCTIAIGFNN YRRTKQVAGMPAKSSSLRSSQ DREMRPGAKAERTRYDSPGSY GVAGPGFLGSRGGSPFGGPGKY NNTITKYALNIAPSAQNQSPHG PKLNRRQETQHALDWLDAGYT FTYSEDQALTPYFKLAYVYDDS NNDNDVNGDSIDNGTEGSAVR VGLGTQFSFTKNFSAYTDANYL GGGDVDQDWSANDLTGITAKD AQMLSVVKPLQEFGKLDKCLS RYGTRFEFNNEKQVIFSSDVNN EDTFVILEGVISLRREENVLIGIT QAPYIMGLADGLMKNDIPYKLI SEGNCTGYHLPAKQTITLIEQN QLWRDAFYWLAWHNRILELRD VQLIGHNSYEQFAHIIFMIAAM QMGSVWGDDFSSGQHSVARKS QLHKPILRVKCHEGFTISANPNS SPRYPTIIEQAEQPRIVDFSIVRF
22511	52879	A	22639	1	852	

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22512	52880	A	22640	1	747	MIIIDPRYTDTGAGREDEWIPIR PGTDAALVNGLAYVMITENLV DQAFLDKYCVGYDEKTLPASA PKNGHYKAYILATD/GVVRTAK STAGHQRYLCSHCRKTWQLQF TYTASQPAGQ*RYTDTGAGRE DEWIPIRPGTDAALVNGLAYV MITENLVDQAFLDKYCVGYDE KTLPASAPKNGHYKAYILATDG WCVPPKAPPDISAISALTAVKH GNCSSLTPLLNPPGSDVIVCAE MDEQWGYVGAKSRQRWLFYA YDSLRKTVVAHVFGERTMATL GRLMSLLSPFDVVIWMTDGWP LYESRLKGKLHVISKRYTQRIE RHNLNLRQHLARLGRKSLSFSK SVELHDKVIGHYLNIKHYQ
22513	52881	A	22641	1722	2463	NPRLAGSEGSCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAGQ*RKLTPGCL FVALKGERFDAHDFADQAKAG GAGALLVSRPLDIDLPQLIVKD TRLAFGELAAWVRQQVPARVV ALTGSSGKTSVKEMTAAILSQC GNTLYTAGNLNNDIGVPMTLL RLTPEYDYAVIELGANHQGEIA WTVTHPPRFVTKQWLCFLPDG LLLFAEARFVIWQMQPAVMAV DVAAFAHLFNQQQYQRFTGRP PDSSKLPWKITCNGECVTFHW WLLGVAVRISRLLPVRVMTAL EGNYNGTEGISALPFNGIILAHS NESEWVTFRNNKNNEAFLDRV YIVKVPYCLRISEEIKIYEKLLN HIFECWQHFLNNPESLQCYIWA ANADFREARQVIFKTFFTVGVE EELGIRQTRTNDFLVTGDNLLRI FRFDVGNEDKVRQQFAVVRIH REVFLVTFHGVNQRFSRHREEF LFEFCVSVTANLTRCFFGIGFNL RLTFFVIGDDFPTLTQNFRILIGV IDGEFRLAHKAVAANHAIGLNA QNGCRNDFVAHAAGSRALAAD GRSLEHAPTVETVVAGPLCESG DVFTQQEGGNVETRALPEVKA AVPPVQLLTGWCVTAKALPDIS AISALTAVKHGNCSSLTPLLNPP GSDVIVCAEMDEQWGYVGAKS RQRWLFYAYDRLRKTVVAHRL

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22514	52882	A	22642	90	1254	KGLCSHSEMVVPSYSATDGVV RNGKSTAGHQRYLCSHCRKTW QLQFTYTASQPAGQ*RDIVLTK LMMVWHSQSGYEKAYAHIQR WWYRAILLLTGWCVTAKALPD ISAISALTAVKHGNCSSLTPLLN PPGSDVIVCAEMDEQWGYVGA KSRQRWLFYAYDRLRKTVVAH VFGERTMATLGRLMSLLSPFDV VIWMTDGWPLYESRLKGKLHV ISKRYTQRIERHNLNLSSTSILVL LNGATQFQDLGDLNKELEETY TDSKNHISCVGNDFGFNDIFSR YVEAVGREGDVLLGISTSGNSA NVIKAIAAAREKGMKVITLTGK DGGKMAGTADIEIRVPHFGYA DRIQEIHIKVIHILIQLIEKEMVN FTGLVQRGGGTGPHKDGWGIT FYEVAFEDVAVNFTQEEWALL DPWQKKLYRDVMLETYRNLAS VGDDDNIPSLREQVAHQRYFKT WHVEREYFSK
22515	52883	A	22643	690	1233	RLQSLHYQGRGKPVPMRSYSLS FLFTISNSAGVFRCPSCSATDGV VRNGKSTAGHQRYLCSHCRKT WQLQFTYTASQPAGQ*RLLGP KNRPREQNWLLWCERGVMSRL QALYLREQGFNNVKVDNFQTK VDSCTRPLAGQQFYPCIPDDAL VQPLFGGNFVFQRREAGHITNR EDIVRHQHGGWRGANSRDDTP GTVELFNGFNQQSAIAKTLRAF NATRQHDHVIFAISHFDQRRIR QQLHAARAGNRQVTIAGDAGS GDFDTAANQQIDSGDGFSLFTT RGEANQCRCAHIHSPFFLPFQT VRVFSAVPPVQLLTGWCVTAK APPDISAISALTAVKHGNCSSLT PLLNPPGSDVIVCAEMDEQWG YVGAKSRQRWLFYAYDSLRKT VVAHVFAVKPYWDTGGGFHC RWIYMQQEKELLQLSLQQGKY NQKRAAELLGLTYHQFRALLK

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22516	52884	A	22644	1314	1483	RIQRYCGKTGCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFT\YTASQPAGQ*RMFNADG SEVAQCGNGARCFARFVRLKG LTNKRDIRVSTANGRMVLTVT DDDLVRVNMGEPNFEPSAVPF RANKAEKTYIMRAAEQTILCGV VSMGNPHCVIQVDDVDTAAVE TLGPVLESHERFPERANIGFMQ VVKREHIRLRVYERGAGETQA CGSGACAAVAVGIQQGLLAEE VRVELPGGRLDIAWKGEELQET LTELDDRAVVDYLIKNPEFFIRN ARAVEAIRVPHPVRGTVSLVE WHMARARNHIHVLEENMALL MEQAIANEGLFYRLLYLQRSLT AASSLDDMLMRFHRWARDLG LAVAMPVTINKGNQIIENQLDT ETITISYEFILCQHLIANTEFSYL ALPENYNRLCLPNSKNQTNNRF KTLNSKAIGRLLAAGGVYNGNI EGFRDTAEKLAVPPVQLLTGW CVTAKALPDISAISALTAVKHG NCSSLYTASQPAGQ

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22517	52885	A	22645	1479	1793	TRYRSCPSCSATDGVVRNGKST AGHQRYLCSHCRKTWQLQFTY TASQPAGQ*RRNACQYRTPAV VASRQKRWHGDLGMIGSRDV MLFISDSVGAKELDLIIPRLEDK SIALLAMTGKPTSPLGLAAKAV LDISVEREACPMHLAPTSSTVN TLMMGDALAMAVMQARGFNE EDFARSHPAGALGARLLNKVH HLMRRDDAIPQVALTASVMDA MLELSRTGLGLVAVCDAQQQV QGVFTDGDLRRWLVGGGALTT PVNEAMTVGGTTLQSQSRAIDA KEILMKRKITAAPVVDENGKLT GAIKLQDFYQGRGLFNPSIPRVS TADAGLANRARRNWVGSSWK QVGQIILQGGPQNAEKSGQRYT VSHDRHRDAERQRVKSGLPRY AECSTYPSCPVALDLAFASHGI HMHAPGEALRMLVTAMDKAA DARTKLARLLATKGITHEIQIPD ISTKEKAQQPIGLNMEQIKPEKQ DFIKPVIPQAGKHNGVNMSVLR SLLTAGVLASGLLWSLNGITAT PAAQASDDRYEVTQQRNPDAA CLDCHKPDTEAVPPVQLLTGW CVTAKAPPDISAISALTAVKHG NCSSLTPLLNPPGSDVIVCAELD EQWGYVGAKSRQRWLFYAYA QSPRTTRCCARIRLHALWRRW

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22518	52886	A	22646	807	1350	NRGCPSCSATDGVVRNGKSTA GHQRYLCSHCRKTWQLQFTYT ASQPAGQ*RLLNRLIEPTRGQV LIDGVDIAKISDAELREVRRKKI AMVFQSFALMPHMTVLDNTAF GMELAGINAEERREKALDALR QVGLENYAHSYPDELSGGMRQ RVGLARAINPDILLMDEAFSAL DPLIRTEMQDELVKLQAKHQR TIVFISHDLDEAMRIGDRIAIMQ NGEVVQVGTPDEILNNPANDY VRTFFRGVDISQVFSAKDIARRT PNGLIRKTPGFGPRSALKLLQD EDREYGYVIERGNKFVGAVSID SLKTAAVPPVQLLTGWCVTAK APPDISAISALTAVKHGNCSSLT PLLNPPGSDVIVCAEMDEQWG YVGAKSRQRWLFYAYDSLRKT VVAHVFGERTMATLGRLMSLL SPFDVVIWMTDGWPLYESRLK GKLHVISKRYTQRIERHNLNLR QHLARLGRKSLSFSKSVELHDK VIGHYLNIKHYQ
22519	52887	A	22647	1	1270	MTAATEQLNASRGLSTREMER QAELAKITTDYINSGGSEGDEK LQNMIKAQNDYYAAEDAKRA DWLAGAESAFADYGDSAMDM YGNVNEIASSALNGMTDMMV QFLTTGKANFADFAKNIISMIIK MIAQMVIFNTSLRNDGRSVSSG GAAVSLAAAAGSVATSGFNAS NSAPKVVTIREVERSVDVSGME ASSTSWITIRSFTAETSTFGPTM TASMTFLPTYCSIIASLLSSFKLA AATDGVVRNGKSTAGHQRYLC SHCRKTWQLQFTYTASQPALA RNPNRDITIYWGGREEQHLYDL CELEALSLKHPGLQVVPVVEQP EAGWRGRTGTVLTAVLQDHAT DGVVRNGKSTAGHQRYLCSHC RKTWQLQFTYTASQPGTHQKII DMAMNGVGCRATAR\IMGVGL NTIFRHLKNSGRSR

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22520	52888	A	22648	381	945	GAPVASVSISCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAGQ*RTENQTPH VLTHKWELNYENPWTQGGEHL TMGLVVGWRGLQEGDPARTN LSYYQANVGSGQHRENKGPIN LGNVGKSNGERGGKSLYRCKIF LESSVTMKDRELPPVYDGVFEV LQWLLFLSAVPPVQLLTGWCV TAKAPPDISAISALTAVKHGNC SSLTPLLNPPGSDVIVCAEMDE QWGYVGAKSRQRWLFYAYDS LRKTVVAHVFGERTMATLGRL MSLLSPFDVVIWMTDGWPLYE SRLKGKLHVISKRYTQRIERHN LNLRQHLARLGRKSLSFSKSVE LHDKVIGHYLNIKHYQ
22521	52889	A	22649	354	1119	RRWRRGAHEAATGGTGRGPAE EAAPGEPAAGRAAPKSGGKRL GGVLGRGGVGRRSGSPDRSGA HSAAPRRCRQLPGRCPSCSATD GVVRNGKSTAGHQRYLCSHCR KTWQLQFTYTASQPAGQ*RSK GAIGEGPPDPRGIVEQNLGGDIS IPCYNGPRPRRSAQKTTLGPLN QPRIPSAQCAGAFPRVAAAGAG GGGGGGSGGSGFCLGWRLRRR RQRRRRWRRGEGEGDGDAGH MRPRPAGRAEARRRRRLRGNP PPGARLPNREGNGSGVSWAAE VSGDGRGARTEAARTRRRPGG ADNYPGAVPPVQLLTGWCVTA KAPPDISAISALTAVKHGNCSSL TPLLNPPGSDVIVCAEMDEQW GYVGAKSRQRWLFYAYDSLRK TVVAHVFGERTMATLGRLMSL LSPFDVVIWMTDGWPLYESRL KGKLHVISKRYTQRIERHNLNL RQHLARLGRKSLSFSKSVELHD KVIGHYLNIKHYQ
22522	52890	A	22650	23	658	VISRPGSSIQVRGLLLSRHGLAL GSAPDLWKLPWVNLVQGMGQ QSQGSSCREGCSRPQCPSAAPC GAAPAHFCSAATFWESEVQSIP R/CRATDGVVRNGKS/TAGHQR YLCSHCRKTWQ/LQFTYTASQP EVIRSSPTSAPRSDGTKTVPPLM GISP*SAHHRLATSDPSLCLSES LCSREPAAVPRASNQQPQGVK DVHHQFTARTSRYPSKC
22523	52891	A	22651	926	1093	

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22524	52892	A	22652	343	817	GGARSRQNPRCGPCMVVVPGQ SGRSVSADSSTEFREQGGS\AI\S FPKSINRAGPELFRFMENPFNSV *YRKNVRELTPAIMAVLPVEFR TRLAPQNDTMSLIASAMKECSE AKQAVLLNAPEHQKMKEVSEG IASLFRLMPEQVGPLMTMVTS MLGVI
22525	52893	A	22653	115	425	
22526	52894	A	22654	747	1173	
22527	52895	A	22655	1	2709	
22528	52896	A	22656	1	2583	
22529	52897	A	22657	636	1029	APSDQKRDFLVPHGADSAMAK SG*CESGNDLLSSSHMNQLR/A/ ESIPEDVIAGASALVLTFIIKFVI AENPQWWQQFLKDHVSILAMN EDEAEALTGESDPLLASDKALD WVDLVLCTAGPIGLYMAGGGD VN
22530	52898	A	22658	1611	3300	QSAWANRHRLVDCGRPGNGSD AGVAARSGRNDGTGRCGLCHS CSRYGDHHRQSDRIYRHYDAG RSPSGAVDYGTQRGNRFSRAV YPVGA/RRWR*GLPLV/QQFQPE NETSAAW\VVGINQPLVDIEAK VDDEFIERYGLSAGHSLVIEDD VAEALYQDVQQKNLITHQSAG GTIGNTMHNYSVLADDRSVLL GVMCSNIEIGSYAYRYLCNTSS RTDLNYLQGVDGPIGRCFTLIG ESGERTFAISPGHMNQLRAESIP EDVIAGASALVLTSYLVRCKPG EPMPEATMKAIEYAKKYNVPV VLTLGTKFVIAKNPQWWQQFL KDHVSILAMNEDEAEALTGESD PLLASDKALDWVDLVLCTAGPI GLYMAGFTEDEAKRKTQHPLL PGAIAEFNQYEFSRAMRHKDC QNPLRVYSHIAPYMGGPEKCNI LGRSGWLLYGRGLDKQRLTQY QSKLGAAMVIVAAWCVEDYQ VIRLAGSLTARATRLAHEAQLD VAPLGKIPHLRTPGLLVMDMDS TAIQIECIDEIAKLAGTGEMVAE VTRTGDARRTRFYRQPAQPCG
22531	52899	A	22659	430	586	
22532	52900	A	22660	1	131	

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22533	52901	A	22661	1	1282	MLPAHLDACVTTLQKIRWTLS VVDPTLALRVPLPALSIRDDPPL RAYLPGRGALKVIRFDDMDFA TIDGINRMLVDIDTNYLFLPRVT SSTIRCLSVPTRRTVPAVTASGR SVKYYPPDFDPSKIPKLKLPKD RQYVVRLMAPFNMRCKTCGEY IYKGKKF\NARKETVQNEVYLG \LPI\FRFYIK\CTRCLGRDSPFKT DP\ENTDYTM/ESLGATRNFQG* EASWEEEEKRV\QK\EREDE/ES LNNPMKVLENRTKDSKLEMEV LENLQELKDLNQRQAHVDFEG\ MLRQHRLSEEERRSQQQEEFEQ KTAALLEEARKRRLLEDSDSED EAAPSPLQPALRPNPTATLDEA PKPKRKVEVWEQSVGSLGSRPP LSRLVVVKKAKADPDCSNGQP QAAPHPRSPAEQEGGQPYTPDA WRVLPEPTGCIPGQ
22534	52902	A	22662	1	412	
22535	52903	A	22663	298	532	MGSWSLPGRTLWKEKVRFLKS KERTNPGSNFFSFPGSQHTREER SQECLSLPVLPSYLATRLSLPDS CPLKGRKAH*QRHSEI*LMGFE PGWPGKL*GWIELAFLLGCLHL TLPLPCPTPLPPKSTKSGCFSLSI ALCFNKQFAVTK
22536	52904	A	22664	1	193	
22537	52905	B	22665	55	281	
22538	52906	A	22666	86	159	
22539	52907	A	22667	63	1036	VRGGLAAGRGRGSAGAAPVVV AAMLGAWAVEGTAVALLRLL LLLLPPAIRGPGLGVAGVAGAA GAGLPESVIWAVNAGGEAHVD VHGIHFRKCIPL*GRVGRALYY GMKLPILRSNPEDQSCYQTE\RS N\EETFGYESPIQREGGLTCWSL KFAE\VYFAQSQQKVFDVRLNG HVVVKDLDIFDRVGHSTAHDEI IPMSIRKGKLSVQGEV\ST\FTQG KLLPLSFSKGYL*PIPKVCAL\YI MAG\TVDDVPKASAFNPGLEK KEEEEEEEEYDEGSNLKKQTNK NRVQS\GPRTPNPYALDNSSLM FPILV\AFGVFIPTLFCLCRL
22540	52908	A	22668	1570	1773	

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22541	52909	A	22669	62	454	NKQLNKKRRRTMIALIQRVTRA S/VTVEGEVTGEIGAGLLV/LLG VEKDDDEQKAN/RDAEGQM/N LNVQQAGGSVLVVSQF/TLAAD TERGMRPSFSQGHHRIRAQAFY DYFVES/CRQQR*YAQGGLSAE FRLLNS
22542	52910	A	22670	1	1930	MAGKPEYDKTISTSIVLNALNA LGVSAEASGRNDLVVKTVEGD RKVSGSAYRETKDRGFHHGTL LLNADLSRLANYLNPDKKKLA AKGITSVRSRVTNLTELLPGITH EQVCEAITEAFFAHYGERVEAE IISPNKTPDLPNFAETFARQSSW EWNFGQAPAFSHLLDERFTWG GVELHFDVEKGHITRAQVFTDS LNPAPLEALAGRLQGCLFSLYN SDLNTVIDNVLRIFPLLLSWISF WLLYSIVPTIRVPNRDAIVGAFV AALLFEAGKKGFALYITMFPSY QLIYGVLAVIPILFVWVYWTCV TVEGEVTGEIGAGLLVLLGVEK DDDEQKANRLCERVLGYRIFSD AEG\KMNLNVQQAGGSVLVVS QFTLAADTERGMRPSFSKGVID DIGFNTEISQTRFHQASHLFKRK GIYRLHFARRRCQQIQRRQRRR RFMQRTAVAITHQQRMKQGIL RLWRNWLLWLLILLLRRNRLL RLLILLLWRNRLLRLLILWLRR NRLLWLLILRLRRNWLLRLLIL LLRCNRLLRLLYRFNNWRKQR FVWTIIQQRFHWRKFKIIQRERI RPSRLFAGITLLLSLRKLTSQFS LCRSICIFCVYGHIMLILFAIALL LCLGELTCQFILLHRIDFIIVVLI
22543	52911	A	22671	377	463	QTISQTTVQSN*NSGLRISPKTA QLHGD
22544	52912	A	22672	129	615	KARQKSCQPVTTDTQCRHTSSS IGKRLAFCQNLTQIHTESTMKP WILLLVMFISGVVMLLPVLGSF WNKDPFLDMIRETEQCWVQPP YKYCEKRCTKIMTCVRPNHTC CWTYCGNICLD/IRRAP*/HQC* TPRFYWPITTVG*RMTIWSKKS AAYFLLGTPTWL
22545	52913	A	22673	3	412	
22546	52914	A	22674	2	390	

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22547	52915	A	22675	180	507	CCGGRARSELCLLNLCIKGAD*I QAW*KFCQWPCERADGRGCRK AER\CPCPKGAYSL/YCRESVCC LPSFVNKNSSSLCVAHNWGRH CYLWTAADVKQFISSHMFPVE HL
22548	52916	A	22676	3	227	GGGRARSELCLLNLCIKGAD*I QAW*KFCQWPCERADGRGS*F DRGAEVCNQTDWQSIRSSQGG RDQRFSTERA
22549	52917	A	22677	567	842	
22550	52918	A	22678	1	1400	MGWGQGPDVQLMNGHERSPS HSPREAKKSGSPLPTDIHCFSPQ SQPAMVITGVPTAPAGASAKM GLCATPITGACPLWLRGFRGWR CEDRCEQGTYGNDCHQRCQCQ NGATCDHVTGECRCPPGYTGA FCEDLCPPGKHGPQCEQRCPCQ NGGVCHHVTGECSCPSGWMLS FPGWRPI*FSKSL*MQGTVCGQ PCPEGRFGKNCSQECQCHNGGT CDAATGQCHCSPGYTGERAAV PDVRK\CQDECPVGTYGVLCAE TCQCVNGGKCYHVSGACLCEA GFAGERCEARLCPEGLYGIKCD KRCPCHLENTHRGDDREKAEF GHLLIALEVQYTEISNCIEKSQE ASCYDIRMLKQPYGETNTEEEL AVNYVYSIYASKEQIRYKHGRS FANGHVKELMEGPSRRIAGSGG EKYKRDEEKNTLLRGQNRGGR GKNPKKTKAWVKIQGQNKIEIS GVGADRKRFFREK

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22551	52919	A	22679	1	2210	MEQKGEFKNDTLIYEFFHIVAK PHPLPIKSSTYTTFQSARVTRFF LDAEKECRCQEGQVEAALIAM GGTCQGTQRLSTAGESESATH MREPAVQCRRDSQCVSVLAGR RRFFQGAASPLHPASVALTQLH VRWASTATIGQVSGFPGKIRVS PTTNLGDSDYIFTASHWGLGHY GPAVHVHSQGGIDERGSNDSG RLYVTNPCGNVPSWTPNIDRLA EDGVKLTQHISAASLCTPSRAA FLTGRYPVRSGMVSSIGYRVLQ WTGASGGLPTNETTFAKILKEK GYATGLIGKWHLGLNCESASD HCHHPLHHGFDHFYGMPFSLM GDCARWELSEKRVNLEQKLNF LFQVLALVALTLVAGKLTHLIP VSWMPVIWSALSAVLLLASSYF VGALIVHADCFLMRNHTITEQP MCFQRTTPLILQEVASFLKRNK HGPFLLFVSFLHVHIPLITMENF LGKSLHGLYGDNVEEMDWMV GRILDTLDVEGLSNSTLIYFTSD HGGSLENQLGNTQYGGWNGIY KGGKGMGGWEGGIRVPGIFRW PGVLPAGRVIGEPTSLMDVFPT VVRLAGGEVPQDRVIDGQDLL PLLLGTAQHSDHEFLMH\YCER VLHAARWHQRDRGTMWKVHF VTPVFQPEGAGACYGRKVCPCF GEKVVHHDPPLLFDLSRDPSET HILTPASEPVFYQVMERVQQAV

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22552	52920	A	22680	185	2091	GSTERDNMLHLHHSCVCFRSW LPAMLAVLLSLAPSASSDISASR PNILLLMA\DDHGVGDIGCYGN NTMRTPNIDRLAEDGVKLTQHI SAASLCTPSRAAFLTGRYPVRS GMVSSIGYRVLQWTGASAGFT TN\ETTFAKILKEKGYATGLIGK WHLGLNCESASDHCHHPLHHG FEHFYGMPFSLMGDCARWELS EKRVNLEQKLNFLFQVLALVA LTLVAGKLTHLIPVSWMPVIWS ALSAVLLLASSYFVGALIVHAD CFLMRNHTITEQPMCFQRTTPLI LQEVASFLKRNKHGPFLLFVSF LHVHIPLITMENFLGKSLHGLY GDNVEEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQL GNTQYGGWNGIYKGGKGMGG WEGGIRVPGIFRWPGVLPAGRV IGEPTSLMDVFPTVVRLAGGEV PQDRVIDGQDLLPLLLGTAQHS DHEFLMHYCERFL\HAARWHQ RDRGTMWESPTL*PPCVSSQEG AGAC\YGRK\VCPCFGEK\VVHH DP\PLL\FDLSRDPSETHILTPASE PVFY\QVMER\VQQAVWEHQR TLSPVPMQLDRLGNIWRPWMQ PCCGPFPLCWCLREDDPQINVC SEKLEPRFLNFVTQIETNQLAM
22553	52921	A	22681	209	392	
22554	52922	A	22682	1	513	
22555	52923	A	22683	3	613	
22556	52924	A	22684	1	2115	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
22557	52925	A	22685	53	1966	VGQPRGLRTLEKLTASVAGGA ANFFGDIERDLGPRDTSRGIRG GNLGDRGCSSAEMAYASWQR WSPVEWARWMWTAVTSSGDS SLLVLQGDSGKRSSDSEEAFET PESTTPVKAPPAPPPPPPEVIPEP EVSTQPPPEEPGWGSETVPVPD GPRSDSVEGSPFRTQAHSFSGVF DEDQPIASTGTDILDFDNIELVD TFQTLEPRASDAKNQEGKVNT RRKSTDSVPISKSTLSRSLSLQA SDFDGASSSGNPEAVALAPDAY STESAKRVVPPASGGGRVQNSP PVGRKTLPLTTAPEAGEVTPSD SGGQEDSPAKGLSVRLEFDYSE DKSSWDNQQENPPPTKKIGKKP VAKMPLRRPKMKKTPEKLDNT PASPPRSPAEPNDIPIAKGTYTF DIDKWDDPNFNPFSSTSKMQES PKLPQQSYNFDPDTCDESVDPF KTSSKTPSSPSKSPASFEIPASA MEANAV\DGDGLNKPAKKKKT PLKTMVEDVMSVCSLFDTFRV KKSPKRSPLSDPPSQDPTPAATP ETPPVISAVVHATDEEKLAVTN QKWTCMTVDLEADKQDYPQPS DLSTFVNETKFSSPTEELDYRNF YEIEYMEKIGSSLPQDDDAPKK QALYLMFDTSQESPVKSSTVR

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22558	52926	A	22686	662	2927	HLRRKRNLPRREGLSPALLEET PLEPAVGPKAACPLDSESAEGV VPPASGGKRCLFTTAPEAGEVT PSDSGGQEDSPAKGLSVRLEFD YSEDKSSWDNQQENPPPTKKIG KKPVAKMPLRRPKMKKTPEKL DNTPASPPRSPAEPNDIPIAKGT YTFDIDKWDDPNFNPFSSTSKM QESPKLPQQSYNFDPDTCDESV DPFKTSSKTPSSPSKSPASFEIPA SAMEANGVDGDGLNKPAKKK KTPLKTDTFRVKKSPKRSPLSD PPSQDPTPAATPETPPVISAVVH ATDEEKLAVTNQKWTCMTVD LEADKQDYPQPSDLSTFVNETK FSSPTEELDYRNSYEIEYMEKIG SSLPQDDDAPKKQALYLMFDT SQESPVKSSPVRMSESPTPCSGS\ SFEETGSPLRNTAA\KNQ\HPVP TRDWAP*PRSSHLAGCQRKSSQ E/VELGGPWGLGHPFQEGDLKF TASPRGSFASADALLSRLAHPV FSL/CGALDYL\EPNFRQKRNPP LFAQKLQREA\VHPTDVSI\SKT ALYSRIRTTEVEKPAGLLFQQP DL\DSALQIARAEII\TKEREVSE WKDKYEESR\REVMEMRKI\LA EYEKTIAQMIEDEQREKSVS\HQ TVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLESFRK NEEVLKRCAQEYLSRVKKEEQ RYQA\LKVHA\EEKLDRANAE\I
22559	52927	A	22687	374	1268	AETNMVWYDWMRPSHAQLHS DYMQPLTEAKAKSKNKVRGV QQLIQRLRLIKSPAEIERMQIAG KLTSQAFIETMFTSKAPVEEAFL YAKFEFECRARGADILAYPPVV AGGNRSNTLHYVKNNQLIKDG EMVLLDGGCESSCYVSDITRTW PVNGRFTAPQAELYEAVLEIQR DCLALCFPGTSLENIYSMMLTLI GQKLKDLGIMKNTQGK*CL/RR LLE/QYCPHHVGHYLGMDVHD TPDMPRSLPLQPGMVITIEPGIYI PEDDKDAPEKFRGLGVRIEDDV VVTQDSPLILSADCP

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22560	52928	A	22688	329	1389	RIWKTQMMRMKKMMMMMMM MMMRTTLFFQQESQEAIFFPFD LFPMCPFGCQCYSRVVHCSDLG LTSVPTNIPFDTRMLDLQNNKI KEIKENDFKGLTSLYGLILNNN KLTKIHPKAFLTTKKLRRLYLS HNQLSEIPLNLPKSLAELRIHEN KVKKIQKDTFKGMNALHVLEM SANPL**/SMGIEPGAF*RG*RCS /YIRIAEAKLTSV\PKGL\PPTLLE LHLDYNKISTVELEDFKRYKEL QRLGLGNNKITDIENGSLANIPR VR\EIHLGNIKLKKIPSGLPELKY LQIIFLHSNSIARVGVNDFCPTV PKMKKSLYSAISLFNNPVKYWE MQPATFRCVLSRMSVQLGNFG
22561	52929	A	22689	1	4608	
22562	52930	A	22690	1	465	
22563	52931	A	22691	1	1542	
22564	52932	A	22692	1	4226	EAVLCSSRGRPDSSMPDCCRNA ALEARSCQSMTSLFSNTVSPTQ DGTSSLPRRQSSFAKPPLRALY DLLIAPMEGGVVESTEPLGTSR SGFASGTALFWLGDNGKAASP PGVSVSSLENEDDNTQCNRLEQ GYREAAVPDWTQDLALCLLPT LQSLKARTAPHLCVPSSCYKA WYTLAVSKVSGMVEGKAWIIL LLLAASTHALLQRPQEGDITPL AGSRAAAVSCQARPFSTFSGLM HSSGPVGRHRQLILVLE
22565	52933	A	22693	2	4197	ALDFPGRRFRPTASFIWASVLFE TIRHEAEVSTDYKLSLFDLQTSS YQALQRVLVSLGHHDEALAVA ERGRTRAFADLLVERQTGQQD SDPYSPVTIDQILEMVNGQRGL VLYYSLAAGYLYSWLLAPGAG IVKFHEHYLGENTVENSSDFQA SSSVTLPTATGSALEQHIASVRE ALGVESHYSRACASSETESEAG DIMDQQFEEMNNKLNSVTDPT GFLRMVRRNNLFNRSCQSMTS LFSNTVSPTQDGTSS
22566	52934	A	22694	1	618	
22567	52935	A	22695	1	3528	

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22568	52936	A	22696	85	1193	RPIEGQLGTCHPGSEPRTIRWRA PGKGLRLYTHPPTSDIAGRTGA AASFPAPLHLPREPRAGVDGTD AERILYPRRAAPAASGVGSRPA GEAVRADEAGAAGLGGFQSER NRSWGGESLGSRQPQKMPAFN RLFPLASLVLIY*VSVCFPVWGE \VPLENGGRARANPMKLRCISC MKREEVEATTVVEWFYRPEGG KDFLIYEYRNGHQEVESPFQGR LQWNGSKDLQDVSITVLNVTL NDSGLYTCNVSREFEFEAHRPF VKTTRLIPLRVTEEAGEDFTSV VSEIMMYILLVFLTLWLLIEMIY CYRQVSKAEEAAQENAPGNSL EGGSQGLQINSTQDGLVTGQQ DVGSHRAREHMPDFEEPPSAK
22569	52937	A	22697	277	527	VRVSWEYFCAPGPAGSPAGPG RGEEKQRLGLLIRDARSPAPPG PPVGSVRG/PKPAPAGRVRAKG RRA*GAACSLAAGAWVEPGI

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22570	52938	A	22698	226	2268	SVKNYTKCHVRNEQICNKLTSC KSCSLNLNCQWDQRQQECQAL PAHLCGEGWSHIGDACLRVNSS RENYDNAKLYCYNLSGNLASL TTSKEVEFVLDEIQKYTQQKVS PWVGLRKINISYWGWEDMSPF TNTTLQWLPGEPNDSGFCAYLE RAAVAGLKANPCTSMANGLVC EKPVVSPNQNARPCKKPCSLRT SCSNCTSNGMECMWCSSTKRC VDSNAYIISFPYGQCLEWQTAT CSPQNCSGLRTCGQCLEQPGCG WCNDPSNTGRGHCIEGSSRGPM KLIGMHHNEMVLDTNLCPKEK NYEWSFIQCPACQCNGHSTCIN NNVCEQCKNLTTGKQCQDCMP GYYGDPTNGGQCTACTCSGHA NICHLHTGKCFCTTKGIKGDQC QLCDSENRYVGNPLRGTCYYK T\LIDYQFTF\SLLQEDDRHHTAI YFIVNPKQSNKNLHISINASNNF NLNITWPC*STAGTISGEETYIV SKNNILEYRDSFSYEKFNFRSNP NITFYVYVSNFSWPIKIQIAFSQ HNTIMDLVQFFVTFFSCFLSLLL EAAVVWKIKQTCWASRRREQL LRERQQMASRPFASVDVALEV GAEQTEFLRGPLEGAPKPIAIEP CAGNRAAVLTVFLCLPRGSSGA PPPGQSGLAIASALIDISQQKAS DSKDKTSGVRNRKHLSTRQGT
22571	52939	B	22699	252	360	
22572	52940	A	22700	1	84	
22573	52941	A	22701	1	404	
22574	52942	A	22702	86	292	NPEMRCREFCLPSCRPELALE* G*SVRDVA*AQMCSVVWAGRP LGFAA*S*GSGHSCGRCSIWGE CWG
22575	52943	A	22703	82	379	HTLQPFISMGSLTKMFKVISEGP MD*RPHPKVRPMT*HSTPAPAN FMGHFFWKIMICTDRTEVATLV AGVVSGASVGGKSPPYRKWNS PEPDVKGPRVL
22576	52944	A	22704	2	382	

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22577	52945	A	22705	1	479	HMPSGETAPLRIVDTGTGTGTV \AYAPTE\LGLHEMHIKYMASHI LESPLRFYVTTPTVPSVSAYGPG LVYGVAN/NTATFTIVTEDAGE GGLDLAIEGPSKAEEPRPRLSRA PGVDGAGASPGLGEDTGPQAP GLQVLTERIPGPSAPTPEFLSVG VSAVC
22578	52946	A	22706	1	590	
22579	52947	A	22707	171	406	
22580	52948	A	22708	269	2477	
22581	52949	B	22709	167	7472	
22582	52950	A	22710	1	520	
22583	52951	A	22711	2218	2472	
22584	52952	A	22712	722	1555	SRNWYEALNNTWGREDICVVD GWQSFRRQDYAFLQERGSGGD LWSSTLAQAMTLVESRHPRHQ ALSTQLLDAIMPYCGNTLRLGV TGTPGAGKSTFLEAFGMLLIRE GLKVAVIAVDPSSPVTGGSILG DKTRMNDLARAEAAFIRPVPSS GHLGGASQRARELMLLCEAAG YDVVIVETVGVGQ\SETEVARM VDCFISLQIAGGADDLQGIKKG LMEVADLIVINKDDGDNHTNV AIARHM/YESALHILRRPPMHR VPRNPKVNLLPGTAMANLLS
22585	52953	B	22713	381	425	
22586	52954	A	22714	1	1185	
22587	52955	A	22715	1	3009	
22588	52956	A	22716	22	527	YEGIVMKPLIIVNPADCIGC\RT CE\VACVVAHPSEQELNADVFL PRLKVQRLDSISAPVMCHQCEN APCVGACPVGALTMGEQVVQT NSARCIGCQSCVSACPFGMITIQ SLPGDTRQQIVKCDLCEQR*EG PACVESCPTQALQLLIERELRRV RQQRIVVTGENPL
22589	52957	A	22717	187	325	

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22590	52958	A	22718	1	2240	MRSDPDTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRFV TLEMKYGRIMLDTAKIIDEQDV PTHILSKLTFTLRNHPEGVVMK NFEVLQPLQNSLSGLPLWVSER ILQQINQLTHYEPVIGIMGKTGA GKSSLCNALFAGEVSPVSDVAA CTRDPLRFRLQIGEHFMTIVDLP GVGESGVRDTEYAALYREQLP RLDLILWLIKADDRALATDEHF YRQVIGEAYRHKMLFVISQSDK AEPTSGGNILSTEQKQNISRKIC LLHELFQPVHPVCAVSVRLHPV VALLQQFRTDDERTHRYHYDS QHRLVDYTRTQYEEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPQVTWYGWDGDRL TTIQNDRSRIQTIYQPGSFTPLIR VETATGELAKTQRRSLADALQ QSGGEDGGSVVFPPVLVQMLD RLESEILADRVSEESRRWLASC GLTVEQMQNQMDP\TEGTTAW Y/AEYDEWGNLLNEENPHQLQ QLIRLPGQQYDEESGLYYNRHR YYDPLQGRYITQDPIGLKGGW NFYQYPLNPISDIDPLGLSMWE VARQMNAIASKLPEGFHIGINFS ASHIISPTFVDECLNFRDSFTRR DLNLVLEVTERDLLNVDESLVQ RLNILHENGFVIALDDFGTGYS GLSYLHDLHIDYIKIDHSFVGRV NADPESTRILDCVLDLARKLSIS

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22591	52959	A	22719	1	2301	MALTSGVHTGEKPYKCAQCEE AFSRKSELIIHQIIHTGEKPYECT ECGKTFSRKSQLIIHQRTHTGEK PYKCTKCGKSFCQQSHLIGHQR IHTGEQPYLGLSVAERPKEYED DRALKMAAPCGNSSREQPCCFL NKASEDAERAKPPS*EPGRLRT P*VAQPH*VPHFMATWVRKHP VHDRQFRLHGQIRELNWDVVR PEQFTGVATNCSGITYPQGGWL CPAELTRNVLELAQQQGLQIYY QYQLQNLSRKDDCWLLNFAGD QQATHSVVVLANGHQISRFSQT STLPVYSVAGQVSHIPTTPELAE LKQVLCYDGYLTPQNPANQHH CIGASYHRGSEDTAYSEDDQQQ NRQRLIDCFPQAQWAKEVDVS DKEARCGVRCATRDHLPMVGN VPDYEATLVEYASLAEQKDEA VSAPVFDDLFMFAALGSRGLCS APLCAEILAAQMSDEPIPMDAS TLAALNPNRLWVRKLLKGKAV KAG
22592	52960	A	22720	1021	1734	
22593	52961	A	22721	1247	2412	RRSHHAANLDIRIRMPQTRQVT LPDPELHPDSTLSMWPD/NRIAR DAHYLYRYDRHGRLTEKTDLIP EGVIRTDDERTHRYHYDSQHRL VHYTRTQYEEPLVESRYLYDPL GRRVAKRVWRRERDLTGWMS LSRKPQVTWYGWDGDRLTTIQ NDRTRIQTIYQPGSFTPLIRVET ATGELAKTQRRSLADALQQSG GEDGGSVVFPPVLVQMLDRLE SEILADRVSEESRRWLASCGLT VEQMQNQMDPVYTPARKIHLY HCDHRGLPLALISKEGTTEWCA EYDEWGNLLNEENPHQLQQLI RLPGQQYDEESGLYYNRHRYY DPLQGRYITQDPIGLKGGWNFY QYPLNPVTNTDPLGLEVFPRPFP LPIPWPKSPAQQQQWYPTFCC
22594	52962	A	22722	1	4767	

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22595	52963	A	22723	668	1922	YPHADSPECWLSSSSERGKSSV TADLSRPRRLRPIPTCHGKPIAC TTTKAKNAFRPIAGASATGRLA NSPIIILPNAAIRQEFGITLDPEEV FTFQGVKLYEYRYFPDCVRSRN EAGILVEQILSTLFSVGEHFSLK RAPFFKVPSLRSFYAFGGLTTG VVRRNGNHGVNTPARKIHLYH CDHRGLPLALISKEGTTEWCAE YDEWGNLLNEENPHQLQQLIR LPGQQYDEESGLYYNRHRYYD PLQGRYITQDPIGLK\GGWNFY QYPLNPVQYIDSMGLASKYGH LNNGGYGARPNKPPTPDPSKLP DIAKQLRLPYPIDQASSAHNVF KTFFRALSPYDYTLYCRKWVK PNLTCTPQDDSQYPGMDTKTA SDYLPQTN/WPVPSSIVSCTTGV VP*VVCQWVFAWPPDISHRRTG
22596	52964	A	22724	25	510	RITDFGVKKIIRVGSCGAVLPHV KLRDV/VI/GMGAC/TDSKVNRI RFKGQAFGGIADFAMGRTAVD PGKALGINARVGNLVSADLFYS PDGEMFDVMEKYGILGVEMEA AGIYGVAAEFGAKALTICTVSD HIRTHEQTTAAERQTTFNDMIKI ALESVLLGDKE
22597	52965	A	22725	415	759	HRRRIVIDDTGIFRPRNTAQQLR QRPIAMSASGVVQIILEGHWRT HSLRNGFHRGFRL*SSPKVGMQ HGSRQVDHRTQRALRFFRQPGI DFLRPVFTPRRQRLAATNHFSR FVEH

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22598	52966	A	22726	2	2329	GTLPGCGAMHTCPSGPATHLV RRRIVRLPACVVTRANVPTPSR PVNATIGAFHSG*MASQGRRLS AQYPWSPFQYA\ARPVPTVPGR LVFTGTSKAPKISVMGPGMGIP SCSISAKELITDFGVKKIIRVGSC GAVLPHVKLRDVVIGMGACTD SKVTRIRFKDHAFAAIADFDMV RNAVDAAKALGIDARVGNLFS ADLFYSPDGEMFDVMEKYGIL GVEMEAAGIYGVAAEFGAKAL TICTVSDHIRTHEQTTAAESQTT FNDMIKIALESVLLGDKEEDRVI RFGKARATRYALLRPYRGIERIP VWRVDDTGKAHKFADIRLCWP QGSCLDVAKAREVIRGSQPLPA WCENWAQEVDARLTKEAQSA LRPVINLTGTVLHTNLGRALQA EAAVEAVAQAMRSPVTLEYDL DDAGRGHRDRALAQLLCRITG AEDACIVNNNAAAVLLMLAAT ASGKEVVVSRGELVEIGGAFRI PDVMRQAGCTLHEVGTTNRTH ANDYRQADFQFDDFVMAFTQN INGPTQNTRALHGGHKRPDFLP LLGAFHGAIDILAPGGLHGYSL PSSFFHALALSAAFPGKRCKLS VHLPFWGLKDGGPLLTAPLGG ALVGIVGGVGGSNLTFPFHTNF LNVRFVIRRISHRHHHFYRIAKL LMNGAQGSNMLIAAVAGVPHQ NGHFPFTVADRFAIVLSEGSIRV
22599	52967	A	22727	1	702	
22600	52968	A	22728	876	1318	RCHLANASPAAGSHAPSPDSLS/ KIR/QEVG/PPLP/PLLAPLIATPP RTSQPLSPLISSSSPSSPASPVGQ VSPFRETPVPPAMSPWPEDPRR ASPPDPSPSPSAASASERVVPSP LQFCAATPKHALPVPGRLPPCA SGHAMPCWRAKIK

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22601	52969	A	22729	485	1455	PVVQRARNASSCQPFSTSVWAI PSISATSVPMCGATHSILSPKKS TVSDRIGSMQISFFPLSRSAEK* ESPCSSDAFHAIFSVLSGLALHS TTTSLCSSTSGQLVCC**TSLPPT TYGMIACAAPVE*SPRCPV*PPA SAI*RCNNVEALCSTPFERQP*E PAK\SMPDHKPHECVYVVGE*D PAPHPNSREQIHPAHECLAGFP VTQESLFAPLEIVPAYCCEPGRE PRSARSFPFAPRELT*VQLELGT GL*RETLDLVVSAGWA*ARRIS GAVTATPETGTLCQLDSGAECH YRETGVELP*RSPRPVGHGSSR HSRRWRT
22602	52970	A	22730	814	5001	PENSSHRPKPIIPMIASTLINANQ NSVSPYKRTFTRLTALMIIKKA AAQIHVGTSGNQYWRKLDFNS PGGSSPVENSDCSTNSRLSFSPE NILIQNQDIVREAAVQGDGQKQ RQPQATDLDSSGTHGSEMLPAT EVTVSGGFSVEETSCGDTGRSG GEALAVANDSTSTPQNANGLW KLKSTTPGGALPECFGTTDTTFS SAFCRKHGETQDTSQSSLPGTL HCYTGIREGGDDTEVESEAFSC SEGSEQQDAPD
22603	52971	A	22731	34	102	
22604	52972	A	22732	584	893	QKLLPNRMGHPVFVKSSQDPV LLSRIAWKDASTVTWVIEQDPV LRRRRRRTRRRRTRMRRRRGR* */SKRRRMR/GRRGRR*CRRRRR RSSRSRPTRRQRNRNQV
22605	52973	A	22733	2	269	IGKLYWFMPPSANLALRELGIV LFLSVVGLKSGLSWIGYGALIT AVPLITVGILARMLAKMNYLT MCGMLAGSMTDPPA*PRFQTN DREEQHDPQLPQREVGAWRHK PVQLAD

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22606	52974	A	22734	3	958	RCYSLLSRAPHPGIYISIAERV/*I RLNSANFTLNSLLPAEKKLAEE FAVSRMTIRKAIDLLVAWGLV VRRHGSGTYLVRKDVLHQTAS LTGLGEVLKRQGKTVTSQVLIF EIMPAPPAIASQLRIQINEQIYFS RRVRFV\EGIPLMLEDSYMPVK LFRNLSLQHLEGSKFEYIEQECG ILIGGNYESLTPVLADRLLARQ MKVAEHTPLLRITSLSYSESGEF LNYSVMFRNATQIQGWRSHFR R\LHPKKSLTVPPERAPPVFGGL IMRKNHSQRIDSGVRERRRTAG WMKIISKRQRRRIGHGTCQHPA HGQVIHFG
22607	52975	A	22735	2	285	GDEMTTSTLQKAIDLVTKATEE DKAKNYEEALRLYQHPVEYFL HA\IKYEAHSDKAKESIRAKCV QYLDRAEKLKDYLRSKEKHGK LCLKDRVT
22608	52976	A	22736	545	791	
22609	52977	A	22737	249	1574	NHKAIDLVTKATEEDKAKNYE EALRLYQHAVEYFLHAIKYEA HSDKAKESIRAKCVQYLYRAE KLKDYLRSKEKHGKKPVKENQ SEGKGSDSDSEGDNPEKKKLQE QLMGAVVMEKP\NIRWNDVAG LEGAKEALKEAVILPIKFPHLFT GKRTPWRGI\LLFRPPGT\GNSN RPKAGAPKATNSTFFSVSS\SDV KSKRLGETEKLV*NLF\ELARQ HK\PSIIFIDEVDSLCGSRNENES\ QAARRIQNGSSLVQIAGGLGIN NDGDSGFFGATNIP\WVLD\SAI R\RKV*KTKFYIPLPEKACPRPD VSRLHLGSTPHN\LRVATFHKL ARKTEGYSGADISIIVRDSLMQP VRKVQSATHFKKVCGPSRTNPS MMIDDLLTPCSPGDPRAMEMT WMDVPGDKLLEPVVCMSDML RSLATTRPTVNADDLL\KVKKF SEDFGQES
22610	52978	A	22738	52	567	
22611	52979	B	22739	1	1293	
22612	52980	A	22740	443	1027	
22613	52981	A	22741	2077	2430	
22614	52982	A	22742	1	504	

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22615	52983	A	22743	3244	3947	RNEITPFRAMMIIRRMAHRFQT EEIKRISFIKRRVGNKDEINPGA RWRRFHDDGITFLRLLDAGLTI PSGKTIVHPLARQRRGLVKIQFL R*LLAKLTRQPLLPLQPVTARL CLNPRLRRQRKIRMPAGTKWQ RLCPLIGDR*RHRQRSAVYALS VRHNPVHHILRKNGDMYSFPIT IGNNVWIESHVVINPGVTIGDNS VIGAGSIVTKDIPPNVVAAGVP CRVILEINDRDK
22616	52984	A	22744	742	1158	
22617	52985	A	22745	439	2882	PDWQAFQSPPFPASLIIHPKPAK LPGWLCIVQWSLLAITRTPTPV RWAQQTTETVGLVVGDVSDPF FGAMVKAVEQVAYHTGNFLLI GNGYHNEQKERQAIEQLIRHRC AALVVHAKMIPDADLASLMKQ MPADKQCESIPDQNNQTGTQY PRGKEPKLLRRLMHMNRKVGP RGPRRMLLRYLDVEFLSVALA VVHLGPQGTCSRLFLVARALV VAVSEMDKSLSAQAQIYFASSN GPVPDLAYQVDFPRLEIGL*F\E YVDTGAETTLVPGDVLYVPAG GWNFPQWQAPATTFSVLFGKQ QLGF/SAVVQWDGKQYQNLAK QHVARRGPRIGSFLLQTLNEMQ MQPQEQQTARLIVASLLNHCR DLLGSQIQTASRSQALFEAIRDY IDERYASALTRESVAQAFYISPN YLSHLFQKTGAIGFNENLSHTR LGHA*TLLKGYDLKVKEVAHA CGFVDSNYFCRLFRKNTERSPS EYRRHRRLHDNRICQFKTPTDN PENPDRYLTFRRIDKETSSLPKK VAPSCKRLSVSRSSPKPSISIRRC MRLMLIEGRRSSFIHPDKDVDG FHPYNVGRLCQRAPRLRPCTPR GIVTLLERYNIDTFGLNAVVIGA SNIVGRPMSMELLLAGCTTTVT HRFTKNLRHHVENADLLIVAV GKPGFIPGDWIKEGAIVMMSGI NRGVATDASCFPLVPFANRVSG
22618	52986	A	22746	2	126	
22619	52987	A	22747	1	465	
22620	52988	C	22748	78	308	

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22621	52989	A	22749	1	2797	MEHPPVLAVQRVALPSRSSEPE LFLNPPTDEETEAHRGMYLDQ GPRTKDWIPVAPGVREPSPLGP GPSSLWLLVVGGTVEEGSRKH RPTCKKDFTKSKTVDQAPTLCA RHQMLNIQFLISDRDPQCNLHC SRTQPKPICASDGRSYESMCEY QRAKCRDPTLGVVHRGRCKDA GQSKCRLERAQALEQAKKPQE AVFVPECGEDGSFTQNTSCIHSS VYQIGENSSLTFLEKREESGHL QRDWFPLWFPRKARVI
22622	52990	A	22750	1	5295	MNLNQEEIPDLPEKEFRRLVIKL IREGLEKGKAQCKEIQKMIQEV KREIFQEIESLKKKPPKIQKTLDI LLKMQNALESLSDRTEQAEEIN SELEDKVFKLTQSNKDKEKITR KYEQSLQEVWSYVKRPNLRIIG VPEEEENTKSLENILGGIIEENFP SFARDLDIQIPEAQRTTGKLIAK RSLLRHIVFRLSKVKMKERILR AVRQKHQATVSQKNKAGGITL PDFKLYYKATVSQKNKAGGITL PDFKLYYK
22623	52991	A	22751	1	891	GSPFEVMPRDDVFFIVDVKI*DI GVYSCTAQNSAGSISANATLTV LETPSFLRPLLDRTVTKGETAV LQCIAGGSPPPKLNWTKDDSPL VVTERHFFAAGNQLLIIGDSDV SDAGKYTCEMSNTLGTERGNV RLSVIPTPTCDSPQMTVL/HLLD DDGWGHCGLYVIIAVVCCVVG TSLVWVVIIYHTRRRNEDCSITN TDETNLPADIPSYLSSQGTLADR QDGYVSSESGSHHQFVTSSGAG FFLPQHDSSGTCHIDNSSEADVE AATDLFLCPFLGSTGPYVFEGK CVWAQNPF
22624	52992	A	22752	1	2947	MSAPSLRARAAGLGLLLCAVL GRAGRSDSGGRGELGQPSGVA AERPCPTTCRCLGDLLDCSRKR LARLPEPLPSWVARLDLSHNRL SFIKASSMSHLQSLREVAGNRIV EILPEHLKEFQSLETLDLSSNNIS ELQTAFPALQLKYLELNRNKIK NVDGLTFQGLGALKSLKMQRN GVTKLMDGAFWGLSNMEILQL DHNNLTEITKGWLYGLLMLQE LHLSQNAINRISPDAWEFCQKL SELDLTFNHLSRLDD
22625	52993	A	22753	2	417	

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22626	52994	A	22754	1	262	VLDIGS/SLTVPDEFSKQE/RAD GMWWKQLVAGAVAGAVS/RT GTAPLDRLKVFMQIKRAILGQQ ETLMCRSASWLAPWLVPQPNH HLPYG
22627	52995	A	22755	1	762	
22628	52996	A	22756	1	1527	RLAAAGADPAGSRGGRGSREA PTEAARCRASPPPRAGAMRGSP GDAERRQRWGRLFEELDSNKD GRVDVHELRQGLARLGGGNPD PGAQQGISSEGDADPNGGLDLE EFSRYLQEREQRLLLMFHSLDR NQDGHIDVSEIQQSFRALGISIL LEQAEKNFAQA/VDRDGTMTID WQEWRDHFLLHSLENVEDVLY FWKHSTVLDIGECLTVPDEFSK QEKLTGMWWKQLAAGAVAG AVSRTGTVPLDRLKVFMQVHA SKTNRLNILGGL*SMVLEGGIRS LWRGNGINVLKIAPESAIKFMA YEQIKRAIPG\E*ETLPVLERFVA GSLAGATAQTII\YPMEVLKTRL TLRRTGQYKGLAGLRRGGILER EGPRAFYRGYLPNVLGIIPYAGI DLAVYETLKNWWLQQYSHDS ADPGILVLLACGTISSTCGQIAS YPLALVRTRMQAQASIEGGPKL SMLGLLRHILSQEGMRGLYRGI APNFMKVIPAVSISYVVYENMK

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22629	52997	A	22757	1	2127	MDQSGLLALRAAVGAVVGSTL AVDIGILVKDWHPRPLGGKHC QLLGAFRCRQHRRGKEERRGE TKEKKGERENERGKRRRIEGER DKYVKENEKQTCVQKERHSCT GNSPNHMATVQAERGALDSHG GWHPWDYCAVQQGRYHQLLL TKEEIEVQRSKKMCLLQAFLIC CQKSHFLGPGCTRSMVPASASG ESLKLLPLMVEDEGEPVTERE\R KREGERERGRERERRRRKRK RRRKRRRKRRRRRRRG*EFLS LG*NERGKRRRIEGERDKYVKE NEKQTCVQKERHSCTGNSPNH MATVQAERGALDSHGGWHPW DYCAVQQGRYHQLLLTKEEIE VQRSKKMCLLQAFLICCQKSHF LGPGCTRSMVPASASGESLKLL PLMVEDEGEPVTEREQEEGGGE RERERERKKEKEKEKEKEKEEK EKEKEKEEERIRVPLPRVELRLT NIAAKQVGNTILDVAAPADHPS ESSCVYVRFVIKIPVAASFRFKK SYVTNNVESCEDGIHYFWKSH MHSENSCSCKLPCPPHLPAAER LGDALEPLLPTMRRQRQCQNT GDCDGRRQIGTRETEMHRDTSL VAVKTQVDTSREGMGEVEPNS CFWRDTHMASGVGAAFEELPH DGTCDECEPDEAPGAEEVCREC GFCYCRRHAEAHRQKFLSHHL AEYVHGSQAWTPPADGEGAGK
22630	52998	A	22758	348	881	WRQPRWPHHQACLWQRAGSS YSQHKDPHFTSFSTPRAVQNFD GFPCPFLRETTTLVLIPSVPLTDP GSFYRAWSFQCGPRSPRPLLGR TLSQKFLLRLRGRPRRPYMSTL TPF*STRIFERAFCQVMGAESGG RIEKTTLCKRSLGPLMEPRV
22631	52999	A	22759	1	347	MVPASASGESLKLLPLMVEDER EPVTERE/REKGRGREREGERE KEREGERERERERGERKGERER RRG*QPPFHNRFSEGQGRSFLCS RRPRVSRRGHTSRGPARVKAAE RRGLG
22632	53000	A	22760	145	258	PENGLIGLS*KIVLSLNIPVNEN DMKVDEVLYEDSSTA

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22633	53001	A	22761	1	1479	MALKEIFCPVRETETCTINCGTR ISPSILHVGLPYPSTPNVKPERE GCGGGVSGNSKQPGALETAESI GKKEGRREEGSRPESASSLSLLL SLAYDVDKSAQICTRIHSSVPLE AVYPGYIHQSIINQADLSALAPY DPCVCQIHKYHGAYNCLQYSV QNTLYSPTTEQYKRCQAPWVL PAIFTIPASGAAASAVPVRAQA QGGQAAGQRRRLATAPLTGEG EPDHGDRTRAGSQGPEARPRIH LGAARGGDRTRGRPGRRGRDW TRLGREMAAAAVSSAKRSLRG ELKQRLRAMSAEERLRQSRVLS QK\V1AHSEYQKSKRISIFLSMQ DEIETEEIIKD\ICQRGK\ICFIPPV RFSRAITMDMVRIGSP\EGNFFN FPKTSWEYSLRLGEG\DVREEG LVPPGGL/EILILPCPQALGLDQ NHGQPRLG\RGQGAYL*CLS*K RLFCSHSGKLKPPTPPGGWLFK EQICPPRSPVNENDMK\VDEVL
22634	53002	A	22762	1	813	
22635	53003	A	22763	1	368	
22636	53004	A	22764	327	4281	SASASRCDPGSGSRREREEELQ WRRRRRRRRRRRRRRQRQRA AAPAAPAGGIEAVNMASASYHI SNLLEKMTSSDKDFRFMATND LMTELQKDSIKLDDDSERKVV KMILKLLEDKNGEVQNLAVKC LGPLVSKVKEYQVETIVDTLCT NMLSDKEQLRDISSIGLKTVIGE LPPASSGSALAANVCKKITGRL TSAIAKQEDVSVQLEALDIMAD MLSRQGGLLVNFHPSILTCLLP QLTSPRLAVRKRTIIA
22637	53005	A	22765	2	271	
22638	53006	A	22766	299	451	IVALFRSLVRHLRGTMAMESTA TAAVAAEL/VSADKIEDAPAPST SADKVES

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22639	53007	A	22767	1	1122	MATESTATAAIAAELVSANKIE DVPAPSTSADKVERIENGVLGN TLDGVHVEEEEGEKTEDESLVE NNDSIDEEARKELREQVYDSM GEKEEAKKTEDKSFAKPETDKE QDCEMEKGGREDMDISESAEEP QEKVDLTLGWLTEISEGAKGG GAPEGPNEAEVTSGKPEQEVPD VEEEKSVSETDVQKECREKGG WEKHREVIVSIEEKPKEVSEEQP VVILEKQGTAVEVAAESLDPTV KPVDVGGDEPEEK/GTVPGSLR PSPCRDPLPAGLGLWVQLSV** GSGTVQQIY*SH*EENGCTKRA GEGG*RIVC*IQERN*GTEGTAT RNYRKDRRCKGVSDYWECS*T GSESYSGGELYFRFHS*WRRLF
22640	53008	A	22768	223	339	
22641	53009	B	22769	341	496	
22642	53010	A	22770	12	1099	VSGVPNCLFFSQALFRSLVRHL RGTMAMESTATAAVAAELVSA DKIEDVPAP\STS\ADKVESLDV DSEAKKLLGLGQK\HLVMGDIP AAVNAFQEAASLLGKKYGETA NECGEAFFFYG\KSLLELARME NGVLGNA\LEGVHVEEEEGEKT EDESLVENNDNI/D*N*RLGRG* *RK**D*RNAK*FSP*KQVSSRK *GGGDWEPRACLGYAGFSKDH F*KARNKRSTALCCPGTS*TRRS *C*I*\KLCASC\GGVPVLP*PTGP VPGSPRPSPCRDPLPAGLGLWV QLSV**GSGTVQQIY*SH*EQNG CTKRAGEGG*RIVC*IQERN*GT KGTATRN*REDRRCKGVSA*W ECS*TGSESYS

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22643	53011	A	22771	11	2485	VSGVPNCLFFSQALFRSLVRHL RGTMAMESTATAAVAADVVS ADKIEDVPAPSTSADKVESLDV DSEAKKLLGLGQKHLVMGGIP AAV\NAFQGAA\SLL\GKKYGET ANE\CGEAFFFYG\KSLLELARM ENGVLGNALEGVHVEEEEG\EK TEDESLVENNDN\IDEEAREELR EQVYDAMGEKEEAKKTEDKSL AKPETDKEQDSEMEKGGREDM DISKSAEEPQEKVDLTLDWLTE TSEEAKGGAAPEGPNEAEVTSG KPGQ\EVPDAEEEKSVSGTDVQ EECREKGGQEKQGEVIVSIEEK PKEVSEEQPVVTLEKQGTAVEV EAESLDPTVKPVDVGGDEPEEK VVTSENEAGKAVLEQLVGQEV PPAEESPEVQTEAAEASAVEAG SEVSEKPGQEAPVLPKDGAVN GPSVVGDQTPIEPQTSIERLTET KDGSGLEEKVRAKLVPSQEETK LSVEESEAAGDGVDTKVAQGA TEKSPEDKVQIAANEETQEREE QMKEGEETEGSEEDDKENDKT EEMPNDSVLENKSLQENEEEEI GNLELAWDMLDLAKIIFKRQET KEAQLYAAQAHLKLGEVSVES ENYVQAVEEFQSCLNLQEQYL EAHDRLLAETHYQLGLAYGYN SQYDEAVAQFSKSIEVIENRMA VLNEQVKEAEGSSAEYKKEIEE LKELLP\EIREKIENAKE\SQR\SG
22644	53012	A	22772	52	161	FQNPTGLY/CDTEYN\RLQKQQ TEKTKQKKTQFHPICN
22645	53013	A	22773	3	115	FFQNPTGLY/CDTEYN\RLQKQQ TEKTKQKKTQFHPICN
22646	53014	A	22774	229	358	
22647	53015	A	22775	257	386	
22648	53016	A	22776	259	294	
22649	53017	A	22777	217	398	KAWWNLLRKSEPKSCGS*GGL STSRERLVECSSPLGLGYCG**L CHLQEPHYGSLHRMSS
22650	53018	A	22778	1	3386	

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22651	53019	A	22779	391	2100	SRRTAGVRLDILCKDPIMWVSA DGHSYQPQYPKAKRATEFHFF NFKALLARAAVGAARGIHIHRC GLTKRPDARRRRVAGAQGREP AISLPGDRAAGARATRTRGPGP APKMPAIAVLAAAAAA\WCFL QVESRHLDALAGGAGPNHG\NF L\DNDQ\WLSTVSQYDRDKY\W NRFRDEVEDDYFRNW\NPNKPF DQAL\DPSKDPCLKVKCSPHKV\ CVTQ\DYQTAL\CVSRKHLLPR QKEWGTWAQKHWGLDL*ILV K\CKPCSRGRSSAMGLAGSDGP LLTAFQVANLEFHACSTGQK/S FATLCDG\PCPCSSQSLEPPKHK GRKGVPCTDKELRNLASRLKD WFGALHEDANRVIKPTSSNTAQ GRFDTSILPICKDSLGWMFNKL DMNYDLLLDPSEINAIYLDKYE PCIKPLFNSCDSFKDGKPFLNNE WCLLPSQNPGGLP/CAQNEMNR IQ\KLSKGKSLLGAFIPRCNEEG YYKATQCHGSTGQCWCVDKY GNELAGSRKQGAVSCEEEQETS GDFGSGGSVVLLDDLEYERELG PKDKEGKLRVHTRAVTEDDED EDDDKEDEVGYIW
22652	53020	A	22780	2	441	HGVQGAGCGEVAAVSIELGAG GPVWRAAPRACSRLQLLRGFG LEGQWFGESCCRRGAS*EGSTR *PPPRRQPWPEWVMSWVPPET REPARISPAPAKQN*PPPAPKSP AAPA\PQAAVAATPSPPGEISEA WDSLESFSKPAFFSQ
22653	53021	A	22781	3	121	

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22654	53022	A	22782	2	1488	FVNNMADGEEPEKKRRRIEELL AEKMAVDGGCGDTETWKDR\ WNHVKK\FLERSGPFTHPDFEP\ STESLQFLLDTCK\VLVIGAGG\ LGCELLKNLALS\GFRQIHVID\ MDTI\DVSNS*IRQFLFRPKDIGR PKAEVAAEFLNDRV\PNC\NVV PHF\NK\IQDFN\DTFY\RQFHI\IV CGTGTLSCARRWINGMLISL\LN YERMVS*DPSSIVPLID\GGTEGF \KENARVIL\PGMTACIECTLEL YPPQVNFPMCTIASMPRLPEHCI \EYVGMLQWPKEQPFGEG\VPL DGDDP\EHIQWIFQKSLERASQY NIRGVTYRLTQGVVKRIIPAVA STNAVIAAVCAT*/EVFKIATSA YIPL*IITWVFNDV\DGLYTYTFE GRKGK\ENCPAC\SQLPQNISVF LHQAKLQ\EVLGIILTNSASLQN EILPAITATLGGEKIGTLYLQSV TSI\EERNRANFFQTIERNWGLL DGPKTGRLLDVTTP\QTVLFQTS ILLLKGKSPT
22655	53023	A	22783	1	1719	
22656	53024	B	22784	199	460	
22657	53025	A	22785	226	1620	NGSGLALATGNRDPGLCPLSAP SCPWR*KSAGASTQQAYSSQSQ /HPAYHRITPT\LTNFALRLYKEL AADAPGNIFFSPVSIS\TTLCLLC LG\AQANNSALILEGLGFNLTET PEADIHQGFRSLLHTLVLPSPKL ELKVGNSLFLDKRLKPRQHYFD SIKELYRAFAFSAHFTDSVTTGR QINDYL*RRTYWPGVDLPFRS/L ARDTFMVLA\NFILFSKAKVKA TLSSRVPDPKSRPVFLVDERTSF \QVPMMHQKEMHRFLYDQDLA CTVLQIE\YRGNALALLVLPDPG KMKQVEAALQPQTLRKWGQL LLPSLLDLHLPRFSISGTYNLEDI LSPNWFSPTYTLNKITSLQSVG G*LNKSISKVSHKSMVDMNEK GDQRPGLLQASSPSPHL*/YTMS DPHAHFNRPFLLLLWEVTTQSL LFLGKVVNPVVWVTMVGGQE LSYLILDQTDRPEPACILGLLCG
22658	53026	A	22786	64	288	
22659	53027	A	22787	1	1923	

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22660	53028	A	22788	309	2286	CAVCHISFQDTPVLVSSNVTMQ FGSKPLFENISVKFGGGNRYGL\ IGANGSGKSTFMKILGGDLEPT LGNGSLDPNER\IGKLRQ\DQFA FEEFTVLDTVIMGHKEL\WKVK QERDRIYALPEMSEEDGYKVA DLEVKYGEMAGYSAEARAGEL LLG\VGIPVEQHYGPMSEVAPG WKLRVLLAQALFADPDILLLDE PTNNLDIDTIRWLEQVLNENNS T\MIIISHDRHFLNMVCTHMAD LDYGELRVYPGNYDEYMTAAT QARERLLADNAKKKAQIAELQ SFIDKIKLEEVKASSRQNPFIRFE QDKKLFRNALEVEGLTKGFDN GPLFKNLNLLLEVGEKLAVLGT NGVGKSTL\LKTLVGNLQPDSG TVKWSENARIGYYAQDHEYEF ENDLPVFEWMSQCKQ*GDDEQ AVRSIFGRLLFSQDVIKKPAKVL SAPFCKDSILEAIDAGIKLIITITE GIPTLDMLTVKVKLDEAGVRMI GPNCPGVITPGECKIGIQPGHIH KPGTGELNITTGGIVKARDTQIA LNDKSKGDVRVDGQNSLLETF NMYVGTSGTGTLTLTNNGTLN VEGGEVYLGVFEPAVGTLNIGA AHGEAAADAGFITNATKVEFG LGEGVFVFNHTNNSDAGYQVD MLITGDDKDGKVIHDARHTVF
22661	53029	A	22789	1	553	
22662	53030	A	22790	1633	2207	ILFFDKGMPAQTPSLQKRWEK M*LVLW*GDREGIKAI/ISEESW GARAPIFLLR/MMEDQGLYSIR MGGARGLPGKSLAL*GAGRGF YSGERTWTLSLPSGNCAP\YQR GGWWYHACA\HSNLNGVWHH GGHYRSRYQDGVYWAEFRGG AYSLRKAAMPHLAPEAVTLCSF GPLGPRGHWSAGAPSCSGHTFF
22663	53031	A	22791	34	210	AAADPLRHLRRGAFIKAGRHA G/PSLPVCLQATA\H*MDLARLA LVLVVRTSASTKSSTRE

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22664	53032	A	22792	397	1168	LLSRISKVSSKLPVRGGAGSLCT GDQRK\RRKFL\ETVELQISLKN YDPQEGQSAFSGHPSRL*V\PSP PLSSLVCVLGGPSKHL*RRLRP VGYPPTMDIEGA*KKLNQELKN LVKKAGPRKYDCVFWPQESLD SSKIPPNPSGPGFK*RAGKVPFP CLTHNGKHGLAQSGIEVEVPTF/ LSFQMKKGVYVWAVAVWSRE R*QTNELVYNIHLACQLSWVSL LKEKNWQ\NVPGPYIIKSTMGQ SPSSHILRHIRINSITS
22665	53033	A	22793	1	377	SVSRVPTRSLRTSTWRLAQDQT QDTQLITVDEKLDITTLTGVPEE HIKTRKVRIFVPARNNMQSGVN NTKKWKMEFDTRERWENPLM GWAST\WSYDIEERKVPKPKSK SYGANFSWNKRTRVSTK
22666	53034	A	22794	183	368	
22667	53035	A	22795	3	623	ILAFACSKMAAVSMSV\VLRQT LWRRRAVAVAAL\SVSRVPT/R RSLRTSTWR\LAH\DQTQDTQLI TS**KIGISLTFNWPFPEEHIKNL EKSGIFVPCSPITCQSGVNNTK\ KWK\MEFDT\RER\WEN\PLMG\ WASTGLIPLS\NMVLNLPVLKE DAVS\FAEK\NGWELWTLEERK\ VPKPKSQVFMGANFS\WNKRTR VSTKIGLALTISPA
22668	53036	A	22796	1	798	MNKVNPTQQDKEDHPELIITSIG DKRQLTLEAASGVCHRGTQTR VKEESKKFLISMSFRGGKPVHK VVERACVCTCLHHTSVPATHN TQRRHTTPTTRKNGRKRRGKK EREKRKDREHNTGRRTKRKKT RNIGGQRTQQKQKQSEDKARR EPGGGRKQGRGREDGTRQRRG GRTRNREEGAQRGRNGR/RGEG RRTEEETHMA*APDITATQQTE QQGHGTRQRDTTLRRHTAEDA QPSEHASADQAHTKKTE*SVSR TNGQYLLT
22669	53037	B	22797	85	322	

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22670	53038	A	22798	165	4733	AATALLTHGQEEGQVEGQDED IPPITCVQNGLRYHDRDVWKPE PCRICVCDNGKVLCDDVICDET KNCPGAEVPEGECCPVCPDGSR VTHRPKKPPGVEGPKGDTGPPR PKGT\PGPPGRDGIPGQPGLPGP PGPPGPPGPPGLGGKLLLPKLSY GYDEKSTGGISVPGPMGPSGPR GLPGPPGAPVSIQDVFICLLGLW SFGGKTGMRAGEMLRDLLGPQ GFQGPPGEPGEPGASGPMGPRG PPGPPGKNGDDG
22671	53039	C	22799	88	392	
22672	53040	A	22800	37	293	
22673	53041	A	22801	55	1917	GGGGVRRRRGTRRSEPGDSRSA MAPIGLKAVVGEKIMHDVIKK VKKKGEWKVLVVDQLSMRML SSCCKMTDIMTEGITIVEDINKR REPLPSLEAVYLITPSEKSVHSLI SDFKDPPTAKYRAAHVFFTDSC PDALFNELVKSRAAKVIKTLTEI NIAFLPYESQVYSLDSADSFQSF YSPHKAQMKNPILERLAEQIAT LCAT\LKEYPA\VRYRGEYKDN ALLAQLIQDKLDAYKADDPTM GEGPDKARSQLLILDRGFDPSSP VLP*I*LFQGMSY*SCLPI\ENDV\ YKYETSGIGGGHGVKGGASGT EDDDLW\IALR\HKHIAEV\SQ\E VTRSLKDFSSSKRMNTGEKTT MRDLSQMLKKMPQYQKELSK YSTHLHLAEDCMKHYQGTVDK LCRVEQDLAMGTDAEGEKIKD PMRAIVPILLDANVSTYDKIRJIL LYIFLKNGITEENLNKLIQHAQI PPEDSEIITNMAHLGVPIVTDST LRRRSKPERKERISEQTYQLSR WTPIIKDIMEDTIEDKLDNK\HY P\YISTRSSASFSTTAV\SARYGH WP*GTRPPGEYRSGP/RVFIIFHP LGGVSLNEMRCALRR*PRANG KWGGA**GSTHILQPHRNLPGH

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22674	53042	A	22802	46	1931	GGGGVRMLCGTRRSEPGDSRS AMAPIGLIAVVGEKIMHDVML NDLNMGEWKALLVDQLSMRM LSYCCLMTDIMTEGITIVEDINK RR*PLPSLEAVYLITPSEKSVHS LISDFKDPPTAKYRAAHVFFTD SCPDALFNELVKSRAAKVIKTL TEINIAFLPYESRVYSLDSADSF QSFYSPHKAQMKNPILERLAEQ IATLCATLKEYPAVRYRGEYKD NALLAQLIQDKLDAYKADDPT MGEGPDKARSQLLILDRGFDPS SPVLHELTFQAMSYDLLPIEND VYKYETSGIGEARVKEVLLDED DDLWIALRHKHIAEVSQEVTRS LKDFSSSKRMNTGEKTTMRDL SQMLKKMPQYQKELSKYSTHL APCLRTCMKHYQGTVDKL\CR V\EQDLAMG\TDAEG\EKI\KDP MRAIVPILLDANVQTY*QIRIILL YIFLKNGITEENLNKLIQHAQIP PEDSEIITNMAHLGVPIVTDSTL RRRSKPERKERISEQTYQLSRW TPIIKDIMEDTIEDKLDTKHYPYI STRSSASFSTTAVSARYGHWHK NKAPGEYRSGPRLIIFILGGVSL NEMRCAYEVTQANGKWEVLIG STHILTPTKFLMDLRHPDFRESS RVSFEDQAPTME
22675	53043	A	22803	2	51	
22676	53044	A	22804	236	451	LHLPLFLGAIRSGQYGLWNLFR VLGWTCSLGIYLGWRVS*NFG RGTKALKVLSTIS/E*RNHHCHP *NNIFVY

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22677	53045	A	22805	3	1173	GAGAPAAGQAGLTSTSAVRAR PVSPARQSQDPAASLSLHLSLPP APGAGCARWRRRGPQAAMAA GAGAGSAPRWLRALSEPLSAA QLRRLEEHRYSAAGVSLLEPPL QLYWTWLLQWIPLWMAPNSIT LLGLAVNVVTTLVLISYCLTAT EEAPYWTYLLCALGLFIYQPLD AIDGKQARRTNSCSPLGELFDH GCDSLSTVFMAVGASIAARLGT YPDWFFSRSFYLGCLVFYC\AH WQTYVS\GMLRFGKVDVTEIQI AL\VIVFVL\SAFG\GATM/WGD YTIPILEIKLKILPVLGFLGGVIFS CS\NYSHVILH\GGVGKNG\STIA GTSVLSPGTPH/MGLIIIL\AIMIY *KVRQLMVF*KSIPCL*YPQCLG CVF\AKVSQKISGSSHDQK
22678	53046	A	22806	2	1091	CPGRRRRRRPGRSRARATALPT PGPRKRGGPAGRKRERPERCSS SSGGSSSSGDEDGLELDGAPGR GKRAAQPVAAGKVGGAAVVV AEPEHTKKHVKLETLLITTEGK LWSWGRNEKAQLGHGDTKRV EAPRLTEGLSHEVIVC\TCARNH TLALTETGSVFAFGENKMGQL GLGN*TDAVPSPVQIMYNSLPIT KMA/CGYGWLGYTEQKDEMV PRLVKLFDFPGHGASQIYAGYT CSFAVSEVGGLFFWGATNTSHE STMYPKAVQDLCSWRIWSLAC GKSSIIVAADESTISWGPSPTFG ELGYRDHKPKSSTAAQEVKTL HGIFSEPVAMGYSHSLVIARDE SETEKEKIKKLPEYSPQTL

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22679	53047	A	22807	1	1409	MSLGLASERLWAGLGLPALPL ADEGGECGETLFVWRSQKLEG SKCKGQLLIFGATNWDLIGRKE VPKQQAAYRNLGQNLWGPHR YGCLAGVRVRTVVSGSCAAHS LLITTEGKLWSWGRNEKGQLG HGDTKRVEAPRLIEGLSHEVIVS AACGRNHTLALTETGSVFAFGE NKMGQLGLGNQTDAVPSPAQI MYNGQPITKMACGAEFSMIMG LQRKPLFLWGALNMGQLGTQL RMGKFHSPGAQRIEYDCELVPR RVAIFIEKTKDGQILPVPNVVVR DVACGANHTLVLDSQKRVFSW GFGGYGRLGHAEQKDEMVPRL VKLFDFPGRGASQI/SCWL/HTC SLCCQ*NGWSVFLGGHQHLP*I YHVPQKQCRTSAAGESGTLAC GKSSIIVAADESTISWGPSPTFG ELGYGDHKPKSSTAAQEVKTL DGIFSEQVAMGYSHSLVIARDE SETEKEKIKKLPEYNPRTL
22680	53048	C	22808	277	518	
22681	53049	A	22809	2	192	
22682	53050	A	22810	1	2946	MAEAGLRGWLLWALLLRLAQ SEPYTTIHQPGYCAFYDECGKN PELSGSLMTLSNVSCLSNTPAR KITGDHLILLQKICPRLYTGPNT QACCSAKQLVSLEASLSITKAL LTRCPACSDNFVNLHCHNTCSP NQSLFINVTRVAQLGAGQLPAV VAYEAFYQHSFAEQSYDSCSRV RVPAAATLAVGTMCGVYGSAL CNAQRWLNFQGDTGNGLAPLD ITFHLLEPGQAVGSGIQPLNEGV ARCNESQGDDVATCS
22683	53051	A	22811	258	362	
22684	53052	A	22812	1	4038	MAEAGLRGWLLWALLLRLAQ SEPYTTIHQPGYCAFYDECGKN PELSGSLMTLSNVSCLSNTPAR KITGDHLILLQKICPRLYTGPNT QACCSAKQLVSLEASLSITKAL LTRCPACSDNFVNLHCHNTCSP NQSLFINVTRVAQLGAGQLPAV VAYEAFYQHSFAEQSYDSCSRV RVPAAATLAVGTMCGVYGSAL CNAQRWLNFQGDTGNGLAPLD ITFHLLEPGQAVGSGIQPLNEGV ARCNESQGDDVATCS

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22685	53053	A	22813	198	380	ASSESDSTPCR*MAYSWPPNSN SSHCIKELPLFMGKIPAAS*DGG PQGLAIFPPGVIVGI
22686	53054	A	22814	1	154	
22687	53055	A	22815	35	486	PARRGRDEC*VLAPFRATRPPS RRTR*SKATYPTPSNDQTRTIRT SRERASMPRSAEPKRPTIPRLHP SPRGIVTVSS/RPRSHALPVSHIH SCHSRTAISDNQVPAFLQVYGE EVRKRAGEVTQAITGFPRYRLF FKMLRCHRSIQVTAST
22688	53056	A	22816	212	365	RCRSGPAPRSAPGARPASPSPPA AGTCR*RPAGHCPAGAAGLLSL CPRCST
22689	53057	A	22817	293	618	QQNPTNCLPPASR*SKT*RARST AGPTRPHLHHPAAPAPGSPACA GEGRLQR/HSPNPLYFNWKKQR FAAKPHFRRPQSSLNPQQWLLA GLLQEESSSLGTDTAPLHSLG
22690	53058	A	22818	3	1129	FCLDDLSSAINEHLSARGRRRRS IVKVSLHPAVIGLKSKFLKKPD QLRKLF\IGGLSFETTDESLRSHF EQ\WGTLTDCVVMRDPNTKRS RG\FGFVTYATVEEVDAAMNA RPHKVD\GRVV\EPKRAVSREDS QRPGA\HLTV\KKIFVGGIKEDT EEHHLRDYFEEIILNSMGKLEV VEIH*LDR\GQWPRKRGFAFVT FDGHDSVDKIVIQKYHTVNG\H NCEVRKALSKQEMASASS\SQR G\RVGSGNFWCGRT\NGFGGND NFG\RGGNFSWSVVAFGG\SRG GVWIWVAVGDGYNGFG\NDGS HFG\GGGSY\NDFGDFH\NQSSK FWTP*RGGNLGGQKLWPPMGG GG\QYFAKPTKPKVAYGRFPAA ASSYGKWPEDFN
22691	53059	A	22819	1	568	MGKMSPGHVRDFHGSCHHNRP GGPGGKSGFMGQALGPG/GCV QPRDLVLCVSATPAMAERGQC GAQAVASEGGSPRPWQLPCGV EPADFRRYMETPGCPGRNL/PA GAGPL*RTSAGAVWKGNVRSE SP/PQSLYWGTASGAVRRGPPSS RNQNGRSTDSLHCMPGKDTQ\P NP*KQPGGRLHPAKPQGRSCP
22692	53060	A	22820	232	389	

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22693	53061	A	22821	3	401	VGVCEKRGAPG\PPLAPGPARG PVAAAVPP/GPGASRARP*DAA AAAGGRGPPEQ*T*KAWGLHP GTGSL/RGHPAPM*PLLRAFPRS PLHPLPPPHPLPRRAA\SNPGTS KCRTAAGTRQWGGRQSQLQRC QCLR
22694	53062	A	22822	1	410	MGKMSPGHVRDFHGRPSHHRP RGPGGKSGFVGKVQGPHAVCS LGTWCLVSQPLHP\G*KGPMYS SG\VASEGGSPKPWQLPRGVEP MGAQKSRTEVWEPLPRFQKIY GNTWMPRIPMCCARDPGGAKG GCSNPSQRR
22695	53063	A	22823	264	979	GPRHADPANFSARNLSRP*DAP GRVQDPRPQAPQL\PPGLGAPSR VRRPPPRRPVDRTLPGGPRPPA AAA\GPTGGRGS\PRAGGTAAA TGPRAGPGARGAAGSAPFLTDP NM\GRPPPPATTTPPGAATAPGP REEAPGKFRVSPPGPSGAGGPP TRASPTPTAAGGGGGDSEGEGP ILLVADAG\PDSARSPPGLPGCV LSAAPRSRRDPDAVGGLAASA AARRLNTTWKLPQLGASTL
22696	53064	A	22824	271	426	
22697	53065	A	22825	546	1296	KMVDCLANSEANTRRISIVENC FGAAGQPLTIPGRVLIGEGVLT KL\CRKKPKARQFFLRNDIVV* GNIVIQKKKYIKQHIIPLENVTID SIKDEGDLRNGWVIKTPTKSF\A VYAATATEKSEWMNHINKCVT DLLSKSGKTPSNEHAAVWVPD SEATVCMRCQKAKFTPVNRRH HCRKCGFVVCGPCSEKRFLLPS QSSKPVRICDFCYDLLSAGDMA TCQPARSDSYSQSLKSPLNDMS DDDDDDDMQ
22698	53066	A	22826	1219	2370	
22699	53067	A	22827	164	601	DRTNIMVGYHQTNQKTDTGKT PTRRPVLVDH\NRLPEGSRGRL AVAVAGDHPAAVQVTMTLVN DTGFDPVFSGSIAESWGQHSGT PSYC*DWEAATMLRAFPLAKK GETKDLRQFPNIDNAYMELGT NRADAVLHDTPNILYFMQF
22700	53068	A	22828	2	91	

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22701	53069	A	22829	1	1188	MGAEPSLLTSLGTLWSGERFQC MRAKIWERSRKGRRFSTDVISP TKDSFAGPFQPISDTLVQHQRIY GLKVCVLPDPCKIRILKPNPQC VGKWEEEVAENEIQVFGGERF DINKYSKSPPPPTPQPLYLTAGF ASCRNHRKSEELREGKGESPGK SKPFHLQANFTVALVTTLQGDK HSQEAFIRPVAKAKTTCTYLSN VCEMKDFKRINCPDPFHKMAP KAKKEA\PAPP\KAEAKAKGFK GPRRQVLK\GVHNHKKRKRKK ERSRTFTHLSRRPGRPLRI\RRQP \KYPSGRAAPRRNKLD\HYAIIK FPLT\TESA\MKKIEDNNTL\VFI\ VELLKATTKNQIKQGC*RSLYD I\DVGQGSTPWISAWMGEKKGI CSQLAPDLPIAFGMFANKIWGFI
22702	53070	A	22830	1413	2197	RVEWRWYNVLPCLDVHSGPVD RRSHVMTAAEKPPFCPAWGQA VSQQSCALEPRTGEEGGKGIQG PASGLFPTGEEISVVPNRWLDA SLSPVILGVQG\GSQCLSCGVGQ EPTLTLEVRLGASSLGTQPQML SLLKPGSPQPWCCGTP*QDSVD GSFASSLRILAKALLCGPGFCPS LTLPSFCRKPVTIME\LYLGAKE S\KSFTFYRRDMG\LT\SSFESAA\ YPGWFLCTEPE\ADQPVRLTQL PENGGWNAPITDFYFQQ\CD
22703	53071	A	22831	100	177	KRDHF*SRLQQVSRSVRWSSSA TDSR
22704	53072	A	22832	610	1080	
22705	53073	A	22833	1169	1308	

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22706	53074	A	22834	1	1889	ACRRRAGTWTPPRPRGSGSRA MAGNCGARGALSAHTLLFDLP PALLGELCAVLDSCDGALGWR GLAERLSSSWLDVRHIEKYVDQ GKSGTRELLWSWAQKNKTIGD LLQVLQEMGHRRAIHLITNYGA VLSPSEKSYQEGGFPNILFKETA NVTVDNVLIPEHNEKGVLLKSS ISFQNIIE\GTRNFHKDFLIGERG E/IFGGYQEGKIQTLTYAVKLFK QEKKMQCKKHWKRFLSELEVL LLFHHPNILELAAYFTET\EKFC LIYPYMRNGTLFDRLQCVGDT APLPWHIRIGILIGISKTIHYLHN VQPCSVICGSISSANILL\DDQFH PKLTDFSMAHFRSP\LEHQSCCI NMPSS\SRKHLWY\MPEEYIRQ GKLSIKTDVYSFGIVIMEVLTGC RVVLDDPKHIQLRDLLRELMEK RGLDSCLSFLDKKVPPCPRNFS AKLFCLAGRCAATRAKLRPSM DE\V*RALESTQASLYF\AGDPP TSLKALRGP\SPLF\LEKVT\SIPV \EDDE\KPNNNLLPS**KALRMK RWPQK\TPF\ECSQP\EVWFLSLE QKAREARENEEACNMPSSS\CE ESWFPKY\IVPS\QDLRPL*GK*K ILSSQA\SGHSC\RTKPVESSCSS KFSWDEYEQYKKE

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22707	53075	A	22835	1	1560	RWERGGKRFRAADPMSALRRS GYGPSDGPSYGRYYGPGGGDV PVHPPPPLYPLRPEPPQPPISWR VRGGGPAETTWLGEGGGGDG YYPSGGAWPEPGRAGGSHQEQ PPYPSYNSNYWNSTARSRAPYP STYPVRPE\LQGQSLNSYTNGA YGPTYPPGPGANTASYSGAYY APGYTQTSYSTEVPSTYRSSGN SPTPVSRGIYPQQDCQTEAPPLR GQVPGYPPSQNPGMTLPHYPY GDGNRSVPQSGPTVRPQEDAW ASPGAYGMGGRYPWPSSAPSA PPGNLYMTESTSPWPSSGSPQSP PSPPVQQPKDSSYPYSQSDQSM NRHNFP/CASVHQYESLGDQ*T MDDSRILLDSPSPSIVPEPSACM GNAHPVTHP\NNQDQSSSLPEE CVPSDESTPPSIKKIIHVLEKVQ YLEQEVEEFVGKKTDKAYWLL EEMLTKELLELDSVETGGQDSV RQARKEAVCKIQAILEKLEKKR IMKGFITKWKPVTNLTKEHLIW LITLFLKCLLMTRSNTFQLFL
22708	53076	A	22836	8	207	TPVPRALRSPAGLEGSHLSSIST MMPAVMSVGKVTENGGSPQGI KSPSKPPGPNRIG*RNQVSVHT
22709	53077	A	22837	459	5520	RQVRPAGLEGSDLSSINTMMSA VMSVGKVTENGGSPQGIKSPSK PPGPNRIGRRNQETKEEKSSYN CPLCEKICTTQHQLTMHIRQHN TDTGGADHSCSICGKSLSSASSL DRHMLVHSGERPYKCTVCGQS FTTNGNMHRHMKIHEKDPTSA TATAPGRGDFASAKSSKRKLSH DAESEREDPAPAKKMVEDGQS GDLEKKADEVFHCPVCFKEFV CKYGLETHMETHSDNPLRCDIC CVTFRTHRGLLRHNAL
22710	53078	A	22838	164	434	
22711	53079	A	22839	23	242	
22712	53080	A	22840	187	325	
22713	53081	A	22841	1	130	NCPMCWPGQSPRVPST*GRRNP PPKRRSVSAES*RHWPQSPSP
22714	53082	A	22842	614	774	QEPMRMCTMLANSSPSSSQATP PGL*SWNQPSLPARTLSRHEWT SCLGSSANL
22715	53083	A	22843	396	560	LFPHDGIKHKGKENP/PKGPPPP THPQTPPRPADAPLVATKSTLD QAWALLAVATS
22716	53084	B	22844	124	205	

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22717	53085	A	22845	1	2355	MVGSRRISGVIPLPFTRRAGIFS DPRANMQPLWAPVPPATFVPTS LPPVPTARPPTSASCHCQQVPC AGLEVALPGNRTICWLSLWPS WQLDEDAQSPALESSSIRQFPT APRSGYPGTLCPSFLFGPRPRTC EYHSKPVLCAPSSRASPSSATTL STRTLWGPGAGSHPFGVHNTR LSPDLCPGKIVLRALKESGAGM PEQHKDPRVQENPDDQRTVPE VTGDARSAFWPLRDNGGPSPFV PRPGPLQTDLHAQSSEIRYNHTS QTSWTSSSTKRNAISSSYSSTGG LPGLKQRRGPASSRCQLTLSYS KTVSEDRPQAVSLGHTRCEKG ADTAPGQTIAPTASRPHINTSLH VEDKAISDCRPSRPSHTLSSLAT GASGGPPVSKAPTMDAQQDRP KSQDCLGLVAPLASAAEVPAT APVSGKKHRPPGPLFSSSDPLPA NSSHSRDSAQVTSMIPAPFTAA SRDAGMRRTRSAPAAAAAAPP PSTLNPTSGSLLN\EWMEAPHIS WPQPQLQHVPRGQ/NVRYNQR SQTSRTRS/CPQTKCQLQLPQLY GRPPGSKAEEG\PASSHCQLALS SSNTVSEDGPQAVSSGHRCENK AGTAPGQTLAPRGGSPRSQASR PHINTALHVEDKAISDCRPSRPS HTLSSLATGASGGPPVSKAPTM DAQQDRPKSQDSLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS
22718	53086	A	22846	1	1200	MPEQDKDPRVQENPDDQRRVP EVTGDARSAFRPLRDNGGLS/PP FVPGPGPLQTDLHTQR\LGYRV TVEDLDREKEAAFQRINSALQV EDKAISDCRLSRPSHTLSSLATG TSGLPAVSKAPSMDAQQERHK SQDCLGLLAPLAPAAEVPSTAP MSGKKHRPPGPLFSSSDPLPATS SHSQDSAQVTSLIPAPFPAASM DAGMRRTSPGTSAPAAAAAPPP STLNPTLGSLLEWIEALHISGPQ PQLQQVPRGQNQRSQTSRTSSC PKRK/CHLQLLQLYGRPPGTKA EEG\PASSHCQLTLSSSNTVSED GPQAVSSGHTHCEKTADTAPG QTLAPRGGFPRSQASRPCRHKF PLLPRRRGEPLMLPPPLELGYR VTAEDLDREKEVAFQRIKSALQ VEDKAI

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22719	53087	A	22847	2	1762	YHSKPVLCAPSSRASPSSATTLS TRTLWGPGAGSHPFGVHNTRL SPDLCPGKIVLRALKESGAGMP EQHKDPRVQENPDDQRTVPEV TGDARSAFWPLRDNGGPSPFVP RPGPLQTDLHAQSSEIRYNHTS QTSWTSSSTKRNAISSSYSSTGG LPGLKQRRGPASSRCQLTLSYS KTVSEDRPQAVSLGHTRCEKG ADTAPGQTIAPTASRPHINTSLH VEDKAISDCRPSRPSHTLSSLAT GASGGPPVSKAPTMDAQQDRP KSQDCLGLVAPLASAAEVPAT APVSGKKHRPPGPLFSSSDPLPA NSSHSRDSAQVTSMIPAPFTAA SRDAGMRRTRSAPAAAAAAPP PSTLNPTSGSLLN\EWMEAPHIS WPQPQLQHVPRGQ/NVRYNQR SQTSRTRS/CPQTKCQLQLPQLY GRPPGSKAEEG\PASSHCQLALS SSNTVSEDGPQAVSSGHRCENK AGTAPGQTLAPRGGSPRSQASR PHINTALHVEDKAISDCRPSRPS HTLSSLATGASGGPPVSKAPTM DAQQDRPKSQDSLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS SDPLPATSYHSRDTAQ

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22720	53088	A	22848	292	2053	GSVAWSPFSPSPSSLCLWDLPV APTLWGPGAGSHPFGVHNTRL SPDLCPGKIVLRALKESGAGMP EQDKDLRVQENPDDQRRVPEV TGDARSA/FLAPAGQWSPLSLC AQSRASADIPPCPEVRNQI*PDIP DHLDELMHQPKCHLQLLQLCG RLAGAKVEEGASGAKEQGRDA *AGQGTPESQQNPDDQRTVPEV TGDARSTVRPLRDSGGLSPFVP RPGPLQTDLHAQSSEIRYNQTS QTSWTSSSTKRNAISSSYSSTGG LLGLKQRRGPASSRCQLTLSYS KTVSEDRPQAVSSGHTRCEKA ADTAPGQTLAPRGGSPRSQGSR PRRRKIALLPHR*GELQVEDKAI LDCRPSWPSHTLSSLATGASGE PPVSKAPTMDAQQDRPKSQDC LGLVAPLASAAEIPSTAPVSGK KHRPPGPLFSSSDPLPATSSHSR DSAQVTSLIPAAFTAASMDVG MRRTRPGTSAPAAAAAAPPPST LNPTSGSLLN\EWMEALHISGPQ PQLQQVPRGQ/NVRYNQRSQTS RTRS/CPQTKCQLELPQLYGRPP GTKGCRHEKNVLCSKLFEGFGF IFVGFFFFAYMGILQLLII

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22721	53089	A	22849	146	1789	RQPSTSGSSRSCPCARRSWWAR TARSGWWWELLGARRSPQTLH CPQATLITLPCPRPSSTTSGSAM T*RGPWRSPGCTTSFCPTSR/PV ERNIDQTDLHAQRSEIRYNQTS QISWTSSCTNRNAISSSYSSTGG LPGLKRRRGPASSHCQLTLSSS KTVNSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTIFDGDGKTYQN VQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITR GSSRPSIREDENGRSQKPVHPEG DMTMNIKKIVNQATVLTFTTAL LAGGATQAFAKENNQKAYKET YGVSHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKGLDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNSIDSWKNAGRVFKDS DKFDANDPILKDQTQEWRGEA
22722	53090	A	22850	500	1034	

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22723	53091	A	22851	1	2396	MDKYLLHGPPRPPPAIASRCLA RVPGCAYSSIMVALSLVPLCAH MPTPSGLEVALPGNRTICWLSL WPSWQLDEDAQSPALESSSIRQ FPTAPRSGISPLCAPHSCLGQGR GPASHPTSTQTLDISGVKTTPRR FSVILQDLCSILGDSCLQFHLHR VPQQVSAVLLRVSGASPSPATT LSTRTLWGPGAGSHPFGVHNT RLSPDLCPGKIVLRALKESRAG MPEQDKDPRVQENPDDQRTVP EVTGDARSAFWPLRDNGGPSPF VPRPGPLQTDLHAQSSEIRYNH TSQTSWTSSNTKRNAISSSYSST GGLPGLKQRRGPASSRCQLTLS YSKTVSEDRPQAVSSGHTRCEK GADTSPGQTIAPTGGSPRSQDS RPRRRKIPLLPRRRGEPLMLPPP LELGYRVTAEDLHLEKETAFQR INSALHVEDKAIPDCRPSQPSHT LSSLATGASGGPPVSKAHTMD AQQHRPKSQDCLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS SDPLPATSYHSRDSAQVTSLIPA PFTAASSDAGMRRTRPGTSAPA AAAAAPPPSTLNPTSGSLLN\EW MEAPHISWPQPQLQHVSRGQ/N VRYNQRSQTSRTRS/CPPRKCQL QLPQLYGRPPATKAEEG\PASSH CQLAHSSSNTVSEDGPQAVSSG HTRCEKKAGAS/RWASRF*STH YGCTAGQTQVPRLPGPTGPPSI
22724	53092	A	22852	1	3392	MDKYLLHDPPRPPPAIASRCLA RVPGCAYSSIMVALSLVPLCAH MPTPSGLEVALPGNRTICWLSL WPSWQLDEDAQSPALESSSIRQ FPTAPRSGYPGTLCPSFLFGPRP RTCEYHSKPVLCAPSSRASPSSA TTLSTRTLWGPGAGSHPFGVHN TRLSPDLCPGKIVLRALKESGA GMPEQDKDPRVQENPDDQRTV PEVTGDARSAFWPLRDNGGPSP FVPRPGPLQTDLHAQSSEIRYN HTSQTSWTSSST
22725	53093	A	22853	40	409	WKMRHETRYNVLVSRGVGCH RLFFLNGVFEHLGRAFVQRRKV DTEHQLLRAAVPANQEHRGLT QSQHVDGHSLLLLTLPNSFLCQI QEPSLG\SGSGALSGNVRIRPQA QEAPEEPSVLTLLW
22726	53094	A	22857	3	220	

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22727	53095	A	22858	1	356	MAGPVKDREAFQRLNFVYQVS LRQGPHGDGARRPRVTAPLPQ AAHCVLAQDPENQALARFYL\H TERTIAKRLVLRRDPSVKEELL CRGCSSLLVPGLTCTPAPRDRC RGQRWTGTDLP
22728	53096	A	22859	2	270	
22729	53097	A	22860	2	364	IFSALPAPRRKVGLNLAPVTEPR DQPWAMIIDVF\SRYSGSRGQPR QT\LT\KGELKVLMEKELPG\FL QSGKDKDAVDKL\LKDPGRPM GDAQGGTFSEVHPCSVAAIT\SA CHK\YFE\KAGLK
22730	53098	A	22861	282	469	DCGSELQAPPPPSLPGPLCPSIM PA/PPYASPPMMPMMGPPFRGM MPVGLAPGPMLLQYNTCS
22731	53099	A	22862	7	522	SVWWNSNGLQSNMPKFYCDY CDTY\LTHDSPSVRKTHCSGRK HKENVKDYYQKWMEEQAQSLI DKTTAAFQQGKIPPTPFSAPPPA GAMIPPPPSLPGPPRPGMMPAP HMGGPPMMPMMGPPPPGMMP VGPAPGMRPPMGGHMPMMPG PPMMRPPARPMMVPTRPGMTR PDR
22732	53100	A	22863	3	455	WFLIHDRTHTGEKPYKCNECV KAFHRSTCLHAHKRTHTGEKP YECNQ*GKAFNSSHSFQIHERT HTGEKPYECKECGKAFKGPSSV RRHERTHSTKKPYECKHCGKA LSYLTSFHNHLGMHTGEISHTC KICGKAFYSPSV\IQTHE*THT
22733	53101	A	22864	1	1665	
22734	53102	A	22865	1	2650	

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22735	53103	A	22866	107	2384	MFGVHGTFLGIESRPPLLSLSPS LLYTCEMFQDPVACEDVAVNF TQEEWALLDISQRKLYREVML ETFRNLTSIGKKWSDQNIEYEY QNPRRSFRSLIEKKVNEIKDDSH CGETFTQVPDDRLNFQEKKASP EVKSCDSFVCAEVGIGNSSFNM SIRGDTGHKAYEYQEYGPKPY KCQQPKNKKAFRYRPSIRTQER DHTGEKPYACKECGKTFISHSG IRRHMVMHSGDGPYKCKFCGK AVHCLRLYLIHERTHTGEKPYE CKQCGKSFTYSATHRIHERTHT GEKPYECQQCGKAFHSSSSFQA HKRTHTGGKPYECKQCGKSFS WCHSFQIHERTHTGEKPCECSK CNKAFRSYRSYLRHKRSHTGEK PYQCKECRKAFTYPSSLRRHER THSAKKPYE/CSFQYHERTHTG EKPYECKQCGKAFRCAPHLRR HGRTH/S/AEKPYECKECGKAFR SASHLQIHERTQTHIRIHSGERP YKCKTCGKGFYSPKSFQRHEKT HTAEKPYECKQCGKAFSSSSSF PYHERTHTGEKPYECKQCGKA FRSASILQMHAGTHPEEKPYEC KQCGKAFRSAPHLRIHGRTHTG EKPYECKECGKAFRSAKNLRIH ERTQTHVRMHSVERPYKCKIC GKGFYSAKSFQIHEKSYTGGKP YECGLQLPRTAAESVDSEKLQG PGKQETHVQLLSLYCLRRVLDC
22736	53104	A	22867	1	391	MKEHIERNPVTIKNVVKPSINT VPLEDMKAHTGEKPYERQKCE LNQRLRDYAFQYHESNSGVVS ADSETKSGHSGCLIKEMKNATK THNGITGGIIFNANHWRETNTIY TRIHI/GEKSCDYKKCGKAFNQ YSSLRRHES\HTGEKPYERQKC ELNQRLRDYAFQYHESNSGVV SADSETKSGHSGCLIKEMKNAT KTHNGITGGIIFNANHWRETNTI YTRIHINKQEKYQATHVSYAAN
22737	53105	C	22868	179	289	
22738	53106	A	22869	3	206	

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22739	53107	A	22870	1	855	MPRAEPRATLGEQEKAGLPLG AWRLYLLRHFRKQTELRRSGSR DVTGALLVAAAVASEAVGSLR VAEGGPNTLLLQVLR\SW\PWC NKELKTMEERKVKRRSPKSFSA HCTQVVNVQKKMSIPVSK\ST\G FSNPASQVNFTSRPKVKKEVM K\EKTKPQGLEEGQRHSSQLPIQ HSFLT\DVSRCSRKMERGLLSL\ LNDFHSWKTFKHFGN\ECSI\EQ MEHVSGELQEKLARLNLELYG ELEELPEDKRKTASDSNLDRLL SDLEELNSSIQKLHLA\DAQDVP
22740	53108	A	22871	67	598	SIRRHCGQRCLVRIRIWPLKLPP RLAVREGLRCGTLRDVMPPSM SGVVVGPPGP\PPGPCGDTTSGP APGTFGQASAPVSPPRRGHGEY LCSSPTPVFFPGLWQPPRAGFTA PERSWSCRGPRWQLRAAWAGR LSSSPVSALLTFKVIILSTGLLFG PLGGWKILSSLPEIFANLAT
22741	53109	A	22872	1	372	
22742	53110	A	22873	1	3961	FALAPEAGFYSLGQQPSTRISGS GCVHPVRVWPFSIEPAIGTLNV GESMQLEVEFEPQSVGDHSGRL IVCYDTGEKVFVSLYGAAIDMN IRLDKNSLTIEKTYISLANQRTIT IHNRSNIIAHFLWKVFATQQEE DREKYSKVTAVFSIAASSNSRF ALYESSYNSQRSPSEWACDDLI KEEKDETDEFFEECITDPLLREH LSVLSRTFANQRRLVQGDSKLF FNNVFTVEPLGWSERKEMAEIR DVQKKDTKV
22743	53111	A	22874	1248	1716	WYAEQSAHEATAQLSTPMAIR RAVVMPPEQRNRTKKEY/SLRI PFGLPGDRMCFFTHRNDD/PTG NEVTPPSLAADLGQQFGGDAT DRQPWMIHQMLIHQGSEQLCF VEHGINMLRLGEILHLAATRHE AHFLAFRQFFNHQRSCFALNLA RQDRITDF
22744	53112	A	22875	478	663	
22745	53113	A	22876	508	884	RQRHPDQRPGRSLFHGHGMCP TTPLQQQVDSQHNGDNNSESA P*QRRADSIHRSSLHIKKRPPSE DVSRCFLCIDLAFRQGFTFNKK GIRVRIPFGLPGDRMCFFTHRN DDRPAMKLLPFAGNKV

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22746	53114	A	22877	1	506	AFCRFSILVGSAFISETDMCLLC PFPIGKAISVRLQYFKHETKQSI CLGNQKSPLVCPFFGEQGLDSS SSLDLPSSPNPAPTLCPCVQPPR GPVSVSVPVSVMGSRLAPLLSA *LFVSVILGRMVILKNPGVLGQ RQAGPSPGAPGLPSPSVRAPLG HKCSERSPSAT
22747	53115	A	22878	621	877	RRRRRRKQRRKQPWSSPARGA *PGPRRPSLRAAGTRRRRKRRA SWTRCSNTCPGRCRTCSRSNQA SCPSLLHLLLLLFGSFFSFY
22748	53116	A	22879	1	1339	MPSYKGCGETQRHATNGTAAP PRRSSCRGDAIKLPHAEKKEGR PPASTSYPLRLGTRSARSSSHC WCTSWEDPPEATAGEEKRHPK SPAVCCGEGTVLTASTVTWRA EPARGEIWARLCPRDRPGSRAA AVIWERPCCDRLIADRTGPPNSS EPHCRAATIPLPTWPLPEGQTLT LKALAKMAAPALLLLALLLPV GAWPGLPRRPCVHCCRPAWP/L WTLCPGEKGEAGVRGRAGRSG KEGAA\GCPGPAGPQSARRGSV GPPGAACRRAYAAFSVGRREG LHSSDHFQAVPFDTELVNLDGA FDLAAGRFLCTVPGVYFLSLNV HTWNYKETYLHIMLNR/QAA/V VLYAQPSERSVMQAQSLMLLL\ RRATPVWSVPEELPAVLPGQDE LGSLQLHAHHPLADGLVRHEL QPGLAGSSRTGHLVFRTDHGLR QHASHGCPVGPLHVPG
22749	53117	A	22880	532	783	VGSTRGIVEGLIFILGEGGECYY PRSLFTVANFTVGKRV\KTLNC PSTDKWINKMCHIHTVEYYSDI KRNEIPMRATCRQTLKA
22750	53118	A	22881	275	720	TPIHNCFKENKIPRNPTYKEHEG PLQGELQTTSQGNKRGYKQME EHSMLMG\GRINIMKMAILPKVI YRFTIPIKLPMTFFTELEKTTSKF IWNQKRARIAKSILSRKNKAG/ AHHAT*LQTILQGYSNQNSMVL VPKQRYRPMEQSPQK

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22751	53119	A	22882	1	609	MGRNQSRKAENSKNQSASSTP KDHSASPATEQSWMGNDFDEL TELGFRKSVMTNFSQLKEDVRT HHKEAKNLEKRLDKWLTRINSI EETLNDLMELKTMARELRDTC TSFSSRFDQVEEGEIQTTIREYY EHLYANKLENLEEMDKFLDTY TLPRLNQEEVESLNRPITGSEIE AIINSLPTKKIPGPDRFTA*RRP* MT*WS*KPWHENYVTHAQASV ADSIKWKKGKYK\HHQRIL*TP LRK*TRKSRRNG*IPGHIHSPKT KPGRS*IPE*TNNRF*N*GNN**P TNQKNSRARQIHSQILPEVQRG
22752	53120	A	22883	191	564	PNARKLRTLKKDHSPD**RRKL RKIK*MQ*KMIKGISQ\RSHRNT NYHQRTL*TPLHK*TGKSRRNG *IPGHIHPPKSKPGRSQIPEYTNN KI*N*GSN**PINQKKSRTGRIHS QILPEVQRGA
22753	53121	A	22884	337	589	TRRSRRNG*IPGHIHPPKTKPGR SRIPE*TNNRL*N*GSS**PTNQK KPRTRETDSRILPEVQRGAGTIP SETIPNNRKRGTPP
22754	53122	A	22885	162	539	TRKSRRNG*IPGHIHPSKTKPGR S*IPEETNNKF*N*GSN**PTNQK KPRTRQVHSRILPEPISHGMGKS WKQSL*KPAQDKAVPSLIAPIQ HIIGSSGQGNQARERNKGYSNR KRGSQIVSVCR
22755	53123	A	22886	329	459	NDDTFRKPHRLSPKSP*AADKQ LQQSLRIQNQCAKLRSIPIHH
22756	53124	A	22887	58	440	GLSRQFSPHSVNKAAGEVPTGR GPPQLSKANVARLPLSIPPLWA GHLWKKGGSPSQGIIDKTLISLG QST*GKGQLWVQLQRT*AFLPA GSEESSGSPSTA\PNSAKGQTPS SSGSLTRASSSSLYLW
22757	53125	A	22888	219	332	NEGKNLKGSQRERNTNYHQRT Q*TPLHK*TRKSRRNG
22758	53126	A	22889	1295	1435	QNQRQKPHDYLNRCRK/W/HFD KIQQPSMLKTLNKLGNDGTYL RIIRDI

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22759	53127	A	22890	2	648	YRFSGPTIRSIQNHTTHNQGRK WHKKGIKKPRAQRYESLKGPE V*PSGQGVTCLLRADWLSPLLG SGTY\VGPKFLRNTRFAKKHNK KGLKKMQANN\AKAMSARAE AIKALVKPKEVKPKIPKGCS/RR KLRFDFAYIAHPKLWGRRCFVA RFCQGASGCSGPKGKAKVPKA KVKVS/PKAKAKAKAKDQTKA QAAAPALV\PAQAPKRTQAPTK ASE
22760	53128	A	22891	3	370	QMYCVFNRNEDACRY/GS/AIG VLAFLASAFFLVVDAYFPQISN ATDRKYLVIGDLLFSG\VLASLA YQRYKAGVDDFIQNYVDPTPD PNTAYASYPGASVDNYQQPPFT QNAETTEGYQPPPVY
22761	53129	A	22892	1	297	
22762	53130	A	22893	3	713	GGGSGGDGDMESGAYGAAKA GGSFNLRRFLTQPQV\VARAVV L\VFALIVFSCIYGEGYSNAHES KQMYCVFNRNEDACRYGSA\IG VLAFLA\SA\FFLVVDAYFPQISN ATDRKYL\VIGDLLF\SALW\TFL WFR/VGFCFLTNQWAVTK\PKT VLVGADSVRAAITFSFFSIFSWG VLASLG\YQRYKAGVDDFIQNY VDPTPDPNTAYASYPGASVDN YQQPPF\TQNAETTEGYQPPPV
22763	53131	A	22894	3	219	
22764	53132	A	22895	1445	1777	PVHLGSTCHQCRQKTIDTKTNC RNPRLLGA/CRGQFCGPCLQNR YGEEVRDALLDPNWHCP\HCR GICNCSFCRQRDGRCATGVLVY LAKYHGFGNVHAYLKSLKQEF EMQA
22765	53133	A	22896	3	337	
22766	53134	A	22897	425	1209	TMSSTQFNKGPSYQLFAEIKNQ LLFKCDPQKQAALCSWIEGLTR LSFSPDFQKSLKEGIVLCTLMN KLGSVPKI/NRLMQNWHQLENL SNFIKAMVGYDMNPMDLFEAN DLFESRNMTQNRIL/P/PLDHSTI SLQMGANKRSSQ/VGMTAPGTP QHIYNTKLGAHKCDNSSMSLH MGDTQSANHSVQGFGLGQQIY YPKYCPQ/GPAASGAPLDAGNC PGPGEAPEDPPCSQEEATTEAPE HAGSLHHRPVWVWGIFLYFRL SFFFL

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22767	53135	A	22898	156	559	QHIRETPGAQVHSCGKWNPQA LWRTAWQLLT/DTKHTLGKPPS /MPHLVIYPLEISC\HTKTCTRML IASFFIITKTWKRPRCPSVDKWK NKPWCIHTGLLSSTVPPGEPGC PIPELSGLLMGLQTTSSRCSVRQ VW
22768	53136	A	22899	161	359	
22769	53137	A	22900	151	383	
22770	53138	A	22901	238	546	PQEHIMEHLEGVINKPRGRRCR PQELQLHYLQKCMDYDGNNLL DGFRTLPQPSTHV\HKEEGSEQ APLMSEDEL\INIIDGVLRDDDK NNDGY\IDYAEFAKSLQ
22771	53139	A	22902	1	819	MAAEDKLLLPQLPELFETSKQL LDDVEVVTEPAGSRIVQKKVFK GLDLLEKAAEMLSQL/DLVAEL ELPKTKNSAE\NHTANFSMAYP SLIAMASQRQAKRERHKQKEL EHRLSAIKSAVETGQADDERVR EYYLLHLQSLEEIESIDQEIKILR ERDSSREASTSNSSRQERPPVKP FILTRNMAQVKVFGAGYPSLAT MTVSDWYKQHWKYGALPDQG IAKATPEEFRKAAQQQEGQEEK EEEDDEQTLYRVREWDDWKGI HPRDYGSQQSMG
22772	53140	B	22903	238	410	
22773	53141	A	22904	1	638	VAELELPKTKNSAE\NHTANFS MAYPSLIAMASQRQAKRERHK QKELEHRLSAIKSAVETGQADD ERVREYYLLHLQSLEEIESIDQE IKILRERDSSREASTSNSSRQERP PVKPFILTRNMAQVKVFGAGYP SLATMTVSDWYKQHWKYGAL PDQGIAKATPEEFRKAAQQQEG QEEKEEEDDEQTLYRVREWDD WKGIHPRDYGSQQSMG

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22774	53142	A	22905	3	1083	RGNSRLRYSHEDELQLPRLPEL F\ETGRQLLDEVEVAT\DPAGFR \IVQEK\VFKG\LDLLE\RAAEML \SQSTLFGRECRFWKDLSPTHLI TFWGP\AFQGA\LPLKQVNPSKR LRIILQR\AREHFI\NYLT\QCH\C YHVGQSFEL\PKT\MNNSAENH TANSSMAYPMLGAM\ASQRQA KIQRYKQKKELEHRLSAMKSA VESGQADDERVREYYLLHLQR W\VDISLEEIESIDQEIKILRERDS SREASTSNSSRQERPPAKPFILT RNMAQAKVFGAGYPSLP/TLW TVSDWYEQHRKYGSITGFRGIA KSAPEGISGKAAQQQEEQEEKE EEDDEPNNFHRAREW\DDWKD TPSLGAYGNRQNMG
22775	53143	A	22906	30	457	
22776	53144	A	22907	401	1509	MWKMNCSLLQSKQMCNQLPP GSTRDGSWKFRQDPRLGKNA/C DCDSCIASEFGVRGYPTIKLLKG DLAYNYRGPRTKDDIIEFAHRV SGALIRPLPSQQMFEHMQKRHR VFFVYVGGESPLKYVTLKEMP AVLVFKDETYFVYDEYEDGDL SSWINRERFQNYLAMDGFLLYE LGDTDLNASSLRERKLILPEDIP LYVGKLVALAVIDEKNTSVEHT SELTVPTVVVLNTSNQQYFLLD RQIKNVEDMVQFINNILDGTVE AQGGDSILQRLKRIVFDAKSTIV SIFKSSPLMGCFLFGLPLGVISIM CYGIYTADTDGGYIEERYEVSK SENENQEQIEESKEQQEPSSGGS VVPTVQEPKDVLEKKKD
22777	53145	A	22908	53	543	LPISSLRTQTLFSSPLFPQHFEHY LALVSVLPFQLGRGRTAPAKKG GEK/RKGHSAINEVVIQEYTINI HKRIHGVRFKKRAPRALREIPK FAIKEVETLSVRIDSRFNKALCA KGIRNVPYRIRVQLSRKRNEDE DSPNKRYTLVTYVPVSTFKNVQ TVHVHEN
22778	53146	A	22909	106	491	IGKGTNELMYGEK/RKGHSAIN EVVIQEYTINIHKRIHGVRFKKR APRALREIPKFAIKEVETLSVRI DSRFNKALCAKGIRNVPYRIRV QLSRKRNEDEDSPNKRYTLVTY VPVSTFKNVQTVHVHEN
22779	53147	A	22910	1	321	

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22780	53148	A	22911	313	402	R*GGEKKKGRSAINEVVTREYT INIHKRIHGVGFKKRAPRALKEI RKFAMKEMGTPDVRIDTRLNK AVWAKGIRNVPYRIRVRLSRKR NEDEDSPNKLYTLVTYVPVTTF KNLQTVNVDEN
22781	53149	A	22912	1	3801	
22782	53150	A	22913	2	535	GGGMADTVLFEFLHTEMVAEL WAHDPDPGPGVSAGLRGEEAG ATKGQKMSLSVLEGMGFRVGQ ALGERLPRETLAFREELDVLKF LCKDLWVAVFQKQMDSLRTN HQGTYVL\QDNSFPLLLPMGSG LQV/YLEEAPKFLAFTCGLLRSA LYTLGIESVVTASVAALPVCKF QVVIPKS
22783	53151	A	22914	1	201	GDLPWEINPLSSCSLLHEKDPPT TSGPQT/DQPKKHHTNFKSGP\T GNRTVQLTWQPLPEPLELWPK AL
22784	53152	B	22915	226	522	
22785	53153	C	22916	1	705	
22786	53154	C	22917	1	462	
22787	53155	C	22918	1	505	
22788	53156	B	22919	1	1059	
22789	53157	C	22920	1	411	
22790	53158	A	22921	1	212	LTSFLHCCLSHHYHGAQIHPRH FLHLICRCHCHQYCHHAYLDPC PQDSHHLHWCWQPLPEPLELRP \RLSD
22791	53159	B	22922	1	864	
22792	53160	B	22923	1	635	
22793	53161	B	22924	1	874	
22794	53162	A	22925	1	566	MPSVRTGDPIILHAHTLNPAVW LAWAVEGEGSLTLNIWICPWQI EPLRHLAYTPGSDATSLTVPTR VISPLCVDSWLFTDPLMKTHAP ERTFLSFPAAAKRQAHLCVLAS NCDKPMYVKLVKAHCAEHQIN LIKGDDNKKLGEWEGPCTIDRE GKPCKVVGCSCAVVKDY/GKE SQAKDVIEQYFKCKK
22795	53163	A	22926	59	602	PTAMVEEGIAAGGVMDVNTAV QEVLKTALIHDGLARGIREAAK ALDKYVYQSQYCGFLQPEQNC HPREEGMEFMVLAQKF*MASV LPET*EK\RQAHLCVLASNCDEP MYVKLVEALCAEHQINLIKVD DNKKLGEWVGL\CKIDREGKPR KVVGCSCVVVKDYGKESQAK DVIEEYFKCKK

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22796	53164	C	22927	135	293	
22797	53165	B	22928	20	325	
22798	53166	A	22929	677	1031	TPTMCLRSHPLPLALVSVILSFP QPSFSSSLINSSWSSPRSSLSSSSS RSPSSGRVNLHPPQTPSSH*SHL SSRSCCSAPLLTYHSSSLLLVCS VPFPFFPGFPGENPLFVLSGSAP
22799	53167	A	22930	1	1011	MCLRVIFTIGAVSVILSFLSLFFII LDQLQLVIPQSSLSSSSNLEDPY SESYYAAARRPDSASTEPPPAG KSSAEYRAHFLAVSTEAERIRA DLVLRARPLGPAHPRTLWPTPP AGPFCRMVAHNQVA\ADNAVS TAAEPRRRPEP/SPSSSSSSPAAT ARPRPCPAV\PAPAPGDTHFRTF RSHADYRRITRASALLDA\LGF YWGPLSVHG\AHEPLRAEPVGT FPVRDS\RQRNCFFALSVKMAS GPTSIRVHFQAGRFHLDG\SRES FDCLFELLEHYRGGSRADLLGA TLRQRRVRPLQELCRQRIRRPP VG\REN\LARIPLNPVLRDY\LSS FPFQI
22800	53168	B	22931	180	1466	
22801	53169	A	22932	1	207	
22802	53170	A	22933	408	3758	CLQQGPGGNQHCSHREEAPAV AACQEPPGHSEPESVLPLGAPP\ SEEDGRQQVGSSRLRHIMAEMI ATEREYIRCLGYVIDNYFPEME RMDLPQGLRGKHHVIFGNLEK LHDFHQQHFLRELERCQHCPLA VGRSFLRHLIGQKQFPESPSGER PGLTSSHAPCPWMPHYLPEGPA CPVLRIPCEAFNWKHVECTDPV VSPPKQSPLLFQEEQFGMYVIY SKNKPQSDALLSSHGNAFFKVI PLGPPPTACPALS
22803	53171	A	22934	3	355	EAAELDAMCTATRQWSRAGQ GVTGRPCQGRLPRCGLRSTITP KPIPGGHRKKPLLGAL\GKHTLS YVERWHWEGHSGI*TRDRQNF ERRLTVPPSRQPFAPTDETRCG DDRISFCNYV

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22804	53172	A	22935	1928	5312	CLQQGPGGNQHCSHREEAPAV AACQEPPGHSEPESVLPLGAPP\ SEEDGRQQVGSSRLRHIMAEMI ATEREYIRCLGYVIDNYFPEME RMDLPQGLRGKHHVIFGNLEK LHDFHQQHFLRELERCQHCPLA VGRSFLRHLIGQKQFPESPSGER PGLTSSHAPCPWMPHYLPEGPA CPVLRIPCEAFNWKHVECTDPV VSPPKQSPLLFQEEQFGMYVIY SKNKPQSDALLSSHGNAFFKDK QRELGDKMDLASY
22805	53173	A	22936	3	306	
22806	53174	A	22937	3	460	LQRQRQHPAAAPAVPVRCFTFC FTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPK PEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENG ET\KAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN
22807	53175	A	22938	3	285	SSCPAREQLQRQRQHPAAAPAV PVRCFTFCFTDIVIMPKRKSPEN TEGKDGSKVTKQEPTRRSARLS /AVFV*FKLSLQKPAPPKPEPKP RKTSA
22808	53176	A	22939	1	413	
22809	53177	A	22940	2	454	AEVQVEEAGLRRALRVSSCSGR GSIQRRFYAVPVRCFTFCFTDIV IMPKRKSPENTEGIDGS\KVTKQ EPTRRSARLSAKPAPPNPEPQPR KTSAKKEPG\AKISRGAKGKKE EKQEAGK\EGTAPAENDETKAE EAQKTESVDNEGRMNCP
22810	53178	B	22941	55	186	
22811	53179	A	22942	2	397	
22812	53180	B	22943	339	470	
22813	53181	A	22944	1	139	
22814	53182	A	22945	1	416	MPLLYHLSRCAYVQQCNFANP VVSALCTCLVKPVVEKCTPYA VLLEALALRNVRQLEDLVIEAV YADVLRGSMDQRNQRLEVDYS IGRDIQRQDLSAIARTLQEWG/C HQHLLSLRSAASQRQQCGYHK LHDKQRLLRG
22815	53183	A	22946	315	570	

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22816	53184	A	22947	933	1841	RPAEPDPGSGHPEPKSPTLSAV MSAEVKVTGRNQEQFLLLAKS A\KGAVLATLIHQVLE\APGVY VFGELLDMPNVRELAESDFAST FRLLTVFAYGTYADYLAEARN LPPLTEA\QKNKLSDTFSVV\TL AAKVKCIPYAVLLEALAL\R\NV RQLEDLVIEAVYADVLRGSLDQ RNKRL\EV\DYSIGRDIQRQDLS AIARTLQEWCVGCEVVLSGIEE QVSRANQHKEQQL\GLKHQIES EVANLKKTIKVTTAAA\AAATS QDPEQHLTELREPAPG\TNQRQ P\SKKASKGKGLRGSAKIW\SKS
22817	53185	A	22948	1	1319	
22818	53186	A	22949	365	1331	RAGGGAPWRFTGTFATVAPET AADLSLHRHLLSRTTSAWGTA CITVPIEPPTWPTWAVPIQWGG SATCIQEDKLRQGILYGYSQQV NQAMDSGLRP\VVDSVNAIRVP QDYVTQSVPLREMNGSLGVLA QQLQNAKLQADAAHSALKQSD DLKPVFDQAFTKVVTTPADAL QPLIPAAQTFTQQLVMVGDYIA QQGTQECGKTFSRASYLVQHS RIHIGKKPYECKECGKAFSSGS YLVQHQRIHTGEKPYECNKCG KAFTVYGQLIGHQSVHTGEKPF ECKECGKAFRLNSFLTEHQRVH TGEKPFKCKKCGKTFRYSSAP
22819	53187	A	22950	2	206	GGGQGATSFGRPESGFIRHQPPP PCRRSSTPTRSKLYTL\SAPE*RS VPTSAPGPQDRPPGSVSKKSW
22820	53188	A	22951	571	1102	MGSVSLGNPQGPFQFTRLPLAN VIHPTFFWETGPRGADSLGAKG RKWQPTFTSRCNLKVYLGRAG SQAATGGPSPSLPNLHVKKLRP RKAEAWPGRRNTGKVSGR/LA ALRAPYGESFARAAGPRDAPS/ QQPRPQPEHAPTLISLGSNFGG MVEESWCRMNPDSGRPKEVAP WPPPSTK
22821	53189	A	22952	1	591	MGPHWKDFKEIDVKKYIDALSI HTYTHTHTHTHADITDGDHGG GALLELEINSHLKVQFRELNITA AKETEDGGGGKAIIIFVPFPQLK SFQKIQVWLRRILPKPTRKSCT\ QNMHWPPRSRTLKAMRDSIPE DLVF\PSEIMCMRIHVKLDGSRL IKAHLDKAQQYHVERNAETFS GVYMKLTGKDINVEFPEFQL

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22822	53190	A	22953	2	508	APPFELPRAAGIRHEGKFSQEK AMFSSSAKIVKPNGEKPDEFES GISQALLELEMNSDLKAQLREL NITAAKEIEVGGGRKAIIIFVPVP QLKSFQKIQVRLVRELEKKFSG KHVVFIAHRRILPKPTRKSRTK NKQK\RPRSRTLTAVHDAIPEDL VFPSEIVGKRNR
22823	53191	A	22954	145	395	
22824	53192	A	22955	536	717	
22825	53193	A	22956	1	729	
22826	53194	A	22957	1	1158	
22827	53195	A	22958	1	2869	MAHLRSCCSSLYQPGHLLPPHN PIQDHPLTAPSLTHLTRRAYFTD EKTKGGQSAYAVSLLRECVKL RPSDPTVPLMAAKVCIGSLRW MAAKHLAGVLLHSLSEECYWS PLSHPLPEFMGKEESSFATQAL RKPHLYEGDNLYCPKDNIEEAL LLLLISESMLANKLLLLEMERV QSPGVESGVDRQLSPYSDTNVN AQNAQIVPVAAKSAQNEVPGY PEETEKSRVQSNLLTQFQDLRL LLAAPECLPPRMSPPS
22828	53196	B	22959	28	139	
22829	53197	A	22960	60	812	LASPFPVPLHRCSAGSQPPGPVP EGLIRIYSMRFCPYSHRTRLVLK AKDIRHEVVNINLRNKPEWYY TKHPFG\HIPVLKTSKCQLIYES VIACEYLDDAYP\GRKLFPYDP YERVRQKMLLELFGKVPHLPK EFPGSVEDVGENAPNLKAALR\ QEFSNLEEILEYQNTTFFG\GTCI SMIDYLPL/WPWFER\L\ECMGY WNCVSHT\PALRLWISAMKWD PTVC\ALLMDKEHF\QGFLNPYF QNNPNAFDFGLC
22830	53198	A	22961	2	251	ILLDFKPWDDETDMAQLEACV CSIQLEELV*GASKLVPMGYGI RKLQIQCVVEDDKVGTDLLEEI TKFEEHVQSVDIAAFNKI

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22831	53199	A	22962	353	1071	APLWPRAERKFYKQMNGPVAS ASRQSSAPG/NDHSELVLQIASL EVENQSLRGVVQELQQAVSNL EAWLN\IRRREKSSPGH/RSTVP QTQHVSPMRQVERPSPRPPYYD PGQEAEDNEDDDIDLDNKEED KEARRLREERLRLYAKKAKNP SLVAKSSILLDIKPWDNKTDMT QLEACVRSIQLDGLVSGASKLA SVGYGIRKMQIQCVVEDDKVG TDLLEEEITKFEEHVQSVDIAAL
22832	53200	A	22963	3	482	PWANEAPAKK/PATPAEG/DAR DDDIDLF\GSDNEE\EDKQAGHS CGEER\LR\HYAGEEGPRKPAL/ VWPKSLPSLLDVK\PWDDDDGP WPSLEACVR\SIQLDGLVWGGF PSLVPVG\YGIRK\LQ\IQCVV\ED DKVGTDFPWRREIT\KFEEARA RSVDIASFSTRS
22833	53201	A	22964	1	2835	
22834	53202	B	22965	571	1337	
22835	53203	A	22966	1	489	
22836	53204	A	22967	1	618	
22837	53205	A	22968	3	5227	SWSRVRPRTRPEGLRQLKMRT GWATPRRPAGLLMLLFWFFDL AEPSGRAVN\DPLTIFHGNTGKC IKPGYGWIVADHCDETEDKLW KWVPQHRLFHLHSQKCLGLDIT KSVNELRMFSCDSSAMLWWKC EHHSLYGAARYRLALKDGHGT AISNASDVWKKGGSEESLCDQP YHEIYTRDGNSYGRPCEFPFLID GTWHHDCILDEDHNGPWCATT LNYEYDRKWGICLKPENGCED NWEKNEQFGRCYQFNTQT
22838	53206	A	22969	3	453	GQSPILVIYHETKRPSGISERFSG STSGNTATLTITGTQAMDEADY YCQAGRDFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKAHSN PVKAGVETTTPSKQSNNKYAA SSYLSLTPEQ*KSHRSYSC
22839	53207	A	22970	2	354	
22840	53208	A	22971	1	315	

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22841	53209	A	22972	1	712	MAWTLLFLTLLTQGTGSWAQS ALTQPASVSGSPGQSITISCIGTS SDIGAYYFVSWYQQYPGKAPK LLIFDVSGRPSGISSRFSGSKSGN TASLTISGLQAEDEADYYCASY ARSSTVVFGGGTSVTVLGQPKA APSVTL\FPPSSEELQANKATLV CLISDFYPGAVKVAWKADGSP VNAGVETTTPSKQSNNKYAAS S\YYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS
22842	53210	A	22973	1	1779	
22843	53211	A	22975	1	2001	
22844	53212	A	22976	292	1497	TGQLNGFHEAFIEEGTFLFTSES VGEGHP\DKI\CDQIS\DAVLDA HLQQDPDAKVA\CETVAKTGMI LL\AGEITSRAAV\DLPRKVVRE SCLNTLEYDDSSKGF*LQRLVN VLVALEQQSPDIAQGVHLDRNE EDIGAGDQGLMFGYATDETEE CMPLTIVLAHKLNAKLAELRRN GTLPWLRPDSKTQVTVQYMQD RGAVLPIRVHTIVISVQHDEEVC LDEMRDALKEKVIKAVVPAKY LDEDTIYHLQPSG/RTFVIGGPQ GDAGLT\GRKII\VDTYGGWGA HGG\GAFSGKDYTKVDRSAAY AARWVAKSLVKGGLCRRVLV QVSYAIGVSHPLSISIFHYGTSQ KSERELL*IVKKNFDLRPGVIVR DLDLKKPIYQRTAAYGHFGRDS FPWEVPKKLIY

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22845	53213	A	22977	67	1579	FFVRSLSHTDTNMNGQLNGFH EALIEEGTFLFTSKADGEGHPD KICDQISEAVLDAHLHQDPDAK VACETVAKTGMILLAGEITSRA AVDYQKVVREAVKHIGYDDSS KGFD\YKTCNVLVALEQQSPDI AQGVHLDRNEEDIGAGDQGLM FGYATDETEECMPLTIVLAHKL NAKLAELRRNGTLPWLRPDSK TQVTVQYMQDRGAVLPIRVHTI VISVQHDEEVCLDEMRDALKE KVIKAVVPAKYLDEDTIYHLQP SG\RFVIGGPQGDAGLTGRIIIVD PYDGWGAHEEGAFSGKDYTKV \SRSAAYGARWVARSLVKGGL CRRVLVQVPGPPKKPDEDLYLE CEPDPVLALTQTLSFQVLMPSG PLPRTSVVPREQQMLPLKDSDL LTQPWYSGNCDRYAVESALLH LQKDGAYTVRPSSGPHGSQPFT LAVLLRGRVFNIPIRRLDGGRH YALGREGRNREELFSSVAAMV QHFMWHPLPLVDRHSGSRELT
22846	53214	A	22978	3	325	
22847	53215	A	22979	15	1014	
22848	53216	A	22980	7	592	LLCSGRHSLQGVMGILSFLPVL ATESDWADCKSPQPWGHMLL WTAVLSLAPVAGTPAAPPKAV LKLEPQWINVLQEDSVTLTCRG THSPESDSIQWFHNGNLIPTHTQ PSYRFKANNNDSGEYTCQTGQ TSLSDPVHLTVLSGQWRKAPG WTWEGQDG*NLLSGRGLQERG VACLLGSIAVSCLSTYQWLFLP
22849	53217	A	22981	32	1150	EKAVTAVLWAPARLQGVMGIL SFLPVLATESDWADCKSPQPW GHM\LLW\TAVLFLAPVAGTPA APPKAVLKL\EPQW\INGGSRED SVTL\TC\RGTHSP\ESDSIQWFH NG\NL\IPTHTQPSLQVSRANNN\ DSGE\YTCQTGQTSLSDPVHL\T VLSEWLVLQTPHLEFQEGET\IV LRCHS\WRDKP\LVKVTFF\HNG KSKKFSRSDPNFSIPQANHSHSG DYH\CTG\NIG\YTLLFIPRLLTIT VQAPSSSPMGIIVAVVTGTAVA AIVAAVVALIYCRKKRISANPT NPDEADKVG\AE\NTITYFTSQW HPGWLWEEPDDQNRILVSIVLA LGIWRRNSEREDLVFPGLKFPL GEDTGRCCQFPKEKVFLPGVIL

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22850	53218	A	22982	1	471	MKSSFQGHNKEKREKKGPSLFS AAYGGGSCLLLSIMAALRPLVK PKIVKKRTKEFIWHQSDQHVKI KCNWRKPRG\QILMPNTGHGSN /KKTKHMLPSGFRKFLVPSVKE LEVLMCNKSPCAEIAHSVSSK\N KTIVERAAQ/LAVRVTNPNARL RSEENE
22851	53219	A	22983	103	564	GIFRGIMAALRPLVKPKIVKKR TKKFIRHQSDRYVKIKRNWRKP RGIDNRVRRRFKGQI\LMPNIGY G\SNKKTK\HMLPKWLSGKFLG SHQRSREL/EKLLA*CCNKFFTC CPRFVSHCFSFQGTGKGLRGER SLPNWAFRVTNPNARLRSEENE
22852	53220	A	22984	3	177	
22853	53221	A	22985	74	735	RFAGAGAIPEARARPPDVQAAE EEKEMDLPDSASRVF/CGDASS NMGEHRMNVNAIIL\AQKNML D\RFEKT\NEMLLNFNNLSSARL ASRLSERFLHHTRTLVEMKRDL \DSIFRRIRTLKGKLARQHPEAF SHIPEASFLEEED\EDPIPTQAPT TTIATSE\QSTG\SC\DTSPDTV\S PSLEPLASEDLSHVQALASPAI\ NGPQPDQIDEEMTGRIALPARC
22854	53222	A	22986	3	275	MRTVAEKVDAVRIVHIHSVI\IL RRSDKRKDRVEISPEQLSAAST EAERLAELTGRPMRVVGWYHS HPHITVWPSHVGKYHGVAMFI VFRN
22855	53223	A	22987	1	886	AKMAVQVVQAVQAVHLESDA FLVCLNHALSTEKEEVMGLCIG ELNDDTRSDSKFAYTGTEMRT VAEKVDAVRIVHIHSVIILRRSD KRKDRVEISPEQLSAASTEAER LAELTGRPMRVVGWYHSHPHI TVWPSHVDVRTQAMYQMMDQ GFVGLIFSCFIEDKNTKTGRVLY TCFQSIQAQKSSEYERIEIP\IHIV PHVTIGKVCLESAVELPKILCP/ QEEQDAYRRIHSLTHLDSVTKI HNGSVFTKNLCSQMSAVSGPLL QWLEDRLEQNQQHLQEL\HQE KEELMQELSSLE

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22856	53224	A	22988	10	988	LKAMSWAKMAVQVVQAVQA VHLESDAFLVCLNHALSTEKEE VMGLCIGELNDDTSRSDSKFAY TGTEMRTVAEKVDAVRIVHIHS VIIL\RRSDKRKDQVEISPGQLSA ASTEAEKLAELTGHPMRVVGW YHSHPHITVWPSHVDVRTQAM YQMMDQGFVGLIFSCFIEDKNT RAGRVLYTCFQSIQAQKSSESL HGPQDFWSSSQHISIEGQKEEER YERIEIPIHIVPHVTIGKACLESA VELPKILCQEEQDAYWRIHSLT HLDSVTKIHNGSVFTKNLCSQM SAVSGPLLQWLEDRLEQNQQH LQELQQEKEELMQELSSLE
22857	53225	A	22989	1	1362	
22858	53226	A	22990	284	542	KLFQKKNKKSSCISDNFFFLLAI MVNLLQIVRDHW\VH\VLVPM GFVIGCYLDRKSDERLTAFRNK SMLFKSFPHRELQPSEEVTWK
22859	53227	A	22991	272	1241	FPGGAACDICWVKEENGSLMS MKMGWKAKSCLPVTVHPRCL TPYSARLSSTFPL*NSITTGP*QS PACKRPF*LTTC*GGSRRNSNR KAA*GPCSPPPPSPPPSPAT\LPR GPAGLQPPGVPVLPPLRPRKHY APGGLP\PPASLLEDDDDTFCTS QAMQPTAPTKLSPPALLPEKDS FSSALDEIEELCPTSTSTEAATA ATDSVKGTSSEAGTQKLDGPQE SRADDSKLMDSLPGNFEITTST GFLTDLTLDDILFADIDTSMYDF DPCTSSSGTASKMAPVSADDLL KTLAPYSSQPVTPSQPFKMDLT ELDHIMEVLVGS
22860	53228	A	22992	1	3234	MELKCVCLKNRSPSAEEQPSLL PEPSAQESHGGHPRSALYGRER LTGQPPSSPHPNPAPWASCPAVI DPVPIYSSVAEAYDSGTEGIPTV PGLR\HVESGSLRATAQRLPPER RV/QQRTTAPPPRQPPRRPLRAS LSAAPPEPREPVVAAGPEPGSL QRPARTALPNRPEPQAASPGTL VEKYAAPVATQDLLDENPCTS RLGVVDLQAVLTLRKLENLRS GAQTPLEGGQSGRVGPHALRW NRGEEEGERLLC
22861	53229	A	22993	307	1906	
22862	53230	A	22994	1	1752	
22863	53231	A	22995	588	704	

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22864	53232	A	22996	3219	3407	DQVVWTKRLQDAILVLV*EFRL HSPALRLCVMKQVGMSQGELE WGQFLKLSSRNRKRSGERI
22865	53233	A	22997	1	588	
22866	53234	A	22998	1	917	
22867	53235	A	22999	1	1692	
22868	53236	A	23000	1	2266	MKRIRDYYERSHANNLDNLEE MDELLETHNLPGLNHEETENLN KPITTSLSPLAGVSSTKKNTKNE LSIVLPFTGSILPVGFATRPRGL ASSNPILLHMVAFLFANGTEEL PVPLMTPTRQKKVIPLIPLMVG LGVSASTIALGTGITGISTSVTTF RSLSNDFSASITDISQTLSVLQA LVDSSAAVVLQGQLRGLDLLT AEKGGLCIFLNEECCFYLNQSG LVYDNIKKLKDRAQKLANQAR QNLDSMLHGTGMKSDSDQKKS ENGVTLAPEDTLPFLKCYCSGH CPDDAINNTCITNGHCFAIIEED DQGETTLASGCMKYEGSDFQC KDSPKAHVRRTIECCRTNLCNQ YLQPTLPPVVIGPFFDGSIRWLV LLISMAVCIIA\MIISSSCFCYKH YCKSISSRRRYNRDLEQDEAFIP VGESLKDLIDQSQSSGSGSGLPL LVQRTIAKQIQMVRQVGKGRY GEVWMGKWRGEKVAVKVFFT TEEASWFRETEIYQTVLMRHEN ILGFIAADIKGTGSWTQLYLITD YHENGSLYDFLKCATLDTRALL KLAYSAACGLCHLHTEIYGTQG KPAIAHRDLKSKNILIKKNGSCC IADLGLAVKFN\SDTNEVDVP\L NTRVGTK\RYMAPEVLDESLNK NHFQPYIMADIYSFGLIIWEMA RRCITGGIVEEYQLPYYNMVPS DPSYEDMREVVCVKRLRPIVSN
22869	53237	A	23001	68	636	GVTSNPKALLGALIAPAFASLPE GRGKRIQALNMFRPKNSWRLG LKYPPSSKEKTQVPKTLISGLPE RKSTTRVGEKLQSAHKMPLSPG LLLLLFSGATATA/APLPLEGGP TG\RDSEHMQEAAGIRKSSLLTF LAWWFEWTS\QASAGPLIGKEA REVARRQEGAPP\QQSARRDRM PCRNFFWKTFSSCK
22870	53238	A	23002	1	144	GIRLPSSADWQKTEAQKRREQL \LLDELVALVNKRDALVRDLDA QEKQ

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22871	53239	A	23003	2	667	RWNSSDPDADRTTLNHADHSS KIVQHRLLSRQEELKERARVLL EQARRDAALKAGNKHNTNTAT PFCNRQLSDQQDEERRRQLRER ARQLIAEARSGVKMSELPP\YG EMAAEKLKERSKASGEQNSKL VDLKLKKLLEVQPQVANSPSSA AQKAVTESSEQDMKSGTEDLR TERLQKTTERFRNPVVFSKDST VRKTQLQSFSQYIENRPEMKRQ RSIQED
22872	53240	A	23004	1	1437	
22873	53241	A	23005	1	2009	MAKPYLYKKYGNQQGVAAIPD VPAAWEAEPSPIPSPVLGRKPN ASQSLLVWCKEVTKNYRGVKI TNFTTSWRNGLSFCAILHHFRP DLIDYKSLNPQDIKENNKKAYD GFASIGISRLLEPSDMVLLAIPD KLTVMTYLYQIRAHFSGQELN VVQIEENSSKSTYKVGNYETDT NSSVDQEKFYAELSDLKREPEL QQPISGAVDFLSQDDSVFVNDS GVGESESEHQTPDDHLSPSTAS PYCRRTKSDTEPQKSQQSSGRT SGSDDPGICSNTDSTQAQVLLG KKRLLKAETLELSDLYVSDKK KDMSPPFICEETDEQKLQTLDIG SNLEKEKLENSRSLECRSDPESP IKKTSLSPTSKLGYSYSRDLDLA KKKHASLRQTESDPDADRTTL NHADH\SSKIVQQDEERRRQLR ERARQLIAEARSGVKMSELPSY GEMAAEKLKERSKASGDENDN IEIDTNEEIPEGFVVGGGDELTN LENDLDTPEQNSKLVDLKLKKL LEVQPQVANSPSSAAQKAVTES SEQDMKSGTEDLRTERLQKTTE RFRNPVVFSKDSTVRKTQLQSF SQYIENRPEMKRQRSIQEDTKK GNEEKAAITETQRKPSEDEKGF KDTSQYVVGELAALENEQKQI DTRAALVEKRLRYLMDTGQNL

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22874	53242	A	23006	145	3217	LDEYEARLTLANLDDFEEDNED DDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPD AAELNPFGDPDSEEPITETASPR\ KTEDSFYNNSYNPFKE\VQTPQ YLNPFDEPEAFVTIKDSPPQSTK RKNIRPVDMSKYLYADSSKTEE EELDESNPFYEPKSTPPPNNLVN PVQELETERRVKRKAPAPPVLS PKTGVLNENTVSAGKDLSTSPK PSPIPSPVLGRKPNASQSLLVWC KEVTKNYR
22875	53243	A	23007	1	165	RPAAPRHERRPAADHGHHRPEP GRGTGQKACSELPSDEACS/GIA IG*SLLCSACSVRSRKRQW
22876	53244	B	23008	26	625	
22877	53245	A	23009	325	526	
22878	53246	A	23010	1946	2224	LLQWRHGLLNPINSPYNSPILPV QKPDKPYRLVQHLCLIYQIVLPI HPMVPNPYTLLSSIPFTTHYSVL DLKHAFFTIPLYPSSQPLFAFTW TDPDTHQAQQITLAVLPQCFIDS PHYFSQAQISSSSVTYLGIILMK THIGLGAVEQGVVLVGEARAA QEPMEWVGGSGMVGCRSRALP RGKAAKARREIERSAVTIVPVL DFNPAFHIIPDTTPDHHDCISLIH LTFTPFPHISFFPVPHLEHTWFID GSSTR
22879	53247	A	23011	1	1479	MEENFIRVFFTTTTMLLLIALIK QGELCESFDGKSLDGRDERVVI CFDAAAGLHRACSIRGEQQNL GTHYFTWQRLFAEVIKLGGLM KPKARNASSLWKEKTKNGFFS LETPEERQTSDLHKYQLAFRLF FIKYKNPAQFMAHLATTLRHFT ALDPESSHNFQNLFSSSHLMHIL SAPRLLRLYSRFVESPTVTIVPG PDFNPASNIIPDTTPDPHDCISLI HLAFTPFPYISFFPVPHPDHTWF IDGSSTRPNCHTPAKAGYAIVSS TSIIEATALPPSTTSRQAELIALT QALTLAKGLRINIYTD/SHILHH HAVLWA/E/RGFLTMQGSSIINA SLIKTLLQAALLPKEAEVIHCKG HQKASDPITQGNAYADKVPSL AHAPTLTLAPVLQCPLREVAGT EDDNGKAVLEIPSNIRKSAHVP VQTWKGWDPTNLLGGWFSNL GGFKTLVGTVIFIIGFLLFLPCVI PRIIKAIKTLVETTVSRQIIQTILL

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22880	53248	A	23012	854	1777	
22881	53249	A	23013	27	496	
22882	53250	A	23014	117	210	
22883	53251	A	23015	124	414	
22884	53252	A	23016	3	627	
22885	53253	A	23017	1	567	
22886	53254	A	23018	44	551	GGGRRSAPLQLGFMSRQAKDD FLRHYTVSDPRTHPKGYTEYKV TAQFISKKDPEDVKEVVVWKR YSD\FRK\LHGD\LAYTHRNLF\R RLEEFPAFP\RAQ\VFGRF\EASV DSRER\RKGAEDLLRFTVHIPAL NNSPQLKEFFRGGEVTRP\LEVS RDLHILPPPLIPTPPPG
22887	53255	A	23019	25	488	
22888	53256	C	23020	9	119	
22889	53257	A	23021	52	241	
22890	53258	B	23022	4	402	
22891	53259	A	23023	249	984	GSTMYKMNICNKPSNKTAPEK SVWTAPAQPSGPSPELQGQRSR RNGWSWPPHPLQIVAWLLYLF FAVIGFGILVPLLPHHWVPAGY AVSLGKRRAGPWNPFLSVSAET ILPQCMGAIFAGHLVVHLTAVS IDPADANVRDKSYAGPLPIFNR SQHAHVIEDLHCNLCNVDVSA RSKHCSACNKCVCGFDHHCKW LNNCVGERNYRLFLHSVASALL GVLLLV/LGGHICLRGVLCQPH ASAHQPTL
22892	53260	A	23024	2	224	
22893	53261	A	23025	111	1368	QQPSGSGALARGSGLPPRPGRL PARSPVQKRKGGWPKGKKRNP PRDLAV\RVPTTGYMIFLNEQRS QLRATHPDLPFTEIMKMLAVQ WAQLSQDKKGRKYAGKALGV TPPPSALTPVALIEEPKQLDIQSL PFQPILDRLKIKDKRQLVPSYLG GMHTVTEGLAGRQVLLQQVQ GGAWESAFLTCPWAMAAAAP GPTLTMLQPSISAVGFSQMAMG PHVQGRASKLSIYVNPRRQLST TTAMGDELNDLYCGTSRQLFSS LCNKKEPAAKAAPAAPLSSPGP PALGHAGHGRQLLLERSLTLFH LYELLKYPRASPGLWPPRVWM PHSLTCGTFWVPMIMMRFCAH VASGLLRPPFNQVFAHLSPAQG RHPGENGIIVLTSRAAVRIRCSS CSRSLTGNLKKILPRTQSTWSL WRKRRDK

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22894	53262	A	23026	2	405	
22895	53263	A	23027	1	391	
22896	53264	A	23028	3	463	
22897	53265	A	23029	74	466	FAFNMPEPAKSAPAPKKGSKK AVTKAQKKDGKKRKRSRKESY SVYVYKVLKQVHPDTGISSKA MGIMNSFVNDIFERIAGEASRL AHYNKRSTITSREIQTAVRLLLP G\EL\AKHAVSEGTK\AVTKYHQ
22898	53266	A	23030	168	597	KEETDFLFWFCHYCFIMPELAK SAPAPKKGSKKAVTKAQKKDG KKRKRSRKESYSVYVYKVLKQ VH\PDTGISSKAMGIMNSFVTTF FE\RIAGEASRLAHYNKRSTITS REIQTAVRLLLPGELAKHA\VSE GTNA\VTKYTSSK
22899	53267	A	23031	18	321	FTATWLNQEVGIVGKYRTRYG VSLQKMVKKIEISQYAKYICSFL WQNSKMKRRAVGIWCCG/SCM KTVKVSSSRNHIVWTYNTTSAV TVKSTIRRLKQLKDQ
22900	53268	A	23032	12	445	FTCRSHVSEVEERCVEAPGLLG SRSITGFSLHSKQAKRTKKVGIV \GKYGNPLWGPSLR\KMVKK\IE ISQHAQVHFALFCGKTKMKRR AVGIWHCGSCMKTV\AGGAWT \YNTT\SAVTVKSAIRRLKEFERP SRTLLYSLRTSLGL
22901	53269	A	23033	3	175	
22902	53270	C	23034	378	434	
22903	53271	A	23035	1	578	MVRCVRLVEAGSVVRYLSTSIC RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAYVRARELHTLEVTGLET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRLGASL/HTSASKHTM VRALTYCSSREETFTAI
22904	53272	C	23037	236	379	
22905	53273	A	23038	178	534	VVQKTEPRLCFAVSPPFSCSLPL PSLFPHSPLLGRPKRQAKPAAD EGFWDCSVCTFRNSAEAFKCSI CDVRKGTSTRYLKICVTWVVV VI*QVFIEHTAICALGVQWYKD RPGPCSYGA

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22906	53274	A	23039	44	1012	VGGGGVQPSMTMGDKKSPTRP KRQAKPAADEGFWDCSVCTFR NSAEAFKCSICD\VRKGTSTRKP RINSQLVAQQVAQQYATPPPPK KEKKEKVEKAGQKRKPEKRPR KFSP/SVVTKKNTNKKTKPKSD\ ILKDPPS\EANSIQSANATTKTSE TNHT\SRPRLEKRGTGGIAQQFG QLTVG\NVTVIITDFK\EKTRSSS\ TSSSTVTS\SAGS\EQQNQRQLR GFRGATDKGSLPVPPNPKGRPC QAVNDESFLKLAHGNCGKLWN SGVWKFQNLPPAHACLHPWEN LSCGTSTSLVDCCQDNFLLCHG HSWPPRDFRHPDDYSGHF
22907	53275	A	23040	1	626	MAGCRNPCKAESHRSKSLLSEA ESLFREAESQHDRGSKNAGHR DESVEVWLSLLSSSQTRAEIER QSRGKQWLRHLLRDTEGPKET VRPELATRAAMDVAEVEFLAE KELVTIIPNFSLDKSYLIGVDNIP KADEIRTLVKDIWDTRIAKLRV SADSFVRQQEAHAKPDNLTLM EINPSGTFLTQALNHTYK/LRTN LQPSESTQSQDF
22908	53276	A	23041	1	951	MDAAEVEFLAEKELVTIIPNFSL DKIYLIGTWELKYREIRWLSQG PHGKPHADPGSSILQNSSGPSG VRTNGKSKPWEPFVAEEFAHQ FHESVLQSTQKALQKHKGSVA VLSAEQNHKVDTSVHYNIPELQ SSSRAPPPQHNGQQEPPTARKG PPTQELDRDSEQEQEEDDEDGE DEEEVPKRKWQGIEAVFEAYQ EHIEERTLERNRSSTAADKAQL LAANRQGHGQPTDPASDNIPKA DEIRTLVKDMWDTRIAKLRVS ADSF\VRQQEAHAKL\DNLT\LM EIHTSG\TFLTQALNHMYKLRT NLQPLESTQSQDF
22909	53277	A	23042	1	626	MAGCRNPCKAESHRSKSLLSEA ESLFREAESQHDRGSKNAGHR DESVEVWLSLLSSSQTRAEIER QSRGKQWLRHLLRDTEGPKET VRPELATRAAMDVAEVEFLAE KELVTIIPNFSLDKSYLIGVDNIP KADEIRTLVKDIWDTRIAKLRV SADSFVRQQEAHAKPDNLTLM EINPSGTFLTQALNHTYK/LRTN LQPSESTQSQDF

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22910	53278	A	23043	2	642	RPRRLLRDAEGPEETVRLWPAA RAAMDAAEVEFLAEKELVTIIP NFSLDKIYLIGGDLGPFNPGLPV EVPLWLAINLKQRQKCRLLPPE WMDVEKLEKMRDHE\RKEETF TPMPKPFTTLELT\KLLLNHASD NIPKQDEIRTLVKDMWDTRIAK LRVSADSF\VRQQEAHAKL\DN LT\LMEIHTSG\TFLTQALNHMY KLRTNLQPLESTQSQDF
22911	53279	A	23044	3	1038	TSSMAAGCSEAPRPAAG\SDGS LVGQAGVLPCLELPTYAAACA LVNSRYSCLVAGPHQRHIALSP RYLNRKRTGIREQLDAELLRYS ESLLGVPIAYDNIKVVGELGDIY DDQGHIHLNIEADFVIFCPEPGQ KLMGIVNKVSSSHIGCLVHGCF NASIPKPE\QLSAEQWQTMEIN MGDELEFEVFRLDSDAAGVFCI RGKLNITSLQFKRSEVSEEVTEN GTEEAAKKPKKKKKKKDPETY EVDSGTTKLADDADDTPMEES ALQNTNNANGIWEEEPKKKKK KKKH\QEVSRTQDPCFSQGQLT S\SGYQSDHKKKKKKRKHSEEA EFTPPLKCSPKRKGKSNFL
22912	53280	B	23045	82	323	

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22913	53281	A	23046	3	1624	QLEIRAPTADEIHVTVGEARNLI PMDPNGLSDPYVKLKLIPDPRN LTKQKTRTVKATLNPVWNETF VFNLKPGDVERRLSVEVWDWD RTSRNDFMGAMSFGVSELLKA PVDGWYKLLNQEEGEYYNVPV ADADNCSLLQKFEACNYPLEL YERVRMGPSSSPIPSPSPSPTDPK RCFFGASPGRLHISDFSFLMVLG KGSFGKVMLAERRGSDELYAI KILKKDVIVQDDDVDCTLVEKR VLALGGRGPGGRPHFLTQLHST FQTPDRLYFVMEYVTGGDLMY HIQQLGKFKEPHAAFYAAEIAI GLFFLHNQGIIYRDLKLDNVML DAEGHIKITDFGMCKENVFPGT TTRTFCGTPDYIAPEIIAYQPYG KSVDWWSFGVLLYEMLAGQPP FDGEDEEELFQAIMEQTVTYPK SLSREAVAICKGFLTKHPGEAP GASGP*WGNLTIRAHGFFPLGF DWERLERLEIPASFSRPRPCGRS GENFDKFFTRAAPALTPPDRLV LASIDQADFQGFTYVNPDFVHP DARSPTSPVPVPVM
22914	53282	A	23047	1	1522	MLRAPRQATRDHHFAHIDIVQV TCFRYLRRSALAPAPAMPSPVR VDRGSFPPVAGGNHTRRRGGTP QEGVTREALAFFDVVATTGAE MMWSNFFLQEENRRRGAAGRR RAHGQGRSGLTPEREGKVKLA LLLAAWAPRWRCCPWAPSSG WTQHLQGQRQRRVRSGPTWG CGRRAPSGCGRRTCPWTGTPA APRSCPEASERNSEHPALICTLP QPHMLKRRARRAPGSMAPPLP RPPQAASVPVFPPDWEPLESRA RSKSPLHSQHRPAQETGRHSRP RTSTRKRQQKHSTEKATHTPER APKPQTRENNPKGRAQGSPAPR DHNPASRHQKTSNDKRSTHDT HKTRKDSQTRRKKTRNNEKQQ PDR/IGPQIIAYQP/YGKSVDWW SFGVLLYE/MLAGQPP/FDGEDE EELFQAIMEQ/TVTYPKSLSREA VAIC/KGCGRSGENFDK/FFTRA APALTPPDRLV/LASIDQADFQG FTYVNP/DFVHPDARSPTSPVPV PASSPTRPQLLENKFGC

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22915	53283	A	23048	505	2345	SIWGMVMMNPTPSSITLRRMM SLFPASLTTKYGGFYINSGTLQF RQASESEDDFIKEKKKKSPKKR KLKEGGEKIKKKKKDDTYDKE KKSKKSKFSKAGFTALNASKEK KKKKYSGALSVKEMLKKFQKE KEAQKKREEEHKPVAVPSAEA QGLRELEGASDPLLSLFGSTSD NDLLQAATAMDSLTDLDLEHL LSESPEGSPFRDMDDGSDSLGV GLDQEFRQPSSLPEGLPAPLEKR VKELAQAARAAEGESRQKFFT QDINGILLDIEAQTRELSSQVRS GVYAYLASFLPCSKDALLKRA RKLHLYEQGGRLKEPLQKLKE AIGRAMPEQMAKYQDECQAHT QAKVAKMLEEEKDKEQRDRIC SDEEEDEEKGGRRIMGPRKKFQ WNDEIRELLCQVVKIKLESQDL\ ERNNKAQ\AWEDCVKGFLDAE VKPLWPRGWMQARTLFKESRR GHGHLTSILAKKKVMAPSKIKV KESSTKPDKKVSVPSGQIGGPIA LPSDHQTGGLSIGASSRELPSQA SGGLANPPPVNLEDSLDEDLIR NPASSVEAVSKELAALNSRAAG NSEFTLPAPSKAPAEKVGGVLC TEEKRNFAKPSPSAPPPASSLQS
22916	53284	A	23049	1	379	AYRNFTSASDVWSYGIVMWEV MSYGERPYWDMSNQD\PNTAL LDPASPEFSAVVSVGDWLQAIK MDRYKDNFTAAGYTTLEAVVH VNQEDLARIGITAITHQNKILSS VQAMRTQMQQMHGRMVPV
22917	53285	A	23050	1	123	
22918	53286	A	23051	3	221	
22919	53287	C	23052	80	379	
22920	53288	A	23053	71	924	AFSVNSSNSWEKA*SQKCLQV NYLSLSSASYLP/CMTCPPSAPL NLISNVNETSVNLEWSSPQNTG GRQDISYNVVCKKCGAGDPSK CRPCGSGVHYTPQQNGLKTTK VSITDLLAHTNYTFEIWAVNGV SKYNPNPDQSVSVTVTTNQAAP SSIALVQAKEVTRYSVALAWLE PDRPNGVILEYEVKYYEKDQNE RSYRIVRTAARNTDIKGLNPLTS YVFHVRARTAAGYGDFSEPLE VTTNTGNKDHPDSVTSEAIFIIQ LNPITVKSKELSVIFGSADILLQ

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22921	53289	A	23054	1	1102	MRWLLKWERKYTLYSSGVLK HKNLLESLLGQFLGPPAQRFDS AGGVRPKNDGRFTVIQLVGML RGIGSGMKYLSDMSYVHRDLA ARNILVNSNLVCKVSDFGMSR VLEDDPEAAYTTRGGKIPIRWT APEAIAYRKFTSA\SDVWSYGIV MWE\VMSYGERPYWDMSNQD VIKAIEEGYRLPPPMDCPIALHQ LMLDCWQKERSDRPKFGQIVN MLDKLIRNPNSLKRTGTESSRP NTALLDPSSPEFSAVVSVGDWL QAIKMDRYKDNFTAAGYTTLE AVVHVNQ/EVSTQRCNTKGDL ARIGITAITHQNKILS\SVQAMR TQMQQ\MHGRMVPRLSTVLNK LKTLEISLPHPCTLIEELHFFNFV
22922	53290	A	23055	148	3229	NAFRFHLLNPAGESHDRLQDLL SAVRSPTKRQEQRWHRRTMAG IFYFALFSCLFGICDAVTGSRVY PANEVTLLDSRSVQGELGWIAS PLEGGWEEVSIMDEKNTPIRTY QVCNVMEPSQNNWLRTDWITR EGAQRVYIEIKFTLRDCNSLPG VMGTCKETFNLYYYESDNDKE RFIRENQFVKIDTIAADESFTQV DIGDRIMKLNTEIRDVGPLSKK GFYLAFQDVGACIALVSVRVFY KKCPLTVRNLAQFP
22923	53291	A	23056	57	450	VGDCLTSRGMSWVQATLLAR/ ALCRAWGGT/CRGALTGTSISQ VPRLAP\RGLHCSA/ASVSSEQS LVPSPPEPRQR/PPGGERDKASF LQTVQKFADTSVVDSGHIDFIY LALRKMREYGVERDLAVYNQL LNIFP

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22924	53292	A	23057	89	1502	VGDCLTSRGMSWVQATLLARG LCRAWGGTCGAAL/SQEPPSLR SLASLPRGLHCSAAAHSSEQV\L VPSPPEPRQEGPPRLLVPFEGPV LGQGAGLGERGQGRAFL/LDGC RNLRTTSVRKRGPH/VDLFYLA LRKMRE\YGVERG/DLAVYNQL LNIFPKEVFRPRNIIQRIFVHYPR QQECGIAVLEQMENHGVMPNK ETEFLLIQIFGRKSYPMLKLVRL KLWFPRFMNVNPFPVPRDLPQD PVELAMFGLRHMEPDLSARVTI YQVPLPKDSTGASKIPPKPHIVG HRACMSPHQESKKSRSSKAAL\ ARHNPS\RPVF\VEGPFSLWLRN K\CVYY\HILRA\DLLPPEEEGK WKRTPEEWE\LYYP\RQLDLEY VRSG\WDNYEFDINEVEEGPVF AMCMAGAHDQ\ATM\VKWI\Q GPAGDQPQTLAQNPPWSFRLRR VQPGELPDILLQGWRSP/HPAR GPPRKKTTTCKRQQQGPELV
22925	53293	A	23058	1	2517	
22926	53294	A	23059	1	927	IIVVEFVSRGLARAPSGPAVFSH LAMARLPLRGVRWGCLLTAVH PEPPTACREKQYLINSQCCSLCQ PGQKLVSDCTEFTETECLPCGE SEFLDTWNRETHCHQHKYCDP NLGLRVQQKGTSETDTICTCEE GWHCTSEACESCVLHRSCSPGF GVKQIATGVSDTICEPCPVGFFS NVSSAFEKCHPWTSCETKDL\V VQQAGTNKTDVVCGPQDRLRA L\VVIPIIFGILFAILL\VLVFIKKV AKKPTNKAPHPK\Q\EPQEINFP DDLPG/SSNTAAPVAGRIFTWG GQPV\TQEDGQRESHFSCRERQ
22927	53295	B	23060	24	439	
22928	53296	A	23061	1	582	
22929	53297	C	23062	1	2607	
22930	53298	A	23063	248	430	ATNYTREQDSMWNCVR*GRTT ATTHSVTQRTDERQRRADTAL TLADYRNTSVTGVFAGLF
22931	53299	A	23064	776	1426	
22932	53300	A	23065	284	598	VFRLLRGQKSEPGKSRPKAL*N KPANTPVQSHISLYAAGIINSDS KVR*SCRQSSARQSGSYL*TSPR SPQNRQQTGEITATVIAFGRTRR TAPDITPHPASAR
22933	53301	A	23066	3139	3792	

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22934	53302	A	23067	2	830	GVPNMAAPQDVHVRICNQEIV KFDLEVKALIQDIRDCSGPLSAL TELNTKVKEKFQQLRHRIQPVL YQRAFIWTASTFFFKLTYSLTDF SSTQHDFNSPTTPVTFSDL\EQL AKEQDKESENQLLLQEVENHK KQMLSNQASWRKANLTCKIAI DNLEKAELLQGGDLLRQRKTT KESLAQTSSTITESLMGISRMM AQQVQQSEEAMQSLVTSSRTIL DANEEFKSMSGTIQLGRKLITK YNR\RELTDKLLIFLALRLFLAT VLYIVKKRLFPFL
22935	53303	A	23068	1231	1458	
22936	53304	B	23069	1	2133	
22937	53305	A	23070	722	957	VFRLLRGQKSEPGQKQAKSTLE QTSEYPSNRGIPIIRQSECSIRTPL PFVRALRD*VRGCGCAPLSSVD SFFCCTEAL
22938	53306	A	23071	2	1137	VPNMAAPQDVHVRICNQEIVKF DL\EVKAPIQDIRD\CSGPLS\AL TELNPKVKEKFQQLRHRPTGP/ VEQLAKEQDKESEKQLLLQ\EV ENHKK\QMLQQFRPSWEGKLN SSPGKICNSDNLEKAELLQGGD LLRQRKTTKE\SLAQTSSTIT\ES LMG/ISGRMMAQQVQQSEEAM QSLVTSSRTILDANEEFKSMSGT \IQLGRKLITKYNRRELTDKLLIF LALALFLATV\LYIVKKRLFPIF VRFPKVPVLAPFNSLFSGICPWF PEAPRLPKAEAHTPLRFAPQLP CRLGWEHQCPPLFLQSSWLVK GEQSPWEEGPGIGMPPLGTYEP PPSHHCALWEAAAAWSTLKSE PPRTRMPLLSPAPIVPLNARSGG GKREER
22939	53307	A	23072	64	665	RVRGGEAELAMAAAEEE\SGAP NVPNRERGGAGRPKTPFECNIC LETAREAVVSVCGHLYCWPCL HQWLETR\PERQECP\VCKAGIS REKVVP\LYGRGSQEAPRIPELK TPPPPPRGQR\PAPESRGGF\QPF GDTGGFHF\SFGVGAFPF\GFFT TVF\NAHEPFRRGTGVDLG\QG HPSLQLGKEFPLPGFSAIFFLFW

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22940	53308	A	23073	1	416	MQRRRRRRLLLLPPRRQTDRAL PPPPSPGSMPPPLPPPP/PPARGG GLRPGDGLYPK/PSPARRGSGA RTSWCTMCAPPSTSAPRASRRP RPSSCATRPPTSKPPPA\GHAPH PPPRDLGGGLDSGVQSDGVLQ HLQRPGH
22941	53309	A	23074	1	1713	
22942	53310	A	23075	1305	1538	LKVKRNCTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAAYRKRKKGHKSSLSLSV KINKTAAANK
22943	53311	A	23076	49	355	
22944	53312	B	23077	253	471	
22945	53313	A	23078	1267	1497	LKVKRNCTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAAYRKRKKGHKSSLSLSV KINKTAAANK
22946	53314	A	23079	3	1237	HEVAGAVPGAIMDEDYYGSAA EWGDEADGGQQEDDSGEGED DAEVQQECLHKFSTRDYIMEPS IFNTLKRYFQAGGSPENVIQLLS ENYTAVAQ\AVNLLAE\WLIQT GVEPVQVQDTVEYHLKSLLIKH FDPRIADSMFTEEGETPAWLE\Q MIAHTTWRDLFYKLAEAHPDC LMLNFTVKLISDAGYQGEITSV STACQQLEVFSRVLRTSLATILD GGEENLEKNLPEFAKMVCHGE HTYLFAQAMMSVLAQEEQGGS AVRRIDQEVQRFAQEKTVLTQE AIITVKGVSLSSYLEGLMASTIS SNASKTIVAAMSNLVPPVELAN PENQFRVDYILSVMNVPDFDFP PEFYEHAKALWEDEGVRACYE RSNEYQLIDCAQYIFVLEMQVP CCEEAQSHPGQHGGVQVGRN
22947	53315	A	23080	1358	1589	LKVKRNCTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAAYRKRKKGHKSSLSLSV KINKTAAANK
22948	53316	A	23081	33	458	GITGSTDASGVTMKFNPFVFSD RRKNRKRHVNAPSHVRRKIMS SPLSKELRQKYNVRSMPIRKDD EVQVVRGHYKGQQIGKVVHV YRKKYVIYIERVQREKANG/DK DRKKILERKAKSRQVGKEKGK YKEELIGKMQEYIEP
22949	53317	A	23082	1	576	
22950	53318	B	23083	37	276	

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22951	53319	A	23084	124	549	NNSLSSPVQADVYFPRLIVPFCG HIKGGMRPGKKVGVMGIVDLN PKSFAINLTCGDSEDPPADGAIE LKAVFTDRQLLRNSCISGERGE EQVSNPLLSIHSTTMPFRVEILC EH\HCFR\VFVDGHQLFDFYHPH SNRYLAI
22952	53320	A	23085	1	215	QGFIKPPLKEENFTLPPPGKFGP PKGSLNSPPS/PSSP*SPGGGILLL VYYLYRALFQKGCKEAAWLEY PLT
22953	53321	A	23086	533	983	PWGPGCNKRWPCLAKDPPPTP QSSGVGQPFGGAEPAGAYIRTG PHLGPPPPPPPDSSTNLHSPNPS DDGADTPLAQSDEEEERGDGG AEP\G\PAASSGPLAYRPDPAGY SPTSRPPGPSPEPLG/AEDPDSLL ASRAPRGGNGWWDCGTLS
22954	53322	A	23087	1422	1670	NRYIDKTGWAWWLTPVIRHFR RPRWVDCLRLGVREQPGQHSKI KSLQKNAK\ISQAWWHAPVDP ATWKADAGGSLEPGSLRLQ
22955	53323	A	23088	2	663	VLLDERSAALDGAKRDGTLAL AAGALCREARAAQVFFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFPV SIPDHSTNSALSYLQSLITTSSHC
22956	53324	A	23089	3	206	

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22957	53325	A	23090	982	2252	LFLEKRRPALGPENRQRAPQGR STLGALRPAMVMEVGTL\DAG GLRAL\LGERAAQLPACLDCRS FF\AFNAGHIAGSVNVRFSTIVR\ RRAKG\AIGALE\HIVPNAELR\G RLLAGAYHAVVLLDERSAG\LD GAKRDGTLALAAGRA/LCREA RAAQVFF/LSKGGYEA\FSASCP\ ELCSKQSTPMGLS\LSLSTSVPD SAESGC\SSCSTP\LYD\QGGPVE ILPFLYLGSAYHASRKD\MLDA LGHRLPWINVLSQIVPNHF\EGH \YQYKSIPVEDNHKADISFWFN\ EAIDFIDSIKNAGGRVFVHCQA GISRSAT\ICLAYLMRTNRVKLD EA\FEFVKQRRSIISP\NFQLHGA SLLQFEFPRMLGPALFRAEAGK PRQMAVL\DRGT\STTTVFNFPV SIPVHSTNSALSVPFRAPLTDLS QLVERPTGR
22958	53326	A	23091	13	287	
22959	53327	A	23092	1	492	
22960	53328	A	23093	1	636	
22961	53329	A	23094	1	506	PTRTWTRGRIPRLSAQPSRGAR GTMADPRVRQIKIKTGV\VKRL V\KEKVLYEKEPKQ\QEEKIEKM RAEDGENYDIKKQAEIL\QES\R MMIP\D\CQRR\LEAAYLDLQRI LENEKDL/EKEAEEYKEAR\LVL DSVKLESLKLFSYGVVFALKPR GPILQSIIFDHVLCVQV
22962	53330	A	23095	1	786	
22963	53331	A	23096	183	1059	VLGAFIWQGLDPSPETAFTDHR ATEWGTNDQSLCLNSP*\DAPS AKHEYQASVSGSVSSKPEIDLQ LYDEVRDQDVPVKRNFARIVV NVSDTNDHAPWFTASSYKGRV YESAAVGSVVLQVTALDKDKG KNAEVLYSIESGSHPPYKTAAD VLLKAPPPGWRPTNTKPVHSTE AQPTQNQRTQQKHNQGASRSP RHSFATSTRAGAGICGCKTRRW MTRWMEESRGSLQTLPSTRLEP GSSAAWLDPEEQAQSLQFSSQE APFLGEGGENHIKGVPHGTKES QQQPLNHRSSL
22964	53332	A	23097	1	1224	
22965	53333	A	23098	1	660	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
22966	53334	A	23099	129	595	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPWHSKPT WIMTL*FPLEKTGALSLTSDTS MFTVVVLTLGGLPLSEA*T/GG NYDSHFDVDKGTGTIIVAKPLD AEQKSNYNLTVEATDGTTTILT
22967	53335	A	23100	1	1782	MAARIEVIHELSIRLLLMKTDL DAATAALLNVQPAKSGDNTSG APFPGKISQTLLKDPHNGYHVV FALAGSPKDADDTSIYMFYQK VGDNSIDSWKNAGRVFKDSDK FDANDPILKDQTQEWSGSATFT SDGKIRLFYTDYSGKHYGKQSL TTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTFEKSNEAADHFKHGGGATIK GRVADNGKPQLSSLTYIDIRVIE ESIYPPAILPLEIFITASGEEYSGG VIGKIHATDQDVYDTLTYSLDP QMDNLFSVSSTGGKLIAHKKLD IGQYLLNVSVTDGKFTTVADIT VHIRQVTQEMLNHTIAIRFANL TPEEFVGDYWRNFQRALR\NIL GVRRNDIQIVSLQSSEPHPHLDV LLFVEKPGSAQISTKQLLHKINS SVTDIEEIIGVRILNVFQKLCAG LDCPWKFCDEKVSVDESVMST HSTARLSFVTPRHHRAARQQ\R GPPLHNPADT*TTARKYNCDKR
22968	53336	A	23101	184	13958	AMGRHLALLLLLLLLFQHFGDS DGSQRLEQTPLQFTHLEYNVTV QENSAAKTYVGHPVKMGVYIT HPAWEVRYKIVSGDSENLFKAE EYILGDFCFLRIRTKGGNTAILN REVKDHYTLIVKALEKNTNVE ARTKVRVQVLDTNDLRPLFSPT SYSVSLPENTAIRTSIARVSATD ADIGTNGEFYYSFKDRTDMFAI HPTSGVIVLTGRLDYLETKLYE MEILAADRGMKLYGSSGISSMA KLTVHIEQANECA
22969	53337	C	23102	56	331	

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22970	53338	A	23103	2249	2680	GEFLKTREFSIYFLEKYTTFPGE NLEHGFWDSSTSPPVLLHPGIPA SRJ/PVSSIFTKVPPKKSATKP/PV SIWGAPPLGPPGFWGCCPTGEQ RGVCHPSEPHPPVVDFRKKPPF LCVSLSLINIFKSNKFLLTTCNL VIFYTCSL
22971	53339	A	23104	739	1672	CQEAASEFGGPLHTPAMFLRRL GGWLPRPWGRRKPMRPDPPYP EPRRVDSSSENSGSDWDSAPET MEDVGHPKTKDSGALRVSRAA SEPSKEEPQVEQLGSKRMDSLK WDQPISSTQESGRLEAGGASPK LRWDHVDSGGTRRPGVSPEGG L\GVPGPGAPLEKPGRREKLLG WLRGEPGAPSRYLGGPEECLQI STNLTLHLLELLASALLALCSRP LRAALDTLGLRGPLGLWLHGL LSFLAALHGLHAVLSLLTAHPL HFACLFGLLQALVLAVSLREPN GDEAATDWESEGLEREGEEQR GDPGKGL

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22972	53340	A	23105	122	2437	RLELKLPLWTMRFTEMELLGH LSIFKITGKQKQLTRTAPGPSGQ LRSNQTTGNSLEPSGQPRSSQTT GNSLEPSGQPRSSQTTGNSLEPS GQPRSSQTTGNSLEPSGQPRSSQ TTGNSLEPSGQPRSSQTTGNSLE PSGQPRSSQTTGDSLEPSGQLRS NQTTGDSVQPNNREQPGTVRS APLQPNNREQPGTVRSAPLQPN NRGQRPTKQQGTTWNRQVSSA PTKQQGTAR\PSGQPRSNQTTG NSLEPSSQLRSNQTTGDSVQPN NREQPGTVRSAPLQPNNRGQRP TKQQGTAR\PSGQPCSNQTTGN SLEPSSQLRSNQTTGDSVQPNN REQPGTIRSAPLQPNNRGQRWD RQVSSAPTKQGTALGPSG\SSAP TKQQGTALEPSSQLRSNQTTGN SLEPSGQPRSNQTTGNSREPSSQ LCSNQTIGNSQDRQVSSAP/IQT TGNSQDRQVSPAPTKQQGTAG NRQVSST/PIQTGNSVQPNNREQ PGTVSGAM/VWVATPVKGPAR VETSAHKVSAAGLPKKKT/QPG VTGGAPRLTLNTVLPKHSRTPS RHEAGSTQALYHNGQAQYALS FPHEAAPMAAFYVVTGIEVTTA LTLEEAPCTVEITTALTLEEPPC TVFWNKTERNTRTLVQDKGSN TKGFVQTATCCFRADCKASRPS PHPPSPHREWTSDLRHKQVSKF PGAHRLPGHPELPIQEAWDRGE
22973	53341	A	23106	605	813	LFVFINFRENPALLRW\AYAR\TI NVYP\NFRPTPKNSLMGALCGF GPLIFIYYIIKTERVSIQTRCLVF
22974	53342	A	23108	273	936	AYSNKVPSWNQKA\PSPTKPAG TLIFDFPAVKTVRNKFVFFINYP VSGYTEDLKKFLKPYTLEEQKN LTVCPDGALFEQKGPVYVACQ SPISLLQACRGMNDLDFGYSQR NPCILVKMNRIIGLKSEGVPRID CVSKNEDIPNVAVYPHNGIIDL KYFPYYGEKLHVGYLQPLVAV QVSFAPNDTGKEVTVECKIDGS ANLKSQDDRDKFLGRVMFKIT
22975	53343	A	23109	104	478	ETEVGGLVEASMSHNCTTALQ PGQHSQKENLQNKPIPGREKY* VSIEFELIYFP/YYCQVGYLQPL VAVQVSFAPNNTGKEVTVECKI \DGSANLKSQ\DDRDKFLG\RV MFQNHSTVHSMSRVSSTE

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22976	53344	A	23110	3	903	LLSPVRAHTMTKNEKKSLNQSL AE\WKLFIYNPTTGEFLGRTAAS WGLILLFYLVFYGFL\AALFSFT MWVMLQTLNDEVPKYRDQIPS PGLMVFPKP\VTALEYTFSRSDP TSYAGYIEDLKKFLKPYT\LEEQ KNLTV\CPDG\ALFEQKGPVYV ACQFP\ISLLQACSGMNDPDFG YSQGNPCILVKLNRIIG\LKPEG VPRIDLCFKRMKDIPNVAVYS\ HNGMIDLKYFPYYGKKTAMF/ VGIYQPIGLLVQVSFAP*QPLGK EVTVE/CAKIDGSSQPKKVQDD\ RDKVFGDEFMFQIHSTVH
22977	53345	A	23111	467	931	SRDSRRGTPLAGGRGRDFAGQ MGHRVQGRHGSRGRLPSGDAR VNAERAEPVGAGAGGPGGGSS VRGFCGRSWSEA/RGRRRAGG GVH\IEP\RYRQFP\QLTQIPRCSQ SEF\FSGLMWFWIF\WRFWHDP K\KVLGHFPV/YPDPSQWTD\EE L\GIPPDD
22978	53346	A	23112	1	390	VTIPTSLAELQGLPHIRVFLDNN PWVCDCHMADMVTWLKETEV VQGKDRLTCAYPEKMRNRVLL ELNSADLDCDPILPPSLQTSYVF LGIG*ALIGAIFLHYRNNGPLTIS SEGGLASLLCKDSRGVPLL

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22979	53347	A	23113	3	1653	PQRIQRGVPTRGEEVAPGRRQE EEREQERGAERPDPPCVLSGGK GRGNRPLREAPGGEGVSQVPA AAPLPRFHERKVFFFQTLPPAR ALRAQPPEPSERAPSQPSSGETR AAMPGGCSRGPAAGDGRLRLA RLALVLLGWVSSSSPTSSASSFS SSAPFLASAVSAQPPLPDQCPAL /CACRSEAARTVKCV\NRNLTE VPTDLPAYVRNLFLTGNQLAVL PAGAFARRPPLAELAALNLSGS RLDEVRAGAFEHLPSLRQLDLS HNPLADLSPFAFSGSNASVSAPS PLVELILNHIVPPEDERQNRSFE GMVVAALLAGRALQGLRRLEL ASNHFLYLPRDVLAQLPSLRHL DLSNNSLVSLTYVSFRNLTHLE SLHLEDNALKVLHNGTLAELQ GLPHIRVFLDNNPWVCDCHMA DMVTWLKETEVVQGKDRLTC AYPEKMRNRVLLELNSADLDC DPILPPSLQTSYVFLGIVLALIGA IFLLVLYLNRKGIKKWMHNIRD ACRDHMEGYHYRYEINADPRL TNLSSNSGCLEEILEDRPRTTLH
22980	53348	A	23114	288	877	ASRLSLPTRTSMRSSSSTSPSSSS SSSSLCRFLLNSRVTDAAFNFLL VWYYCTLTIRESILINNGSRWG RAGPEGGEHGMGCQGPSGKGR EQGAGG*WWVFCSRV\KGWW VFHHYVSTFLSGVMLTWPDGL MYQKFRNQFLSFSMYQSFVQF LQYYYQSGCLYRLRALGERHT MDLTVGESGVALASGHSPFLPS

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22981	53349	A	23115	1	1273	MAPLHSILGNRVGLCQASVRA CPGATVSSQCRASLRSRLAWRG SELPANRGRTWPGPGGLRLQA APRLAYLGRATLLVLTPYYDLP PNVRFTSMPASPHTYFLVLGAPI FLLLRSTWSYYHACRFEYATPN DRNTTYLAISGPTRRTYDVATF AYKDEYEKFKLYLTIILILISFTC RFLLNSRVTDAAFNFLLVWYY CTLTIRESILINNGSRPDGLMYQ KFRNQFLSFSMYQSFVQFL\QY YYQSGCL\YRLRALG\ERHTM\D LTVEGFQSW\MWRGLTFLLPFL FLW/YNSGQLFNALTLFKPGPR DPQLQGVGRCLCCGFPFLL\LFL GNFFTTLRVVHHKFHSQRHGS KKDLRLGLSPCRPRRGFLVPVC FWEGDWEGAPSSVRVSGGLFY SPLGFMGRCGPGKEDPGPSCPQ
22982	53350	A	23116	238	398	
22983	53351	A	23117	1	386	
22984	53352	A	23118	13	580	
22985	53353	B	23119	39	1171	
22986	53354	A	23120	381	795	PPSSKAPSSKGPAKIVCIYWALI LQSNEVTITEDKFNNLIKAAAV TVEPFWPSFFAKALASVNIGSLL CNAGVG/SMAPAACTAQAGGP ATSTTAASASFRNHNPRIAPKFR GVLAHEQYLSERATWVWAPNP NPKSLF
22987	53355	A	23121	1	960	
22988	53356	A	23122	2	3952	
22989	53357	A	23123	1058	1494	KSVRLVVN/YLRTQKAVVRVSP EVPLQNILPVICAKCEVSPEHVV LLRDNIAGEELELSKSLNELGIK ELYAWDNRRVPSAVPMQGPWP AEHFLQVNEQPPAGSPSPCPSSS SSSSGLRGGMQTANGPACALTP TCAQTDCPCPTSH
22990	53358	A	23124	195	398	TDSSSALQPQHRGRPALRQRTP PRRSP/SPGLSPPRGASPAS\SGA PARGVAFGGDEPPIGAEAMYSK P
22991	53359	A	23125	2	155	
22992	53360	A	23126	1	339	

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22993	53361	A	23127	150	1017	LGRWRQDQVPHGLECRSQSEW SCTDSRQHSSS\YSDSRRQEIGK MRYVSVRDFKGKVLIDIREYW MDLKRLPRKPRTGEAGSGSLSS PGADTPVEAAVTWRLGLGSVD VGSFRAWQRGKSAAVGHTVSP RWPRWQGGDSSALSMASLSTL TCSWGLRYSALSPTTSAQREEG SALYRHLSPPSLRFYPTVKWAT LAITRPRPPAPRSHSHHPQPRAL CPVWVLFQHPKTHGENLGDRW KEGSALVSSKGTPAKLSSGRIR NALQNTLGEVSVARIQTHRGIF VETTEARL
22994	53362	A	23128	1	584	APIECGGIPSLPVLCQSRANDQE GVRLLEPSEAMPKSKELVSSSSS GSDSDSEVDKKLKRKKASLL/P ENPVKK\QKTGETS\RALSSF*TE PASSRDDNMFQIGKM\RYVSV\ RDFKGKSA*FDIREYWMDPEGE MKPERKGISLNP\QQWEPSLKE QISGPLIDASKKTCKISEPILIKPC TVPVVLICLVTVAVCF
22995	53363	A	23129	186	687	LLWARGLGRAKSAVPTVSTML GLPWKGGLSWALLLLLGSQIL LIYAWHFHEQRDCDEHNVMAR YLPATVEFAVHTFNQQSKDYY AYRLGHIFNSWKEQVESKTV\F SMELLLGRTRVWEYLKTTIDNC HFQESTELNNTFTCFFTISTRPW MTQFSLLNKTCLEGFH
22996	53364	A	23130	232	402	LFKAWECFFLIFLQVVITRLKLD KDRKKILERKAKSRQVGKEKG KYKEETI\EKMQE
22997	53365	A	23131	637	758	NVEEKNRKKILERKAKSCQI\K KEKGEYKEETIGTMRECGL

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22998	53366	A	23132	1	1095	IVFLLYLETCLEVMDDKPNPEA LSDSSERLFSFGVIADVQFADLE DGFNFQGTRRRYYRHSLLHLQ GAIEDWNNESSMPCCVLQLGDI IDGYNAQYNASKKSLELVLW\Q FKRRKGPVHHTWGNHEFYNFS REYLTHSKLNTKFLEDQIVHHP ETMPSEDYYAYHFVPFPKFWFI LLDAYDLS/ALGAWDQSSPKYG GSVWKILEGSHNP\NTGNWNSS SRDFSEA/RSLFQFNGRVSAQEQ LNWLNEVLTFSDTNQEKVVIVS HLP\LYPGPPFDNVCLAWNYRD ALAVIWSHECV\GVSLLGHTHD GGYSEDPFGVYHG\NLEGVIET APDSQRFGTVHVYPDKMMLKG RGRVPDRIYELQGKEEPSHC
22999	53367	C	23133	235	382	
23000	53368	B	23134	63	293	
23001	53369	A	23135	160	330	
23002	53370	B	23136	1	870	
23003	53371	A	23137	2	1013	
23004	53372	A	23138	1	1552	
23005	53373	B	23139	120	1034	
23006	53374	A	23140	1	584	RTRGRRSLAFLLLAERGAAAA VLWSGCRRFRARLGCLPGGLR VLVQTGHRSLTSCIDPSMGLNE EQKEFQNAAFDFAAREMAPNM AEWDQKELFPVDVMRKAAQL GFGGVYIQTDVGGSGHVRLDT SVIFEALA\TGCTSTTAY\IRHPQ CPQSQHSFVQEGGTHYKAGHL CCRQWGPRACLPPGRPCHRGA
23007	53375	A	23141	2	412	
23008	53376	A	23142	47	487	
23009	53377	A	23143	77	459	GWKGIEHTLGRCLEAQGVINY RMLLSWRRWLVAHPVF*SFSCE VGPVGQS*RMTMLHCRHSDPV AKRLSCRRGDFASVVVLCPPPQ RLRTLKHFLFFGGLPLSIDFVMT VDFCCHLHLTDFSSNFGF
23010	53378	A	23144	1	304	KVAGSPSPTPAGQQVLDVNSCL DSSVLDSSFLTFSGLHAE/AEGS TGGPAALAYLGLKTLCTSQQAF AGQMKSDLFLDDSKSDLEEPW ELRKEGAPRSRDRE
23011	53379	A	23145	1	207	
23012	53380	A	23146	1	3009	
23013	53381	A	23147	3	298	
23014	53382	A	23148	1	636	
23015	53383	A	23149	1	795	

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23016	53384	A	23150	125	1527	SSPRQQTQLARVHP/DGRAQ/LA PSCLPGLGLCPLPVCPPVCNCPA CPCHEHCGEAP*GVA\AKRGAL RVHPHPSCGGPRAMTVTLHGQ DVLMLPGDLVGLQHDAGPGAL LHCSPAPGHPGPQAPYLSANAS SWLPHLPAQLKGTWACPACAL RLLAATEQLTVLLGLRPNLGLR LPGRYEVRAEVANGVSRHNLS CSFDVVSPVAGLRVIYPAPRDG RLYVPTNGSALVLQVDSGANA TATARWPGGSVSARFENVCPA LVATFVPGCPWETNDTLFSVVA LPWLSEGEHVVDVVVENSASR ANLSLRVTAEEPICGLRATPSPE ARVLQGVLVVLLAGSSGYLVG FKFLESHGSDSGSANSFHCLISQ NEFKTLLPDLTRAPRYSPVVEA GSDMVFRWTINDKQSLTFQNV VFNVIYQSAAVFKLSLSADSAP RPRWRLQSPRVGRLSPDPGFFG SPGPCQPRLQAFLI
23017	53385	A	23151	648	1387	ASTQSLLAWCPAWLSIPSTWPS SFSSGCPG/CKAQPVYEVSRSSY VYLEGRCLNCSSGSKRGGYTFT LT\VLGRSGEEEGCASIPLSPNRP PLGGSCRLFPLGAVHALTTKVH FECMGWHDAEDAGAPLVYAL LLQRCRQGHCEEFCVYKGSLSG YGAVLPPGFRPQFEVGLAVVV QDQLGAAVVALNRSLAITLPEP NGSAMGLTVWLHGLTASVLPG LLRQADPQLVIEYSLALVTVLN ETYTESL
23018	53386	A	23152	2	654	DKHIWLSIWDRPPRSCFTRIQRA TCCVLLICLFLGANAVWYGAV GDSAYSTGHVSRLSPLSVDTV\ AVGLVSSVVVYPVYLAILFLFW MSRSKV\AGSPSPTPAGQQVLDI DSCLDSSVLDSSFLTFSGLHAEV INTLADHQHRGTDFGGSPSVLI TVSLRSYKFAISLCTTYLWVINT LADHRHRGTDFGGSPWLLIITV FLRSYKFAISLCTTYLC

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23019	53387	A	23153	2	4072	SRDPAGSYHLNLSSHFRWSALQ VSVGLYTSLCQYFSEEDMVWR TEGLLPLEETSPRQAVCLTRHL TAFGASLFVPPSHVRFVFPEPTA DVNYIVMLTCAVCLVTYMVM AAILHKLDQLDASRGRAIPFCG QRGRFKYEILVKTGWGRGSGT TAHVGIMLYGVDSRSGHRHLD GDRAFHRNSLDIFRIATPH\SLG SVWKIRV\WHDNKGLSLALGFL Q\HVIVRDLQTA\QSTFFLVNDW LSVETEANGGLVEKE
23020	53388	A	23154	1	10922	MPPAAPARLALALGLGLWLGA LAGGPGRGCGPCEPPCLCGPAP GAACRVNCSGRGLRTLGPALRI PADATALTAMAKADGDVKKY GSKRGALALTHGHSLLRDVSH NLLRALDVGLLANLSALAELDI SNNKISTLEEGIFANLFNLSEINL SGNPFECDCGLAWLPRWAEEQ QVRVVQPEAATCAGPGSLAGQ PLLGIPLLDSGCGATLVGPHGPL ASGQLAAFHIAAPLPVTATRWD FGDGSAEVDAAGPAAS
23021	53389	A	23155	3887	14184	HVLCAWVTYMVMAAILHKLD QLDASRGCAIPFCGQRGRFKYE ILVKTGWGRGSGTTAHVGIHA VWGGQPERPPAPGTATEPSTAT VWDIFQIRHPAQPGVACWKIRV FGTTTKGSALPRFPCSTSSSGTC RRHAAPSSWSMTGFRWRRRPT GAWWRRRCWPRVRPRSVFPLR HAALLRFRRLLGAELQRGFFDK HIWLSIWDRPPRSYFTHIQRATC CVLLICLFLGANAVWYGAVGD SAYSTGRVSRLNPLSVY
23022	53390	A	23156	1	442	GGASGMGGIT\ASTVNQ\SLLSP LVLEVDP\NIQAVRTQEKEQIK\ TLNNKFASFIDKVRFLEQQNKM LETKWSLLQQQKTARSNMDN MFESYINNLRRQLETLGQEKLK LEAEFTTWGPPLPMPPATKQFN CFFFLVQNKTSASSANVK
23023	53391	A	23157	1	497	
23024	53392	C	23158	208	422	

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23025	53393	A	23159	81	1339	ELSSPRSSFSAPSRISAWFGPPAS TPASTMSIRGTQKSYKGSTSGP RAFKQAAS*QRSGPGFRISSSSF SRVGSSNFRGGLG\GGYGGASG \MGGITAVTVNQ/SRALLSPLVL EVDPNIQAVRTQEKEQIKTLNN KFAS\FI\DEVGFLEQQNKMLGT KWSLLDQQKTA\RSNM\DNMF\ ESYINNLRRQLETLAQEKLKLE AELGNMQGLVEDFKNNYED\EI NKSTETENEFVLIKKDVDEAYI NELYEEEIRELQSQISDTSVVLSI DNSRSLDTDSIIAEVKTEISEMN RNISWLQAETEGLKGGRISLEA GIADAEQRRELVIKDANAKLSE LEAALQQTKKLLE\MENMSIHT KTTSGYAGGVSLAYGGLTGSG LSYGLSSSSRSGAGSSSFSRTSST RAMVVKKIKTRDGKLLTLSLR
23026	53394	A	23160	1	651	MTAFNSGKVDIVAINDPFIDLN YMVYMFLYDSTHGKFHGTVK AENGTLVINGNPITIFQDQDPS KIKWAP/LAKVIHDNFGIIEGFM TTVHTITATQTINGPSGKLSRDG CRALQDIIPVSTGAAKPVGKVIP ELNGKLTGMAFHVPTANVSVA DLTCRLEKPA/KYDDIKK\NTHS STFDAGAAIVLKDHSVKLISWY DNEFGYSNRVVHLMAHNASKE
23027	53395	B	23161	1	382	
23028	53396	A	23162	3	1151	ASAHASAVRQSAAIFFCVASRA HIAETPLGKVKVGVNGFGRIGR LVTRAAFNSGKVDIVAINDPFID LNYMVYMFQYDSTHGKFHGT\ VKAENGKLVINGNPITI\FQE\RD PSKIKWG\DAGAEYRRGSPLGV FNQPWRKAGGSICKGGSQKGSS ISAPSAECPPCFVMGCEPMKKY DKQAFKI\ISN\ASCTNQLL*HPL AKG*FHDNFGNSLEGLHDHKS MAITANPRKTVD\GPSRGKLWP LMGRGAL\QNIIPASTG\AAKAV GKVIPELNGKLTGMAFRVPTAN VSVVDLTCRLEKPAKYDDIKK VVKQASEGPLKGILGYTEHQV VSSDFNSDTHSSTFDAGA\GIAL\ NDHFVKLISWY\DNEFGYSNRV V\DLM\AHMGFQGS
23029	53397	A	23163	160	236	
23030	53398	A	23164	931	1124	
23031	53399	A	23165	132	303	

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23032	53400	A	23166	20	171	
23033	53401	A	23167	1008	1262	HELQCSLLPVRHATAGHTNGQ NRLHWGHVAHSNYGAALKTN GVEVR*FTAAIARCDGNPYESF RKDVRADFQTRIDAIVRCLPK
23034	53402	A	23168	732	1162	RCHEKGRKGHQAPTGSTRPDG TLSACRSCQQGQGMPASAGVP ARQMGSTGNLPHLV*PYFLGLS SKAQHTG*LHKKR
23035	53403	A	23169	2	1093	
23036	53404	A	23170	236	496	
23037	53405	B	23171	22	3084	
23038	53406	A	23172	305	522	LRDGRGSMSSSSPNSASGSAICP ASSVMPETVSVSRVMPNVTKP A/MTAKQTRIRNQMVAITYIES DAWNRSYQ
23039	53407	A	23173	177	386	
23040	53408	A	23174	3	200	GAVAPMHPLAHPVPGAAAQPP PA*QPATPCHQPA*GQPAPPDV PGEPSAGRSLHHAHICLAPNEQ
23041	53409	A	23175	171	535	
23042	53410	A	23176	190	505	VPTDRIRTRLTSVCKRRCEVHQ LEDRPFEVYQVA/PRRD*SFETS VWNHMRKQ/PPLDVRQLAS*N VLHRQLDIMDSAVASMYSIHLS IKMGIGFSGVTTVVKGTPK
23043	53411	A	23177	349	1272	
23044	53412	A	23178	518	1451	VSSSIIMFGPLSQFPRQQVGSSV KRPSNVVCPGLMFSFFSSAA*IP **PLI*QPGV
23045	53413	A	23179	2436	2894	TSPDVLRAGPRVPSVQGTSPSQ SCPGQRPHGPNSKAYGR/LSVM AQYYCNVIPVLE/VPPSAFTPPP KVDSAVV/RLVPHATMPHPVK DVRVLSRITTEAFNQRRKTIRNS LGNLFSVEVLTGMGIDPAMRA ENISVAQYCQMANYLAENAPL
23046	53414	A	23180	1846	2557	IPVSERQGSDWRFFSVYVVNKA GGLIYQLDSYAPTGLRLEKTF\S YPLDLLLKLHDERVLVAFGQR GRHPEWGHAVL\AINGMDVNG RYTAD\GKKVLEYLG\NP\ANYP V\SYLFAQPRL\TSNDKLMLAL MFHSLFAIGSQACLP\EQGKPQG IENAWKTDTFKLH\CYQTLT\GI KFVVLADPRQAGIDSLLRKIYEI YSDFALKNPFYSLEMPIRCELFD QNLKLALEVAEKAGTFGPGS
23047	53415	C	23181	34	225	
23048	53416	B	23182	105	381	
23049	53417	A	23183	1	837	

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23050	53418	A	23184	3	744	HEASCRSERRRQMADFDTYDD RAYSSFGGGRGSRGS\AGGHGS RSQKELPTEPPYTAYVGNLPF\N TVQGDIDAIFKDLSIRSVR\LVR DKVTGKFK\GFCYVEFDEV\DSL K\EALTYD\GALLGDRSL\RVDF AKGRKTKIRVAFGF\RKGGPDD R\GFRDDF\LGGRGGSRPGD\RR TGPPMGSR\FRD\GPPLRG\SN\M DFREPTEEERAQRPRIQ\LKPRT VWRPLNQVANPNSAIFGGARPR EEVVQKEQE
23051	53419	C	23185	1	1038	
23052	53420	A	23186	1	1486	MGRNQSRKAENSKHESTYSPP KDHSSSQAMEQSWTENGFEKL GFRRKEALYYLDLTASCQSQEL FQLYAGMSVVGTSMPVQAVCP YCGNRIITVTTFVPGALTWLLC TTLFLFGYVLGCCFLAFCIRSLM DVKHSCPVCQRELFYYHRLRQ MELASSARTVVAPSRPCAGREG RGDANGKNSSPTAGSAMSSEPP PPPQPPTHQA\GVGLLDTPRSRE RSPSP\LRGNVVP\SPLPTRRTRT FS\ATVR\ASQGPVYKGV\CKCF CRSKG/HIGFNYPPAGWAGPDIF PGTSLDVGRGSY\VPSGKGDEV TLLKCAPIPTPKNE\KLAGPWEV VHHSPWHPGT\KHET\WSG\HVI SFLGGLVESTPLSLCFVGDFAG RRQQTLEDDILPHETGLQRGNG PSQVSPGGKGYGGAGVGCGVF PAISTAYGPLQQPLHHLKSIKSH LKRRGAHWWLSGGSNPIPGSGS RVGISSQLAQTHGLNPQNPSSS WSWRPQIPRSGPLAA
23053	53421	A	23187	2	617	
23054	53422	A	23188	1	993	
23055	53423	A	23189	779	1210	AAAGSEAGRRRGADPTRGPHV LPGSRQRRP/PIFPSLDLSGFFLF CSEFCPEIKSTNPGISIGDVAKE KKKLGEMWNSLNDSEKQPYFT KAAKLKEKYEKDVADYKSKG KFDGAKGPAKVARKKVEEEDE QEEEEEEEEEEEDE

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23056	53424	A	23190	116	522	KAPYSTNSLSLPPFPILFMGSGY RKGPTFQEPKPLPGAAARGPGC DPTQPPRHSAPRDHGPP\SPRCS PRPARPRASPAWLPPRAPTPPSP PAPAAAPRSCRGHARASSGRSG TTATPRRRRGGLWNQSPMDIK G
23057	53425	A	23191	1	152	
23058	53426	A	23192	1	676	MWSAGRGGAAWPVLLGLLLA LLVPGGGAAKTGAELVTCGSV LKLLNTHHRVRLHS\HDI\TYGS GSGQQ\SVTGVEASDDANSYW RIRGGSEGGCPRGSPVRCGQAV RLTHVLTGKNLHTHHFPSPLSN NQEV\SAFGE\EGEGDDPGTLW TVRCSGTA/HWEREAAVRFQH VGTF\VFLSVTGEQYGSPIRGQH EVHGMPQCQ\QHNTWKAMEGI FIKPSVEPSAGHDEL
23059	53427	A	23193	1	1044	
23060	53428	A	23194	1	1083	MTATLAAAADIATMVSGSSGL AAARLLSR\SFLLPHNGIRHCAY TA/SLRQHLYVDKNTKIICQGFT GKQG/TPFHSQQALEYGTKLVG GTTPGKGGQTHLGLPVFNTVK EAKEQTGATG\SVIYVPPPFAAA AINEAIE\AEIPLVVC\YPRGIPQP GLGHSSSHKTCGPGKDKAYWG PNCPGV\INPGECKIGIMPG/HIF HKKGRIGIVSTSGTLTYEAGH/Q TTQKLGLGQSLCVGIGGDP\FN GTDFID\CLEILFERFLPQEGIILI G\EIGGNA\EENAAEILEPLYSGS KF/ARPVVS\FIAGLTAPPGRRN GVMPGAIISGREKVGAKRERSS ALQSAGVVV\SMSPCTAGEPRF YKEFEKREDRL

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23061	53429	A	23195	1173	2110	FFTELEETILKFIWNQKRACISK ARVNTNDKSGGITLPDFKLYNE AIVAKTTWYWYKSRHIDQEKR REEKKE*KKDPSVPETLKKKQR NFTELKIQCLSKKFAQKMLQTA RRKLIYEKVKHCHKEYRKMYR TEIRMARMATKAGNFYVPAEP KLAFVIRIRGINGVSPKVRKVLQ LFLLYQIFNGAFVKLNKASINM LRIVEPYIA/WRYPNLKSVNELI YKCGYGKINKK*IALTDNALTA RSLGKYGIICREDLIHEIYTVGK CFKEANNFLWPF/K/LSSPRGGM KKKTTHFVEGGDAGKREVQIN RLIRRMN
23062	53430	A	23196	3	571	GTMEGVEEKKKEVPAVPETLK KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRT\EIRMA\RMARK\AGN F\YVPARTQIWRFVIR\IRGINGS EPQRFRKVLQLLRPFVKIFNG/T PFVKLQQGFRFNMLRDCRSHIL AWG\YPN\LKSVNELIYK\RGYG QNQFDLHFPTEKRSHPGSQ
23063	53431	A	23197	2	340	PRVRPRVRDSKMASVGEVSGP QYPVKDKKLL\EVQTGGSFPSW \ILMRGPSSPSGIFG\AFQRGLLR GTYNKYI\NVKKGSDLGGFTMV L\ACY\VLFSYSFSYKHLKH\ER\ LRKYH
23064	53432	A	23198	2	48	PRVRLRC*MVDEYCGCEWGK* LNGGRVLWM
23065	53433	A	23199	123	693	QACIMREYKLVVLGSGGVGKS ALTVQFVQGIFVEKYDPTIEDS YRKQVEVDAQQCMLEILDT\AG TEQFTAMRDLYMKNGQGFALV YSITAQSTFN\DLQDLREQILRV KDTDDVPMILVGNKCDLEDER VVGKEQGQNLARQWNNCAFL ESSAKSKIYVNEIFYDLVRQINR KTP\VPG\KAPQKSPSCQLL
23066	53434	A	23200	461	1422	SPHGEPLLGQCRREMWGWSLH TESPLG\QWGSQILKLQNDLL
23067	53435	A	23201	232	331	TPL*KWLRGVMAVTVVTPQTG IIAIPDPHHEWGSTGYPRLPA

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23068	53436	A	23202	5	1223	GLDSGPESGLRAQPGLLAGKRK MSVLRRMMRVSNRSLLAFIFFF SLSSSCLYFIYVAPGIANTYLFM VQARGIMLRENVKTIGHMIRLY TNKNSTLNGTDYPEGNNSSDYL VQTTTYLPENFTYSPYLPCPEKL PYMRGFLNVNVSEVSFDEIHQL FSKDLDIEPGGHWRPKDCKPR WKVAVLIPFRNRHEHLPIFFLHL IPMLQKQRLEFAFYVVEQTGTQ PFNRAMLFNVGFKEAMKDSV WDCVIFHDVDHLPENDRNYYG CGEMPRHFAAKLDKYMYILPY KEFFGGVSGLTVEQFRKINGFP NAFWG\WGGEDDDLW\NRV\H YAGY\NV\TRPEGDLGKYKSIPH HHRGEVQFLGRYKLLRYSKER QYIDGLNNLIYRPKILVDRLYT NISVNLMPELAPIEDY
23069	53437	A	23203	78	495	CTFEKAPPFQLGRGRMVPAKK GGEKKTGR\AINEVVTREYTINI HKRIHGVGFKKRAPWALKEIR KFAMKEMGTPDVRIDTRLNKA VWAKGIRNVLYRIHVRLSRKR NEDEDSPNKLYTLVTYVTVTTF KNLQTVNVDEN
23070	53438	A	23204	138	360	KNQKRQLSGGHCADQTSLVLA RLAPLF\PTTMSDKPDMAEIEKF DKSKLKKTETQEKNPLPSKETT EQEKQAGKS
23071	53439	A	23205	145	728	KRQPTSAMKDPSRSSTSPSIINE DVIINGHSHEDDNPFA\EYMWD GKMEGRNFNR\QIGRRELWGR KD\FLNRCFPKE\MLGEEGKEG ALNWVLFPSFEILPHQTMGPNP RTSFNDPCLSSDGSFSWEDLVV KS\NLNPNAKEFVPGGEVRKYL SRRGPLLVDVAQFPHCEGSIRR LNCKSSLGHCVTLYAIAQSFC
23072	53440	A	23206	530	707	
23073	53441	A	23207	1	515	MDFSKVPPHAAFRAQPPPALT WGLAKGSGRGAGEGGERPDRR R/PAARTGTPAWRPAGRRRLPP RSPPPAPVPVRPALPHPVRPGKE TGKTRRRRHYSPGRPLRGAAA AAAAAAVAQTASPSWAEGGRS GAGGSAESPAFSSPALPCPEGLL CPSAVPVPSKQSVSEVLAIF
23074	53442	A	23208	3	713	
23075	53443	A	23209	1	704	

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23076	53444	A	23210	2	1631	GLPRRPTRPPTRSGVSPPWPGPH SGVLFPLLLHCTGSLSQAVLTQ PSSLSASPG\ASVKLTCTLRSDIN VGSPFIYWYQQKPGSPPQFLLR YKSDSDNQQGSGVPSRFSGSKD ASANAGILLISGLQSE\VRDDYY CQAWDSSTAHSDTGRCGIVGRP PVRQCWPLLLLGLAMVAHGLL RPMVAPQSGDPDPGASVGSSRS SLRSLWGRLLLQPSPQRADPRC WPRGFWSEPQSLCYVFGTGTK VTVLGQPKANPTVTLFPPSSEEL QANKATLVCLISDFYPGAVTVA WKADGSPVKAGVETTKPSKQS NNKYAASSYLSLTPEQWKSHR SYSCQLQWGLGLGASQGGFLY EPVSQCVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAA SSYLSLTPEQWKSHRSYSCQKP NHASHGTSRMPSVSAPVSGLKS CWSGTGDRSALGQMPGPCHGI PDPMQQASDSGQPKAAPLGSL CSKPSSEELSGQQGPHWCVS
23077	53445	A	23211	1	959	VFLLLYLVAMPDPAKSAPAPK KGSKKAVTKAQKKDGKKRKR SRKESYSVYVYKVLKQVHPDT GISS\KAMGIMNSFVNDIFERI\A GEASRLAHYNKRSTITSREIQTA VRLLLPGELAKHAVFIENLLNY RKYLVKSSEKDRNYPCPLPGLK SKVDICTPYCLLLLPQPRHYPG KDTKEETEDFPNSPPPINREEDK RYTTVMGPCLRQAALEGELLA CPVMEDQQANWVHEPITFNTF KEIRKSIRENGPASPFTRGLIEVI ADSSDLVASTQKLTQPKETPSA PYNDISDLTNQDSWFIGFPPIWN AGETDLSNNKTT
23078	53446	A	23212	3	463	
23079	53447	A	23213	74	464	
23080	53448	A	23214	41	490	
23081	53449	A	23215	2	369	PDPAANAPAAAKPAAAKALPV FLLLLSGGAGPAHPMRAPGC*G ELGYTEQLFQFLQATAQEEGIF EYTDPKLAISAVWTFRDLGVLQ QTPSPAGPRLHLSPTFASLDNQE KLEQFIRQFICS
23082	53450	A	23216	124	301	

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23083	53451	A	23217	3	2426	PGVLSTATFRESGLSPCSKLKHP GPRGRLQYSPPTAGQGRLENG AGHPQSTGPVATLSVAEYGTQ GGASGPARIPIGSRGCLLAGRA EASLWSSGFGMKLEAVTPFLG KYRPFVGRCCQTCTPKSWESLF HRSITDLGFCNVILVKEENTRLF SWALLRVLKLLFLNVQLHKGQ MKMVQKAAQQVGQVGTSLWL SPEQGLPLVLLSTHKTLLDGILL PFMLLSQGLGVLRVAWDSRAC SPALRALLRKLGGLFLPPEASLS LDSSEGLLARAVVQAVIEQLLV SGQPLLIFLEEPPGALGPRLSAL GQAWVGFVVQAVQVGIVPDAL LVPVAVTYDLVPDAPCDIDHAS APLGLWTGALAVLRSLWSRWG CSHRICSRVHLAQPFSLQEYIVS ARSCWGGRQTLEQLLQPIVLGQ CTAVPDTEKEQEWTPITGPLLA LKEEDQLLVRRLSCHVLSASVG SSAVMSTAIMATLLLFKHQKG VFLSQLLGEFSWLTEEILVRGFD VGFSGQLRSLLQHSLSLLRAHV ALLRIRQGDLLVVPQPGPGLTH LAQLSAELLPVFLSEAVGACAV RGLLAGRVPPQGPWELQGILLL SQNELYRQILLLMHLLPQDLLL LKPCQSSYCYCQEVLDRLIQCG LLVAEETPGSRPACDTGRQRLS RKLLWKPSGDFTDSDSDDFGE ADGRYFRLSQQSHCPDFFLFLC
23084	53452	A	23218	169	955	ASSQLPCSMAQCCATWAPLKM RWLCSTAWSTSSLSLPPSWSSL QASQPSCCHATSLAPPCAGQCL ARAWPVLSFLCTCALGLLASIA MTFATQGKALLAACTFGSSELL ALAPYCPFDPTRIYSSSLCLWGI ALRCSAWAENVFAVRCAQLTH QLLELRP\WWGKKQPTHMMRE NPELVEG\RDLLSCT\SSE\PLTL CRDDVLPRP\DGQLRTLQATLL CDPGPGFLGAGLRGLKWTLGG P\SGAFQPSSPTTPAHLHLKIETL F
23085	53453	A	23219	1	344	

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23086	53454	A	23220	214	1355	FCSSWLRSLADSSLSWKMFLVG LTGGIASGKSSVIQVFQQLGCA VIDVDVTARHVVQPGYPAHRRI VEVFGTEVLLENGDINRKVLGD LIFNQPDRRES\LNAITHPEIRKE MMKETFKYFLRGYRYVILDIPL LFETKKLLKYMKHTVVVYCDR DTQLARLMRRNSLNRKDAEAR INAQLSLTDKARMARHVLDNS GEWSVTKRQVILLHTELERSLE YLPLRFGVLTGLAAIASLLYLLT HYLLPYAYTASAIPPSGAASRG PGARCSAIRKRAPARPTSAVSPP GAPRSPARGLRAIDRAAGTRNL NATLPPPGPPAPPSPPSPPSSITL HVFHQLQPDITRGREGTDFQWE KFPGRVLVADSRRALRCLAPAP TWLV
23087	53455	A	23221	2	1231	TPLFLRKGTADGSARTTVIHLG FTKGKQRCVETQAAAVAGDVG RTAAGGRVGKESGVISSDDRPG LPVGQSQPEGGEQEATDTVSVH ATTSQAWPGGADSKELSSKAE ERETGKDQQTELPLCLPLRDFP DSAPVMSSDSGHATESLHLASS DSKPPMPTPNEGPGSTVGHAGP PRTVKADLCTEPQLALRGLQVS LPRLHLVGVIYAEHQASGLEGC GHAGSCSPDGSPRAPGATLCLS KPLSFRTKRCLPCWLPASAPVGI PGAPVHIPGAPVCIPGAPACISN APVHIPGAPVGIPGAPVCIPGAA VCVPNTPMCIPSAPMCIPNTPVC IPNTPVCIPNTPVCIPGAAVCILG A/PRAHPWCSSCVHPGAPECYL GCGLTQADRLEPAVLDAGLQE PLFALCGQALPS
23088	53456	A	23222	2	408	
23089	53457	A	23223	62	251	

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23090	53458	A	23224	2111	3003	TQKAICMCLGLCKKIHHLLSLQ CLISQIKMIMGAGWQ/SSGFTDE KETSKIKADPEKLKKLQESLLE EDSEEEGDLCRICQIAGGSPSNP LLEPCGCVGSLQFVHQECLKK WLKVKITSGADLGAVKTCEMC KQGLLVDLGDFNMIEFYQKHQ QSQIKTEATVVEHKDIYNVTET QLVPEARSVLLVGAGQMLLTG ANRALNSDYSSMRPKVKAQNE LMNSGLYLVLLLHLYEQRFAEL MRLNHNQVERERVRVTRVLGG LSPNVSCGVVSGVGSFQWVRG LTDLKNEASDLHAQIPAE
23091	53459	A	23225	1	594	MIAAFNPGKVDTVTTNGPFIDL NYMVYMFHYDPTHGKFHDVP MFVMGMNHKHENKLTVISNAS CTTNCLDPLAKVIHDNFGIREG LMTTVHSIIATQKTVDGPSRKL WHDSHGAFQNTIPASTGAAK\I KKVVRQA/SQGPLKGILGYTEH QVVPLEFKSNTRPSTFEAGAGI AVNDHFVKLISWYGNEFAYSN KVIKPM
23092	53460	A	23226	3	232	
23093	53461	A	23227	1078	2221	QQTLQPAALPCPFPPPTHPPEVL PTAMNTTSSAAPPSLGVEFISLL AIILLSVALAVGLPGNSFVVWSI LKRMQKRSVTALMVLNLALAD LAVLLTAPFFLHFLAQGTWSFG LAGCRLCHYVCGVSMYASVLL ITAMSLDRSLAVARPFVSQKLR TKAMARRVLAGIWVLSFLLAT PVLAYRTVVPWKTNMSLCFPR YPSEGHRAFHLIFEAVTGFLLPF LAVVASYSDIGRRLQARRFRRS RRTGRLVVLIILTFAAFWLPYH VVNLAEAGRALAGQAAGLGLV GKRLSLARNVLIALAFLSSSVNP VL\YACAGGG\LLRSAGVGFF\A KLLEG\TGSEASSTP\RGGSLGQ TV\KSGPAALEPGPSESLTASSP LKL\NELN
23094	53462	A	23228	6125	6319	ASVVPVTSALAMCSPKSGIGDG FAVLRVEDVAQK***KAALGV ASSPAWQQTREREHVQGNSPL
23095	53463	A	23229	1	1347	

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23096	53464	A	23230	1	1124	MRECISIHVGQAGVQIGNACWE LYCLEHGIQPDGQMPSDKTIGG GDDSFNTFFSETGAGKHVPRAV FVDLEPTVVDEVRTGTYRQLFH PEQLITGKEDAASNYARGHYTI GKEIVDLVLDRIRKL\FGGGTGS GFASLLMERLSVDYSKKSKLEF AIYP\APQVSTAVVEPYNSILTT HTTLEHSDCAFMVDNEAIYDIC RRNLDIERPTYTNLNRLIGQIVS SITASLRFDGALNVDLTEFQTN LVPYPRIHFPLATYAPVISAEKA YHEQLSVAEITNACFEPANQMV KCDPRHGKYMACCMLY\RGDV \VPKDVNAAIATIKTKRTIQFVD WCPTGFKV*LGDMEAFQQAAD AQNNTGLEGPHPLGRLSLFHGL
23097	53465	A	23231	1	2918	MDVYCAHESLRHTKSPEATGQ TSGQRPEALQAFWPAFGSSPVT GSSPVTEVTTKGRWSSSRQVL WDRIPLAKSRPAISNRQSQRTNI PWWESCPPILNLEREQPPRFAQP GTYASRWKALEEMEKQQREQ VDRNIREAKEKLEAEMEAARH EHQLMLMRQDPGLALVSCMQ QGQSMSRSPKKVFKHLYELNL TKLQSLGSRSRLRWKDSPFWGE EAGGKRPPLVSLALHRSPSLLL LFVPKHPSKGRPDCTVQRS
23098	53466	A	23232	1	158	
23099	53467	A	23233	1	414	LGGLKGTWGETKPAMAAAEEE DGGPEGPNRERGGAGATKTLL YTGNHLFSPQWLETRPERQECP VCKAGISREKVVGEKSLLTFSL HFLRLKTPQICRLPV*LFLPP*GF QPFGDTGGFHFSFGVGAFPFGF FNSPSY
23100	53468	A	23234	1	663	
23101	53469	A	23235	2	667	SWAGGGFWFVGACVCVFGGTE GYVGRNKTGHGSSRRRRSGAP NVPNRERGGAGRPKTPFECNIC LETARELVLSVLANLYFWTISH QV\LE\TRPE\RQECP\VCKAGISR EKVVP\LYGRGSQEAPRIPRLKT PPPPPRGQR\PAPE\SRGGF\QPFG DTGGFHF\SFGVGAFPFGFFTTV F\NAHEPFRRGTGVDLG\QGHP A\SSW\QD\SLLLFLAIFFFF\WLL
23102	53470	A	23236	363	476	
23103	53471	B	23237	224	364	

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23104	53472	A	23238	1	1324	MRQRRAELLSKDKRVRTDGNN KCSPSAIGKRKERGTNDWIEGD NNQESQGLNCSDTLNRDLGPN TRGFLYAGLSGLDPDPSLPTPD MSSEVLEDNLDTLSLYSGKDSD SVKLLEEYADSESQASLQGRSR CWQHPHPAPLSYPPAASGSQLS LQGKFPSAKPPLLGGYTCTAQR TQWALTKRSLRATRESVSRQQ GVYGLVGRKRTRHHRGVLGLL GIPSARPERPGTGSEAGPTRLPG AAVARRRPARPVRGRLGDPAP TAAQTSGPASLPPPPPPRSYGDP HQNGYPDPDPAPSASPDLPPAA GDTRGSGGRRKKRRTGTARLN TPGRKA\PKQKAAAGRKGRAH QPAPRTPEPQRRRPIRPPNQTDR LRHPHRRAGRGPPPGGAGGTA NPSTGANGGAATARRTAGART RGARGASERAGRHGSRPASWL TATPPPGT
23105	53473	A	23239	1	433	PTRPSSPEETDGPWDPEGHPGG PLTDPPNAPVLALPPAIPGLSLS MADGSSDAAREPRPAPAPIRRR SSNYRAYATELQDLCRQLHAR VDKVDEERYDIEAK\VTKNITEI ADLTQKIFDLRGKFKRPTLRRV RISADAMMQALL
23106	53474	A	23240	2	409	
23107	53475	A	23241	3	490	SSPEETVGPWDPEGHPGGPLTD PPNAPVLALPPAIPGLSLIMADG SSDAVRAAG*GVAGTPRARAR EPRPAPAPIRRRSSNYRAYATEP HAKKKSKISASRKLQLKTLLLQ IAKQELEREAEERRGEKGRALS TRCQPLELAGLGFAELQDLCRQ LHARVDK
23108	53476	A	23242	149	846	VSAWRNGSSDAAREPRPAPAPI RRRSSNYRAYATEPHAKKKSKI S\ASRKLQLKTLLLQIAKQE\LE REAEERRGREGARSLAPRC\QP\ LELAG\LGFADLPGLCCRQFHA RV\DKVDEERYDIEAKVSKNITE IAN\LT\QKIFDLRSKFKRPTL\RR VRISADAMMQALLGARAKESL DLRAHLKQVKKEDPEKENREV GDWRKNIDALSGMEGRMKKW RELSLPAYCPCPEEGH
23109	53477	A	23243	1	487	
23110	53478	A	23244	80	511	

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23111	53479	A	23245	427	1417	KTMWKVEFGVRFSITRLLLEHQ PKQTMYIPLPK/PPLWPEEPKTE APKQTPRAPPKPKTSPRPRIPQT QPEETDQSTQEPFTTKIPRTTEL AKTTQGLEMLSCLIHNPKMHK DSTNEQIAASLQACYYEQLLM YIRVTDVDSVGPGNGKEAVTA PQAPTLFWLNHKAQLAKDWA GKDVNITPTFATSKKENKPPNN LQICNVSKIHQRAKVAGKPEIK DKHIQKEMPLDAIEASKINLVKI FNEFLKAWKCRLSFEYRIPENQ GHKGSFYLLVGSSRTSWLLTEK IGSSKRVLRMPPMDILKTTQILL SFLWSINLTPRGKNNHLVAPAH
23112	53480	A	23246	3	1011	
23113	53481	A	23247	2	334	PIQSFFLVLKKPPLRKGVYLSSK SLSRWFFKVQAN*RSQPQKAFS RLSCHC
23114	53482	A	23248	1	642	
23115	53483	A	23249	854	1150	KEDTNKWKNIPCSWLGRINIVK MAIMPKVNL*IQCHPHQATNDF SSQNWKKTTLKFIWEPKKEPAL PSQS*AKRAKLGGITLPDFQTIT YKATVTKTA
23116	53484	A	23250	1754	2393	PSNRREFGESWPETQAPGALRP LLPAPGTPRARERPAGWPARPM EVYIPSFRYEESDLERGYTVFKI EVLMNGRKHFVEKRYSEFHAL HKKLKKCIKTPEIPSKHVRNWV PKVLEQRRQGLETYLQ\AVILE NEELPKLFLDFLNVRHLPSLPK AESCGSFDETESEESSKLSHQPV LLFLRDPYVLPAASDFPNVVIE GVLHGIFYPHLQPR
23117	53485	A	23251	1	265	AGNRLRFQLELEFVQCLANPNY LN/WYPQCLHMLELLQYEHFR KELVNAQCAKFIDEQQILHWQ HYSRKRMRLQQAL\AKQQQQN NTSGK
23118	53486	A	23252	1	987	
23119	53487	A	23253	1	491	RGFRNFARVSGLLLCQAGGVL VSSFVMAAAVAMETDDAGNR LRFQLELEFVQCYANHNTLIFLP QR\GYF\KDKAFVNYLKYLLYW \KDPEYAKYLKYPQCLHMLGA APNMEHFRKEAGWNAQC\AKF IGWNRQVSTLGKHYS\RKRM\R LQQALAEQQQQNNTSGK

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23120	53488	A	23254	73	355	HEGQVHVLLASAHVDVAIVLG AGSMVEGEARPEQAAQHHQGI APLHLDAPGPSWTQSRSPRNRA NQNHTCSEAT*SHPEQLPQTLW ECHAPRSP
23121	53489	B	23255	1	441	
23122	53490	A	23256	528	698	HGQRFLHGPV/H/HHSHYDN/PH HSLHHHRCLHHCHLHHHRHHL HHHPLHCYHHHPGQNG
23123	53491	A	23257	1	403	
23124	53492	A	23258	509	4547	LYLTTSRREEHLKSLVVETQDL ASPVLRSVSICTKVEEAFRQAH VIVVLDDSTNKEVFTLEDCLRS RVPLCRLYGYLIEKNAHESVRV IVGGRTFVNLKTVLLMRYAPRI AHNIIAVALGVEGEAKAILARK LKTAPSYIKDVIIWGNISGNNYV DLRKTRVYRYESAIWGPLHYSR PVLNLIFDSEWVKREFVAILKN LTTTGRQFGGILAAHSIATTLKY WYHGSPPGEIVSLGILSEGQFGI PKGIVFSMPV
23125	53493	A	23259	56	290	
23126	53494	A	23260	468	993	VLLACFWPGSDFWPRSRRKTY GTAPQSCYSFYVALDCGGVSRL VIFVSWRNPQVAPTSAHQNRPS RNPVSRPPNTQRVARRKHYAL ADGYTERRWTNAPCRAESSFPP NCPSAAPIPDSYDK*PSRATLFT SHLTVEAFPVWSYLYPGETPRL HPRAHTRTVPAAIRYPDRQTPN GLRGANTMHSQMDTLNGDGR THLAGQRARSPRTARPQRQYRI HTTSDLPGLVRKYASGCCLRIW YCCAWIERALSLQVGGGVFGD PLSEGQAECDHGST
23127	53495	A	23261	1	3114	
23128	53496	A	23262	3	401	TSSLSLSGKSGRYIVFLRRSVGI QSPSAVATVRLLLAGSDRRFAA GSAGCAVLSRAERS*EPGCCYR IRRSAFRLRAGSIGNRDKPVAW PDTGSGDNTEVYFRAHQAGILP DTVLAGPAQRVAVSGGTPVDW
23129	53497	A	23263	2874	3062	

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23130	53498	A	23264	2766	3323	MPDLVEGREKSDKGAQPQPRT QSRSARTNGSGVRILHSLWRIIG IPLLLGYSLVCSRVLLACFWPG SDFWPRSRRKTYGTAPQSCYSF YVALDCGGVSRLVIFVSWRNP QVAPTSAHQNRPSRNPVSRPPN TQRVARRKHYALADGYTERR WTDAPCRAESSFPPNCPL*RQY RIHIVDASVCGP
23131	53499	A	23265	968	1440	
23132	53500	A	23266	3	640	LSVVRSRIHMGVGVGVGCPVR YRNQDDHELQITHGNKILCGIV CDKGAQPQPRTQSRSARTNGSG VRILHSLWRIIGIPLLLGYSLVCS RVLLACFWPGSDFWPRSRRKT YGTVPQSCYSFYVALDCGGVS RLVIFVSWRNPQVAPTSAHQNR PRRNPVSRPPNTQRVARRKHYA P\ADGYTERRWTIAPCRAESSFP PNCPSAAPIPDSYDK
23133	53501	A	23267	1	3140	MVYKMRYRSQHPYSIKEKQMK SEVLSVKEKIGYGMGDAASHII FDNVMLYMMFFYTDIFGIPAGF VGTMFLVARALDAISDPCMGL LADRTRSRWGKFRPWVLFGAL PFGIVCVLAYSTPDLSMNGKMI YAAITYTLLTLLYTVVNIPYCA LGGVITNDPTQRISLQSWRFVL ATAGGMLSTVLMMPLVNLIGG DNKPLGFQGDLSPMFSTPEEIA RPGPYENDVHVVGASSLAAGH KTLIPELVRSAEQHMGTR
23134	53502	A	23268	750	1340	ILHAPAPPFSASASHEQPEWSD KGAQPQPRTQSRSARTNGSGVR ILHSLWRIIGIPLLLGYSLVCSRV LLACFWPGSDFWPRSRRKTYG TAPQSCYSFYVALDCGGVSRLV IFVSWRNPQVAPTSAHQNRPSR NPVSRPPNTQRVARRKHYALA DGYTERRWTNAPCRAESSFPPN CPFAAPIPDSYDK*PFRIVS
23135	53503	A	23269	93	699	RASVQQKKLSTDDKGAQPQPR TQSRSARTNGSGVRILHSLWRII GIPLLLGYSLVCSRVLLACFWP GSDFWPRSRRKTYGTAPQSCYS FYVALDCGGVSR\RSYLYPGET PRVAPTSAHQNRPSRKPG\TRPP NTQRVARRKHYALADGYTER\ SATNAPCRAESSFPPELPVPQVP NTGFIRQVTFRDCFVNTPQAAA SGFW

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23136	53504	A	23270	1000	1530	QRYSDNPPNDKGAQPQPRTQSR SARTNGSGVRILHSLWRIIGIPL LLGYSLVCSRVLLACFWPGSDF WPRSRRKTYGTAPQSCYSFYV ALDCGGVSRLVIFVSWRNPQV APTSAHQNRPSRNPVSRPPNTQ RVARRKHYALADGYTERRWT NAPCRA/VEPFPPNCPWEAQYRI
23137	53505	A	23271	242	711	LKQKRDKEDRSSRVSAVLLIK/ HRRPLPLPIGLKACHCSCTAKC LGGCESPRKGGQLLIFEGHVKI DLEIFTKSLWLTRQLIVKKETEK AVKHASNICIMRTGLTFQSHKIE DGLFGLLVIATEAEWSYVCQST NPVDVYPLTAVPACCIISASDVP
23138	53506	A	23272	2	459	CVNSQIGRGHKITTYPFSPRKSG RKGMAQSQGWVKRYIKAFCK GFFVAVPVAVTFLDRVACVAR VEGASMQPSLNPGGSQSSDVVL LNHWKVRNFEVHRGDIVSLVS AKNPEQKIIKRVIALEGDIVRFP *DFCMPMPHISCGPQSAGRNW
23139	53507	A	23273	1	474	
23140	53508	A	23274	358	948	PLTPFSPRKSGRKGMAQSQGW VKRYIKAFCKGFFVAVPVAVTL LDRVACVARVEGASMQPSLNP GGEPV/ASDVVLLNHWKVTEF/ SEVHRGDIVFIG\APKNPEQKIIK RVICSLKGDIFQNHRTQKP\DVK VPRGSHLGLEGDHSWDTVFDS NSFGPVSLGLLHAHATHILWPP ERWQKLESVLPPERLPGTERRG MTA
23141	53509	A	23275	90	664	NKYRLQPSPPRLALWDRASDPP APPEDPETAPAMEEDQELERKI SGLKT\SMVEG\ERKTT\LELV\Q AAG\TDRP\CVTFVLHEEDHTLG \NFLRY\MIMKNP/EKVEFCGYT YG/HPSFQRAKLNLPHSRFRGYP FPAVEPISREALNELM\NVC\QP CAFTSFRASIKDYKESKSKQEM ESTFLVLLWQFYKGGTVL
23142	53510	C	23276	108	320	
23143	53511	B	23277	446	625	
23144	53512	A	23278	1	3042	
23145	53513	A	23279	1	3156	

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23146	53514	A	23280	518	2076	QQRR*MCQNLMTH\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGYVSNSLT GPYKPLNKTGLVLQMGLDPND VTFTYSHFAVPQAKGNNVVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTW LQVAKRAGLGGGQSGRTVLRE RVRIEIASTHIALAVECVSVRV WKVPRLPSRQKYAKHASQLVS NQKSEEEEYMKTFNISQQDLEL VEVATEKITMLYEDNKHHVGA AIRTKTGEIISAVHIEAYIGRVTV CAEAIAIGSAVSNGQKDFDTIV AVRHPYSDEVDRSIRVIPTYGT DEWEQWWNAFNEENLFCSEE MPSSDDEATADSQHSTPPKKKR KYIYVLVIAITMVMRFWQYING
23147	53515	A	23281	299	457	
23148	53516	A	23282	584	1185	QQRR*MCQNLMTH\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTSEKSNEAADHFKHVPQAKG NNVVITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QGQLTVN
23149	53517	A	23283	1	3618	
23150	53518	A	23284	191	819	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV

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23151	53519	A	23285	2	2556	WRKIYQAN/GKTKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSYTIIMGDFN TPLSTLDRSMRQKVNKNTQEL NSALHQADLIDIYRTLHPKSTEC TFFSAPHHMYSKIDHIVGCKAL LSKFKRTEIITNCLSDHSAIKLEL RIKKLTQNCSTTWKLNNLLLND YWVHNEMKAEIKMFFETNENK DTTYQNLWDTFKAVCRGKFIA LNAHKRKQERSKIDTLTSQLKE LEKQEQTHSKASRRQEITKVRA ELKEIETQKTLQKINEFRSWFFE RINTIDRPLARLIKKKREKNQID AIKNDKGDITTDPTETQTTIREY YKHLYANKLENLEEMDKFLDT YTLPRLNQEEVESLNRPITGSGI VAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEEEGI LPNSFYEASIILIPKLGRDIAKKE NFRPISLMNIDAKILNKILAHRI QQHIKKLIHHDQVGFIPGMQG WFDIRKSINVIQHINRTKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLVLEVLVRAIRQEKEIKCIQL GKEEVKLSLFADDMIVYVENPI VSAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKSIKYLGIQLTRHVKD LFKDNYKPALNEIKEDTNKWK NIPCSWIGRINIVKELEKTTLNFI
23152	53520	A	23286	1	3087	
23153	53521	A	23287	1	741	MLGKKKPVCEVGGDSGVPKKE FQEGRQVLFKLWRGQANKVG DNSIDSWKNAGRVFKDSDKFD ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTT AQVKVSKS/V*HTQNQRSGRSQ NDF*RRRKNIS*RSAVYR*RQL YIRRQPYAERPS\HVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQSA KKRDAELANGALGIIELNNDYT LKKVVKPLITSN

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23154	53522	A	23288	849	1688	QQRR*MCQNLMTH\QNQPSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGYVSNSLT GPYKPLNKTGLVLQMGLDPND VTFTYSHFAVPQAKGNNVVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEPGQLAV
23155	53523	A	23289	1	3171	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLKELEKQEQRHSKPSRRQE ITKMRAELKEIETQ
23156	53524	A	23290	1	3255	
23157	53525	A	23291	1	3924	
23158	53526	A	23292	1	3139	
23159	53527	A	23293	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
23160	53528	B	23294	1	3127	
23161	53529	A	23295	1	3325	
23162	53530	A	23296	1	3145	

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23163	53531	A	23297	191	819	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
23164	53532	A	23298	1	3352	
23165	53533	A	23299	1841	2679	QQRR*MCQNLMTH\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFTDSRGSK MTIDGINSNDIYMLGYVSNSLT GPYKPLNKTGLVLQMGLDPND VTFTYSHFAVPQAKGNNVVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTV
23166	53534	A	23300	1207	1533	YVHCKPSGWTVRTFDKPRKRFI AFFIAGILFRAIKNHFLPRETLQ CLPYILTGFRRGQSEYFSIFSNM DLADTVMFL*GAIRFSDLVNEQ IQHTFLIPGETICRLSEVV
23167	53535	A	23301	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
23168	53536	A	23302	1	3095	
23169	53537	A	23303	2	2678	

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23170	53538	A	23304	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
23171	53539	B	23305	1	2293	
23172	53540	A	23306	1	3810	
23173	53541	A	23307	255	1215	CVGQLAAAKR*RNSS*IQRLSR CVCSCGKPERR**HINLHVLSK GRRQLN/QTAGKTRAVSLKTAI SSTPTIRS*KIRRKNGPVLQPLH LTEKSVYSTLTIPTKAINTLYSK PTREQKTDTKAKNLYLTKRTT AAARTSSVKKARSFSRALKNA MLS*RTAPSVS*S*IMITH*KK** SR/CITSNTVTDEIERANVFKMN GKWYLFTDSRGSKMTIDGINSN DINMLGYVSNSLTGPYKPLNKT GLVLQMGLDPNDVTLTNSHFA VPQAKGNNVVITSYMTNRGFF EDKKATFAPSFLMNIKGNKTSV VKNSILEQGQLTVN
23174	53542	A	23308	1	4539	
23175	53543	A	23309	1	3229	
23176	53544	B	23310	1	3552	
23177	53545	A	23311	1	3139	
23178	53546	A	23312	1	3057	
23179	53547	A	23313	1	3215	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLRDIIQENFPNLARQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKDRSTRQ KVNKDTQELNSA

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23180	53548	A	23314	1	1921	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTN\HSKASRRQEITK IRAELKEIETQKTL*KINESRSW FFERINKIDRLLARLIKKKREKN QIDAIKNDKGDITTDPTEIQTTIR EYCKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITG AEIVAIINSLPTKKSPGPDGFTA KFYQRYKEELVPFLLKLFQSIEK EGILPNSFYEASIILIPKPGRDTT KKENFRPISLMNIDAKILNKKL AKRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDKIQQPFML KTLNKL\GIKYLGIHLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKMCL* RRWTPLCLLTAAASLNRE*ERL VQPLLWRQMYCGPRHCRQVPQ HRRLNWSPSLRLS
23181	53549	B	23315	1	2907	
23182	53550	A	23316	584	1278	QQRR*MCQNLMTH\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFTDSRGSK MTIDVPQAKGNNVVITSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQGQLTVN
23183	53551	A	23317	1	3345	

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23184	53552	A	23318	2	3366	WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPTFI QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSDHSAIKLELM IKNLTQNHSTIWKLNNLLLNDY WVHKEMKAEIKMFFETNENKD TT\YQNLWDTFKAVCRGKFIAL NAHKRK\QER
23185	53553	A	23319	1	2611	MGDFNTPLSTLDRSTRQKANK DTQELNSALHQVDLIDIYRTLH PKSTEYTFFSAPHHTYSTTDHIL GSKALLSKCRRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYGVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQK\INES RSWFFERINKIDRPLARLIKKKR EKNQIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLHTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEFDQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASIILIRKPGR DTTKKENFRPISLMNTDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIHKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLSKLGIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIRQ EKEIKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSQLPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTFKFIWN QKRARITKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN

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23186	53554	A	23320	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
23187	53555	A	23321	911	1539	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
23188	53556	A	23322	191	820	VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
23189	53557	A	23323	965	5050	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETK\ENK\DTTYQNLWD AFKAVCRGKFIALNAHKRKQE RSKIDTLTSQLKELEKQEQTHS KASRRQEITKIRAELKEIETQKT LQKINESRSWFFERINKIDRPLA RLIKKKREENQ
23190	53558	A	23324	1	2787	
23191	53559	A	23325	1	902	
23192	53560	A	23326	1	3640	

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23193	53561	A	23327	1	3686	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRSLRSRCDQLEERVSV MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLKNTLQDIIQENF PNLARQAKVQIQEIQRMPQRYS LTRATPRHIIVRFTKVE
23194	53562	A	23328	1	3433	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAIKNDK
23195	53563	A	23329	1	3070	MEGEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLLN DYWVHNKMKAEIKMFFETNEN \KDTTYQNLWDA

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23196	53564	A	23330	3	2372	TTNCLSDHSAIKLELRIKKLTEN HTTTWKLNNLLLNDYWVDNE MKAEIKMFFEINEKK\DTTSQNL WDTFKAVCRGKLIALNAHKRK QERSKIDTLTSQLKK\LEKQEQR NSKASRKQEITKIRAELKEIETQ KKTLQKINESRSWFFEKINKIDG PLARLIKKKREKNQVDAIKNDK GDIITDPTEMQTTIREYYKYLY ANKLENLEEMDKFLNTYTLQR LNQEGIESLNRPITGSEIEAIINSL PTKKSPGPDGFTAKFYQRYKEE LVYPEPRSESECLSNIREFLRGC GASLRLESIREDRNGRSQKTVH TEGDMNMNIKKIVKQATVLTF TTALLAGGATQAFAKENNQKA YKETYGVSHITRHDMLQIPKQQ QNEKYQVPQFDQSTIKNIESAK GLDVWDSWPLQNADGTVAEY NGYHVVFALAGSPKDADDTSI YMFYQKVGDNSIDSWKNAGR VFKDSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTIFDGDGKTYQN VQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG
23197	53565	A	23331	2	2987	APRFIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVHKDT QELNSALHQADLIDIYRTLHPK STEYTCFSAPHHTYSKIDHIVGS KALLSKCKRSEIITNCLSDHSAI KLELRIKKLTQNRSTTWKLNNL LLNDYWVHNEMKAEIRMFFET NENKDTTYQNLWDTFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAELKEIETQKTL\QKINE\SR SWFF\ERINK
23198	53566	A	23332	339	701	PDKEGNEIWVDMYTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFSIFSNMDLADTVMFL*G AIRFSDLVNEQIQHTFLIPGETIC RLSEVV
23199	53567	A	23333	190	502	

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23200	53568	A	23334	4472	8032	KKSGNNRLMRVHGKKRFLWQ KQGVCEVEIQAQRESARDGTD REDAESPHAEVTVPRGTRTEILT LWASRDRPASACGVTVPKGST THPGGMDRVCGVDTAVLHWM KQVQGISNLEVETGPRRRDMD EAGSRHSQQTNIGTENQTPHVL THKWQLNRNSACDKLHKPHSV PGGVAAGDVGGKTISNPGVCAI EYQVDGSPHIWEDVNKGVYIEE DRAPLMERSSSPAMEQSWMEN DFDELREEGFRRSNYSELRED
23201	53569	A	23335	1	2374	MVSISDLVICPPRHPKVLGLQGP PGLDSISDPSAGAGFLDWGEIG MPGPGRAGHQALCKCDCQCLE KTTTKAPGKMPKSTRSGPVRV RLADGPNRCAGRLECGMPDAG EQCVMTTGTSGRHCGLLGTGL WKGYTDLTIIPPGPGTPPQERTC QGDYHSGGTWTHSPLETTRRP GSSSPAIRRLPAQMLLLPARPPH PRSSSPEAMDPPPPKAPPFPKAE GPSSTPSSAAGPRPPRLGRHLLI DAN/GVYPYTYTVQLEEEPRGP PQREAPPGEPGPRKGYSCPECA RVFASPLRLQSHRVSHSDLKPF TCGACGKAFKRSSHLSRHRATH RARAGPPHTCPLCPRRFQDAAE LAQHSWGTPRGPLLAAACNCE VARGRLESPGPERLLHGYGGRE EEGGWGRAAGGLDRVEGFISS KAHHYLLIDTQGVPYTVLVTRS HRGSQGPVGLQARKVLQLPRV LKGLRVHVHLQRHSITHSEVPQ DFAGSLDSFQTPGESLRLVFRA LDTTQSSRISKAEPCLKEEPLSL GDLPYMHTTLCFCRKRRASPGP GTLQRGALAWPDWASPRALPV PSLSSTTRSPAAPLFAVPLSGRT TQAMAFDGIIFQGQSQRSAGLT TTSRFLACQRPLRLCAWWASRS PRCTLRRPVGLRPGVHPRPRLV YRDLKPENVMASGQPRDRPQP WFAWPPRPTRFCGGCWTLTPK

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23202	53570	A	23336	853	1602	PGAAWSRPDLRGCCTEPQPALR MLVLASPCPQPLAFSSVETMEG PPRRTCRSPEPGPSSSIGSPQASS PPRPNHYLLIDTQGVP\YTVAW LDEESQREPGASGAPGQKKCYS CPVCSRVFEYMSYLQRH\RFSH SEVKPFE\CDICGK\AFKRSQHL/ SARHHSIHLGGWVGGPTACRFC PRRF\RDAGELAQHSRVHSGER PVSVSTLPSPLYGAEHTAETHA VEASHEAGLPGAPGTHRTLQG ALDSCPDTW
23203	53571	A	23337	1	1144	MGHHLMIDKLVALGGLYYAIQ RHYATKCSVLKNDQILVIGLFM IQNVIYRKHFANPLSALFLQQGI ELFAAIAEIHITTVAERNHAITQI RLEAQTIFDSLKEWHNAIRKSL DYEALQAFEFRVGATDRGFPAL SSEALVRVLVLDANDNSPFVLY PLQNGSAPCTELVPRAAEPGYL VTKVVAVDGDSGQNAWLSYQ LLKATEPGLFGVWAHNGEVRT ARLLSERDVAKHRLVVLVKDN GEPPRSATATLQVLLVDGFSQP YLPLPRAAPAQAQADSLTVYL VVALASVSSLFLFSVLLFVAVR\ LCRRSRAAPVGRCSVPECPFPG HLVDVSGTGTLSQSYQYEVCLT GGSGANEFKFLKPVIPNLLSRDS
23204	53572	A	23338	1	1260	MVCYIQENLPFLLKPSVENFYIL ITEGALDREIRAEYNITITVTDL GTPRLKTEHNITVLVSDVNDNA PAFTQTSYTLFVRENNSPALHIG SVSATDRDSGTNAQVTYSLLPP QDPHLPLASLVSINADNGHLFA LRSLDYEALQAFEFRVGATDRG SPALSREALVRVLVLDANDNL\ PFVLYPLQNGSAPCTELVPRAA EPGYLVTKVVAVDGDSGQNA WLSYQLLKATEPGLFGVWAHN GEVRTARLLSERDAAKHRLVV LVKDNGEPPRSATATLHVLLVD GFSQPYLPLPEAAPAQAQAEAD LLTVYLVVALASVSSLFLLSVL LFVAVRLC\RRSRAASVGRCSM PEGPFPGRLVD\VSGTGTLFQSY QYEVCLTGGSETGEFKFLKPITP HLPPHRGGKEIEENSTLPNSFGF

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23205	53573	A	23339	123	5794	SSSDSGSLKGACTEVKMEPAGE RFPEQRQVLILLLLLEVTLAGW EPRRYSVMEETERGSFVANLAN DLGLGVGELAERGARVVSEDN EQGLQLDLQTGQLILNEKLDRE KLCGPTEPCIMHFQVLLKKPLE VFRAELLVTDINDHSPEFPERE MTLKIPETSSLGTVFPLKKARD LDVGSNNVQNYNISPNSHFHVS TRTRGDGRKYPELVLDTELDRE EQAELRLTLTAVDGGSPPRSGT VQILILVLDANDNA
23206	53574	C	23340	20	313	
23207	53575	A	23341	119	247	RSRCISASPRRPASFRKSIPEEED ESLNI*KGQVSILFFYIK
23208	53576	B	23342	55	288	
23209	53577	A	23343	1	3576	MAFLFEFSDLVSLLSIGTMLAY SLVAFSVLVLRYQPDENFSKNE KPKEEVVEMNSVPKAESPACVP EASSTPASLWSPVSTIPTPRWGR IVYGCAFLLVVLLSMLCLVLAH WPKRLFSGELIYIAAAVLLLVLI VGFTFTVWRQPQSNTPLYFKPP HISTSQNLSLPEHPMEYLLRTGI EPDVRGVLTVNALPAGPPVACS PLVSISAHVYLMMQMTTETWA QCGVWMLIALECPNLKLKKPP WLHMPLAMTMYA

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23210	53578	A	23344	3	1762	SVRPGPGHVRV\RFFSLSPLPLR PWPLCPAARRTMGSILSRRIAG VEDIDIQANSAYRYPPKSGNYF ASHFFMGGEKFDTPHPEGHLFG ENMDLNFLGSRPSQFPYVTPAP HEPVKTLRSLVNIRKDSLRLVR YKDDADSPTEDGDKPRVLYSL EFTFDADARVAITIYCQASEEFL NGRAVYSPKSPSLQSETVHYKR GVSQQVSLPSFKIDFSEWKDDE LNFDLDRGVFPVVIQAVVDEG/ DSVVEVTGHAHVLLAGFEKHM DGSFSVKPLKQKQIVDRVSYLL QEIYGIENKNNQETKPSDDENS DNSNECVVCLSDLRDTLILPCR HLCLCTSCADTLRYQANNCPIC RLPFRALLQIRAVRKKPGALSP VSFSPVLAQSLEHDEHSCPFKK SKPHPASLASKKPKRETNSDSV PPGYEPISLLEALNGLRAVSPAI PSAPLYEEITYSGISDGLSQASC PLAAIDHILDSSRQKGRPQSKAP DSTLRSPSSPIHEEDEEKLSEDV DAPPPLGGAELALRESSSPESFI TEEVDESSSPQQGTRAASIENVL QDSSPEHCGRGPPADIYLPALG
23211	53579	A	23345	35	3134	RPREGPTWPQLPGSSPRRLFPW SPGSSSRGLFPWSPGSSSRGLFP WSPGSSSRGLFPWSPGSSSRGLF PWSPGSSSRGLFPWSPGSSSRGL FPWSPGSSSRGLFPWSPGGSSR GSSRGHPGPPPGGSSRGHPGPPP GALPVVTRVLLPGLFPWSPGSS SRGLFPWSPGSSSRGLFPWSPGS SSRGLFPWSPGSSSRGSSRGHPG PPPGALPVVTRVLLPGLFPWSP GSSSR/RTLPVVTRLLLSGTLPV VTRVLL
23212	53580	A	23346	3	91	
23213	53581	A	23347	3	174	
23214	53582	A	23348	3	360	
23215	53583	B	23349	158	368	

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23216	53584	A	23350	3786	4928	PPPARTRPCASLTPEKAKWWRS KPGLTRAPARCGLSSPQTGSCS APASAG*VSGNSRSGTRRGLRP TRG*GPCGPSSRARAISSPRAS/L RMSQRELGLWDPNNFEEPVAL QEMDTSNGVLLPFYDPDSSIVY LCGKVLTAGQGEQGTGWRCG GPCPGAPLNRLILQGDSSIRYFEI TDEPPFVHYLNTFSSKEPQRGM GFMPKRGLDVSKCEIARFYKLH ERKCEPIIMTVPRKSDLFQDDL YPDTPGPEPALEADEWLSGQD AEPVLISLRDGYVPPKHRELRV TKRNILDVRPPSGPRRSQSASDA PLSVRSALLHSGPIYISPNRPYTT RPLCPPPQQQHTLETLLEEIKAL RERVQAQEQRITALENMLCELV
23217	53585	A	23351	1	1898	MSRKGPRAEVCADCSAPVGPD FALAISELVSPDIFMQSHSENAIS VKEIVTEIESISQGVGQIQLKGDI LPNPCHTPKKNSIHELLLERAQT PENKPGHMEQDEDSCTAQPEL AKDSGMCNPEGCLTTHSSIADL EEGEQLRGNKSSRAQGCTQNS KNDSSVADLAPKGKSDEAPPEH SFVLKEPEMSKGKGKYSGSEA GSLSHSEQNATVPAPRVLEFDH LPDPQEGPGPEASNGLKVSQKS EGSQPSSSRSPLEFLKEAGVPNQ TLSSGTPDPYFMALLGPKLNSR RPHLHPVSHTLDLGNSPPLPQQ FAKCQRGRKGPEGKYPLHYLV WHNRHRELEKEVRAGQTLITQ TLSQANPTAITAEEYFNPNFELG NRDMGRPMELTTKTQKFKAKL WLCEEHPLSLCEQVAPIIDLMA VSNALFAKLRDFITLQIPIFHILN ARITFGNLNGCDEPVPSVRGSPS SETPSPGSDSSSVSSSSSTSEAPR ENACPSALPGVASCRGCEISPAL FEAPRGYSMMGGQREAATRDD DDDLLQFAIQQSLLEAGSEYDQ VTIWEALTNSKPGTHPMSYE/R SPTGQGQVPAATCSG/RYDEQL RLAMELSAQEQEERRRRARQE EEELERILRLSLTEQ
23218	53586	A	23352	341	711	

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23219	53587	A	23353	57	719	TSDLMAEIIQERIEDRLPELEQL ERIGLFSHAEIKAIIKKASDLEY KIQRRTLFKEDFINYVQRIGYSF KKDEIENSIVHRVQGVFQRASA KWKDDVQLWLSYVAFCKKWA TKTRLSKVFSAMLAIHSNKPAL WIMAAKWEMEDRLSSESARQL FL\RALRFHPECPKLYKEYFRM ELMHAGKTGGRRRKNLKKPV WMWRILIILKKSLRASWHGSST
23220	53588	A	23354	27	352	TESVVTIMSLLNKPKSEMTPEE\ REEEEFNTGPLSVLTQSVKNNT QVLINCRNNKKLLGRVKAFDR HCNMVLE\NVKEMLTEG/DRYI SKMFL\AGDPVIVVLRNPLIAGK
23221	53589	A	23355	32	575	STRLDLPKCWDYRSLFNKP\KS EMTP\EELQKREE\EEFNT\GPTP LCLTQS\VKNNTQSAQSTC\RNN KKLPGAA*RPFDRASPPCSPPGT CNMVL\ENVK\EMWT*GTQEV GKGKEGSSKP\VNKDRLTSSKM FPGGGGFSSFVVPCGNPFHSAG QIRGPPVLFDKNSHPLVLLKTA CHLVFENY
23222	53590	A	23356	103	713	VTSGCGKKKVWLDPNET\NEIA NANFRSADPGRLIKDGLIIRKPV T\VHSRARLPEKTPLARCKGHG TLGIGKRKGTANA\RMPKEGHH GMRRMRILAPACSRRYRESKKI D\RHMYHSLYLKVKG\NVFKNK ADFSWEHIHKAEGRARPRKEAS WLDQAEA\RRSKDQGKHGKRR EERLPGQRKEEINQRLYSKEGR RPRNKNLTL
23223	53591	A	23357	1	2847	
23224	53592	A	23358	1	2823	
23225	53593	A	23359	3	2858	AMFGFQRRGLGTPRLQLWLLL LEFWEVGSGQLHYSVSEEAKH GTFVGRIAQDLGLELAELVQRL FRVASKTHGDLLEVNLQNGILF VNSRIDREELCGQSAECSIHLEV IVDRPLQVFHVNVEVKDINDNP PVFSLREQKLLIAESKQSDSRFP LEGASDADIEENALLTYRLSKN EYFSLDSPTNGKQIKRLSLILKK SLDREKTPELNLLLTATDGGKP ELTGTVRLLVQVLDVNDNDPE FDKSEYKVSLMEN

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23226	53594	A	23360	194	931	NSPVVPVMASGQFVNKLQEEVI CPICLDILQKPVTIDCGHNFCPQ CITQIGETSCGFFKCPLCKTSVR\ RDAIRFNSAVAEIWWEKIQALQ ASEVQSKRK\EAT\CPRHQEMF HYFCEDDGKFLCFVCRESKDH KSHNVSLIEEAAQNYQGQIQEQ IQVLQQKEKETVQVKAQGVHR VDVFTDQVEHEKQRILTEFELL HQVLEEEKNFLLSRIYWLGHEG TEAGKHYVEIPLMPTVERSQEA
23227	53595	A	23361	2	381	AINWTSARPVSQCWDP\CPPSQ VVCLAGLPP*RVCQNPVKGP\N CPLAHTSEPTGHCLL*TRGMCF PSLCGQLCP*SGPPDCPSPRALH HTGFCPVALLVAESQVRARAC GPEPHRAGRASRWCLHAG
23228	53596	A	23362	213	574	PQTHTGNHSERGRQPITRSPEKP EP\CPSKRAPQTQQP\PWAPSLC PPALGPCKGTRRPRVQVHRPTS SQKCPLPAWFHHLPLWPTSAAR SSSTETPTGQQMRKLRHPAAPR SANALSLGE
23229	53597	A	23363	21	456	
23230	53598	A	23364	2	98	
23231	53599	A	23365	64	241	PWPLASNPRGCLP*PSTLN*PTP SSQPGMSLDSLDRHPP*TRETAS GIGGQRPGSDPARTPHFISQTQ
23232	53600	A	23366	209	353	

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23233	53601	A	23367	1766	3292	SSCPTTRVLIMKGAGHPCYLDK PEEWHTGLLDFLQGLQLWLMH MQQLMSLAVVSGRLSRGQCGT ERPSRRAAAAAAAGQPQRGHF QHIEERLETNVQNCQSPDTLCP THCSPVLNEPCPEVSVVAVAPA SPDRMSGSDGGLEEEPELSITLT LRMLMHGKEVGSIIGKKGETV KRIREQSSARITISEGSCPERITTI TGSTAAVFHAVSMIAFKLDEDL CAAPANGGNVSRPPVTLRLVIP ASQCGSLIGKAGTKIKEIRETTG AQVQVAGDLLPNSTERAVTVS GVPDAIILCVRQICAVILEGFSV QGQYGAVTPAEVTKLQQLSSH AVPFATPSVVPGLDPGTQTSSQ EFLVPNDVSRGWDGWRLIGCVI GRQG\TKINEIRQMSGAHIKIGN Q\AEGAGERHV\TITGSPVSIALA QYLITACLETAKSTSGGTPSSAP ADLPAPFSPPLTALPTASPLAC WAHPMPSPSPTLIGFKAHALLG FTTCFPRAAAGLGGLHRQDGSS
23234	53602	B	23368	1	363	
23235	53603	A	23369	486	947	LDGAGLLAPVKAHLQKKGPRL GTRGCAMPRLGSTPFLKGQCL ANSRNTLEAVSLTESSASRVPP APVLGSRRPHSPSPWP/P/YYTP VPPPPRMALVPPNMHGQGTVG LTSVPLACTVAMLGSYKQAGA FGPLANCYGGLGHAQCWGQEF CPTQCP
23236	53604	A	23370	38	680	GSRLRRLQAAAARPALPLPLPP WEWKHLPHVPEAKWWLTTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESLDLAEFAK KQPWWRKLFGQESGPSAEKYS VATQLFIGGVTGWCTGFIFQKV GKLAATAVGGGFFLLQLANHT GYIKVDWQRVEKDMKKAKEQ LKIRKSNQIPTEVRSKAEEVVSF VKKNVLVT\GGFFGGFLLGMAS
23237	53605	C	23371	30	200	
23238	53606	A	23372	14	161	

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23239	53607	A	23373	69	715	APALPGCEHMMAIRELKVCLL GDTGVGKSSIVWRFVQDHFDH NISPTIG\ASFMTKTVP\WENDFT KFLIWDTAGQERFSFIGLPLYYS RLQLAAVYSCYGYLPSRDFIFIT LKE\WV\KRLKELGPE\NIVMAI AGNKCDLSDI\REVPPEGMLKE Y\AESIGAIVVETSAKNAINI\EE LFQGIS\RQIPPLDPPMKNGKQW DHQKLRSQPMQASRRCC
23240	53608	A	23374	3	293	VTSTMAYRAQGQKV\QKVMV QPINLIFRYLQNRSRIQVWLYEQ VNMRIEGCIIGFDEYMNLVLDD AEEIHSKTKSRKQLGRIMLKGD NITLLQSVSN
23241	53609	A	23375	3	393	HESCSQRQRAGCALCENSHPW RSRGPGVQKSAEGLWCQPICRT SSSRYL\QNRIAGFQVWLYEQV NM\RI\EGCIIGF\DEYVNLVLDD AEEIHSKTKSRK\QLGR\IMLK\G DNITLLQTCLPPRMVHGSGEIV
23242	53610	C	23376	129	425	
23243	53611	A	23377	470	635	ENSSSHHIIKPFSSGCSIHGFSGH INVTSVTIL*PIKSCHIRCHF*CA QYMVADN
23244	53612	A	23378	71	566	PLFPPCLSPVVAGWARGHMLG QSHQQVAAPLKHRPITPTELCQ KCLSLIKKTKFLNAYITVSEEVA LKHAEESEKRYKNGQSLGDLD GIPIAEKDNFSTSGIETT\CASNM LKGYIPPYNATVDQKLLDQGA LLMGKTKLNDFAMGSGSTDGV FGPVKNPWSYSK
23245	53613	A	23379	255	1042	ILAARMGKQNSKLRPEVMQDL LESTDFTEHEIQEWYKGFLRDC PSGHLSMEEFKKIYGNFFPYG\D ASKFAEH\VF\RTFDANGDG\TID FREFIIALSVTSRGKLEQKLKW AFSMYDLDGNGYISKAEMLEIV QAIYKMVSSVMKMPEDESTPE KRTEKIFRQMDTNRDGTWVPH LALIYRTAEGGFAVQRASVSFY PPPSAGNAMVNEAAVFLEIPLG SSPGQVSAVCHSGRKLSLEEFIR GAKSDPSIVRLLQCDPSSAGQF

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23246	53614	A	23380	1	721	MDGNLRKIRFEKHAITEEFRTT EPGLAALRLPSTWIRGVRTSES KREVGKGGQSQQYENRDTEGE GHVMTKARDWSKAAASQRLP ANHLKLRLCIDGFRSHSLPEEGP KKPCQHHAAQEEPCTRSGRLPQ AHEGSISDCCTSSEQGSMDIGSV EPGTGYNLLVCHLL/STLEKRSI WAGVSRFSRYHLSRLPLARK\G NPLTPCASQLLLPLPSTTQKRQS GHALYSFPYRPQPKNDNLVMP
23247	53615	A	23381	80	562	DRAMWGDLWLLPPASANPGT GTEAEFEKAAEEVRHLKT/RSPS DEEMLFIYGHYKQATVGDINTE RPGMLDF\TGKA\KWD\AWNEL KGTSKGDAVEA\YLNQV\EELK KKYGDMERLDLVTVPCVYPKP ETIPFFFSNTVDGWEFRENNPV KPATQRLLTHTGS
23248	53616	A	23382	380	1041	EVTINSGFIFIMLFMEHPEHYTI MHKWILTWILPTLLYRSCFHIIC LVGTISLACND\MTPEQMATNV NCSSPERHTRSYDYMEGGDIRV RRLFCRTQWYLRIDKRGKVKG TQEMKNNYNIMEIRTVAVGIVA IKGVESEF\YLAMNKEGKL\YA KKECN\ED\CNFKELILENHYNT YASAKL/WTHNGGEMFVALNQ KGIPVRGKKTKKEQKTAHFLP MAIT
23249	53617	A	23383	127	549	SSPKMAATMKKAAAEDVNVTF EDQ\QKINKFARNTSRITELKEEI EVKK\KQLQNL\EDACDDIMLA DDD\CL\MIPY\QLGDVFISHSQE ETQEMLEEAKKNLQEEIDALES RVESIQRVLADLKVQLYAKF\G SNINLEADES

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23250	53618	A	23384	1	2050	MEYESMVISFDDRVMEKTEYG PIFTVFAMGNRMTFVTEEEGIN VFLKSKKVDFELAVQNIVYRTA SIPKNVFLALHEKLYIMLKGKM GTVNLHQFTGQLTEELHEQLEN LGTHGTMDLNNLVRHLLYPVT VNMLFNKSLFSTNKKKIKEFHQ YFQVYDEDFEYGSQLPECLLRN WSKSKKWFLELFEKNIPDIKAC KSAKDNSMDSDEDPVNLQSRS ALVCEMLHVQRSSSDADAIGPH ADHSLSNRWEVILADEHGIIAD DMISRYALSEKSQVELSTQVIKS ASSKSVNKSDIDTSVFLNWYNP EKKMIRAYATVIDGPEYFWCQF ADTEKLQCLEVEVQTAGEQVA DRRNCIPCPYIGDPCIVRYREDG HYYRALITNICEDYLVSVRLVD FGNIEDCVDPKALWAIPSELLS VPMQAFPCCLSGFNISEGLCSQ EGNDYFYEIITEDVLEITILEIRR DVCDIPLAIVDLKSKGKSINEK MEKYSKTGIKSALPYENIDSEIK QTLGSYNLDVGLKKLSNKAVQ NKIYMEQQTDELAEITEKDVNII GTKPSNFRDPKTDNICEGFENP CKDKIDTEELEGVSQKAQESMC TEDMRKSSCVESFDDQRRMSL HLHGADCDPKTQNEMNICEEEF VEYKNRDAISALMP\FSLRKKA VMEASTIMVYQIISQLNYRTPTL
23251	53619	A	23385	3	602	TRPPTRPGLSPDPTSPTEADRGV CERPHRCFLLPQITHPSSGRRCL CLLSPTSFDFSLLYESQSDRAIF GVGTEPDQEPPPPYHEQVPVSV YHPT\P\SQTWVATQLTEEEQIRI AQRIGLIQHLPKGVY\DPWRDG SEKKIRECVICMMDFVYGDPIR FLPCVHEWYHLDCIDDWLMRS FTCPSCMEPVDAALLSSYETN
23252	53620	A	23386	33	512	TAARCQGGPTHVPAFVGTACP TRIPGHAPARQCREYYY*YYYD F/WKEPRRCHALLLPPWAGLEV GMPPSHTQLGMHPAPPPPHLEV KAQG\PSNRQRTDGCRWCSGR ASALGGGRQDSRLRERGGGYD H/HCPICRSLKIQLKCHPASGPQ TVGLGRLASVS
23253	53621	A	23387	1	1731	
23254	53622	B	23388	1	706	

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23255	53623	A	23389	1	1986	MGIGEGPTTSEGCRESVEYSHQ KSELPLSGDSQVPGPIGCNCDP QGSVSSQCDAAGQCQCKAQVE GLTCSHCRPHHFHLSASNPDGC LPCFCMGITQQCASSAYTRHLIS THFAP/GDFQ/GFA/LVNPQRNS RLTGEFTVEPVPEGAQLSFGNF AQLGHESFYWQLPETYQGDKG EAYFARMRRAHQNRTSLSEEQ LRAAVTAGRIPEPPEGRDWAQR ASQFSLSYEGFSLLPGSLYYWQ LPRAFLGDKVAAYGGKLRYTL SYTAGPQGSPLSDPDVQITGNNI MLVASQPALQGPERRSYEIMFR EEFWRRPDGQPATREHLLMAL ADLDELLIRATFSSVPLAASISA VSLEVAQPGPSNRPRALEVEEC RCPPGYIGLSCQDCAPGYTRTG SGLYLGHCELCECNGHSDLCHP ETGACSQCQHNAAGEFCELCA PGYYGDATAGTPEDCQPCACP LTNPENMFSRTCESLGAGGYRC TACEPGYTGQYCEQCGPGYVG NPSVQGGQCLPESSELHFPSVQ PSDAGVYICTCRNLHQSNTSRA ELLVTEAPSKPITVTVEEQRSQS VRPGADVTFICTAKSKSPAYTL VWTRLHNGKLPTRAMDFNGIL TIRNVQLSDAGTYVCTGSNMF AMDQGTATLHVQGSAEAGERS MYSISVLLKYTS
23256	53624	A	23390	3	13319	PASGRLRAARSGRRGASERESG AGRAMGWRAPGALLLALLLH GRLLAVTHGLRAYDGLSLPEDI ETVTASQMRWTHSYLSDDEYM LADSISGDDLGSGDLGSGDFQM VYFRALVNFTRSIEYSPQLEDA GSREFREVSEAVVDTLESEYLKI PGDQVVSVVFIKELDGWVFVE LDVGSEGNADGAQIQEMLLRVI SSGSVASYVTSPQGFQFRRLGT VPQFPRACTEAEFACHSYNECV ALEYRCDRRPDCRDMS

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23257	53625	A	23391	41	1323	HYLVFFLPSLRRYTVSLSPNSTS YQLLVPGPSY/SALPISSAASLY AGA\GGSGSRMSVSHSTSLRDG ISSGGLA/TGMARGLGGMGGIQ NKKETTQSLNDSLAVRVRSLET ENRKLESKIREHLEKKGPQVRD WSHYFKTIEDLRAQIFANTVDN VRIFLQIDNARLAADDFRVKYE TELAMRQSVESDIYGLHKVIDD TNVINGCSFFMKKNHGEEVKC LQAQIASSGLTMEVDAPKSQDL AKITADISTRYDELARKNREEL DKYWSQPIEESTTEVTMQSAKV RAAEMTFMELRRTVQSLEIDLD LMRNPKASLENSLREVEACYA LQMEQLNLDP/GILLHLESELTQ TRAEGQL\QAQKYKALLNIKNK LEAEIATYCLLLEDGKDFNLGD TLDSSNPMQTIQKTTTSRIVDG KVVSETNDTKVWRH
23258	53626	A	23392	1	771	
23259	53627	A	23393	732	1656	SCSWTSPAAWPPNASLHSCLKR RNQDHLLLWDWRFLDFPSSMA SKCQSPLLPQKKKPRPLPALGP EKTSASAGLPKKGEKEQQETIE HIHEVQNEMDRLNEQAK\RSEL ISKIPDFWVTIFVNHPEVSALPG EEDEEALHYLTRVEMTDFDDIK SGYRIDFYFDENPYFENNILAKE FHLNESGDPSSKSTEIKWKYGK DLMKRSSQTQNKAHRKRQHEE PESFFTWFTDHSDVGADELGEV IKDIWPNPLQYYLVPDMDNEEG EGEEDDDDEEEEGLEDIDEEG DEDEGEEDEDEGEKGEEDEGE
23260	53628	A	23394	3	923	ARRLVVWFWDFPNSMAPKRQS PLPPQKKKPRPPPALGPEETSAS AGLPKKGEKEQQEAIEHIDEVQ NEIDRLNEQASEEILKVEQKYN KLRQPFFQKRSK\LSAGIPNFWV TTFVN\HPQVS\ALLGEEDEEAL\ HYL\TRVEVTEFEDIKSGYRIDF YFDENPYFENKVLSKEFHLNE\S GDPSSKSTEIKWKSGKDLTKRS SQTQNKASRKRQHEEPESFFTW FTDHSDAGADELGEVIKDDIWP NPLQYYLVPDMDDEEGEGEED DDDDEEEEGLEDIDEEGDEDEG EEDEDDDEGEEGEEDEGEDD

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23261	53629	A	23395	732	1656	SCSWTSPAAWPPNASLHSCLKR RNQDHLLLWDWRFLDFPSSMA SKCQSPLLPQKKKPRPLPALGP EKTSASAGLPKKGEKEQQETIE HIHEVQNEMDRLNEQAK\RSEL ISKIPDFWVTIFVNHPEVSALPG EEDEEALHYLTRVEMTDFDDIK SGYRIDFYFDENPYFENNILAKE FHLNESGDPSSKSTEIKWKYGK DLMKRSSQTQNKAHRKRQHEE PESFFTWFTDHSDVGADELGEV IKDIWPNPLQYYLVPDMDNEEG EGEEDDDDDEEEEGLEDIDEEG DEDEGEEDEDEGEKGEEDEGE
23262	53630	A	23396	3	924	ARRLVVWFWDFPNSMAPKRQS PLPPQKKKPRPPPALGPEETSAS AGLPKKGEKEQQ\EAIEHIDEVQ NEIDRLNEQASEEILKVEQKYN KL\RQPFFQKRSK\LSAGIPNFW VTTFVN\HPQVS\ALLGEEDEEA L\HYL\TRVEVTEFEDIKSGYRID FYFDENPYFENKVLSKEFHLNE\ SGDPSSKSTEIKWKSGKDLTKR SSQTQNKASRKRQHEEPESFFT WFTDHSDAGADELGEVIKDDI WPNPLQYYLVPDMDDEEGEGE EDDDDDEEEEGLEDIDEEGDED EGEEDEDDDEGEEGEEDEGED
23263	53631	A	23397	1	1393	MGKQKGGGPQAWEAEGLGRE WMRMPQEGKGSQRKSTQKQT KREIDAYIVQAKERSYETVLSF GKRGLNIAASPAVQAATKVLW APSPPAAPIPPLRPFGLIQLLCQG AQRWQPGSREVKGRLCQARLA ETSSIAGNLRVQSYERPVDPGV TMDPLLPGRTIVFAAGDHTLW RAPVSSCAQRSGVWSLDNMGV NSGSVPFHGVRIQASQLISLSFN FSFCEADLKTPLHGFLILPAGPK EEVTVKKEKRERDRDRQREGH GRGRGRPEVIQSHSIFEQG\PAE MMKKKGNWDKTVDVSDMGPS HIINIKKEKRETDEETKQILRML EKDDVDHHALSEHLVTTATFSI GSTGLVVYDYQQVECGGHVRA DLKTQDLYSHAQFGDNNYPGG VDWYRAGGLQDSDTEDECWS DTEAVPRAPARPREKPLIRSQSL RVVKRKPPVREGTSRSLKVRTR KKTVPSDVDS
23264	53632	A	23398	297	584	

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23265	53633	A	23399	2	149	CMKFGAVTPIGGPPLGDQSPVL LLFAL*KRSTYNLGSSDPPAQGI SHQF
23266	53634	A	23400	1	170	PAGIRHEERSTYDLWSSDRPGQ GTSHQF*IIRFQIPWNSGPRLSE* LLPRSSRLSS
23267	53635	A	23401	1	1077	
23268	53636	B	23402	289	1359	
23269	53637	A	23403	3	2233	
23270	53638	A	23404	1	1491	
23271	53639	B	23405	76	511	
23272	53640	A	23406	1	2706	
23273	53641	A	23407	273	862	
23274	53642	A	23408	1	1080	
23275	53643	A	23409	134	675	MHYFHSSVQIGLPLTRRSQVLIL PQPLLPNPIILLSPPLLTPVPAYS FIL/PTSPPPPARQFPLKKVAEAK GIVKQLKTDTARSPRKPTGPSQ TLWVTLTVEDLKHAFFTIPLHP SSQPLFAFTWTDPDTHQAQQIT RAVLPQVFTDSPHYFSQAQISSS SVTYLGIILIKTHVLSLLIMSG
23276	53644	A	23410	1	895	MEVHKHPFNTLALRHESGCEL VWAEKHRNQIFPFPKSTASPKQ WDTGRHNSDAKQQEPGGREER NTMEMETKETHFIRGPKTLASV TDWEGSLPLVFNHCRGTSLIIHP RFKGVRPRRDACLGPSPLAASP AFLGKGQHALKGLKPVITRLLQ HGLLKPINSPFPS\PILPVLKPDK AYKLVQNLRLINQIVLPIHPVVP NPYTLLSSIPPSTTHYSVLDLKH AFFTIPLHPSSQPLFAFT*TDPDT H*AQQITWAVLPQGFTRQPPLL QLSPNFILICYLSRHNSHKNTRA LPADRV
23277	53645	A	23411	1	930	MIQEHADKQVQRLQGVLLGSIP TAASRARLHPGEINNHVAHTEP VWWSLHMDAYEIWCRGSDRR TSLGRSIPLPPALCSLRRIHLRPQ VLRSTSPRNISPISNPGHLSDYTP TFQGCQTMQGRLPWSFTLSGK SRFSGEGATQRQYPIPQQALKG LMPAITRLLQHGLLKPINSPYHS PILPVLKPDKPYKLVQDLRLINQ IVLPIHPMVPNPYTLLSSIPASTT HYSV\LYVKHAFFTIPLHPSSQP LSTFTWTDPDTHQAQQIT*AVL PQVFTDSPHYFSQAQISSSSVTY LGIILHENTRALPADHV

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23278	53646	A	23412	299	1028	RLGSFSSNHPYLGQRQYPIPQQ ALKGLKPVITCLLQHVLLKPVN SPYNSPILPVQKLDMPYRLVQD LCLINQIVLPIHAMVPNPYTLLT SIPPSTTHYSVLDLKPAFFTIPLR LSFQPLFTFSWTDPDTHQAQQI TRAVLPQSFTDSPHYFSQAQIS* RLGSFSSNHPYLGQRQYPIPQQ ALKGLKPVITCLLQHVLLKPVN SPYNSPILPVQKLDMPYRLVQD LCLINQIVLPIHAMVPNPYTLLT SIPPSTTHYSVLDLKPAFFTIPLR LSFQPLFTFSWTDPDTHQAQQI TRAVLPQSFTDSPHYFSQAQISS SSVTYLGIPGFAILTKPLYKLTK GNLADPIDPKSFPHSSFRSLKTA LETAPILALPVSSQPFSLPTAEV WAAQSEFLHKNRDRTE
23279	53647	A	23413	157	202	RSECARWMEK*CPWL
23280	53648	A	23414	184	482	EGVSVFLLLSPYQGQPQVSRRC S/RQVSQRCPHRGRGPRCPQVS RSHGPSWVGHPGMPLYGS\EQF YCGAPGLAGPPNGSRGESLKIS VWIFPCRDFGNFN
23281	53649	B	23415	13	862	
23282	53650	A	23416	1	11342	MATRWFYYGHPPRDARVPRIV AEAKEKNLTPGKIIEVDVTIEAQ IRQEFLDAERDTGGFVKFFRITK KKLQEFFLGEEEEQVPHVSPVE LGAKPTAFNAFIANAVGKTLAV QHASLKAPEPEMTVTHERFYG NYAVWITDVDPRNHRIEVIHVI REISGRTSEYVNNLLAQPTPFK VFDWLTETQAKEFVRRLNNTQ GVISVYNKLEDGIPVKVAVKAT EPTNKEKLEAASTKLKAMGAV ATDAYEFHTDLNENE
23283	53651	A	23417	7597	7883	LSSLAWVWQWNHRISVLFHSN SVRTNLVPQFNQLVITESNSCPE FFNQTSAFFKT*VESGCM/CLQD *GIEWFRLRLDVYNSRLVFLTG ATDYCTG
23284	53652	A	23418	3	1573	
23285	53653	A	23419	6692	6793	GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS
23286	53654	A	23420	1	17727	
23287	53655	A	23421	6687	6785	VNTGNRTWWEPLFRK*KKTQR EDTTEKKTKGR
23288	53656	A	23422	1	2856	
23289	53657	A	23423	1	7194	

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23290	53658	A	23424	7460	7561	GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS
23291	53659	A	23425	1468	1857	
23292	53660	A	23426	1	1985	MEPVGIDIIAISWIGAPEYPDNV KRAINAKVEATQKTLQREQEIQ QRVAEANMEREQAKGVADAIR LRGEALTENPNVMQLEAINKW NGLVPFITSSPGMGKSAIVRQIA EDFGLKLIDHRLSTSAPEDLSGL PRFKENGRAEFAPFDELFPLEG DAVPEGFNGWLLFLDEFNSAR KEIQAAAYKLVLDRMTGQKKL HPYVAIVCAGNKATDRAITNNL STAMQSRLIHLEMETDFDVFME DVAIPNKWDERVIAFLNANPNK LNDFEPDHQEKTFCCSRTWEFV NKIVSILPPGPINSEMTLLLAGTI TSGVATSFVQFTQVYSNMVSL NEILDNPKKARMPEDNNLLWA VVTSLINNTDEDNHSKIFDYVE RMPFTFKVLYYRSRKTDMSMT DAQLTREYDRCQAKAFMGKTA AFFGSLLCSLKFRWVKDGCDT AQTDGEHLEWNPDWFESLLPE SRVTVLMHELWHVGLLHSVR MGSRDPEVWNYACDIYINNQLI QDGYSFIGIENCWKDPKYAGW AEEQIYHDLMSKHPRPPKASGA FGTGSGGDMKPSTSKASLKLSG GSLPGVLPGKMEEVITQFLKPV VPWQVLLERFFNDLQETYYSW QRPNRRYPDMYLPSSMDDDCR LEHLAYFL*NEADLTGLLVLK* TDDGQSVSGQNLLQSDEQLQIY
23293	53661	A	23427	2365	2784	
23294	53662	A	23428	5789	5980	DQNMRFDNTFETYYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL
23295	53663	A	23429	1	6819	
23296	53664	A	23430	376	2052	SKVCGNDGFADDLKHLLIFTGA QSGEDIVPFQLEDGHSLGEVVL LHGGSGVESGQR/CGRTSAGSC Y*SPGKICCCNLLVTKTEGFFAP VPIQLENTNQVTNCSDNW
23297	53665	A	23431	2	2189	
23298	53666	A	23432	2	1583	
23299	53667	A	23433	2142	2242	GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS
23300	53668	A	23434	3	1188	
23301	53669	A	23435	470	862	
23302	53670	A	23436	1	1352	

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23303	53671	A	23437	1837	1955	SKCSIGLYQRYPYSNGC*NSGCI CRVY*CCREHRGYVRN
23304	53672	A	23438	1447	1565	SKCSIGLYQMYPYSNGC*NSGC ICRVY*CCREHRGYVRN
23305	53673	A	23439	773	823	
23306	53674	A	23440	3	1529	
23307	53675	A	23441	1	1794	
23308	53676	A	23442	236	427	DQNMRFDNTFETYYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL
23309	53677	A	23443	8510	8611	GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS
23310	53678	A	23444	516	669	ATSELKRKASLGLMEPDVSRK* ARCSSLPSSSIGDGRYISGYLRL GRCHE
23311	53679	A	23445	410	593	FLNLIQPQGKRKLLLKRCRSLLP KN*CQHSKQHKLSISSVVILNIT NS*PNKVKLMPILAM
23312	53680	B	23446	1	2286	
23313	53681	A	23447	1418	1723	CNTNIIFNCHFPTKLGCICKAMK VVSPLIHNSIVILLNQITIDFFSTL AQICTFICLTYSKQTTTRIASFK KVIEEFLSLAPIEKVELKEHS*YI SISEKV
23314	53682	B	23448	1	6167	
23315	53683	A	23449	1	3199	
23316	53684	A	23450	1	5733	
23317	53685	A	23451	709	1099	
23318	53686	A	23452	5039	5230	DQNMRFDNTFETYYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL
23319	53687	A	23453	664	993	
23320	53688	A	23454	1	19859	MASIDSIAVCNPRQVRKFVEHC IRSGLVPFITSSPGMGKSAIVRQI AEDFGLKLIDHRLSTSAPEDLSG LPRFKENGRAEFAPFDELFPLEG DAVPEGFNGWLLFLDEFNSAR KEIQAAAYKLVLDRMTGQKKL HPYVAIVCAGNKATDRAITNNL STAMQSRLIHLEMETDFDVFME DVAIPNKWDERVIAFLNANPNK LNDFEPDHQEKTFCCSRTWEFV NKIVSILPPGPINSEMTLLLAGTI TSGVATSFV
23321	53689	B	23455	74	240	
23322	53690	A	23456	143	384	
23323	53691	A	23457	1	3267	

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23324	53692	A	23458	2	550	KRSSEHIQRIDRDVSGTLRKHIF FRDRYGTKQRELLHILLAYEEY NPEVGYCRDLSHIAALFLLYLP EEDAFWALVQLLASERHSLQG FHSPNGGTVQGLQDQQEHVVA TSQPKTMGHQDKKDLCGQCSP LGCLIRILIDGISLGLTLR\LWDV YLVEGEQAFMPITRIAFKVQQK RLTKTSR
23325	53693	A	23459	72	630	
23326	53694	A	23460	1	2835	MDALMLALGALMLALGLGDP KSAQVSDPDGAEPGPGRATGT DPLVQIHWKLGISEALSIPGGRL YRDLWSLTPVCLHIPGIAHHGP FTLGRMDVVEVAGSWWAQER EDIIMKYEKGHRAGLPEDKGPK SFGSYNNNVDHLGIVHETELPP LTAREVKQIRREISRKSKWVKM LGEWDTYKNSRKLIDRAYQGIP MNIRGPMWSVLLNIEEIKLKNP GRYQVRSARAQPTGQAVSGAQ VSSWRERQDHPGELGVKI

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23327	53695	A	23461	1	832	MGWRARWLMPVISALWEAED PIPPELTRLLQQSQDPLLMGLFP TNPKEKTQEEPPGQSRAPVLTV VSKFKVLAGLLHLGNIQFAASE DEAQPCQPMDDAKCEGQGVG WAGPVRKASLEQLLQVLHSTT PHYIRCIKPNSQGQAQTFLQEE AGAGRRRQRRRQKQQRRRRRQ LGGGGDGGNGSVGDDGATRGS RGCALEKECVATPRRGLLFSRP HKLAFAVGGSVTSVGPKPRAP MDVVEVAGSWWAQEREDIIM KYEKGHRAGLPEDKGPKPFRS YNNNVDHLGIVQDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMQLARQV SRLESGHFYDAHNPFLPPPSMS KQAKKTGVPSEGLCRPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AVSATQLIGLQLILLGEVLQKV LTASYPAQSSVPLTSGPVRQIM KEKGKRSSEHIQRIDRDISGTLR KHMFFRDRYGTKQRELLHILLA YEEYNPEVGYCMDLSHIAALFL LYLPEEDAFWALVQLLASERHS LQAARAPAAIGAHERADQAQIS LGLTLRLWDVYLVEGEQALMP ITRIAFKVQQKRLTKTSRCGPW ARFCNRFVDTWARDEDTVLKH LRASMKKLTRKQGDLPPPAKPE
23328	53696	A	23462	3	497	SSECLTMAWIPLLLPLLILCTVS VASYELTQPASVSVSPGQTASIT CSGDVLAKKKYARWFQQKPG QAPVLVIYKDSERPSGIPERFSG SSSGTTVTLTISGAQVEDEADY YCYSAADNNGWVFGGG\TKLT\ VLSQPKAAP\SVTLFP\PSSEELQ ANKAHTGVSQ
23329	53697	A	23463	1	393	FRSGSELVKAGLRAFFENAAED LEKTSENLKLGKFTHSRTQIKG VSQNINYTTVALLPILTSIFEHV TQHQFGMDLLLGDVQISCYHIL CSLYSLGTGKNIYVE\ILGMPDT VEDMCPDIPQLECLMKEIN
23330	53698	A	23464	319	508	
23331	53699	C	23465	94	222	
23332	53700	A	23466	1	636	
23333	53701	A	23467	1	483	
23334	53702	A	23468	1	1797	

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23335	53703	A	23469	1	4275	
23336	53704	A	23470	1	1848	
23337	53705	A	23471	122	14928	ARSWRRRWRTRTKRRRRKSAA AVSARRAAAGGSRGAGGWGT ADASGAMAEGGEGGEDEIQFL RTEDEVVLQCIATIHKEQRKFC LAAEGLGNRLCFLEPTSEAKYIP PDLCVCNFVLEQSLSVRALQEM LANTGENGGEGAAQGGGHRTL LYGHAVLLRHSFSGMYLTCLTT SRSQTDKLAFDVGLREHATGE ACWWTIHPASKQRSEGEKVRIG DDLILVSVSSERYLHLSVSNGNI QVDASFMQTLWNVHPTC
23338	53706	A	23472	134	1063	RPPGLTRSPSSPAPARSPTRRQS TRRRSGATTSCSQRLWATWNG CD/VCLNQSLREIPTDDKGFTAI HFAAQWGKLACLQVLVEEYKF PVDLLTNNSQTPLHLVIHRDNT TVALPCIYYLLEKGADLNAQTC NGSTPLHLAARDGLLDCVKVL VQSGANVHAQDAMGYKPIDFC KIWNHRACARFLKDAMWKKD KKDFAREMTKMKMFKSQLTL MEHNYLIEYQKEHKILREAAIR KWLHGKLHPGHSLVSNTKQAR ATALSKTPEQRESQRSRSFHPSV DARLQCIPQPTEMPKPIYRKPTV KRPHNVEC
23339	53707	A	23473	1	1280	MAGLGFWGHPAGPLLLLLLLV LPPRALPEGPLVFVALVFRHGD RAPLASYPMDPHKEVASTLWP RGLGQLTTEGVRQQLELGRFLR SRYEAFLSPEYRREEVYIRSTDF DRTLESAQANLAGLFPEAAPGS PEARWRPIPVHTVPVAEDKLLR FPMRSCPRYHELLREATEAAEY QEALEGWTGFLSRLENFTGLSL VGEPLRRAWKVLDTLMCQQA HGLPLPAWASPDVLRTLAQISA LDIGAHVGPPRAAEKAQLTGGI LLNAILANFSRVQRLGLPLKMV MYSAHDSTLLALQGALGLYDG HTPPYAACLGFEFRKHLGNPAK DGGNVTVSLFYRNDSAHLPLPL SLPGCPAP\CPLGRFYQLTAPAR PPAHGVTCHGPYEAAIPPAPVV PLLAGAVAVLVALSLGLGLLA WRPGCLRALGGPV

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23340	53708	A	23474	133	672	AVGWESGKWDSGRGQGGGQE QMWSCQSDMLYPPDQVGAWG LPGPTGPKGDAGSRGPMGMRG PPGECPQCCPTAPLAIPSTRWAL PCSWPPGPPGPPGPPAPVGPPHA \GSPSMVSPPGIPAGGGGGGVAI STVPATIKTRRQEVSPELPRP/PG PAPPPGPDVRPWLLRPPGPMGK LSPGQG
23341	53709	A	23475	135	677	AVGWESGKWDSGWGQGGGQE QMWSCQSDMLYPPDQVGAWG LPGPTGPKGDAGSRGPMGMRG PPGECPQCCPTAPLAIPSTRWAL PCSGPPGPPGPPGPPAPVGPPHA \GSPSMVSPPGIPAGGGGGGVAI STVPATKKTRRQEVSPELPRP/P GPAPPPGPDVRPWLLGPPGPMG KLSPGQG
23342	53710	A	23476	220	745	TVIQRTGLHSVGPGDPQQGLRE AKLGTMVRLVLLPTPRRTTEVR TGPERELSMVLEAILGSLLETAC DHRQTPPSSKPQA/GSSRLREGT SAGQPCS/LRLRLGPRAGGRRC CRDIERSSSSSVCGRKCKRKKR KRGMCQSRHKHGCRRPQEGPR CNDGRALCSPRPQTTPGPLSTA
23343	53711	A	23477	1	2433	
23344	53712	A	23478	3	803	FPGRRFRVRACVAGGSHCLFNS CCCCTSASLPARERHEWPGPAA AAAAAAAAARRSQTQREGLFA GWGGGFAMSDDDSRASTSSSSS SSSNQQTEKETNTPKKKESKVS MSKNSKLL\SPRAKGIQKEL\AD ITLDPPPNCSAGPKGDNIYEWR STILGPPGSVYEGGVFFLDITFTP EYPFKPPKVTFRTRIYHCNINSQ \GVICLDILKDNWSPALTISKVL LSICSLLTDCNPADPLVGSIATQ YMTNRAEHDRMARQWTKRYA T

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23345	53713	A	23479	372	1839	GEAGGTEAEPENGAGGPRVPG WWGWSSTSSPRGCWDSGRSAA AIMDFLWDKRTGLAARKMPHP RRYHSSERGSRGSYCEHYRS/R K/HKQRRSRSWSSSSDRTRRRR REDSYHVRRRCSRTFSRSSSQH SSRKAKSVEDDTEGHLIYHVGD WLQERYEIVSTLGKGTFGRVV QCVDHRRRGARVALKIIKNVE KYKEAARLEIKVLEKINEKDPG KNLCVQMFDWFDYHGHMCISL ELLGLSTFDFLKDNNHLPYPIH QVHHMASQLCQAVKFLHDNK LTHTDLKPENILFVNSDYELTY NLEKKRHERSVKSTAVRVGDF GSATFDHEHHSTIVSTRHYRAP EVILELGWSQPCDVWSIGCIIFE YYVGFTLFQTHDNRQHLATME RILGPIPSRMIRKTRKQKYFYRG RLDWDENTSAGRYVRENCKPL RQYLTSEAEEDHQLFDLIESML EYEPAQRLTLGEALQHPFFSRL WAEPPNKLWDSSQDISP
23346	53714	A	23480	28	941	QSARPSLKRARSQRGRPLPSRA LVFLFLFFFFFFNFLPIHTQPSAH KDMTTNAGPLHPYGPQHL\RLD NFVPN\DRPTWAYTGLGLFSVT GGLRSWTTWAVVQGRAAGCPI GDFGRATVPCCWVLQCVGFIH LVIEGLVPFSNYERPCFGDQSLL NLKLW\KEYGQGETARLHPGG DKFHSVALGTITSFA\WGEPFSL WVVIA\FLLQHPL\RFIL\QLVVS VG\QIYG\DVF\YFLKEHPRRDS KHGKPGPTPLLLPGFSFVFHEM PLWLVPAPGSPLCLDA\VKAPS THAPEHAWNAKGPQKPKSKKN

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23347	53715	A	23481	1	1386	MWRNLKLPRDLLNGFDQNADS DMDNEVQAEVVTDGDEELIGN WSKGHSCYILAKRLAAFFPCPK DLWKFELERDDLGYLAEEISSS EAFKSVSYEKAHAWNPLESTC RHASLALAVVLQRRDWENP\G VTQL\NRLAAHPPFASW\RNSEE ARTDRPSQQLRSLNGEWRLMR YFLLTHLCETLVKVKDAEDQL GARVCVLERQIFDFLGYQWAPI LANFVHIIIVILGLFGTIQYRPRY ITGILSFPKHQESLSLKFTCLTEA ERDTDALLHLENACRESTATQR IQGFFLKDKKRKKQQPQQQKQ QQWAKVQLGPWLQRVQAPSL GSFHGVLSLRVHRSKELRFRNC CLDFRGCMEMPGCPGRGVLQA QNPRGEPLLGQCRREMCGGSP YIVPTGALPSGAVRRRPPSSRPH NGRPTDSLHCVPGKAADTQHQ PLKAARRAAVPCKATGSELPK
23348	53716	A	23482	3	732	SPLTPTATSGNPSKASSPGGLGS LVSTASSLPAGEKNSPRTGPGP RRAG\AGIPNSGPDTVEGPYNL CGRQGRWGGLIISLASEMKLQT LQTSVTTAKATLLELFVPLGGL VASLASEVRLQIFPRGGHLQSA KCGLLLHFSLPTSRSGRRKANR PMAVTVLLVLIRDCADLLAVK AVIHCYQDQWPLRGSSRPANTP PPKASVSRRPPGHRGVRRGSPL LQVGARRVGAEAPALLELQSPS
23349	53717	A	23483	1	234	
23350	53718	A	23484	1	256	MLNLQGKEWLELEEDAQKAYI MGLLDRLEVVSRERRLKVARA VLYLAQDGEKFCPKRDCTNNS/ RY/NSI*MIQMMRFGTLELMRL
23351	53719	A	23485	1	3333	
23352	53720	A	23486	1	2661	
23353	53721	A	23488	3	433	

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23354	53722	A	23489	3	990	EKMNTADQARVGPADDGPAPS GEEEGEGGGEAGGKEPAADAA PGPSAAFRLMVTRREPAVKLQ YAVSGLEPLAWSEDHRVSVST ARSIAVLELICDVHNPGQDLVIH RTSVPAPLNSCLLKVGSKTEVA ECKEKFAASKDPTVSQTFMLDR VFNPEGKALPPMRGFKYTSWSP MGCDANGRCLLAALTMDNRL TIQANLNRLQWVQLVDLTEIYG ERLYETSYRLSKNEAPEGNLGD FAEFQRRHSMQTPVRMEWSGI CTTQQVKHNNESRDVGSVLLA VLFENGNIAVWQFQLPFVGKES ISSCNTIESGITSPSVLFWWEYE HNNRKMSGLIVGSAFGPIKILPV NLKAVKGYFTLRQPVILWKEM DQLPVHSIKCVPLYHPYQKCSC SLVVAARGSYVFWRLLLISKAG LNLHNSHVTGLHSLPIVSMTAD KQNGTVYTCSSDGKVRQVIPIF TDVALKFEHQLIKLSDVFGSVR THGIAVKPCGAYLAIITTEGMIN GLHPVNKNYQVQFVTLKTFEE AAAQLLESSVQNLFKQVDLIDL VRWKILKDKHIPQFLQEALEKK IESSGVTYFWRFKLFLLRILYQS MQKTPSEALWKPTHEDSKILLV DSPG\MGNADDEQQEEGTSSKQ VVKQGLQERSKEGDVEEPTD\D SLPTTG\DAG\GREPMGRRNSW GNSKGKIRSCWEMRLTREHMK
23355	53723	A	23490	1218	1446	RCTDSQV\RSPTPLHLAAQACSL ETTVCLLCSKADYTLSEKRGW MPIHFAAFYDNVCIIIALCRKDP SLLEAEATAE
23356	53724	A	23491	2	632	NMAKTYDYLFKLLLIGDSGVG KTCVL\FRFSE\DAFNSTFIFTIRI DFKIRTIELDGKRIKLQIWDTAG QERFRTITTAYYRGAMGIMLVY DITNEKSFDNIRNWIRNTEEHAS ADVEKMILGNKCDVNDKRQVS KGS/GENKLALDYGIKFMETSA KANINVENAFFTLARDIKAKMD KKLDGNSP\QGSNQGVKITPDQ QKRSSFFRCVLL

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23357	53725	A	23492	1	1018	MVFYHVGQAGLELLTSGPHCP DSQAADKAESATLLSRARLGA YCACASLERRWPHFPSGRECN MAKTYDYLFKLLL\IGDSGVGK TCVLFRFSEDAFNSTFISTIGIDF KIRTIELDGKRIK\LQIWDTAGQ ERFRTDHNRPTYRGAMGI\M\L VYDITNE\KSF\DNIRN\WI\RNIE EHASAD\VEK\MILGNKCDVND KRQVSKERGEKLALD\YGIKFM ETSAKANINVENAFFTLARDIK AKMDKKLGPARPHGTLLGKGE EFAGVAGASASGSASLGTLPKQ TRPCPVNPQASREHTAFSIPLKG QKDNMEGNSPQGSNQGVKITP DQQKRSSFFRCVLL
23358	53726	A	23493	1	130	
23359	53727	A	23494	1	1392	
23360	53728	A	23495	445	649	YPSLTNSKLLVHH\FMELC\WD KCVEKPQGIALDSRTENCLS\SC \VDRFIDT\TLAITSRFAQIVQKG GQ
23361	53729	A	23496	210	397	VIYAPGKKAQRTQK/APKTKTK KPHLSPCPSP/WRSRSCQPMQQS WSGAQVHIPQPPHTTCITWA
23362	53730	A	23497	55	286	QASSSPPISSVTCRKALPPGQTK KGLVASGDPEPVSMGTSSPTPS LAPEHSSRASLEPSSSA*PSLAT* SRAGGSQA
23363	53731	A	23498	780	1022	QAMHGRSPGVTVRASGLRNEG DGPLGSVPTQARATGAPGHSAT PSPAWRAW\SSSSKAS/WLPDA AGPPTPPWSGPSPPTSW
23364	53732	A	23499	1	782	
23365	53733	A	23500	275	688	

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23366	53734	A	23501	1166	2271	LRCILTLISRWCS*VSTVANLPP GISKWGANWQRCEMKE*CWSP AVTWCITCAQRSG/IGDSSPYPG ATSFNEYVKANLTWRGPVEQH PLVNYLDHERGTLSNPTARHYL PVLYVLRAILWARTPLPIPGRTT VSKVKMKKRILRAMRQKQQVL PLLVGLGLDELSMSAPSIPAAK ARMAQLDSRECRKLLNQAMA CRTSLEVEHLLAQFRMTQQDA PLVTAECITLESDWRSKEEVLK GMTDNLLLAGRCRYPRKLEAD LWAREAVFSTGLGFSFAIPHSK SEHIEQSTISVARLQAPVRWGD DEAQFIIMLTLNKHAAGDQHM RIFSRLARRIMHEEFRNALVNA ASADAIASLLNMNWTVKEHHE
23367	53735	A	23502	1	2604	
23368	53736	A	23503	306	468	TRHCDRRQPRRGHRRAGT/CNQ I*KGCCCVRTKQPLSSVLISPNF CPCSSFLKNS
23369	53737	A	23504	102	509	AAQQGTMARSLLLPLQILLLSL ALETAGEEAQGDKIIDGAPCAR GSHPWQVALLSGNQLHCGGVL VNERWVLTAAHCKMNEYTVH LGSDTL/E/ADRKAQRIKPSKSF RHPGYFTQTHVNDLMLVKLNS QARLSSMVK
23370	53738	A	23505	1	1032	MMQATVGFEDGDAATSQVSPS VNKVHSSIYFLDFFEEYIVIAFKI LRRGPDISCSQIINGEDCSPHSQP WQAALVMENE/LFCSGVLVHP QWVLSAAPVSRKYNRPLLAND LMLIKLDESVSESDTIRSISIASQ CPTAGNSCLVSGWGLLANDPT SR\LPPPLECRNPVPQLLLPPEKP RTAPDTLGSSPVPKSRTGSSGSS FLLPAPPSPFPRPHHGTPPTSCG QDVDVPALAGGSLGSPAGEAL PRLAAPERLSRHHGKIPSPAPAD LTAILALETAGEEVPFPLTSCA WMSSSSPPGLHEGLQGLTGKFH AVRWHPRLQEKRLQSVPSPDSR IPGARRPAAR
23371	53739	A	23506	303	393	

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23372	53740	A	23507	391	1170	GSFFFFFKYFAYSPMPKNSKVV KRELDDDVTESVKDLLSNEDA ADDAFKTSELIVDGQEEKDTDV EGK\SEVEDERPAWNSKLQYIL AQVGFSVGLGNVWRFPYLCQK NGGVVEPECEQSSATTYYWYR EALNISSSISESGGLNWKMTICL LAAWVMVCLAMIKGIQSSGKV NTYDRVTMSATVLALQEQWQT FSPIRSGNGHLTGSGAQRTPCRI RRGGSQLRVCDGGKQQWWTV SQSSARAITNTDQKSVQLQDLIE
23373	53741	A	23508	45	546	EGGGSRSLWFRELIGQPVQSFIE PVAAGGAVALNVQ/RSCGVVS AAPACL*SRPHSWRWGGPACW RTPGG/LASRSSSSASILMSSSRA SFTRSLSLLSTHKDQGLVCSGSS GATGAGSC/LWPPTSHTVKLMF LYSTVSTLKPMVGMVVTISPSL SL*RIVVFPAASRPT/YEDAHFFF CQKGP*RGSWSSLQHPGPP
23374	53742	A	23509	1367	2142	VRRPQGCLGKRSLLSRVCALVP WGIWP/WSLAVGPQYSSLGSQP ILCASIPGLVPKQLRFCRNYVEI MPSVAEGIKIGIQECQHQFRGR RWNCTTVHDSLAIFGPVLDKG YFGYLETITVPSDSVVSTKAETP DKGVCGRELGFRGGWLPELQS LDEISMGWALCSRLQIKATRES AFVHAIASAGVAFAVTRSCAEG TAAICGCSSRHQGSPGKGWKW GGCSEDIEFGGMVSREFADARE NRPDARSAMNRHNNEAGRQV GSPPARVLGKKEPPQQGVCPGS LGHMARSLAVGPQYSSLGSQPI LCASIPGLVPKQLRFCRNYVEI MPSVAEGIKIGIQECQHQFRGR RWNCTTVHDSLAIFGPVLDKG YFGYLETITVPSDSVVSTKAETP DKGVCGRELGFRGGWLPELQS LDEISMGWALCSRLQIKATRES AFVHAIASAGVAFAVTRSCAEG TAAICGCSSRHQGSPGKGWKW GGCSEDIEFGGMVSREFADARE NRPDARSAMNRHNNEAGRQ

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23375	53743	A	23510	2094	2619	ASPASPAPCSGIPRT*SPYPSPSR TQ\APRARGPAIHAHPGP/RGCT ALPRQGPPTPGSARAPPRIPAHR APTSPTLNFCLASSRQSMPPAPR PPPVPATNPVTPGCGRPPPTLGC RNPQTLRPPPGLPSPALLRRPLP PPARVGMPPHQPPLPTTPACWR PVDWARAEGAGRAVC
23376	53744	A	23511	3050	3317	PARTSPSASGPP**DLISALWTPS QPRAPTRQSLNSLSSSAPSSSTIG PSPSPPAPGPAPPLPWLPPSPSSL PRLSQVSRRPHSHLHPQ
23377	53745	A	23512	862	2954	AEHTLLVCFLNTSLTTTSTHVES FGGQLRGSQIGHPRRPNKMPYA WSIPQDPPLKPERDPGGPLGVS LSLPVNQYGESEEPMGDDDYD EYSKELNQYRRSKDSRGRGLSR GRGRGSRGRGKGMGRGRGRG GSRGGMNKGGMNDDEDFYDE DMGDGGGGSYRSRDHDKPHQ QSDKKGKVICKYFVEGRCTWL YHTTGNCINGDDCMFSHDPLTE ETRELLDKVEMTGSSVFDYIHP GDHSEVLEQLGLRTPTPGPPTPP SVSSSSSSSSLADTPEIEASLTK VPPSSLVQERSFFVRMKSTLTK RGLHVKASGYKVIHVTGRLRA HALGLVALGHTLPPAPLAELPL HGHMIVFRLSLGLTILACESRVS DHMDLGPSELVGRSCYQFVHG QDATRIRQSHVDCETHLHPPSL PTTPQTRASHSLVPGSPSSGLPT VPPAAPTAPGTPFSIGRAARRLS DASGLLDKGQVMTGYYRWLQ RAGGFVWLQSVATVAGSGKSP GEHHVLWVSHVLSQAEGGQTP LDAFQLPASVACEEASSPGPEPT EPEPPTEGKQAAPAENEAPQTQ GKRIKVEPGPRETKGSEDSGDE DPSSHPATPRPEFTSVIRAGVLK QDPVRPWGLAPPGDPPPTLLHA GFLPPVVRGLCTPGTIRYGPAEL GLVYPHLQRLGPG\PALPEAFYP PLGLPYPGPAGTRLPRKGD

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23378	53746	A	23513	1319	2211	GSKVYGSLFHINHGNPFNMEVL VDSWPEYQMVIIRPQ/ETVRGE EKVQGNDLTFHHPTQEMTDDM DSYTNVYRVFSKDPQKSQEVL KNSEIINWKQKLQIQGFQESLG EGIRAAAFSNSVKVEHSRALLF VTEDILKLYATNKSKLGSWAET GHPDDELESETPNFKYAQLNVS YSGLVNDNWKLGMNKRSLRYI KRCLGALPAACMLGPEGVPVS WVTMDPSCEIGMGYSVEKYRR RGNGTRLIMRCMKYLCQKNIPF YGSVLEENQGVIRKTSALGFLE ASCQWHQWNCYPQNLVPL
23379	53747	A	23514	234	858	SVPLQESPLPPPPTHQADC*SPC GAQGGWVTLAVASASS*AHTA SPLPRSPQAQGRAPSPAPPQIHL TTPSSFSSQGT/SHGGLGSTPGA DDPNTSSS\PPPGGSTPRWSAGD SAHSGGEVDGWS*SFP*SVPSY GT*SPFCPWPSSGQRSFHGIASG WEPDGIPDGSSRWEPCGKPQES ETGVEGRQHFPKQLCLGSCRA VASPRVARA
23380	53748	A	23515	1	3582	
23381	53749	A	23516	628	4254	RLPESRAHDVAGADERPWPVH AGIFKSPAAGAAMSPAAAAAG AGERRRPIASVRDGRGRGCGGP AGAALLGLSLVGLLLYLVPAA AALAWLAVGTTAAWWGLSRE PRGSRPLSSFVQKARHRRTLFA SPPAKSTANGNLLEPRTLLEGP DPAELLLMGSYLGKPGPPQPAP APEGQDLRNRPGRRPPARPAPR STPPSPPTHRVHHFYPSLPTPLL RPSGRPSPRDRGTLPDRFVITPR RRYPIHQTQYSCPGVL
23382	53750	A	23517	1	392	KVHMNGLRYALYIMGPALTRG CHQVLIMLCCEVIERILT/VMM KEAYFGEVDIMDDLPT\GNISA NVTGRLYKCGVINHTVDLRRM KT/EKWQNNLLPSRQFGFIVLTT SAGIMDHEEARRKHTGGKILGF
23383	53751	A	23518	227	352	

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23384	53752	A	23519	3	507	SFRAATMVRMNVLADALKSIN NAEKRGKRQVLIRPCSKVIVRF LTVMMKHGYIGEFEIIDDHRAG KIVVNLTGRLNKVGVQWRDLG YCNLCLPGSSDSSASASLVAEIT \CGVISPRFDVQLKDLEKWQNN LLPSRQFGFIVLTTSAGIMDHEE ARRKHTGGKILGFFF
23385	53753	A	23520	279	653	ARAQRFSSQVDVFYLIQSVIFCR LALAEFEIIDDPQSLGKLL*TLT GRLKQ/CLGVISPRF\DVQLKRP WKKWHEIIL/PSNPAKFGF\IVLT TSAGLHG/HHEGRQDRKHTGG KILGILLYRDVIHIFT
23386	53754	A	23521	1	392	KVHMNGLRYALYIMGPALTRG CHQVLIMLCCEVIERILT/VMM KEAYFGEVDIMDDLPT\GNISA NVTGRLYKCGVINHTVDL/PPY ENGKWQNNLLPSRQFGFIVLTT SAGIMDHEEARRKHTGGKILGF
23387	53755	A	23522	108	371	LSYIGKFEIIDDHRAGKIVVNLT GGLNKCGVISLRFDVQLKDLEK WQNNLLPSCQFGFIALTTSAGI MDHKEAR*KHTAGKILEFFF
23388	53756	A	23523	252	378	
23389	53757	A	23524	3	518	HASAFRAATMVRMNVLADAL KSINNAEKRGKRQVLIRPCSKVI VRFLTVMMKHGYIGEFEIIDDH RAGKIVVNLTGRLNKVGVQWR DLGYCNLCLPGSSDSSASASLV AEIT\CGVISPRFDVQLKDLEK\ WQNNLLPSRQFGFIVLTTSAGI MDHEEARRKHTGGKILGFFF
23390	53758	A	23525	279	709	ARAQRFSSQVDVFYLIQSVIFCR LALAEF*NPLMTHQSLGKFVVN PHRAGLNKCG\VISPQILTVQLQ RPWKKWAGLILLP\SRQVLGF\I VLTTSAGI\MDHEEARPKTPRR GKSWGFFFLGDVNYILFYKLKC LMDSGASTWSF
23391	53759	A	23526	207	564	SMAKEAISINRSLWAGPAKISSP AETE\IESLISLFQKYVGKGGYN CTLSKTEFLSFMNAELAAFTKN QKDPGVLHRMMKKLGTNNDG QLDFSEFLNLIGGLAMACHDSF LKAVPSQKRT

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23392	53760	A	23527	1	407	FREKQSQELSQYGAMGAGQSF NSQFLQHGGPRGPSVPAGMNP TGIGGVMGPSGLSPLAMNPTRA AGMTPLYAGQRLPQHGYPGPP QAQP/PAPTGGQENLL*GVSRA AVSARSLPGPFRAIPVSHLAGNP TPPMNPH
23393	53761	A	23528	3	315	
23394	53762	A	23529	1	763	DYEEITIDPTCSWKPVPVKPDM HIKEEPDGPALKRCRTVSPAHV LMPSVMEMIAALGPGAAPFAPL QPPSVPAPSDYPGQGSSFLGPGT FPESFPPTTPSTPTLAEFTPGPPPI CYQSDIPSSLLTSEKST/SLPLQA RR/PPAGHLDPTHNPGTPGLHTS NLGAPPGPQLHHSNPPPASRQS LGQASLGPTGELAFSPATGVMG PPSMSGAGEAPEPALDLLPELT NPDELLSYLGPPDLPTNNNDDL LSLFENN
23395	53763	A	23530	1	2901	MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARIVP GFIRIARPRDGSFAYESVPWQQS ATQPAGSLSVVTTVWGVGNAT QSQVLGNPMGPAGSPSGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQQGVYSRGGYP GAPGFTTGYAGGPGGLGLPSH AARPSTDFTQAAAAAAVAAAA ATATATATATVAALQEKQSQE LSQYGAMGAGQSFNSQFLQHG GPRGPSVPAGMNPTGIGGVM
23396	53764	A	23531	80	412	KPGNGACAGREWCDGGGAAW NWRDPGLPVGDSGVWDRVLLE LLGPRSPRPLDVGGPAAGTPGV LSR/HLPVDCGLGPEALLCSSAP AARRPSLCGGHGRVMRGFRLG CGFRP
23397	53765	A	23532	1	192	RPLDVGGPAAGTPGVLSR/HLP VDCGLGPEALLCSSAPAARRPS LCGGHGRVMRGFRLGCGFRP

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23398	53766	A	23533	1	2094	RPLDVGGPAAGTPGVLSRPCPS TAALAPKPFCAAPRPQPDAPAC AGATGGSCADFDSGVDFVRRR SSGLWGPQPPLFPVKNYTEMFQ DPVAFKDVAVNFTQEEWALLD ISQKNLYREVMLDTFWNLTSIG KKWKDQNIEYEYQNPRRNFRS VTEEKVNEIKEDSHCGETFTPV PDDRLNFQKKKASPEVKSCDSF VCGEVGLGNSSFNMNIRGDIGH KAYEYQEYGPKPCKCQQPKKA FRYRPSFRTQERDHTGEKPYAL LKNDGKKPLFYHSSIQRHMVV HSGDGPYKCKFCGKAFHWLSL YLIHERTHTGEKPYECKQCGKS FSYSATHRIHERTHIGEKPYECQ ECGKAFHSPRSCHRHERSHMGE KAYQCKECGKAFMCPRYVRRH ERTHSRKKLYECKQCGKALSSL TSFQTHIR\MHSGERPYECKTCG KGFYSAKSFQRHEKTHSGEKPY KCKQCGKAFTRSGSFRYHERTH TGEKPYECKQCGKAHERTHTG EKPYECKLYGKALSRLISFRRH MRMHTGERPHKCKICGKAF\SS PSSFQRHERSHTGEKPYKCKQC GKAFTCFHF\FQYHERTHTGEK PDGCKQCGKAFRSAKYIRIHGR THTGEKPYECKQCGKAFHWVS SFHRHERTHAGEKPYECKHCG KAFTCSIYIRIHERIHTGEKPYQ CKECGKAFIRSSYCRKHERTHTI

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23399	53767	A	23534	48	1317	CGLMDELVHDLTSALEQTSEQ NKLGELWEEMALSPRQQRRQL RKRRGRKRRSDFTHLAEHTCC YSEASESSLDEATKDCREVAPV TNFSDSDDTMVAKRHPALNAI VKSKQHSWHESDSFTENAPCRP LRRRR\KVKRVTSEVAASLQQK LKVSDWSYERGCRFKSAKKQR LSRWKENTPWTSSGHGLCESA ENRTFLSKTGRKERMECETDEQ KQGSDENMSECETSSVCSSSDT GLFTNDEGRQGDDEQSDWFYE GECVPGFTVPNLLPKWAPDHCS EVERMDSGLDKFSDSTFLLPSR PAQRGYHTRLNRLPGAAARCL RKGRRRLVGKETSINTLGTERIS HIISDPRQKDFWLPSAGKRERN QFNPLSPLYSLDVLADASHRRC SPAHCSARQANVHWGPPCSRDI KQEAETSGHSIFV
23400	53768	A	23535	225	403	
23401	53769	A	23536	1	403	REQEFLHMAPGEVTITVR\LIRS LEHR\NFKPVVYHGVNLDQTV KEFIVFLKQDIPLRTNLPPPFRN YKYDALKIIHQAHKSKTNELVL SLEDDERLLLKEDSTLKAAGIA SETEIGIF\REEDYRNYKANPISS
23402	53770	A	23537	2	239	
23403	53771	A	23538	2	214	
23404	53772	A	23539	1	1341	
23405	53773	A	23540	1	1677	
23406	53774	A	23541	1010	1509	
23407	53775	A	23542	1	6355	
23408	53776	A	23543	223	10504	VKMPIGSKERPTFFEIFKTRCNK ADLGPISLNWFEELSSEAPPYNS EPAEESEHKNNNYEPNLFKTPQ RKPSYNQLASTPIIFKEQGLTLP LYQSPVKELDKFKLDLGRNVP NSRHKSLRTVKTKMDQADDVS CPLLNSCLS\ESPVVLQ\CTHVTP QRDKSVVCGSLFHTPKFVKGR QTPKHISESLGAEVDPDMSWSS SLATPPTLSSTVLIVRNEEASET VFPHDTTANVKSYFSNHDESLK KNDRFIASVT
23409	53777	B	23544	137	709	
23410	53778	A	23545	1	1974	

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23411	53779	A	23546	207	1622	MACCL\SDEVKESKRINAEIEKA AAAETRRDARREL/RRLLLLGT GESGKSTFIK\QMRIIHGAGYSE EDKRGFTKLVYQNIFTAMQAM IRAM\ETL\KILYKVRSRTRANA L\LIRGGGTLEKVTTFGAFSYVQ LPLKDLFGRDPGIQE/CAYERQP RSYQLSDSAKYYLTDVDRIATL GYLPTQQ\DVPAGSRVPTT\GIIE YPFDLENIIF\RMVDVGG\QRS\E RRKWIHCFENVTSIMFLVALSE YDQVLVESDNENRMEESKALF RTIITYPWF\QNSSVILFLNKKDL LEDKI\LYSHLVDYFPRSSMGPQ R\DAKAAREFILKMFVDLNPNS DKII/YTSHFTCPHRHRRTSRFVF PAVKDTILQLNLEEYKPGLSAP GPGRRDGDTGQDLPSTEPAAA RAGGAAESGPGPLPAGGDFFFF IFLTNGFYFTVIRGCTSLPPYTSR TFSPFVNGKGSLFLALTYGSLFS KKKKKKKE
23412	53780	A	23547	1	401	KKVPGRLSEMSFSLNFTLPANT TSSPVT\DCGPSLGLAAGIPLLV ATALLVALLFTLIHRRRSSIEAM EESDRPCEISEIDDNPKISENPRR SPTHEKNTMGAQEAHIYVKTV AGSEEPVHDRYRPTIEMERRR
23413	53781	A	23548	584	1071	PCRLPLHLILVEDLSFSLNFTLP ANTVSTAAPIHQAT/PEKTSAEF TDCGPSLGLAAGIPLLVATALL VALLFTLIHRRRSSIEAMEESDR PCEISEIDDNPKISENPRRSPTHE KNTMGAQEAHIYVKTVAGSEE PVHDRYRPTIEMERRRGLWWL VPRLSLE
23414	53782	A	23549	25	654	LFLQMKDTSPIIFVRKELTIRQC TKKVPGRLSEMSFS\LNFTLPAN TTSSPVTGGKETDCGPSLGLAA GIPLLVATALLVALLFTLIHRRR SSIEAMEESDRPCEISEIDDNPKI SENPRRSPTHEKNTMGAQEAHI Y\VKTVT\KSEEPVHDRYRPTIE MERRRGLWWLVPRLSLGMMP TSNQGSHQTWHLGTGLKTQGF VLGEERCQAAS
23415	53783	A	23550	108	413	RRSGSMALWRAYQRALAAHP WKVQVLTA/GLLGRKAALLAP CQ*LYLPTQASWTEGHASCSSL QEATSCPSAFCA*NSKATKQLV ERRGLQEHQRGRTLTMVS

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23416	53784	A	23551	1	146	
23417	53785	A	23552	2	442	GREARRSRSMALWRAYQRALA AHPWKVQVLTA\ASGEEGSTA GPMPVAIPADPGLLD*RTRFLLL TPRSHFLPLCLLRMKLKSHKRS LMGLGDIISQQLVERRGLQEHQ RGRTLTMVSLGCGFVGPVVGG WYKVLDRFIPGTTKVDA
23418	53786	A	23553	3	675	RHSRFGAQGSMALWRAYQ\RT LF\ALPWK\VQVLTAGSLMGLG DIISQQLVERRGLQEHQRGRTL E/TMVSLGCGFVGPVVGGWYK VLDRFIPGTTKVDALKKMLLD QGGFAPSFLGCFLPLVGALNGL SAQDNWGQTTAGELG/RDYPD ALITNYYLWPAVQ\LANFYLVP LHYRV\AVVQCVAVIWNSYLS WKAHRALSLPHSIVSTLQVMQ LDPWNGSDNPPQKWA
23419	53787	A	23554	512	1227	LQGHLMGIMAASRPLSRFWEW GKNIVCVGRNYADHVREMRSA /VWLSEPVLFLKPSTGVRAQRA RPILMPAYTRNLHHELEL\ALVI GQ\RCRAVPE\AAAMDYVGG\Y ALCL\DMTAWDVQ\ASARKKG LAWDSGE/DAFTASCPVQRVSL PKEKIPDPSQ\LKALGFKVNGEL RQEGETSSMIF\SIPYIISYVSKIIT LEEGDIILTGTPKGVGPVKEND EIEAGHTRAGQYDHLKVEKAQ
23420	53788	A	23555	192	436	RTSDHECFREGQICSVCLRERL NLNPEEACLLSQAPCMLFVLQY LNTVIPYEKKASPPSV\EDLQML \TNILFAMKEDNEKVP

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23421	53789	A	23556	94	1252	ARMEAPLVSLDEEFEDLRPSCS EDPEEKPQCFYGSSPHHLEDPSL SELENFSSEIISFKSMEDLVNEF DEKLNVCFRNYNAKTENLAPV KNQLQIQEEEETLQDEEVWDA LTDNYIPSLSEDWRDPNIEALN GNCSDTEIHEKEEEEFNEKSEN DSGINEEPLLTADQVIEEIEEMM QNSPDPEEEEEVLEEEDGGETSS QADSVLLQEMQALTQTFNNNW SYEGLRHMSGSELTELLDQVEG AIRDFWE\ELVQQLARRDELEF EKEVKNSFF\TVL\IEVQNKQK\E QRELMKKRRKEKGLSLQSSRIE KGNQMP\LKRFSMEGISNILQSG IRQTFGSSGTDKQYLNTVIPYEK K\AYPPSVE\DLQMLTNILFA\M KEDNEKVPYFA
23422	53790	A	23557	391	1169	GSFFFFFKYFAYSPMPKNSKVV KRELDDDVTESVKDLLSNEDA ADDAFKTSELIVDGQEEKDTDV EGK\SEVEDERPAWNSKLQYIL AQVGFSVGLGNVWRFPYLCQK NGGVVEPECEQSSATTYYWYR EALNISSSISESGGLNWKMTICL LAAWVMVCLAMIKGIQSSGKV NTYDRVTMSATVLALQEQWQT FSPIRSGNGHLTGSGAQRTPCRI RRGGSQLRVCDGGKQQWWTV SQSSARAITNTDQKSVQLQDLIE
23423	53791	A	23558	321	568	CLWCGASWPRRHSSPGRPAGD HRGDRP/EGPDTQGPGRPEPSTE PAFNPQSSLDQGGGPAAPAVD DDTRRGHGGVCGDGGAGEA
23424	53792	A	23559	510	690	LRSPQ\RGVAAPPFLGSPVPFGG FRVQGGMAGQPSAPPALQTDD PYSKAHSVTPKSTPRVT
23425	53793	A	23560	25	480	
23426	53794	A	23561	84	292	VRAVQSLHFHFPWRR/ISCPSES TRSIHVDRLPRRNSASLSLSAFP VSAGALINGEAWVRMGQVPIP KAP

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23427	53795	A	23562	1138	1924	CRSSATWTPWTTTGCRGDLTK TYSLEAYDNWFNCLSMLVATE VCRLLLSPGSAMLRSPATFQVV KKKHRTRMLEFFIDVARECFNI GNFNSMMAIISGMNLSPVARLK KTWSKVKTAKFDVLEHHMDPS SNFCNYRTALQGATQRSQMAN SSREKIVIPVFNLFVKDIYFLPQ NP\SNHLPNGHINFKKFWEISRQ IHEFMTWTQVECPFEKDKKIP\S YLLTAPHPTARKLSSSPSFESEG PENHMEKDSWKTLRTTLLNRA
23428	53796	A	23563	3	260	
23429	53797	A	23564	1	1386	
23430	53798	A	23565	137	611	MKVNLGDSQNLACVFCRKHD DCPNKYGEKKTKEKWNLTVH YYCLLMSSGIWQRGKEEEGVY GFLIEDIRKEVNRASKLKCCVC KKNGAFIGCVAPRCKRSY\HFP CGLQRECIFQFTGNFASFCWDH RPVQIITSNNYRESLPWHHLLG NLFEPIPSY
23431	53799	A	23566	181	486	DPQGEAKGAAPAEGGGGPV*W N\GLQGPAGVPGRDGSPGANGI PGTPGIPGRDGFKGEKGECLRE SFEESWTPNYKQCSWSSLNYGI DLGKIAECTFTKMRS
23432	53800	A	23567	600	888	QYNGMCSPGPAGVPGR\EGSPG ANGIPGTPGIPGRDGFKGEKGE CLRESFEESWTPNYKQCSWSSL NYGIDLGKIAGRNCWHILAPVP NIVSLYFGS
23433	53801	A	23568	91	1170	ISLHRRPGPTCSMESPASSQPAS MPQSKGKSKRKKDLRISCMSKP PAPNPTPPRNLDSRTFITIGDRN FEVEADDLVTISELGRGAYGVV EKVRHAQSGTIMAVKRIRATV NSQEQKRLLMDLDINMRTVDC FYTVTFYGALFREGDVWICME LMDTSLDKFYRKVLDKNMTIP EDILGEIAVSIVRALEHLHSKLS VIHRDVKPSNVLINKEGHVKM CDFGISGYLVDSVAKTIN\AGCK VKHGHESLN\PDLNRKGCDVKS HVWSLGITMIEMAFLRFPYESW GTPFQQLKQVVEHPSPQLPAGR FSPEFVDFTAQCLRKNPAERMS YLELMEHPFFTLHKTKETDIA\A FVKEILGEDS
23434	53802	B	23569	111	193	

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23435	53803	A	23570	312	696	RP*SAHPEPGDCPSPPHPPRCGG VAQTAQVPDAPAPV*AG\QHSR SYMEDHLKNKNRLEKEWEALC AYQAEPNSSFVAQREENVPKN RSLAVLTSQPTRNQCLPFLQHG PGDICTPVSISSIVLCHRVT
23436	53804	A	23571	1	2974	QAAGMGPPLPLLLLLLLLPPR VLPAAPSSVPRGRQLPGRLGCL LEEGLCGASEACVNDGVFGRC QKVPAMDFYRYEVSPVALQRL RVALQKLSGTGFTWQDDYTQY VMDQELADLPKTYLRRPEASSP ARPSKHSVGSERRYSREGGAAL ANALRRHLPFLEALSQAPASDV LARTHTAQDRPPAEGDDRFSES ILTYVAHTSALTYPPGPRTQLH EDLLPRTLGQLQPDELSPKVDS GVDRHHLMAALSAYAA
23437	53805	A	23572	1	3202	ASRRLPRGHGLSAAGQAAGMG PPLPLLLLLLLLLPPRVLPAAPSS VPRGRQLPGRLGCLLEEGLCGA SEACVNDGVFGRCQKVPAMDF YRYEVSPVALQRLRVALQKLS GTGFTWQDDYTQYVMDQELA DLPKTYLRRPEASSPARPSKHS VGSERRYSREGGAALANALRR HLPFLEALSQAPASDVLARTHT AQDRPPAEGDDRFSESILTYVA HTSALTYPPGSRTQLREDLLPR TLGQLQPDELSPKVDSG

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23438	53806	A	23573	1	1459	MPLTSQDVDQKTAAWVPTNRD STVPSDPWDCKRRPWPLLVLRP LAPGTKAPPGGQNGRGRQKGS PCSRRLLLEPAGPLGPASVRCIR TTTPQLLIITTSLRFPSLEAAVGY GSNTCIFANACQMVFIMITWPY LQCIPYSVLLKDLEMRNLRELE DLIIEAVYTDIIQGKLDQRNQLL EVDFCIGRDIRKKDINNIVKTLH EWCDGCEA\ALLGIEQQVLRAN QYKENHNR/TLQQQVEAEDVYI LPQSGNDCRGLRFVSSLIGGVR CVHLKHKGDAVVWEAIEEGEA LPGKYRLKGGRSVWAAAVRA VCMDQVTNIKKTLKATASSSA QEMEQQLAERECPPHAEQRQP TKKMSKVKGLVSSSPLGPAGA AGTHQAWVRWGGDTKGPFPPL STCSEFQTCPSPHQRLPTLLVLF QKNCYSPSPTPSFPSCSLQTQGL HQCHPKTGSDTAQLPSRRFLSL CKGLVSLPVFLLLPRHFVRLVIK
23439	53807	A	23574	2	396	
23440	53808	A	23575	1	1014	
23441	53809	A	23576	110	212	
23442	53810	A	23577	1	747	
23443	53811	A	23578	323	495	GRAGKWHTQPE*SLRKAM*MF QILMMKMIVALARATSGTEAV AGRSWASGLRRSGRV
23444	53812	A	23579	26	229	
23445	53813	A	23580	1	574	
23446	53814	A	23581	889	1189	
23447	53815	A	23582	170	625	GAAVALVRPNGGTAASHVVCR EMRPLRPLQSRRCSRRRTGISN MRALENDFFNSPPRKTVRFGGT VTEVLLKYKKGETNDFELLKN QLLDPDIKDD\QIINW\LLEFRSS VMYLTK\DFE\QLISIILRLP\WL NRSQ\TVVEEYLAFLGNLVSA
23448	53816	A	23583	166	455	RWKPSGTWPRNPMERPGH*ES VPKPGD*AKKSGGET\RGRKEG NEHRETFSQIPDCHLNKKSQTG VKPCKCSVCGKVFLRHSFLDRH MRAHAGHKRS
23449	53817	A	23584	3	3706	

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23450	53818	A	23585	1	1970	MVTDRKAAAGTHGEARPCWG SGSRVHTYRGAGERAMRVHRP MPREDSERVREADGGKHEQRS FGDLHPTAAPAPAASGCGTQPG RVKQPGEWQHREAPQQRQPPV RPHGSHQLVTVRYERRPGGKE RARLRPGLGCPSGRTPQGRAPQ GTALPTAAAAAIFPSAALTSGQ RNASLPKFYFRGGTWGTSQSEA LCGKLSNQFLGEPLVPRIRLILS CGTCSGCSSPRKDPGHPEAGNG PSRDFFQLPSEERDSVAFEDVA VNFTQEEWALLSPSQKNLYRD VTLETFRNLASVGIQWKDQDIE NLYQNLGIKLRSLVERLCGRKE GNEHRETFSQIPDCHLNKKSQT GVKPCKCSVCGKVFLRHSFLDR HMRAHAGHKRSECGGEWRETP RKQKQHGKASISPSSGARRTVT PTSMRPYE\TKVCGKA\FIS\PIYF QIHQRTPTEKRSYKCREIVRAFT VSSFFRKHGKMHTGEKRYECK YCGKPIDYPSLFQIHVRTHTGE KPYKCKQFGKAFISAGYLRTHE IRSHALEKSHQCQECGKKLS\CS SSLHRHERTHSGGKLYECQKC AKVFRCPTSLQAHERAHTGERP YECNKCGKTFNYPSCFRRHKKT HSGEKPYECTRCGKAFGWCSSL RRHEMTHTGEKPFDCKQWVKS
23451	53819	A	23586	86	390	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQT\TSPRNISPISNPELA THAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP ELLELWPKVL
23452	53820	A	23587	1	502	MLLTQSLFGGLFTRTHMKFGA VTQIRGPPLGDKSPVLLLFALER QRRHVLSMDPKLRCWSRTGKA AFPWCLIIAEMPDYSPTFQRCQ TTQGRLPWSFTLSSKSRFSGEG ARACYKCQKSDHQAKECPQPG IPPKPCPICAGP\TGNRTVQLTW QPLPEPLELWPKAL
23453	53821	B	23588	1	663	
23454	53822	A	23589	233	496	
23455	53823	A	23590	2	378	ERQRRHVLSMDPKLRCWSRTG KAAFPWCLIIAEMPDYSPTFQR CQTTQGRLPWSFTLSSKSRFSG EGARACYKCQKSDHQAKECPQ PGIPPKPCPICAGP\TGNRTVQLT WQPLPEPLELWPKAL

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23456	53824	A	23591	3	452	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLIS LRPNPLCPHPDLVSLCPDPFPAF LEAHKNFQTPEPQQPGIPPEPPP PGACYKC/HEI*PPGQGMPAAQ DSS*AMS/LSVRDPTGNQTVQL TWQPLPEPLELWPKAL
23457	53825	A	23592	1352	1540	
23458	53826	A	23593	177	383	EAMEPWKGVPLGRVNTEQIAP FSEAEGPREIH*GSRKVRKAAQ GLNEGPRELFWQPLPEPLELWP KAL
23459	53827	A	23594	1478	1744	
23460	53828	A	23595	23	178	SCLEVCDEQGPEK\TRQRALRG VSSVTEDTLNICRLCWQPLPEPL ELWPKAL
23461	53829	A	23596	1	282	
23462	53830	A	23597	34	241	SGDLPWEINPPSSCSLLREKDPP MTSGPQT\TSPRNISPISNPDPTG NRTVQLTWQPLPEPLELLPKAL
23463	53831	A	23598	121	286	AASFYSSPTSLTIPQPLSPFNLGV TLQSLPSLNFNSF\LFWQPLPEPL ELWPKAL
23464	53832	A	23599	144	488	GYEIWCRDSDQGTFPWEINPPS SCSLLREKDPPTTSGPQT\TRPR NISPISNLVSGLFLLSSPPSLTIPQ PLSPFNLGATLQSLPSLNFNSFH FLVETKETRFIRGAKIPAPVTD
23465	53833	A	23600	471	677	
23466	53834	B	23601	67	555	
23467	53835	A	23602	1	1440	
23468	53836	A	23603	860	1209	IPGNCRDSSGVGIKERETNAGS QHMH/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPENPVYEKKPK KEVKKKRWNRSKMSLAQKKD WVAQKKASFLRA

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23469	53837	A	23604	1	966	MGFVKVVKNKAYFKRYQVKF RRRREGKTDYYARKRLVIQDK NKYNTPKYRMIVRVTNRD\IICQ IANA\RIEG\DMIVCAP\YAHELP KIWV*RVGLTNYAAA\YCTGLL AGPAGFFHRFGMDQIYE\GQV\E LTGDEYNVESIDGQPGCLHPAY WDARPLPRTYPLAIKVFGCP*R GA\VDGGLVLFP\HSTKTIPPGY DS\ESK\EFNAES/IHRKPHPWAQ NVARLHAPTLMEEDEDA/YTK KQFSQYIKNSVTPDMMEEMV/Y RKAHAAIRENP\VYEKKPKKEV\ KRKRWNRPKMSLAQKKDRVA PKKASFLQSSRSGLLESLTPAIFP
23470	53838	A	23605	1	644	ANSSPVNPVVFFDVSIGGQEVG RMKIELFADVVPKTAENFRQFC TGEF/RVSFRCV*LLCLLQRGVL GLQ*GYR*TTCWP*MIAGDSDR RKDGVPIGYKG\STFH\RVIKDF MIQGGDFVNGDGTGVASIYRG PFADENFKLRHSAPGLLSMANS GPSTNGCQFFITCSKCDWLDGK HVVFGKIIDGLLVMRKIENVPT GPNNKPKLPVVISQCGEM
23471	53839	A	23606	638	1391	CPAYKGAHGIQCVYCTLPPPLL QTTRRVRRNPTLPTSASGSEPW RLANSSPVNPVVFFDVSIGGQE VGRMKIELFADVVPNYAENFR QFCTGEFRKDGVPIGYKGSTFH RVIKDFMIQGGDFVNGDGTGV ASIYRGPFADENFKLRHSAPGL LSMLTWPGKLTAGIFGFHQANS GPSTNGCQFFITCSKCDWLDGK HVVFGKIIDGLLVMRKIE\GMPC IFQPTWTHFLPVITTACSALGSM LAAERGTKN
23472	53840	A	23607	2	591	ARAEFGTSRVGAMAVANSSPV NP\VVFFDVSIGGQEVGRMKIEL FADVVPKTAENFRQFCTGEFRK DGVPIGYKGSTF\HRVIKGF\MI\ QGGDFV\NGDGTGSRPVFTRGP ILQMKIFKL\RHSAP\GLLSMAN SGP\STNGC\QFFITC\SKCDW/V WDGKHVVFGK\IIDGLLVMRKI E\NVPTGPNNKP\KLPVVISQCG
23473	53841	A	23608	6	424	

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23474	53842	A	23609	3	470	DAWVSGRLTELPSSCFFPPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKKDGKKRKRSRKESYS VYVYKVLKQVH\PDTGISSKAM GIMNSF\VNDIFE\RIAGEASRLA HYNKRSTITSREIQTAVRLLLPG \ELCKHAV\SEGTNA\VTKYTSS
23475	53843	A	23610	93	421	
23476	53844	A	23611	2	1173	DHAAPRRRSRASVATVTRAGR CPTMSVRVARVAWVRGLGASY RRGASSFPVPPPGAQGVAELLR DATGAEEEAPWAATERRMPGQ CSVLLFPGQGSQVVGMGRGLL NYPRVRELYAAARRVLGYDLL ELSLHGPQETLDRTSQVQSPGT GIPRRVRAHVLHLSPQVIENC/V VS/AGLAFSPSFCALIFPNALL/F WPGLYAVKIRAEAMQEASEAV PSGMLSVLGQPQSKFNFACLEA REHCKSLGPVNGQICKGGFLGH CSAETSFLPQALRFLQKNSSKF HFRRTRMLPVSGAFHTRLMEP AVEPLTQALKAVDIKKPLVSVY SNVHAHRYRHPGHIHKLLAQQ LVSPVKWEQTMHAIYERKKGR GFPQTFEVGPGRQLGAILKSCN
23477	53845	A	23612	187	425	
23478	53846	A	23613	1	1258	MKAYLLLGAAPPLPWFPGQAV FRPCPPPAGLWRTAQLVELEHG PVPREDLIPCSRPFSISFLGPERV DGLAFPRIQALGIAAARGMEPK GAPGKSDSGNSRSAGGRVLGC QGAALEVECSAGRGGPVRLAV GCVLLRAPERGWRRGEGAARG IPAGRSSESLGALSPQVGVRSDI GINGNIWHPGVQTDFSSLKRSQ GLYAVKIRAEAMQEASEAVPS GMLSVLGQPQSKFNFACLEARE HCKSLGIENPVCEVSNYLFPDC RVISGHQEALRFLQKNSSKFHF RRTRMLPVSGAFHTRLMEPAV\ EPLTQALKAVDIKKPLVSVYSN VHAHRIQGIPGHIHKLL\AQQLV SPVKWEQTMHAIYERKKGRGF PQTFEVGPGRQLGAILKSCNMQ AWKSYSAVDVLQTLEHVDLDP

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23479	53847	A	23614	2	1050	GRCPTMSVRVARVAWVRGLG ASYRRGASSFPVPPPGAQGVAE LLRDATGAEEEAPWAATERRM PGQCSVLLFPGQGSQVVGMGR GLLNYPRVRELYAAARRVLGY DLLELSLHGPQETLDRTVHCQP AIFVASLAAVEKLHHLQPSVIE NCVAAAGFSVGEFAALVFAGA MEFAEG\LRFLQKNSSKFHFRR T\RMLPVSGAFHTRLMEPAVEP LERKLLKAVDIKKPLVSVYSQR PTRIRLQAFPGNIQQSCLAQQLG LPK*KWEQ\TMHAIYERKKG/R RGFPQTFEVGP\GRQLG\AILKS CNMQAWKSYS\AVDVLQTLEH V\DLDPQEPPKMTGRGLKCNDP LCPPEERL
23480	53848	A	23615	600	905	QAPASGSPWLSGGPQQVEDAG AGYGFAPGQPPPPPRTQPRSAC SRRAAG/TPVPRAPPAPSAG\PK ARAPRSLGCGSLGRFSTGVRPD KCIFPPETENAAGCF
23481	53849	A	23616	390	722	QAPASGSPWLSGGPQQVEDAG AGYGFAPGQPPPPPRTQPRSAC SRRAAG/TPVPRAPPAPSAG\PR AAAPRSLGCGSLGRFSTGVRPD KCIFPPETEMSYLLFRNTVSRCR C
23482	53850	A	23617	1	673	MGQVKGHKLCLDFTLLSPDGG AAEGRCLELGWQAKEVEETIE GMLLRLEEFCSLADLIRSDTSQI LEENIPVLKA\KLTK\MRGIYAK VDRIKAFVKMVGHHVAFLEAN VLQAERDHGAFPQALRRWLGS AGLPSFRNDPTAPLRQVFEASP DPRLARTVTIQTQQPVRVSGPL SGQRKEKSLQKGAQVFQTNVP ETLLEGAAISPAPACGGPLTSGD GFRHVRK
23483	53851	A	23618	1	651	
23484	53852	A	23619	195	497	DQFLENTKKCDGLNQLSFDPA NNNKPLEFGRARGPLVTEGLIE NGGESSKKRRRTNSSSADNSRT LNVDSTAMTLPMSDPTAWATA M\NNFGMAPVRIVGH

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23485	53853	A	23620	241	1823	NDDRAKFTVEDHTMQRDFRW LWVYEIGYAADNSRTLNVDST AMTLPMSDPTAWATAMNNLG MAPLGIAGQPILPDFDPALGMM TGIPPITPMMPGLGIVPPPIPPDM PVVKEIIHCKSCTLFPPNPNLPPP ATRERPPGCKTVFVGGLPENGT EQIIVEVFEQCGEIIAIRKSKKNF CHIRFAEEYMVDKALYLSGNR ELKKFLNKEDNYFRKINLTALY KTVLEERCEKRRGGYRIRLGSS TDKKDTGRLHVDFAQARDDLY EWECKQRMLAREERHRRRMEE ERLRPPSPPPVVHYSDHECSIVA EKLKDDSKFSEAVQTLLTWIER GEVNRRSANNFYSMIQSANSH VRRLVNEKAAHEKDMEEAKEK FKQALSGILIQFEQIVAVYHSAS KQKAWDHFTKAQRKNISVWC KQAEEIRNIHNDE\LMGIRREEE MEMSDDEIEEMTETKETEESEL KKLEGIVDGSVEVSAEALRKLL NEYERQVKEEQKVGYRIWGTI HNKGEGKKEEFAEELEKSSSER
23486	53854	A	23621	996	1512	RPVHLASPAKEQQGTRKGRRA PARLPVPTTGRGLEKGPESQAP PSFRQATGRFSRSGSSGGPTPSK NSRDCSHTPQLPTPRGNPYVFPS PGHPEPSRPVEMPAPG\EPRTRQ LCRERTRKACPPKPRPPLGLPG DPTGPVTHHAPPVSPTGASGQE RRAEPGAVSYAHASATK
23487	53855	A	23622	293	1140	PRGILHQDKNLVVINK\PYGLPV HGWPWG\QLCITDVLPILAKML HGHKAEPLHLCHRLDKETTGV MVLAWDKDMAHQVQELFRTR QVVKKYWAITVHVPMPSAGVV DIPIVEKEAQGQQQHHKMTLSP SYRMDDGKMVKVRRSRNAQV AVTQYQVLSSTLSSALVELQPIT GIKHQLRVHLSFGLDCPILGDH KYSDWNRLAPQKLSVGTLKKL GLEQSKARYIPLHLHARQLILPA LGSGKEELNLVCKLPRFFVHSL HRLRLEMPNEDQNENNEAKCL

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23488	53856	A	23623	1	1328	MAVDLGSHTPGSSGVTAATFR GRRLVNTREESVVLGAGGEVL SGVPGTWDALGPGASFGIKGM FPKGTVIMSTSPMCEGPVPRRK PCASSVGQQNSRSRKKAGRKTP TLAGRHVPVKIKKEAIQQKPLP ASSFSPALTRSGAIFGPCPALTS APVLEYPLQKVVENEAFKVFN NRDEESKRQKQAEFRMLTSAIR GPAGPRGHSSTRKPPSNPPPPGA CFKCGNEGHRSRQCPNPGTTSQ EAELIALTRALTLAAGQQINIYS NSHYVFHIVHSHSSIWKERGILT AKNTPAINGSLINKLLKAARLP QKVAIIHCRGHQTPDNPILAGN VLADQVAKQVALQPVQGQFLS LSLFSPLYSSEEKEDFRAQNLQ KQGPW/LQSQGARLLVPAACAS KVAEAGRKPAGRHVPLKIQKE AIWSSPFSVPMATRAAASTSPT
23489	53857	A	23624	475	622	IHSKVLFSASSSSC*NTNNSWFR ASIKKNPEKQNKNMQSAIPQHG LWKI
23490	53858	A	23625	17	992	GRGEVLRGRGRGQLDAVLSRE HCGGSRQSEQPWSRRSSSSSSR RRLRSAAEPAMALSMPLNGLK EEDKEPLIELFVKAGSDGESIGN CPFSQG\LFMILWLKGV\VFSVT TVALKRKPADCQNLVPGTPPP\ LILFSSEVKTDVNKIEEFSEEVL\ CPPKYLKLSPK\HPRSNTAGMDI FA\KFSAY\IKNSRPEANEALER GLLKTLQKLDEY\LNS\PLP\DEI DENSMEDIKFSTRKFLDGNEMT LADCNLLPKLHIVKVVAKKYR NFDIPKEMTGIWRYLTNAYSRD EFTNTCPSDKEVEI\AYSDVAKR LHQVKSRLLKEVSFMSSP

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23491	53859	A	23626	1	1128	MALASGEGLPVALSHGRRGNG QERVPYLKLRDTCAYRVAWRC NRLARAKVKRTSYRSGYGNGF EPGVEPDCVVLLALGVENDLV RISSKAEKYSLYEFSFPLRVSRE CEEECRKEPWFNPGQKPSVLIT SGQILGQEEQKTLLFPGLLSLVF QFNVENSDLRCLSLAENLEISAL LSLSCSSVIRLILINLEVTISPPITI LKHAPPLTSLEASSSSSGIEKKIH NNFRQGPFPSSATRSTFLMNHT SFDSYVVVSNIVPRLNLYPQVL DVLQSLHKIHQLASNAKWTIQG PAKPDLGLELGLHRYPDWEKE ERKKKRKRSVSPEKSITTHNKP TSSGIFY/RPRRCGCDLGRPPAP GPHPSSPPHSPPQPSRCPPV
23492	53860	A	23627	3	453	SLGKDIRPRSARAACKGVGLWS GCFGKMAGSGVRQVTSTASTF VKPIFSRDMNEAKRRVRELYRA WYREVPNTGER*RLVRPAVLK HSYVANRSF
23493	53861	A	23628	3	695	PYASRRKFRVDPRVRAWSGCF DKMAGSGVRQATS\TASTFVKA HFSVGDMNE\AKREGARVLTAP WYR\EVPNT\VRVHQFQLDI\TV KMGRDKVREMFMKNAHV\TDP RVVDL\LVIKGK\IE\LEETIKVL KQ\RTHVMRFFH\ETEAPRPKDF LSKF\YV\GHDPLKSFSGKDAR WILFLGAQIKLTIQWSLCDRIPL MNQFSAASFCLSKWGPWVLHI TCSFPFSWKCGVCCKLD
23494	53862	A	23629	82	441	SLPINPVPTACTLQPAGLLRPPG SDVRTPMLPPSAPSQPSYPTSRP PLWPTWPAGPVFRRSQPLAQPN LPRSYHQQAPGGQTPVALGLE\ CPKATNQPFGTLQRDPKSPAKV PPFEEFSL
23495	53863	A	23630	3	504	DRSSSSTMSTGGDFGNPLRKFK LVFLGEQSVGKTSLITRFMYDS FDNTYQATIGIDFLSKTMYLED R/TNVNSFQQTTKWIDDVRTER GSDVIIMLVGNKTDLADKRQVS IEEGERKAKELNVMFIETS/AKA GYNVKQLFRRVAAALPGIMPS VLFQIIPSQALTRYLC

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23496	53864	A	23631	416	1239	GGGRSSSSTMSTGGDFGNPLRK FKLVFLGEQSS\GKTSLITRFMY DSFDNTYQATIGIDFLSKTMYL EDRTIRLQLWDTAGQERFRSLIP SYI\RDSAAAVVVYDITNVNSFQ ANYKSGIDDVRTERG\SDVI\IM LVGNKTDLADKRQVSIEEGERK AK\ELNV\ILMETSAKAG\YNVK QLLSTCKQPALPGMESTQDRSR EDMIDIKLEKPQE\QPVSEGGLF LTNLPCHLQPFFQKLTGFWPPY SFIDCSVNIGLMPFPFSNNVLRFI IAACPAWR
23497	53865	A	23632	1	493	PKPATAPPPPSL/RARFLCPQRRP ERAR/PRARGASPRPEKTAGAR KRRRGSCERPHPGG/RPPAPG*I SSRPTLGFFWILNFFFLKKLGRI KDVPWQDSTKEHLSVCRGLRG TWSVPSASDPLHPAWRRTCFRV PPTTGAREWWLHLPPPALQRPP DSRQCHRIPVC
23498	53866	A	23633	1	560	MESIWAGLWTAQDTTVLADDF EFILWTLKRRPERAR/PRARGAS PRPEKTAGARKRRRGSCERPHP GGLRRLPGARDQRAPPRSDAG RSPGRLRRLPALLCAGPLSPGRE PRRWEPRAGVARPAGQQWGFF WPGNQQGASICSLILWFLLECG SRSTGGPCSGTELGHFSRERPTV LLSRLGTVKRP
23499	53867	A	23634	32	327	LTQRLFGGLFTRTHMKFGALTR IG\DLPWE\INPLSS\CSLLPEKDP PMTSGPQTDQPKEHLTNFKSAA RRSSRTSSHRNLLHVLEIWQLD QGMPAARDF
23500	53868	A	23635	2	424	LTPFSDSAHLHPGEINSPVAHTK PVGGLFTRMRVTFGAKTQDRS TP\QETSPLSSPS\PVTSGPQTNQ PKEHLTNFKLGKQSFHSSHASL ATLQSSSLATLQSPCPSNSNSFS SLVETRRRPGAVARLQSQLSGR LRGGRIA
23501	53869	A	23636	31	246	TALLLTQSLFGGLFTRTHMKFG AVTRIG\DLPWGINPLSSCSLLR EKDPLTISGPQTHQPKEHLTNF KSGPH

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23502	53870	A	23637	125	464	TAVFLTQSLFGGLFTRTRMKFG TMTRI/RGDLPWEINPLSSCSLL HEKDPPTTSGPQTNQPKKHLTN FKSRKVERTKGLLKTHLTKLSH QLKKAWTILLPLSLLRIQACPR NAT
23503	53871	A	23638	1064	1304	TAMLLTQSLFGGLFTQMCMKF GAVTRIG\DLPWEINPLSSCSLL HEKDPPTTSGPQTDRPKEHLINF KSGACYTCRKSGH
23504	53872	A	23639	539	747	TAMLLTQSLFGGLLTRTRMKF GALTRIG\DLPWEINPLSSCSLL HEKDPHTPSRKIHIRPQGNHESQ KGL
23505	53873	A	23640	709	950	TALLLTQSLFGGLFTRTHMKFG AVTQIG\DLPWENQSPVLLCSLL REKDPPTTSGPQTDQPKEHLTN FKSGKWSFHSSPAF
23506	53874	A	23641	1	1257	MGKKVLGIASQLLGAVRCEPD GRRVLPEDWPECLSLVTHGTW FTRQGDKNIQMADNSFSDGVPS DFVEAAKNASKTEKLTDQVMQ NPGVLAALQERLDNAPHTPSSY IETLPKAVKRRINALKQIQVRC AHIEAKFYEEVHDLERKYAAL YQPLFDERREFITGDVEPTSDM ESEWHRENEEEEKLAGDRKNK VVITEKAAATAEEPNPKGIPEF WFTIFRNVDMLSELVQEYDEPI LKYLQDIKFHFQPNDCFANSVL TKTCKMKSEPDKADPFSFAGPE IMDCDGCTIDWKKGKNVTVKT IKKKQKRKGPGTVRTITKQVSN ESFFNFFNPLKASGDGESLDKD SEF/ASDFEIGHFFRER\PQAVLY FAGEALKDDDNFDEGEEEEDEL EGDEEGEDEDEVEINPNKEPSQ
23507	53875	A	23642	132	1277	
23508	53876	A	23643	1	515	RVRHRSVSVGSTHASAHAYGE GSLRIIPVTRSPLVTMNHIVQTF SPVNSGQP\PNYEMLKEEQEVA MLGAPHNPAPPTST\VIH\IRSET SV\PDHVV\WSLFNT\LFMNTCC LGFIAFAYS\VKSRDRKMVGDV TGAQAYASTAKCLNIWALILGI FMTI\LLIIIPVLVVQAQR

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23509	53877	A	23644	243	643	NHTVQT\FFSPVNSGQPPQRMR CIKEEHEVAVAGG\PHNPAPPTS T\VIHIRSETSVP\DHVVWSRVQ TPSSMNPC\C\LGFIAIRLTP*SLR DRKMVGDVT\GAQA\YAST\AK CLN\IWAHDSGASVMTILLIVIPS
23510	53878	A	23645	3	1498	RCNFLRSSRIRVHPTPAASTMPP KFDPNEIKVVYL\RCTGGEVGA TSALAPKIGPLGLSPKKVGDDIA KAMGDWKGLRITVKLTIQNRQ AQIEVVPSASAMIIKALKEPPRD RKKQKNIKHSGNITFDENGNIC STDMR/HRSLSRELSGTTKEILG TAQSVGCNVDGRHPHDIIDDIN SENDKQPRKSKMRTSFSPQIPG HEHFHYLLLLQHVHCQLALTL RARKEGSSTHHQKLSTYYFKEG NSKEPKKIQRCRNTELRKEEGG GGSGKAPGSEIKLESPACSGASL GEMTAWTMGARGLDKRGSFF KGPLPNTCGHFWEMVWEQKSR GVVMLNRVMEKGSVVEFVTEL FFYVALPKMFPVHYIVILLASKL EEVTFNFPPPPDLCTPFLQNYLR VAFQEVNSGCTGKTLLVRPYIT TEDVCQICVEKFKVGDPEEYSL FLFVDETWQQLAEDTYPQKIKA ELHSRPQPHIFHFVYKRIKNDPY GIIFQNGEEDLTTS
23511	53879	A	23646	361	918	GCTGSRGTVPLSALGPQRIGPP GSCLQIKSWVNDICQRQPG\DW KGP*GFTVKLTHSRTGQAPDCT RVP/VLPSCP*FIQSPSREPPKRPE KKPEKTFKHQLGIFTFLNEICST LLRQMR\HRSLSPEKLSWNPT* RDSWGIAQFSGAVNVDG\RH\P HDI\IDDIQQWVLWKCPRQLST KENIFNKGII
23512	53880	A	23647	1	642	

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23513	53881	A	23648	894	2438	VETKRIQPQPPDEDGDHSDKED EQPQVVVLKKGDLSVEEVMKI KAEIKAAKADEEPTPADGRIIY\ RKPV\KHPSDEKYSGLTASSKK KKPNEDEVYQDSVKKNSQKLII NSSLLSFDNEDENDTEKSMENL TGKIRKLQLRIVDPTFLPKLSNK GKDPVAVARLETGKGNKGAFR VLRDISRWATLCTSPQHSSSEA KNIIPYQATQFQNEVHKWYKK KGGLKISKRKALFFLTQDIQKK LQKLALGPNTPTPDILKIASLVF YNQDQEEKERAQQNERQKEKL YWLSYKSASPFQVALRILSQET THKDELPTDLPNNPEVQAPGIP GNTIMAMPVAIQLKDPSSYPCR IIKVPEIASWIHRTQVKLWKSPE TSELEPTPSVIEYTREALEDLKF LFKQKDNSSAKTPGRAYAASPR DWTSIEAELHIFYQWDPNLKG MFKPASLLAKVKQDFPDIHKES PIFRAIFSNITLMGIAPICVTGKTI KKRTRQHHTTPKSNLREQASQ GSLNWEGN
23514	53882	A	23649	200	1727	RTATSLDSVLYKSDYMTWKYR VSFFYILSCRLLKK/QCTDNEHV YMELSKKLYKYCPKEWKKEAS KVRQYEVTWVVSKRGKDYILK HIPNMHKDQFALTASEAHLKYI KEAVRLDDVAVHYYRLYKDK REIEASLTLGLTMRGIQIFQNLD EEKQLLYDFPWTNVGKLVFVG KKFEILPDGLPSARKLIYYTGCP MRSRHLLQLLSNSHRLYMNLQ PVLRHIRKLEENEEKKQYRESYI SDNLDLDMDQLEKRSRASGSS AGSMKHKRLSRHSTASHSSSHT SGIEADTKPRDTGPEDSYSSSAI HRKLKTCSSMTSHGSSHTSGVE SGGKDRLEEDLQDDEIEMLVD DPRDLEQMNEESLEVSPDMCIY ITEDMLMSRKLNGHSGLIVKEI GSSTSSSSETVVKLRGQSTDSLP QTICRKPKTSTDRHSLSLDDIRL YQKDFLRIAGLCQDTAQSYTFG CGHELDEEGLYCNSCLAQQCIN IQDAFPVKRTSKYFSLDLTHDE
23515	53883	A	23650	182	423	RLSIMASSLNEDPEGSRITYVKG DLFACPKT\DSLAHCISEDCRM GAGIAVLFKKKFGGVQELLNQ HYKEKGLRTSQLYG

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23516	53884	A	23651	1	249	
23517	53885	A	23652	435	494	
23518	53886	A	23653	163	578	RVTWLKKHLNSGNSDSVCMAS SLNEDPEGSRITYVKGS\LFEGP KTDFLAPCISEDCRMGAGIT\VL FKKKF\GGVQELLNQQKKS\GE V\AVLKRRWGRLYIFTWITKRK RAFAQSPLYENLTEEFRGQLKS HLSEEWSH
23519	53887	A	23654	1	2238	
23520	53888	A	23655	26	1941	RDAGTKWQRLGHLSCHCRKQA AREIINMHFQAFWLCLGLLFISI NAEFMDDDVETEDFEENSEEID VNESELSSEIIYKTPQPIGEVYFA ETFDSGRLAGWVLSKAK\KVD MDEEISIYDGRWEIEELKENQV PGDRGLVLKSRAKHHAISAVLA KPFIFADKPLIVQYEVNFQDGID CGGAYIKLLADTDDLILENFYD KTSYIIMFGPDKCGEDYKLHFIF RHKHPKTGVFEEKHAKPPDVD LKKFFTDRKTHLYTLVMNPDD TFEVLVDQTVVNKGSLLEDVV PPIKPPKEIEDPNDKKPEEWDER AKIPDPSAVKPEDWDESEPAQI EDSSVVKPAGWLDDEPKFIPDP NAEKPDDWNEDTDGEWEA\PQ ILNPACRIGCGEWKPPMIDNPK YKGVWIPPLVDNPNYQGIWSPR KIPNPDYFEDDH\PILLTSFSALG LELWSMTSDIYFDNFIICSEKEV ADHWAADGWRWKIMIANANK PGVLKQLMAAAEGHPWLWLIY LVTAGVPIALITSFCWPTKVKD\ RHSDLEYIIPDICIPQTKGVLEQE EKVEKAALEKPMDLEEEKKQ\N DGEMLEKEEESEPEEKSEEEIEII EGQEESNQSNKSGSEDEMKEA DESTGSGDGPIKSLRKRRVRKD
23521	53889	A	23656	297	398	
23522	53890	A	23657	286	430	TAGARCSSRTSSPGSCFNCQKS GHWAR\NARSPGFLLSRVPSVN WIHI
23523	53891	A	23658	405	524	ARMSVACLPGLFFICLRGDFKQ NLTAYCWKCYQL*RSLGTHS
23524	53892	A	23659	1	657	
23525	53893	A	23660	22	334	ALKHFCLCSLIFSVTTMKFLAV LVLLGVSIFLVSAQNP\TTAAPA DTVSSLLVLLMMKPLDAETTA AATTATTAAPTTATTAASTTAR KDIPVLPKWVGDLPNR

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23526	53894	A	23661	1	270	
23527	53895	A	23662	1	284	
23528	53896	A	23663	111	281	
23529	53897	A	23664	229	363	
23530	53898	A	23665	250	586	PVRHGAFFQDKSSDKKVQTKG KRGAKGKQA\EVAN\QETKEDL PAENGETKTEESP\ASDEAGEKE CQCLINNHIPCLISGPCLPSCTIQ RNIFINYFVNASFLVALETFLKK
23531	53899	A	23666	3	478	APAVGLSSSGGGRSGSGKAARF REGCRRAAARMQQAPGTRLPR RHPARAFPAATMPKRKVSSAE GAAKEEPKRRSARLST\KLPAK V\EAKPKKAAAKDKSSDKKV\Q TKGKRGAKGKQA\EVANQETK\ EDLP\AENGETERLEEESSLLIEA GEKEKPKS
23532	53900	A	23667	1	252	
23533	53901	A	23668	328	414	
23534	53902	A	23669	1	3156	
23535	53903	A	23670	1887	2036	
23536	53904	A	23671	3	212	
23537	53905	A	23672	22	539	YEGIVMKPLIIVNPADCIGC\RT CE\VACVVAHPSEQELNADVFL PRLKVQPIWTAVSAAR*CCPFSS ENAP\CVGA\CPVGA\LTMGEQV VQTNSARCIGCQSCVSACPFGM ITIQSLPGDTRQQIVKCDLCEQR EEGPACVESCPTQALQLLTERK LRRVRQQRIVVSGENPL
23538	53906	A	23673	135	302	PIHMKTRQPRDQFSADCVFLQS TCPVPC*RNRL*TPGGYWRTRR DYLRCDRSVHV
23539	53907	A	23674	175	794	LSTHSQPIADAADPPPHLHTGEL LCSAHQADFAVSAEPARPANN NAATTAPVHAVAITPPAYPDCF RTLPKSLSHQDSTQRLYGIARL LLRISTSGPPPSRLKVQRLDSISA PV/MCHQCENAPCVGACP/VGA LTMGEQVVQTNSARC/IGCQSC VSACPFGMITI/QSLPGDTRQQI VKCDLCGALRDCVAVLRQRRN SRVVLDACTRA
23540	53908	A	23675	2	434	LISLPFPPDSLAHRPPSSAPTEPQ GLFTVAAPTPGAPSPPATLAHL LPTPAMYSLLETELKNPVGTPT QAAGTGGPAAPG/GRKMALEN PKMHNSEISKRLGADWKLLTD AEKRPFIDEAKRLRAVHMKEYP DYKYRPRRKTKTL
23541	53909	A	23676	3	264	

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23542	53910	A	23677	1	2377	MDDTFLNYKYKNKCGPKHIKK KEEEEEEDNNSNDSKNKDKTLT TGSSGSAKIFLMRGGRRQLLLP TLSLCLLSVQRSPGSHESGPPQS MNPRLSPQGKYLKNDFLDVIG MCDIACHLVVELLVGNNGNFL AHAFAHVEVVAQQNQRENAA RPNGGSVMIGQGASLRTCQSRV LRVARGGPSPNPGESEQGLFTV AAPAPGAPSPPATLAHLLPAPA MYSLLETELKNPVGTPTQAAGT GGPAAPGGAGKSSANAAGGAN SGGGSSGGASGGGGGTD\QDR VKRP\MNAFMVWSRGQRRKM APENPKMHNSEISKRLGADWK LLTDAEKRPFIDEAKRLRAVHM KEYPDYKYRPRRKTKTLLKKD KYSLPSGLLPPGAAAAAAAAA AAAAAASSPVGVGQRLDTYTH VNGWANGAYSLVQEQLGYAQ PPSMSSPPPPPALPPMHRYDMA GLQYSPMMPPGAQSYMNVAA AAAAASGYGGMAPSATAAAA AAYGQQPATAAAAAAAAAAM SLGPMGSVVKSEPSSPPPAIASH SQRACLGDLRDMISITGRENIFV VGDPAACLLPIEMEETFLPWPL GFEDRLHLEGPRPVQEIPSFLRK VPNCGQWLLQTPSVEPADPWE NPQAFPPSLQQEQPCLSLIVGIF VEAFGGRGRWGSKGKKPKRYR TVEWMRIHQPSICCLQETHLTR
23543	53911	A	23678	1	399	

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23544	53912	A	23679	3	1216	LGNKRAGLRRADGEAPSALPY CYFLQKDAEAPWLSKPAYDSA ECRHHAAEALRVAWCLEAASL SHRPGPRSGLSVSSLRPTRKMA TTFLAHEKIWFDKFKYDDAERR FYEQMNGPVAGASRQENGA\T VILRDIARARENIHKSLAGSSGP\ GAS\SGTSGDHGELVVRIASLEV ENQSLRGVVQELQQAISKLEAR LNVLGKELRLAHRGTAPQTQH VSPMR\QVEPP\AKKPATPAEDD EDDDID\LVGRDNE\EEDKEAA QL\REER\LR\HYAEKKAQESLP LGGQVPPSLLDVK\PWDDESDM AQLEACVRSIQ/LGTGRSWGAS QMVAVGYG\IRKLQIQCVVEDD KVGTDLLEEEITKFEEARARSV DIASFSTRSEALKCVYVAHVRE GPCTRSKDLRPAKKKKKK
23545	53913	A	23680	1	2066	MAAALRAPTQVSAASSRPPLPS PPETEGRVKGFLQPGPHCPAQC LCSGDDGSNEDLEQKREVIFPR PHEAPVAEHRQQTVGLRELVAI PKRKEETTAIVQVFVAFEDVAI YFSQEEWELLDEMQRLLYRDV MLENFAVMASLGCWCGAVDE GTPSAESVSVEELSQGRTPKAD TSTDKSHPCEICTPVLRDILQMI ELHASPCGQKLYLGGASRDFW MSSNLHQLQKLDNGEKLFKVD GDQASFMMNCRFHVSGKPFTF GEVGRDFSATSGLLQHQVTPTI ERPHSRIRHLRVPTGRKPLKYT ESRKSFREKSVFIQHQRADSGE RPYKCSECGKSFSQSSGFLRHR KAHGRTRTHECSECG\KSFSRK THLTQHQRVHTGERPYDCSEC GKSFRQVSVLIQHQRVHTGERP YECSECGKSFSHSTNLYRHRSA HTSTRPYECSECGKSFSHSTNLF RHWRVHTGVRPYECSECGKAF SCNIYLIHHQRFHTGERPYVCSE CGKSFGQKSVLIQHQRVHTGER PYECSECGKVFSQSSGLFRHRR AHTKTKPYECSECEKSFSCKTD LIRHQTVHTGERPYECSVCGKS FIRKTHLIRHQTVHTNERPYEC DECGKSYSQSSALLQHRRVHT GERPYECRECGKSFTRKNHLIQ HKTVHTGERPYECSECGKSFSQ

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23546	53914	A	23681	1	468	MAAQVGAVRVVRAVAAHEEP DKEGKEKPHAGVSPRGVKRQR RSSSGGSQEKRGRPSQEPPLAPP HRRRSQPPTSWAAAVNDM/PAP TVPGPVEPLLLPPPPPPSLAPAG PADDAPLPAPSTSGLFTFSPLTA SAAGPKHKGTQGAAQAPSPPRP RW
23547	53915	A	23682	950	1326	RPESQRANGVDSGPNLKTVPQP DTRKGSVLKWISKRGKPLAVEI EESHCL\CLPLRTECLGIKP\IVH LFSCTRPVIVPSLELNYDVDSIA HMFVADLLLMITLPSYDIPFYC LVFQNLLVLEFQYL
23548	53916	A	23683	271	918	NQGLRDLGLCRICLVNKMFTSS ILGKGHRHSLVSIKQEHSALRK AAG\PLPLKVGYC\QGFSPCDSL KYG\SWDEKDLTVPQPDTHKGS VLRWISKRGKPLAVEIEEG\HCL PELPPGELECPG/ILKHGLYHWS SSEMGE\NRPMVG\ARHVYSNA ALLFFTALRIFGQRRNINLGLRA HPG\IVPPLELNYDIDSSAHM/FF LADLLLIITLPSYYIPFC
23549	53917	A	23684	1	942	
23550	53918	A	23685	346	1753	TWIPLSRTGRRFPVFSCSSSRYV AAISFHKRWKEGRCFGRTRGE MGWEGRSRSLKELNTRNDWNP GERELDFWRKITRFKEAASWTL EALEEAGSTARRRVWLEDGRR TCEILSVLCTSSLSSNCASLDCV TYKALSTTRLYDSVYWNKKPE RSSSPATEQSWTENDFDKLREE GFRRI\NYSELKEEARTHGKEVI NLEKK\LDERLTRITNAEKSLKD LMELKTMARELRDECTSFSSQF DPLEERVSVMEDQMNEMK\QE EKFREKRIKRN/EKQSLQEIWDY VKRPNLHLIGVPESDRENGTKL ENTLQEIIQENFPNLARQANIQI QEIQRTPQRYSSRGATPRHIIVR FTKVEMKEKMLRAAREKGRVT HKGKPIRLTADLLAETLQARRE WGPIFNILKEKNFQPRIAYPAKL SFISEGEIQYFADKQMLRDFVTT RPALKELLKEALNMERNNWYQ PLQKHAKW
23551	53919	A	23686	73	327	GALQPTAALWEPLSGLAKAAA RSLSLQGGVEGDARAGTGAAR GACGPAGVPGGRGLGGPALGA AGRPGP*LPSRGAGLGTAARHA

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23552	53920	A	23687	322	402	DQEPTNSGHIGNLEQCLGHGYQ R*LFP
23553	53921	B	23688	545	3063	
23554	53922	A	23689	1	579	MKHEKRDRCAELTAILLNEQAS PMCTIVLGYTGTSTITLPRTSCH FAPRLSNSQQHSSYQVGHKPES YCVRNWWVLGLTDFKNEAAD PHNSGGQLASPSGSRTGAAGG\ VPASPAPCARTPQPLGGRWDW AP\GTGGGIRRGGSGCTGTHGG GGRLRHGGLQSGGLPRGKAAK ARREIESSAGYSNSSSKCSII
23555	53923	A	23690	399	592	KCIHFPGPTPKFVCGVIVVTAVP /TFGM*TVYV**LPFSILAQNVG *RDDCDPGWKLNLFYAKKKK
23556	53924	A	23691	3	268	DRV/RPLRKNFQRNDQTAAFTV HENPLLCSYRCWYPGKQEQKK IKPQRGGKNRAEKLETLKSRAP LLFQRNAVPHQQRNKAGWRM TLTS
23557	53925	A	23692	29	484	CSFFLVSMVFTFWHDFAAAGTS CSFPCLVLSFRSSFRAGLVVTKS LSICLSVKYFISSSLMKLSLAGY EIVG*KFFSLRMLNIGPHSLLAC RVSAERSAVSLMGFSLRVTRPF SLAALNIFSFISTLVNLTIMCLG VALLEKYLCGILCVS

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23558	53926	A	23693	182	2076	MQEWLRLTARKTELSRDSRSC GQLKTSLLISLLVESTQGRH*SF L/VWTQTHSGGDGWRVAKAW RPKYHDTQLGGEKEEPQGHHA SDCRWRAQPHCRTLSAAVVNV AGFTVTFELRCLTLMKMREKD HHLCDNDIVLFPPDTAFPLDCL LSCIHSTVHGLLRWNAIQYLAS RSESHPERSEGGTPDRNGHPAL SLASFNGAQQDRRTVQSLGEKP GLPEEMAAFMAGTEKEQNELG IEFFQLIIPASKRTHSENALFSHS GDDTECSRSGQGSPPSYSRGPP RRTFILATQPLCSKEAQTSPHEQ PTRTEKNRGSHLYHKSPCDHAS PGMSVTMSGMQQALPRQLTTL TFYPPAFRSIKIFRIMILKTEMLH THARSQEALLKDSSKTMLHSTL PSCVRKSNYHHRERKIKTKEAF PAKIHRSRNQGMKVEVAPLTIT SSDPLAEFLLPVTVTLCSASLEV LAPEGGMLSPGDATMIPLNWK LTLPPGHSGLLLPLSQQVKKRV PVLVGVIDLDYQDEIDYYSSMK ERSSSPATEQSWMENDFDELRE EGFRRSNYSELREEIQTKGKEV ENFEKNLEECITRITNTEKCLKE LMELKTKVRELREECRSLRSRC DQLEERVSAMEDEMNEMK
23559	53927	A	23694	933	1118	RVERRRLQTIKLLRATGGNSNQ RQRS*KL*KKFRRMYN*NNQY REVLKGADGAESQGSRTT
23560	53928	A	23695	2	250	WCHTKLDGLSLFGESVALEEA GGQTALWLMRFLSRKANYVD KITTREVGHRE*LMSSRLHSR* WAASSVCSSSCVLLPSSHS
23561	53929	A	23696	1017	1230	
23562	53930	B	23697	62	1069	
23563	53931	A	23698	216	582	ILVPTLFWLGEFLLRDPLLV*W ASI*G*PD/AFSLAALNIFSFISTL/ RESDNYVSWSCSSRGVSL*RSL YFLNLNVGLPCQIGEVLLDNIL QSVFQLGSILPVTFGYTNQMQI WFHFIHFIFHH
23564	53932	A	23699	434	681	TLACLARLGKFSWIISCRVFSNL VPFSLSLSGTPIRRRFGLFT*SHI SWRLCSFLFILFSLNFPSRFISFV SSSITDTLSSS

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23565	53933	A	23700	290	1231	RSFRAIGEVGSIRGWGGGYAAQ LQSPSRLPVLGGGKKGGSRGV GQGSSRAEVGLGSQRERSGTCG AEAAAAAAQLIAGTGSSLPYQG PGQNQTAIAPTCAPLSPCKAAA VIMGNIFGNLLKSLIGKKEMRIL MVGLDAAGKTTILYKLKLGEIV TTIPTIGFNVETVEYKNISFTVW GCGVARDK\IRPL\WRH\YFQN\T QGFDILWSDSN\DR\ERVNEA\R EEL\MKNAGAETSLRDAVLPFL/ FGNKTDLRNAMNAAG\IQDKL G\LHSLRHRNWYI\QATCATRG N\GLYEGLHWLANSVPKQEVES RTALTKHPNRP
23566	53934	C	23701	164	208	
23567	53935	C	23702	1	381	
23568	53936	C	23703	43	276	
23569	53937	C	23704	1	462	
23570	53938	C	23705	38	121	
23571	53939	A	23706	77	202	QKNYTQRPLPLHGLLELEVTCR CWSWQPLLEPLELRP\RLSD
23572	53940	A	23707	123	209	
23573	53941	C	23708	1	411	
23574	53942	A	23709	1400	1809	SSNPLSRPPLPTPVTPCPLLRLSL LRACCCCLFLPLRFFSCPLLCFL LCFFFSVCSPAHKNFKMPKPQW SGIPTGPPPSGSCFKCQKSGHW A\RNACSPGFLLSHVPSVWDPT GNQTVQLAWQPLLEPLEL*P\R LSD
23575	53943	B	23710	76	358	
23576	53944	B	23711	1	606	
23577	53945	C	23712	272	388	
23578	53946	A	23713	1	259	PGVRGAQGGPSIPRQCEESAIGP KFAWIISSFHWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGFIWQPLPEPLEL*P\RLSD
23579	53947	A	23714	684	917	GDFGLRQWGFLNIQSCHLQTGT I*LPLFLIEYPLFLSPA*LPWPELP TLCCIGVVREGISVLCQFSKGM LPVFAHSV
23580	53948	A	23715	618	683	
23581	53949	A	23716	306	710	DRVSLLTPRLGVQWPDPGSLQP RPPGFKRFYCLSLPSS*DYRHEP LLPAYFFPYRIIGWSRL
23582	53950	A	23717	2	88	

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23583	53951	A	23718	972	1967	FPPGRGRGPGRPAGCSRGRARA CPKPVDHVKRPMNAFMVWSR AQRRKMAQENP\QMHNSEISKR LGAEWKLLTESEKRPF\IDEAKR LRAMHMKEHPDYKYRPRRKPK TLLKKDKFAFPVPYGLGGVAD AEHPALKAGAGLHAGAGGGLV PESLLANPEKAAAAAAAAAAR VFFPQSAAAAAAAAAAAAAGS PYSLLDLGSKMAEISSSSSGLPV LNMPNMHINSLGKNLALNLFV YNDANSMLDLCYDGVDGKGPI CFCATQGYEDIFKAGYGSVVD YYNDGSDLTTPLEIATVIPTFSN HPLMSQRPSTWRQNPPLAKRLP LTEDSDGDDH
23584	53952	A	23719	2	144	RPQRRP/LPPPTGSPLKHPGGAS GAAGAPIGEPQHPGAVVSVRA WSLCS
23585	53953	A	23720	219	897	PGRAGGTLGLGSRRDGTREKG VEETPHRLHARTDTTAPGCCGS PIGAPAAPEAPPGCFEG\PRWVE GVKKASPPLPAELIGWLVNFPL ARPVRPPSLSPGPPRRPPEGVCG SWPGRSEGERGKAKNTAESTPR QNLHRKYTIIVTHYQRNRKGQ NISFSLVCEFHPSLADWTTVTA LTWTSPKDNSLTEESWLREGN VHRGMDEYVRAQSFLILMTLE NSGGSVVSK

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23586	53954	A	23721	937	2730	TNPHCHDHYYHHHHHCHHCH HHHHHCHHHHYHHHHHCRDH HYHHHHHCHHCHHHHHHCHH HHYHHHYHHHCHDHHYHHHH HCHDHHYHYHHHHCHDHHYH HHHHCHDHHYHYHHHHCHDHH YHHHHHCHDHHYHHHHHHCHD HHYHHHHHCHDHHYHYHHHC HHHRYHHHHHCHHCHHHHH/P HHHHHHHHHCHHHHYHHHHHC HHHHYHHHHHCHHHHYHYHC HHHHYYHHHHCHHCHHHHYH HHHHCHDHHYHHHCHHCHHH HYHHHHHHYHDHHYHHHHHCH HCHHHHHHH\DHHHHHHLHCHH HYYHHHHHHHHHHHYHHHHHH HLHCHHHYYHHHHHHHHHHY HHHCHHCYHHHYHHHHYHCH HHYHHHHHYHPYHYHQHHHH YHPHHYHHHYYHCHHHHDYH HPHHCHHHHHYHQHHYYPITII TTTITTITTIIITVTTTTFTTTTNT TAPTTTPVTAITTTTTTTTTITTT TPITITTITNITTTTVTTTVIITTTF TTTIHPYHHHHHHHHPVTITTTIT TATIITTTTSITSITTITTTIVTTIII TTTAATHHHYHPYYHHYHHHH HHHHTHSYYHYHHHHHHHCF HYHHHHYHHH
23587	53955	A	23722	2348	2571	
23588	53956	A	23723	4919	5142	
23589	53957	A	23724	2	370	
23590	53958	A	23725	588	701	
23591	53959	A	23726	295	521	
23592	53960	A	23727	2837	3061	
23593	53961	A	23728	272	436	
23594	53962	A	23729	239	514	
23595	53963	A	23730	105	367	TGRPPELLLHLRSLSPPLL/CSSP/ TPPPQLPPPPVSLASGYPLLHPL ARYPACPLPPRRARTEQRGGEQ PGVGASPLPIPGRWPGTEAT
23596	53964	A	23731	999	1145	
23597	53965	A	23732	1084	1893	

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23598	53966	A	23733	1605	2296	HSIHSSVDHPENRIYRRKIEELS KRFTAIRKTKGDGNCFYRAL\AI PYLESLLGKSREIFKFKERVLQT PNDLLAAGFEEHKFRNFFNALR AGRAQFYSVVELVEKDGSVSSL LKVFNDP\GASDHIVQFLR/LCF TSAFIRNRADFFRHFIDEEMDIK DFCTHEVEPMATECDHIQMTA LLQALSIALQVEYVD\GWIPALT QHVFLEAATPSVYMLYKTSQY NILYAADKH
23599	53967	A	23734	529	1830	AGYGDRTMLARKSIIPEEYVLA RIAAENLRKPRIRDRLPKARFIA KSGACNLAHKNIREQGRFLQDI FTTLVDLKWRHTLVIFTMSFLC SWLLFAIMWWLVAFAHGDIYA YMEKSGMEKSGLESTVCVTNV RSFTSAFLFSIEVQVTIGFGGRM MTEECPLAITVLILQNIVGLIINA VMLGCIFMKTAQAHRRAETLIF SRHAVIAVRNGKLCFMFRVGD LRKSMIISASVRIQVVKKTTTPE GEVVPIHQLDIPVDNPIESNNIFL VAPLIICHVIDKRSPLYDISATDL ANQDLEVIVILEGVVETTGITTQ ARTSYIAEEIQWGHRFVSIVTEE EGVYSVDYSKFGNTVKVAAPR CSARELDEKPLPSLFRPSQKSEL SHQNS\LRKRNS\HRRNNFHRRN N\SIRRNN\SSLMVPKVQFMTPE GNQNTSES
23600	53968	A	23735	968	1243	
23601	53969	A	23736	541	1010	SVTSCLKVTSVCLTSAAASCRH RRSVEEYLVS*KLPM/WSRRRK AAALTES/V/CIVFWLASWMMS RWLHYPDWVTIIAQQVLMNVV SVMQADCRMNLLEIFLRWLMR KIFHNILRHFSQLLNVPITRPFS WILRPF
23602	53970	A	23737	766	1910	LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFSICFVI CSRTLILKGSSLMYVFCLPNTAI GGSSRVDRCRAATSRGSSRVDL TL*KYSLVGPSVPLVSSV**SDW PLKLLLMTMMS

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23603	53971	A	23738	581	1434	KLPMGVAVVKLLHLPKVIIVFW LASWMMSRWLHYPDWVTIIAQ QVLMNVVSVMQADCRMNLLEI FLRWLMRRASDICSSIHGD*EPL L/YAVFGKQNTYIRLEPFKINVL EQITKHIEKLQCGGVVKQLSRR GNNQHISSTYDINRADTQVRRA VNNYDIIVMSNSFNGQSEHQV WIDRKAGECLLHEYEDLVPIRD TLRLFPGGRYLPRAKHVAPSEP DPEQDEQKLRFCKRHLYGKQP RSPVERVWDHGPTRIVGLIISLG PRSHSYRRSDNQTGTTVPLVSS
23604	53972	A	23739	515	774	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIS GTTVPLVSSV*LLVWDHGPTRI VGLIIRLGPRSHSYRRS
23605	53973	A	23740	322	763	CRMC*LFPRLLSCLTTPPHCSFSI CFVICSRTLILKGSSLMYVFCLP NTAIVMALSPRGWRSKFGMPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPVCGRDVKSTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDL
23606	53974	A	23741	1	127	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEK*RRL SPLHSLMMTARKRGK*PGAGE
23607	53975	A	23742	9	437	WLGLGNWKERLGTQTRMIWS QKTARRLCRTFSGIPAYSMCI/CI GMAERMWCDRNRERHTVSSSG GNRLPNPDWAPGPPRIVGLNIS LGPTVPTRIVGLIISLGPRSHSYR RSDNQTGTTVPTRIVGLILVLGP WSHSYRRSDY
23608	53976	A	23743	766	767	LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFSICFVI CSRTLILKGSSLMYVFCLPNTAI GGSSRVDRCRAATSRGSSRVDL TL*KYSLVGPSVPLVSSV**SDW PLKLLLMTMMS
23609	53977	A	23744	573	1085	VCHQILTHLPALLSGARMMWD QLWRGRP*RRCQQPQCGG*WH CFWATAHHSPLDSTLNHLHCLP RGP
23610	53978	A	23745	2	379	WLTRSSCSWRLPPRRKKKGAL V*PVWLPPGGVAVLLQLGCCV LQDVSCKRLCYNRKGQSEIVL MS*ITMWKLFPRPPLLPFSTCIC *KTCGKRGRSK*KVDILVLSIRF SAIKLEPLDCHENAWL

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23611	53979	A	23746	575	576	TGIDSDQLNGRDWRRALSVSPA PDSGFPRCNGDEQAGI*LLGTG WAEKCHRLAFPPAGSTAGR
23612	53980	A	23747	1	723	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVCSWKERPPGNSL NVSRMVWDHDPTRVVGLIIGL GPRSHLYCRSDYQQRS\TSVCG CMPAVDCCCVLLIHNILRTVM WTKYLVTQAVPAR*PGCIRCKC
23613	53981	A	23748	1	1101	
23614	53982	A	23749	5	205	YCSSLSFTAAITSRAFLPDRRITT PPATSPSPFSSAMPRRISGPIWTF ATSRR*TGTPFSLAFKTM
23615	53983	A	23750	1	761	
23616	53984	B	23751	56	2188	
23617	53985	A	23752	627	1272	
23618	53986	A	23753	448	2218	VRRQRSDPERSDARMVRFCNL YI*RKNPFILH*LFR*TLRQTKPD NSAGKCVKI
23619	53987	A	23754	171	959	AASRGPDAPGLEMAGNCSWEA HPGNRNKMCPGLSEAPELYRR GFLTIEQIAMLPPPAVMNYIFLL LCLCGLVGNGLVLWFFGFSIKR NPFSIYFLHLASADVGYLFSKA LFSILNTGGFMGTFADYIRSVCR VLGLCMLLTG\VLLMPAGWDE RGVRSERAWCTVETGRVHRSR VRVSRNTARDPANGLGHLLQS LGMPALEPGPTLGSALRWEFLQ TASPQLPVQPLHPAAATPQRSL RGRGRGPKARALGLGPRSTSYR
23620	53988	A	23755	664	838	
23621	53989	A	23756	2732	3007	
23622	53990	A	23757	1522	1706	CHYFACMWSGCEVYS*SAPG** C*EDLSGLVRCRCLHSNAETPI* FAANADTSPRGPFLCR
23623	53991	A	23758	537	795	ADCPLHMGRPCLID*GPCRTE*P RCAVVCLLWIAAVSCLSTT/SLR TGI/DGPKYLVTQAVPARYPGCI RCKCVAVDELASSDMRLPCS
23624	53992	A	23759	2074	2276	
23625	53993	A	23760	36	206	ECWIWCELGAELHHQP*ASSH WKSSYRQQSSLPRCRASQRTLH LLLQGWAVLGPLE
23626	53994	A	23761	444	725	
23627	53995	B	23762	1	1212	

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23628	53996	A	23763	11	972	RFSKSLLDSGVQLASPSGSRTG ATGGAAHSPARAPALHSPWAV DGTRGRLAGTAGLWSPRPAFH FKVSLSLPFSCVSSPFPGPPLGPS PRKHQMADDAGAGVGGRRPR GPRMG/NRGGFRRGFGSGIRHQ GCGCGQGQGQGRGVRGGKAE YKEWMTVTKLGHLVKDIKIKS LEEIYLFSFFKTSSSLKDEVLKI MLVQKQTHTSQCTRFKAFVAT GDYNGHISLGIKCSKEVATAIC GAIILAKLSIVPACRGYWGNKIS KPHTIPCKVAGCCGSVLVCLIS VPRGTGIVLAPCEGDRGLRKSS PASLSPESCKDGSHSRSF
23629	53997	A	23764	2	260	LLEECRSLRSRCDQLEERVSAM EDEMNEMK*EGKFREKRISPKR APERSAKHGKEQPVPAAAKSC QNVNTIETRKKLHQLTSKITS
23630	53998	A	23765	3	1150	
23631	53999	A	23766	1	1521	
23632	54000	A	23767	1	753	
23633	54001	A	23768	1	3351	
23634	54002	A	23769	1	1740	
23635	54003	A	23770	1	1353	
23636	54004	A	23771	1	1932	
23637	54005	A	23772	1	1221	
23638	54006	A	23773	1	1214	MAKKQNRKTGNSKKQRASPPP KECSSSPATEENWTENDFDELR EEGFRQSNYSELWEDIQTKGKE VENFEKTLEECITRITNTEKCLK ELMELKTKAQELRKECRSLRSR CDQQQERASVLEVLEVLAR\QL GRKRK*RVFN*EKRKSNCPCLQ TT*LYI*KTPLSQPKISLS**ATS AKSQDTKSMYKNHKHSYTPTT DKQRAKS*VNSHSQLLQRE*NT *ESNLQES*NWISSLHLIQKSIQD GLKT*TLDLKPSKP*KKT*ALPF RT*AWARTSCLKHQKQWQQRT KLTNWI*LN*RASA/PAKESTV/S SEQATYNMGENFHNLLI*QRAN IQNLQ*TQTNLQEKNKQPHQKV GEGHQQTLLKRRHLCSQKTHE KMSIITGHQRNANQNHNEIPSH TSYNGNH

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23639	54007	A	23774	1157	2085	QGRPTDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLIAAGTTGFPTGKRAVS ATQLMTQFSPAREQSWRKN/DF DELRKE/GFARSNYS\EKCLKEL MELKTKARELREECRSLRSRCD QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQENFPNLARQANVQIQE IQRTSQRYSSRRATPRHIIVRFT KVEMKENMLRAAREKGWVTL KGKPIRLTADLVAETLQARRE WGPIFEEP
23640	54008	A	23775	1	1707	
23641	54009	A	23776	1	1899	
23642	54010	A	23777	1	2781	
23643	54011	A	23778	1	831	
23644	54012	A	23779	1	3264	
23645	54013	A	23780	1	882	
23646	54014	A	23781	1	1853	
23647	54015	A	23782	1	550	
23648	54016	A	23783	1	831	
23649	54017	B	23784	64	3436	
23650	54018	A	23785	1	1422	
23651	54019	A	23786	1	773	MGKKQSRKTGNSKKQSATPPP KERSSSPATEQSWTENDFDELR EEGFRRSNYSELQEETQTKGRE VENFEKNLDECITRTTNTEKCL KELMELKAKAWELREECRSLR SRCNQLEERVSVMEDEMNEMK REGKFREKRIKRNEQSPQVIRD YVKRPNLRLIGVPESDGKNGTK LENTLQDIIQENFPNLARQANIQ IQEIPRTS/QRYSSEEHSIIGLIGR FPS*RTDMFRAPKKREQKRNNR KIQKEEGGRTAPTGI
23652	54020	A	23787	1	2775	
23653	54021	A	23788	1	2712	
23654	54022	A	23789	1	1590	
23655	54023	A	23790	1	547	MGKKQNRKTGNSKKQSASPPP KECSSSPATEQSWTENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLSSR CNQLEERVPAMEDEMNEMKE D/GNRYDDRRQ/RKEEIMIKSW RFCCRHLIRVVRGWGPSKYLWI TMVVTLAGNPQ
23656	54024	A	23791	1	710	

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23657	54025	A	23792	1	895	
23658	54026	A	23793	1	1938	
23659	54027	A	23794	1	1413	
23660	54028	A	23795	985	1219	LCSGSVERCTESYLHSSHCLVQ QAGVTGDEGGSCY*DPPSHHRS HPRKLKKLCEQEFSVTSAPWRK CRSLHGRFPGLP
23661	54029	A	23796	1	3570	
23662	54030	A	23797	1	634	
23663	54031	A	23798	1	4551	
23664	54032	A	23799	1	4721	MHPSQRTPYQSRSPATIFATVST FKSHKSNLETKHPQQVPLSSLG LAANISSEDIESEAEDNGKWES VDRTSFFPALTSFQQSMIHKKI MTVFKSVEPEDGLGRPTLAFHE DRCQLSIQNSLDAGGGCPSMA APPAEVHELASGLISAAALLLSP AASGRVSKHQHIPTGFPDPPKA LHKGKLTTRKDIYTENPSVHHH HQRPKVDKTTKMGKKQNRKT GNSKTQSASPPPKECSSSPATEQ SWMENDFDELREE

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23665	54033	A	23800	1	2152	MDILGWASRAHKWKGRATGT HVFNLMREYLISLQCCASEQAA SPEHGASFRVWKSLGFQKLILS LICPQCLQSLTRETWMRFKSKK TKGPDLRLVMDANKWEFRRH ALRPALTFPNEGGDLGVEALPV ALPPEAHVGGVVLPAALVRGA HGEQLPAIPGPEEFALPAVQAR AARPERQVVVIVVNEAGVDPA GVEGLAPVPVLPGVRLEATAPK QPPRLPARLRAPLPSGRKLNAK CPRLRWGFFVQDGDGTELACL SEGDGGCCQEAPLDHRPRRLRG LAGSAGAREAREPRLRPGDWG NRIARVRAPEEAAAALSRPARV AAALAKTHRREHRARSQKLVM SSVQQGKLTTRKDIYTENPSVH HHHQRPKVDKTTKMGKKQNR KTGNSKKQSAF\PPPKECSSSPA MEQTWT\DNDFDELREEGFRGS NYSELREDIQTKGKEVENFEKD LEECITRITNTEKCLKERMELKT KARELREECRSLRSRCDQLEER VSAMEDEMNEMKREGKFREK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENTLQDII QENFPNLARQANVQIQEIERMP QRYSSRRATPRHIIVRFTKVEM KEKMLRAAREKGRVTLKGKPI RLTAVLSAETLQARREWGPIFN ILKEKNFQPRISYPAKLSFISEGE IKYFIEKQMLRDFVTTRPALKE
23666	54034	A	23801	1	2109	

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23667	54035	A	23802	1	2544	MSVHSWKPSWIRPIRSLSPKRPL GTQGTSEVPPDTHICQTKFHSLS SGPLLLSVHPVGKLSAVVGRVF IHILSQRERRRRRVISAFPSEVPG SSHQGVPDSGCRSVGAHPVREP KQGEALPHSGSPREGKLTNRKD IHTKNPSVHHHHQRPKVDKTT KIGKKQNRKTGNSKTQSASPPP KECSSSPATEQSWMENDFDELR EEGFRQSNYSELRKDIQTKGKE VENFEKNLEECKTRITNTEKCL KELMELKTKARELCEECRSLRS RCNQLEERVSVMEDEMNEMK REGKFREK\RIKRNEQSLQEIWD YVKRPNLRLIGVPESDVENGTK LENTLQDIIQENFPNLARQANV QIQEIQRTPQRYSSRRATPRHIIV RFTKVEMKEKMLRAAREKDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEII TNYLSDHSAIKLELRIKNLTQSR STTWKLNNLLLNDYWVHNEM KAEIKMFFETNENKDTTYQNL WDALKAVCRGKFIALNAHKGK QERSEIDTLTSQLKELEKQEQT HSKASRRQEITKIRAELKEIETQ KTLQKINESRSWFFERINKIDRP LARLIKKKREKNQIDTIKNDKG DITTDPTEIQTTIREYYKHLYAN KLENLEEMDTFLDTYTLPRLNQ EEVESLNRPITGSEIVAIINSLPT

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23668	54036	A	23803	1	1886	MKENFKHRHVVAFISSQEAQE DSREEEDRLESRFYFLFLLELSY KTTGLNREPTVSLNSKSGTPMD QNEHSHWGPHAKGQCASRSEL RIILVGKTGTGKSAAGNSILRKQ AFESKLGSQTLTKTCSKSQGSW GNREIVIIDTPDMFSWKDHCEA LYKEVQRCYLLSAPGPHVLLLV TQLGRYTSQDQQAAQRVKEIF GEDAMGHTIVLFTHKEDLNGG SLMDYMHDSDNKALSKLVAA CGGRICAFNNRAEGSNQDDQV KELMDCIEDLLMEKNGDHYTN GLYSLIQRSKCGPVGSDERVKE FKQSLIKYMETQRSYTALAEAN CLKGALIKTQLPKVDKTTKIGK KQSRKTGNSKKQSTSPPPKERS SSPAMEQSWTENDFDELREEGF RRSHYSELPEDIQTEGREVENFE KSLEECITRITHTEKCLKELMEL KTKARELREECRSLRSQCDQLE ERVSAMEDEMNEMKREGKFKE K\RIKRNEQSLQEIWDYVKRPN LRLIGVPESDAENGTKLENTLQ DRIQENFPNLARQANGFCRFRN HHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINRSWH DRFPDWKAGTGLKSAIFAWE
23669	54037	A	23804	1	4134	
23670	54038	A	23805	1815	1849	

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23671	54039	A	23806	1	4016	MGKKQNRKTGNS\KTQSAFP\P PKECSSSPATEQSWMENDFDKL REEGFRRSNYSELR\EDIQTKGK EVENFEK\NLEECIT\RITNTEKC LKELMELKTKGSRNYVKECR\S LRSRCDQLEERVSAMEDEMNE MK*EGKFREKRIKRNEQSLQEI W\DYVK\RPNLRPIGVSESDGEN GTKLENTLQDIIPENFPNLARQA NVQIQEIQRTPQRYSSRRATPRH ILVRFTKVEMKEKMLRAAREK GQVTLKGKPIRLTADLSAETLQ ARREWGPIFNILKEKNFQPRISY PAKLSFISEGEIKYFIDKQMLRD FVTTRPALKELLKESLNMERNN WTSKQIIQEDGYSEEEGWLCRA VIYSHTLQAIMAIVKATGNLQT DFANPFHTDDARQQFAMSYTV VGQGALPEDLSRCHLQTEAVQ RHPESLGCPLDLLHGMPVSSCF GYPQDTSSTV
23672	54040	A	23807	2059	3153	
23673	54041	A	23808	6	188	
23674	54042	A	23809	3	1014	VACRPLPRRRAQPATFIPRVAV KMALVASVRVPARVLLRAGAR LPGAAFGRTERAAGGGDGA\RP \FGSQRVLVEPDAGAGVAVMK FKNPPVNSLSLEFLTELVIS\LEK LENDKSFRDVILTSD\RPGVFSA GLD\LTEMCG\RSPAHYAWVLE RPVQELWLRLYQSQL\VLVSAI NGA\CPAGG\CLVALTCDYTIL\ AGNPRYCIGLNE\TQ\LGIIAPF\ WLKDNPWRTPIGHRAAESA\LQ LGLPLPPPAEALQVGIVDQ\VVP \EEQVQSTALSAIAQWMAIPKP MAHK\LTKAIMRKGQGPPAWS RKGYADVQNF\VSFISKDSIQKS LQMYLERLKEEKG

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23675	54043	A	23810	1	2665	MTTSIRQFTSSSSIKGSSGLGGG SSRTSCQLSGGLGAGSCRPGSA GGLGSALGGSSYSSCYSFGSGG GYGSSSFEGVDGLLVGGEKAT MQNLNDRLASYLDKVRALEEA DTELEVKIRDWYQRQAPGPAR DYSQYYRIIEELQNKPPPSDDLT TLPSPLILTATVDNANILLQNDN AHLAAADFRTKFETEQALCLSV EADINGPCRVLDELTLARADPE MHIENLKEELAYLKKNHEEMN APRGQVGGEINVEMGAAPGVD LSRILNEMREQYEKMAEKNRK DAEDWFFSKTEELNREVATNSE LVQSGKSEISELRCTMQALEIEL QSQLSMKASLEGNLAETENRY CMQLSQIQGLIGSVEERLAQLL CEMEQQNQEYKILLDMKMRLE LEITTYHRLLEGEDAQTVQHTP GSPCVPEWAHDRCSLPAQLDE WSCQAQRGICGHRRENCWERIP SQSCFYRPTARSLTSLLGTMST CSHQFTSSRSMKGSCSIGGSIGG GSSRISSVLAGGSCHAPSTYGG ASCGLGGGYGGGFGSSSSFASG FGGGYGGGLGAGFGGGLGAGL GGGFAGGDGLLVGSEKVTMQH LGDRLASYLDKVRALEEANAD LEVKIRDWYQRQRPSEIKDYSP YFKTIEDLRHKIIAATIENAQPIL QIDNARLAADDFRTNYEHELAL QQTVEAGVNGLCREMLALRGQ
23676	54044	A	23811	222	548	TLPCGDHHHSQDPARLPSWHD LLQERSEKCGSQDWQRDSVQP GVSYQFCCVPWPAGRSPQPRH CWGCCGTEASYDSGI*SLSTPG GGQLQGSV*GPDGAGLQNSHR
23677	54045	A	23812	2	165	
23678	54046	A	23813	1	665	
23679	54047	B	23814	1	1673	

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23680	54048	A	23815	1	331	ARQLRTSAMTMPVNGAHKDA DLWSSHDKMLAQPLKDSDVEV YNIIKKESNRQRVGLELIASENF ASRAVLEALGSCLNNKYSEGYP GQRYYGGTEFIDELETLCQKRA LQAYKLDPQCWGVNVQPYSGS PANFAVYTALVEPHGRIMGLDL PDGGHLTHGFMTDKKKISATSI FFESMPYKVNPDTGYINYDQLE ENARLFHPKLIIAGTSCYSRNLE YARLRKIADENGAYLMADMA HISGLVAAGVVPSPFEHCHVVT TTTHKTLRGCRAGMIFYRKGV KSVDPKTGKEILYNLESLINSAV FPGLQGGPHNHAIAGVAVALK QAMTLEFKVYQHQVVANCRA LSEALTELGYKIVTGGS/CVISG GAGKPG*FSHQDGTGTSQDGG RRPFLHHTLSY
23681	54049	A	23816	3	1709	SHPTPRETPTGVEGQATPSVLG AAPASQAKATPTLGRPHASDR GEVAQLDEWSCQAQRGICGHR RENCWERIPSQSCFYRPTARSLT SLLGTMSTCSHQFTSSRSMKGS CSIGGSIGGGSSRISSVLAGGSC HAPSTY/GGGLCVSFSRFSFGGA CGLGGGYGGGFGSSTNFWS\GF GGGYGAGLGAGFGGGLGAGL GGGFAGGDGLLVGSEKVTMQH LGDRLASYLDKVRALEEANAD LEVKIRDWYQRQRPSEIKDYSP YFKTIEDLRHKIIAATIENAQPIL QIDNARLAADDFRTKYE\HELA LRQTVEADVNGLRRVLDELTL ARTDLEMQIEGLKEELAYLRKN HEEEMLALRGQTGGDVNVEM DAAPGVDLSRILNEMRDQYEQ MAEKNRRDAETWFLSKTEELN KEVASNSELVQSSRSEVTELRR VLQGLEIELQSQLSMKASLENQ L\EETKGRYCMQLSQIQGLIGSV EE\QLAQLRCEMEQQSQEYQIL LDVKTRLEQKYCHPTAALLEG EDAHLSSQQASGQSYSSREVFT\ SSSSSSSRQTRPILKEQSSSSFSQ
23682	54050	A	23817	2	365	

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23683	54051	A	23818	1	464	RRWRICSTWTRSFATAWLPPAP SANFPRTDRSQGDRGAPAGFAL APILEFFLWDTSSQKFLQKPHCF MHGRERAKMGRRAQQESAQA ENHLNGKNSSLTLTGETSSAKL PRCR/QGGWAGDSVKASKFRR KASEEIEDFRLRPQSLNGSDYG GDIP
23684	54052	A	23819	384	805	
23685	54053	A	23820	3	392	MKYSAIQTLDGEIDLKLLTKVL APEHEVR*VQWWQQFPGLSTL AIPINPAELPGLALCLP*RPWNG REKVSLQLREKALSLSYPAKPF L\EDDVGWDWDHLFTEVSSEV LTE\WDPLQTEKEDPAGQARHT
23686	54054	A	23821	63	785	GPIRGPWGPGFGGWGGATPPAP TSLRRLRAAGLAPRRRAKMGR RAQQESAQAENHLNGKNSSLT LTGETSSAKLPRCRQGGWAGD SVKASKFRRKASEEIE\DFR\LRP QSLNGS\DYGGDIPI\IPDLEEVQ EEDFVLQV\AAPPSI\QIKRVMT YRDL\DNDLM\KYSAIQTLDGE D/IDLKLLTQK/VLAPEHEVRER NPSWQDDVGLGTWGPICSTEV SLRRSFTEWDP\LQTEKEDPGG Q\ARHT
23687	54055	A	23822	1	441	MSFNCSTRNCSSRPIGGRCIVPV AQVTTTSTTDADCLGGICLPSSF QTGSWLLDHCQETC/CGCQPLG GISSVCQPVGGISTVCQPVGGV STVCQPACGVSRTYQQSCVSSC RR\PAKCVGASERIKTPRPASCF QDLPACCLSLNSSS
23688	54056	A	23823	1	538	PTRPLQQATCSPLSDIMSFNCST RNCSSRPIGGRCIVPVAQVTTTS TTDADCLGGICLPSSFQTGSWL LDHCQETCCEPTACQPTCYRRT SCVSNPCQVTCSRQTTCISNPCS T\PTAGRSP/CVSSGSQPLGGISS VCQPVGGISTVCQPVGGVSTVC QPACGVSRTYQQSCVSSCRRTC

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23689	54057	A	23824	832	1885	AEWDAADKAHVGPGRSPRQPL PHVGRRRAAHTTGRGRRTAGC APAPARTLCILSILGPWCVLPHL PTLCLGQAQAASCSQGAHGCF AGCSCT/GTSASHPV/CCKCPLH PVCTLADVHGCITSGFSVISLPQ TCAPWTSWRKWSLSDSWQVD ACPESCCEPPCCATSCCAPAPCL TLVCTPVSCVSSPCCQAACEPSP CQSGCTSSCTPSCCQQSSCQPA CCTSSPCQQACCVPVCCKPVCC VPVCCKPVCCKPICCVPVCSGA SSSCCQQSSRQPACCTTSCCRPS SSVSLLCRPVCRSTCCVPIPSCC APASTCQPSCCRPASCVSLLCRP TCSRLSSACCGLSSGQKSSC
23690	54058	A	23825	1	3097	MDEKRTRLQPEEADVPAYPKV ATVPQSEKKPSKYPLCSADAAV STTPPGSPPPPPPLPEPPVLKVLS SLKPAAPSPATAATTAAAASTA ASSTASSASKTASPLEHILQTLF GKKKSFDPSAREPPGSTAGLPQ EPKTTAEDGVPAPPLLDPIVQQF GQFSKDKALEEEEDDRPYDPEE EYDPERAFDTQLVERGRRHEVE RAPEAAAAEREEVAYDPEDETI LEEAKVTVDDLPNRMCADVRR NSVERPAEPVA
23691	54059	A	23826	67	442	VKFFCLYLQSNEKPMKNFKQG SNNQLLMRSFWLLCGIDYKKPP PPPAPGPESVAPALSGPPPPAHS RGPRAVVRA\PPPPGPRHRSPAE PPPPPGTEPSVATYSIKASKRVS QQDRCHNLMKSQE
23692	54060	A	23827	3	657	GERSRRWGPACGPGAAEKTPP CDAGAAGAAPGAPGHAGNPGL GSGPDYD\GEATCMHLHPDDPC PAGAGCCPGSFEVAFPDAAEK MKKSLHSLKKGCYSRVCDLPL DCPGCDSDSGRQAMFSCIVNFQ LPKEESPIPGSSQEESSGPSHSEC DSVGVDWRGQRVSRKLQAPNH SLVLLVTSLFQETTKSHLNRTN DAVSPRKFKRLGALYWGKVEA
23693	54061	A	23828	141	246	
23694	54062	A	23829	1	609	
23695	54063	A	23830	1619	1752	

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23696	54064	A	23831	54	470	CSTMNPSEMQRIAPPRRQRHRS RAPSAHKMNRMVMSEEQMKL PSTKKAEPPTWAQLKKLTQLA KKK\LENTKVTQTPENMLLAAL KTVSTVSAGVPSSSEESDHRER AMMTTVVLSKRRGKCGEKKEI SDCYCVYVERS
23697	54065	A	23832	213	572	IQWYPYQDTIDFLHRIRKNFFKF HMEPKKSLHCQDNPKPKEQSW MHHTT*LQTMLQGYSNQKRMP PHLGSEERLCPAAPSGR*GAPLP GRCAIFQV*SDSLSAGVPNSSEE TATIENGP
23698	54066	A	23833	296	583	
23699	54067	A	23834	2452	4557	
23700	54068	A	23835	3	266	
23701	54069	A	23836	31	499	ARVTAAVSAAAVAKRVWRDG FDCSGYYSLTTILLVQPTKRP\E GRTYADYES\VNECMEGVCKM YEEHLK\RMNP\NGPSI/THNTTS QLFDFID\DLADLSCLVYRA\DT QTY\QPYN\KDWIKDEDPTVLLS SGKAQQAREIIVVGSHWGGWG GAWDTGV
23702	54070	A	23837	3	323	
23703	54071	A	23838	366	892	PCVYSQFPAGEQCLKLHSPAEA SPPALEASEAQTRKAPECGSGV PEVAGGSCPCLLLCLPRHQAVP TQGPGTYSPCTSHQPHIFPRPAA PHHLGLLQNPHNAASCIQCLYP AGVATTMPRRKAEGDAEGD/K AKVKDEPQRRPAKLSAKPAPPN PEAKPKNAPGVTLSLRGTATRF

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23704	54072	A	23839	201	1412	LWKSRLTFKLAMSRVPSPPPPA EMSSGP\VAESWCYTQIKVVKF\ SYMWDPSITLAFCREEMG\EV\I KSSTFSSGANDKLKWC\LRVNP KG\LDEESKDYLVTFTCYLVSC\ PKSEVRANFKFSILNAKGEETK AMESQR\AYRFVQGKDWGFKK FIRRDFLLDEANGL\LP\DDKLTL FCEVSVVQDSVNISGQNTMNM VKVPECRLADELRGLWENS\RF TDCCLCVAGHEFQAHKAILAA RSPVFSAMFEHEMEESKKNPSL KSMDV\EPEVFKE\MMCFIYTG KAPNLTKMA\NDLLAAADKYA L\ERLKVMCEDALCSNPV/SVEN AAEILIL\ADLH\SADQLKTQAV DFINYHA\GDVLETSGWKSMVL SHP/HNLVAEAYRSLAS\KQCPF LGTPTQNALKQSLKILLCC
23705	54073	A	23840	1	575	FRHRKIIY*NLLKQEDSINVTEM TSIRASVDILIPDPPPKDDEMDT DKQEKKEVPKCGFLPGNEKVL SLLAMVKPEVWTLKEKCIVVIT WIQHLIPKIEDGNDFGVAIQEK VLERVNAVKTKVEAFQTTIS/K MDYRALVHERDEAAYGELRA MVLDLRAFYAELYHIISSNLEKI VNPKGEEKPLMYPTRD
23706	54074	A	23841	1	1092	
23707	54075	A	23842	130	397	EGVHSQVNLFPIKGNQTHVPAS HGTDSALPPTLQMDYRALVHE PD*AAYGELRAMVLDLRAFYA ELYHIISSNLEKIVNPKGEEKPF
23708	54076	A	23843	20	334	VRLPGSTHAGGDRSSMAKPCG VRLSGEARIQVEVLRQNLFQEA \EEFLYRFLPQKIIYLNQLLQEDS LNVADLTSLRAPLDMPIPDPPP KDDEMETDEQEKKEGK

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23709	54077	A	23844	1	898	MKQKVAAEAGRGQILQAKVLP SGTLSRLAEALFGVQTYDQDA YGFLTPSAQSMKVFCCLWKLV CKQLEGDVAQGLAIDGDVKKH SGLEWQVETIQNLVDSYMAIV NKNMQDLMPKTIIHLMINNTKE FIFSELLANLYSRGEQNTLMGE SAEQAQGRNEMRRMHHVLRE APSIIGDIKTTIVSTPTGSPKSSPT TQCRLPAVPPARPGLRSPAPGPL PAASTLGEAPVVPSTPGASPDPL GPPP\QVPSRPSRGPQPQDRMPC GLAGDLTVGFLEPTLQAIIRWS LLLRPPANSPESQS
23710	54078	A	23845	99	429	FSDAAAVARQPSFGKALGAPQP ADTQPTPSMPPRCPGGSETKPK KAAGKDKSSDK\KNKTKKQMK AEKGGKEKQAEVADQETKDLS AENGDTENKESPASDEATEKDT KSD
23711	54079	A	23846	1	390	TWMFIAAVFRIASTWKQPRYFS VGKQDQKRTSRKLQQTCSRGA *WLEGKLTNRKE*HQYQRKGH PRKNTIQRSPTLKTKANIILNGQ KLEAFPLKTGTRQRCPLSPLLFN MVLEVLARSIRQEKEIKVFK
23712	54080	A	23847	522	733	ASAADTQANRVWSGPP/RKLQ QTCS*GS*LLQGKLTNRKDIHT KTPSVHHHHQRPKTLNQQRSK ETKKAIT
23713	54081	A	23848	46	330	
23714	54082	A	23849	1	873	MAEKKDPTKEPEKKHLLAWM NKLLYELDPKYKNDSNTDGSA VVHKIIIACDKPVSPPPSAMIGSF PRPSSEADAGAMLCVQPARTKI LGILGLKATSLQYLRLHTGKPL LPKIDESTKMGRNQPKKAENSK NQNASSPPKDHNSSPVREQNR MQNEFDELTEVGFRRDRSSKR NSVVIKALPRHLINQGRSQEWR LGIGARDSPKTSGRRGKSPAGP NRTTVPEDEQA/GSRPRPIPTRQ ADPRTPPPTRSEKE/AQLSLATD QMCPSLAPLIK*PQES**WKQRI SI*MEHL
23715	54083	A	23850	1075	1350	AIITANVFKFVSIDRGLVCNMEL EGSNCFIDVCSWTSEMKSKGTS RR*KIT*GNSSGSLPRDTQRSGH RNSSLCCERSKYGGSRVDIRRK VF

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23716	54084	A	23851	1	956	MEVLARVFRQEKEMKGIHIGK EEHKLFLFADNMTLCLEKTKDS VKKLVEQPSSFGSVDWLCLSSC SGSTHTPRPADVSPGSLPGPGQ TFGTREPPQAVSTKEASSSNLH APERTVAGLTFTTEQVRALEGV FRHHQYLGPLERNWLAREMQL SEVQIKTWFQNRRMKHKRQM QDSQLNGPLSGSLHGPPAFHSP SSGLANGLQLLCPWAPLPGS/L WLPLGSFWGLRQMDQEALASS WASCCGQPLAYHPPRPGSGAH KLGPALSTGPRGLCALPETGDA FEETPPTTCLPHKRSVQIASDAY PEDSAVLFTSWRHLSP
23717	54085	A	23852	1	846	MEAFDANYTFQSGPSAAGLLV FAGGPLQALCAWVSAVEAAEQ WILQPSSFGSVDWLCLSSCSGST HTPRPADVSPGSLPGPGQTFGT REPPQAVSTKEASSSNLHAPER TVAGLTFTTEQVRALEGVFRHH QYLGPLERNWLAREMQLSEVQ IKTWFQNRRMKHKRQMQDSQ LNGPLMGSFPGAPWLSTHHFLA LAKGLQ\LLCPWA\PLPGSPGCP LGSFWGTP\QMDQEALASSWA GCCG\QPLAYHPPRPGSGIDLPK GTQLSLRLFQDISSTRGDHRSG
23718	54086	A	23853	3	239	
23719	54087	A	23854	10	1154	RRAGFGGVRASGAMGTPPGLQ TDCEALLSRFQETDSVRFEDFT ELWRNMKFGTIFCGRMRNLEK NMFTKEALALAWRYFLPPYTF QIRVGALYLLYGLYNTQLCQPK QKIRVALKDWDEVLKFQQDLV NAQHFDAAYIFRKLRLDRAFHF TAMPKLLSYRMKKKIHRAEVT EEFKDPSDRVMKLITSDVLEEM LNVHDHYQNMKHVISVDKSKP DKALSLIKDDFFDNIKNIVLEHQ QWHKDRKNPSLKSKTNDGEEK MEGNSQETERCERAESLAKIKS KA\FSVVIQASKSRRHRQVKLD SSPLDSASGQGQVKATRKKEK KERLKPAGRKMSLRNKGNVQN IHKEDKPLSLSMPVITEEEENES LSGTEFTASKKRRQH

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23720	54088	A	23855	16	447	VNCDKANCSTTCFNGGTCFYP GKCICPPGLEGEQCEISKCPQPC RNGGKCIGKSKSVCEPGCGAH GTCHEPNKCQCQEGWHGRHCN KRYEASLIHALRP\AGAQLRQH TPSLKKAEERGDPPESN\YIWVE LPTSGNVLSYTKFI
23721	54089	B	23856	103	1989	
23722	54090	A	23857	3	1295	SGRGVSRHMADYLISGGTGYV PEDGLTAQQLFTGAAARDRLT YNNFLILPGFIDFIADKVDLTSA LTWKITLKMPLISSPMDAVTEA DMAIAMALMGGIGFIHHHCTPE FQANEVRKVKKFERGFIMDPV VLSPSHTVG\DVLEGKMRHGFS G\IPITETGTMGSKLDSHKQLLC GAAVGTREDDKYRLDLLTQVG VDVIVLDLSQGNSLYQMAMVY YIKQKYPHLQVIGGNMVTAAQ AKNLIDAGVEGLHVGMGCSSIC ITQEVMAYSWPQGTAVYKVAE YARHFDHGEHGKALALGASTV MMGSLLAATTEVPSKYFFSDG VWLKKYRGMGSLDALEKSSGS QKQYFMEGDKLKIAQGVSSSIQ DKGSIQKFVSYLIAGIQHGCQD TGVCNLSVLLSMMYSGERKFE KWTMLAQIKGGVQGLHSYKK
23723	54091	A	23858	770	1008	LAPSPCVRSKGRKESPDSR/RPL WLRPIAPALGPSGRRGLAPDSR LNPHRSLLGTGNYDVNVIMAA LQGLGLAAVWWDRRR

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23724	54092	A	23859	1	1489	MTRWSSYLLGWTTFLLYSYESS GGMHEECVFPFTYKGSVYFTCT HIHSLSPWCATRAVYNGQWKY CQSEDYPRCIFPFIYRGKAYNSC ISQGSFLGSLWCSVTSVFDEKQ QWKFCETNEYGGNSLRKPCIFP SIYRNNVVSDCMEDESNKLWC PTTENMDKDGKWSFCADTSNL GMGVGPTPRHHRRASTRHSRPP PADPDGGGERPRTADDRQDDA TEDDGTRCRGRQTRTQATNAN ANHKKSNRTKPPPRHKPNKAK RHTKKETPQNT/CGTQDKNPDS GRPKLFRRACITSTGTRGELWT RSREHPAK\QGRRSGKQRLRPW DRMLSPDWHRAQRIAQVWKPE QEDGLSIGFGDQPGPHSDTSSR QQVRRSKATEMHVGGRVDFD DFVELMTPKLLAETAGMIGVQ EMRDAFKEFDTNGDGEITLVEL QQAMQRLLGERLTPREISEVVR EADVNGDGTVDFEGDIDGAWG RHGTQGPHWPWGLGDVRGEPL
23725	54093	A	23860	283	490	GDIWMGTQPKPYHS\PPGPSPN\ PCPPHFKNQSMPSPKSPPKVFNS FPALTQKVHTSKVSSETRQVPS HL
23726	54094	C	23861	82	222	
23727	54095	A	23862	27	454	VDGRIAGEITRRGSRARPRPGPQ CPPGRPGTAMIKAILIFNNHGKP RLSKFYQPYSEDTQQQIIRETFH LVSKRDENVCNFLEGG/LVFVE TLDKCFENVCELDLIFHVDKVH NILAEMVMGGMVLETNMNEIV TQIDAQNKL
23728	54096	A	23863	1	403	RGSRARPRPGPQCPPGRPGTAM IKAILIFNNHGKPRLSKFYQPYS EDTQQQIFRETF/HLGSKKEEKG WNFLKGGLLIGGSDNKLDYRH YATVYFVF\GGDFSKRELGFLN LIQEFGEPLDKCFEKVWELDLIF
23729	54097	A	23864	215	599	

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23730	54098	A	23865	2	683	GRIAGEITRRGSRARPRPGPQCP PGRPGTAMIKAILIFNNHGKPRL SKFYQPYSEDTQQQIIRETFHLV SKRDENVCNFLEGGLLIGGSDN K\LIYRHYAT\LYFVFCVDSSE\S ELGILDLIQVFV\ETLDKCFGNV\ CEL\DLIFHV\DKV\HNIL\AEMV MGGMVLETNMNEIVTPIDAQN KLEKSEAGLAGAPA\RA\VSAV KNMNLP\EIPRNINIG\DISIK\VP
23731	54099	B	23866	94	726	
23732	54100	B	23867	94	1146	
23733	54101	B	23868	1	360	
23734	54102	B	23869	1	1371	
23735	54103	B	23870	1	639	
23736	54104	B	23871	280	2391	
23737	54105	A	23872	3	244	
23738	54106	B	23873	103	285	
23739	54107	A	23874	70	378	MPLRILLMHGEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE\ EEEEEEEEEEEEEEEEEILQIKTK HYTTKEQEKEEQGIKLVQGSNN D/QEQEKKGEYKNTGEKNSMK
23740	54108	A	23875	5	156	RKKGGG/EREEEGEGEEEEEEE EEEEEEEEEEEEEEEEEEEVVL LTPGTGAEDFKKH

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23741	54109	A	23876	1	1808	MEVLSIDNLAGHKVFYQKESHS WKQQKQDLMSGKRLSAANPLP ALLLPVLWTTGQAPSPGPGGDP ILQLWDDAQQMAGSPRTKKKG CTRNSQAARLSFQSRGGQGSLT EKMIFEQRFGGGKGESRKDAIA IIVVDIVTLQPCRTVEWVPTRPF RSLQGHFQGGLRRQQMMVME GVWVLSCAMDLTSPRDCLPFC VSLPVLLLSAPLCSCSTAGGSPV TSPHHFPVEGGLGRVRRCYINE PVVTTLGWESVCWVSFWLLLR IRYSTSGQAACHAESQELNPRG FGCLGHRNVTWVKCLLPALQP EGSVPFLELLEPFIFASASKTFV AANLVTWVACFLLVQAAFQLS EYRQGVGIPVADRTGDAPTLGL SYEADVAEGHGFFLDQESVIQII PEPLPQFYLCLLDAELTGVQGE PALPSMQIFSSPEAATGVHNDR GAEHFPVSRQPSAELGLRPMQA SQERKINFPGPSPGFPPKRQNKT LSRREKKEEEKEEKEEEEEEE/E GEEEKEKEEEEEKEEEEEEEEEE GGEEEEEEEEEEEEEEEEEEEE KWLYQYDPEDKAQSKQWLSR GGSGPVKAKADWWRAKEIHSL QPRQVIPGIPSM
23742	54110	A	23877	459	636	IPGGSNGLEAEGPPPPPLPVAAV LA/AGSGGLAVASCAFTICALR WPGVPCSRVPIWTPS
23743	54111	C	23878	183	254	
23744	54112	A	23879	103	335	LGSGDLPWEINPLSSCSLLHEK DPPTTSGPQTDRPKEHLINFKSG ACYTCRKSGH*AKECLQPGIPIK PHLICVGPH
23745	54113	A	23880	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPKEHLTNFKSAA ED
23746	54114	C	23881	80	106	
23747	54115	A	23882	317	427	
23748	54116	A	23883	353	511	
23749	54117	B	23884	1	320	
23750	54118	A	23885	1	624	
23751	54119	A	23886	224	355	
23752	54120	A	23887	872	1003	
23753	54121	A	23888	1	603	
23754	54122	A	23889	2	214	
23755	54123	A	23890	459	601	DVDRHVRGSNFHHNEIRSLAAT PRAPGTLAQ/GLTDSFPDLLGLA AED

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23756	54124	A	23891	2	267	QWDGWGARKGMEWEDDLPLE FGRPTASLLSDRPQPNSSRGSDV PFL\PPSLPCHSSACLAATPRAPG TLAQGSLTDSFPDLLGLAAED
23757	54125	A	23892	72	299	
23758	54126	B	23893	1	1470	
23759	54127	A	23894	134	1276	
23760	54128	A	23895	2	847	PPPPRVLRTGGGASLTAQAPGT PRRPQEGEPVTPGRSLGLRSSCQ ASVSLLLPVIVACASLEPGRGR AFRDEGAWNTRVSAAVISSQA QLLSSILVNSRRLSFSAHHTAFG TVALGEYAFRMF\RLSARLFG\E VT\RPTNS/RSLMKVVKLFSE/IW PLAKKKETYDW\YPNHHTY/AL ELMAGRLRFLGTLTEDEAFRDF MGMEAKTDLKEAFVGKGGNP KEREKGKRAAKKGNSCLVPSR RGDFLSSVAERRKLHLLSFPHIG GDVIFLNGSLFGRNTSHLLGEI
23761	54129	A	23898	3	1224	MRRNKPRQRGVREARPAGGAG PGWRGARCSGAGEGGGGERRG SPPAALALAPASGPRRNFPPDA RCLIYQQIHQGAFLLAGSASLS AVTGVPEGEARFTEDYCPEEK MFGFHKPKMYRSIEGC\CISGA KSSSSRFTDSKRYEK\DFQ\SCFG LHETRSGDI\CNACVLLVKRWK KLPAGSKK\NWNHVVDARAGP S\LKTTFEPK\KVKTLSG\NRIK\S TQISKLQKEFK\RSNSDAHSTTS SASPAQSPCYSNQSDDGSDTEM ASGSNRTPVFSFLDLTYWKRQK ICCGIIYKGRFGEVLIDTHLFKP CCSNKKAAAEKPEEQGPEPLPIS TQEWTECPDLSLVVSWRPPLSS LPAGCSLHGLAADWTTDMITV TTSKCREPSCQQEGSFQRRKAF PKRLPKMAEVQVLVL
23762	54130	A	23900	69	355	
23763	54131	A	23901	316	830	VSLSQTLHPPMTLQLSRYSRGW GLSSDRPRGAKAKVPSCFGTAP R/GPEAAPRLLAHHLVPAGRGS/ ARAPAPGWRLGSP\GAGRKGR DFRLPASGLAVSGEWDPIPWGY VGEVGGCSCQWFSPGVQQKRR RRKVWLGQPQDLPGPSALADK GPALAKADGQRVNVASVGLQP

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23764	54132	A	23902	1	1044	MSYKVTQEISKELRWISAVLVT WDLRGETGTRVCIAMGVSRMQ YSIMAKIVGSGNNLELNPAADK LDNLGAQCGLASVKVSARAAP PFAPATLVALLEARAAELPLPPP PGVSLRCVEAPDVRGRGRGGG EGSGVTRLLLPPPPPSGASFLQR GRPVTPALFQAGWGRAADRPG PADLAGGAGGRSGGRRMLPRS PGAALRDRSALEDGIVEGYGPL GEPEEGSRSSFLESKVAFNYCN KVAPLDFGNEAVEQCHTMSDR KAVIKNADMSEDMQQDAVDC A\TQAMEKYNIEKDIAAYIKKEF DKKYNPTWHCIVGRNF\GSY\V PHTEDKHFIYFYLGQVAIL\LFK
23765	54133	A	23903	33	427	
23766	54134	A	23904	72	777	EWKQAGEGGGGQRRGSPPAVL ALAPASCPRREMSYLPTNPPGSI LICWLGVSLSSHRSAGGGSAIY G\SYYPEEKMFVFHKPKMYRSI EGYCICRAKSSSSRFTDSKRYEK DFQSCFGLHETRSGDICNACVL LVKRWKKLPAGSKKKTGIMCN QSDDGSDTEMASGSNRTPVFSF LDLTYWKRQKICCGINYKGRF GEVLIDTHPFKPCCSNKKAAAE KPEEQGPEPLPISTQEW
23767	54135	A	23905	234	989	PKTSDQAYYCPEEKMFGFHKP KMY\RSIEGC\CISGAKSSSSRFT DSKRYEK\DFQ\SCFGLHETR\SG DI\CNACVLLVKRWKKLPAGSK K\NWNHVVDARAGPSLKTTLK PKKVKTL\SGNRIK\STQISKLQK /ENFKR\HNS\DAHSTHPQVPSP\ AQSPLFTVNQFRWTGSDTGVG FPGSNRNHPVFSFLDL\TYWKR QKICCGI\IYKGRFGEVLIDTHLF KPCCSNKKA\AAEKPEEQGPEP LPISTQEWVTEVFM
23768	54136	A	23906	3	1059	

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23769	54137	A	23907	1	1697	MRPCALCWRSAVTAAPERAVL ESRGGAPDTPRRLHSFTQTRSLS PQAHAGPHTRLHPRQGHAHMR GGGRVTDTRRHIPNADVPRYK LTCTGGVTTFVALYDYESRTET DLSFKKGER\LQIVNNTKGDW WLAHSLSTGQTGYIPSNYVAPS DSIQAEEWYFGKITRRESERLLL NAENPRGTFLVRESETTKGAYC LSVSDFDNAKGLNVKHYKIRK LDSGGFYITSRTQFNSLQQLVA YYSMSHCPPFSAAGWYGGGCP EEPQKHADGLCHRLTTVCPTSK PQTQGLAKDAWEIPRESLRLEV KLGQGCFGEVWMGTWNGTTR VAIKTLKPGTMSPEAFLQEAQV MKKLRHEKLVQLYAVVSEEPI YIVTEYMSKGSLLDFLKGETGK YLRLPQLVDMAAQIASGMAYV ERMNYVHRDLRAANILVGENL VCKVADFGLARLIEDNEYTAR QGAKFPIKWTAPEAALYGRFTI KSDVWSFGILLTELTTKGRVPY PGMVNREVLDQVERGYRMPCP PECPESLHDLMCQCWRKEPEER PTFEYLQAFLEDYFTSTEPQYQP
23770	54138	A	23908	1	736	MDPGAALQRRAGGGGGLGAG SPALSGGQGRRRKQPPRPADFK LQVIIIGSRGVGKTSLMERFTDD TFCEACKSTVGV\DFKIKTVELR GKKIRLQIWDTAGQERFSSITSA YYRSAKGMILVYDITKKETFDD LPKWMKMIDKYA\SEDADLLL VGNKLDCETDREITRQQGEKFA QQITGMRFCEASAKDNFNVDEI FLKLVDDILKKMPLDILRNELS NSILSLQPEPEIPPELPPPRPHVR
23771	54139	B	23909	84	441	
23772	54140	A	23910	6	254	
23773	54141	A	23911	1	230	
23774	54142	A	23912	3	187	
23775	54143	A	23913	3	143	
23776	54144	A	23914	3	481	
23777	54145	A	23915	1	711	
23778	54146	A	23916	55	381	

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23779	54147	A	23917	240	875	GLSAESTPTSIMSMTLGYWDIR GLAHAIRLLLEYTDSSYEEKKY TMGDAPDYDRSQWL\NEKFKL GL\DFPNLPY\LIDGAHKMHPEA TPFLCYI\ARKHNLLLGETGRRE KISSWDIL\ENQAMDVSNQLAR VCYSPDFEKLKPEYLEELPTMM QHFSQFLGKRPWFVGDKITFVD FLAYDVLDLHRIFEPNCLDAFP NLKDFISRFEVSCGIM
23780	54148	A	23918	64	774	CLSAESAPTSTMPMTLGYWDIR GLAHAIRLLLEYTD\SSYEEKKY TMGDAP\DYDRSQWLNEKFKL GL\DFPNLPYLIDGAHKITQSNA ILRYI\ARK\HNLCGGDRRREKIS CWDILENQVM\DNHMELVRLC YDPDFEKLKPKYLEELPEKLKL YSEFLGKRPCFLG\DKITFVDFL VY\DVLETK\QVFEPK\CLDAF\Q NLKDFISRFEGL\EKISAYMKSS\ RFL\QELVFSKMAVWGNK
23781	54149	A	23919	163	317	LSPNNYYRKLPQKVKLE*RYHR LALFSFPTKKLTPEKVSLCCRFL EMGYIF
23782	54150	A	23920	62	255	VRLTAQKSLGPLTSTHSLWGSA \RARHREPVGSVCGCDPCEQLL LLVSQLRAPGVDSAAAGRPV
23783	54151	A	23921	173	467	KSRFCFFGVVLKLPKKLHIR*WI GATL*NQP*TIFQTDGDCSHQSL GPLPACDLWDQLHLRSKQGGS VCGCDPCEQLLLLVSQLRAPGV DSAAAGRPV
23784	54152	A	23922	35	548	PRSCPSLSPGLSCLLQ/RLVNYQI SIKCSNQFKLEVCLLNAENKVV DNQAGTQGQ\LPAVGQARWGS GCRGAHTW\PLAVIGAADCTG QRGWEGV*AFPGLTEPVSSLFC GQDGD/CSPHSM*VLSHVVLWL LNGLC\SLVLGSVCGCDPCEQL LLLVSQLRAPGVDSAAAGHPV
23785	54153	A	23923	1	599	MSPAGLVNYQISVKCSNQFKLE VCLLNAENKVVDNQAGTQGQL KGRPDGAQAV/VGAHTWRFGC RRCG*LHRSHWGL*LLHTPCGR PHCARHREPVAHSLLCSRAISGS EPHFWQCSVQ*PQLCVPGRVAT PLGELDSGDGDCSHQSLGPLPA CDLWDQLHLRSRQGGSVCGCD PCEQLLLLVSQLRAPGVDSAAA GRPV
23786	54154	A	23924	290	528	

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23787	54155	A	23925	274	571	KSRFCFFGVVLKLPKKLHIR*WI GATL*NQP*TIFQTDGDCSHQSL GPLPACDLWDQLHLHSRQGGS VCGCDPCEQLLLL\VSQLQAPAI DSAAAGRPV
23788	54156	B	23926	204	410	
23789	54157	A	23927	29	330	YLGVELVKSAYPFFQIHLSFPSC MWLCGLFLLFYIDFLTLMCGD KPLICKKHQLSASTCA/CTIC*G ALTLLMEIEQGPCDLSCASREV STARSLAELFSGP
23790	54158	A	23928	259	699	ETSHQVMDRSNPVKPALDYFL NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGQLKV LGANLWWPYLMHEHPAYLYS WEDGDCSHQSLGPLPACDLWD QLHLRSRQGGSVCGCDPCEQLL LLVSQLRAPG\VDSAAAGHPV
23791	54159	A	23929	245	695	
23792	54160	A	23930	302	745	ETSHQVMDRSNPVKPALDYFS NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGQLKV LGANLWWPYLMHEHPAYLYS WEDGDCFTPKALDPLPACDLW DQL\HLRSRQGGSVCGCDPCEQ LLLLVSQLRAPGVDSAAAGRPV
23793	54161	A	23931	2	293	VFCHTDLRKNLTVDEGTMKVE VLPALTDNYMYLVIDDETKEA AIVDPVQPQKVVDAARKHG\V KLTTVLTTHHHWDHAGGNEKL VKLESADLGIRLF
23794	54162	A	23932	1	441	
23795	54163	A	23933	1	630	
23796	54164	A	23934	3	265	
23797	54165	A	23935	3	1062	SAVQPGPVMVVGRGCSRRSLA ALGAACARRGLGPALLGVFCH TDLRKNLTVDEGTMKVEVLPA LTDNYMYLVIDDETKEAAIVDP VQPQKVVDAARKHGVKLTTVL TTHHHWDHAGGNEKLVKLESG LKVYGGDDRIGALTHKITHLST LQVG\SLNVKCLATP\CHTSGHI CYFVSKLGG\SEPFVVFTGDTLF V\AGCGEVLMKGLRDEMCKAL LEV\LGRLPPDTVGSASLRAGR VYCG\HEYTIKQTSKFAR\HVET GNA\AIREK\LPWA\KEKYSIGEP TVPST\LAE\EFTYNP\FIKVREER RCKQH\AGETDPVTTMRPVRRE KDQ\FK\MPRDLRPPLHLQQDL GIKALLDRLF

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23798	54166	A	23936	107	750	SHLWSPVSEPLQACSFC/VIRDK YRYFACLMRARSEEHTNEKDM MKAIRLLKEAEEEFWYHQHPQ PCIFPDSPRGTSYVTHECYKVPE WCLDDWHPSEKAMYPDYFAK RKQWKKLRRESWKREVKQLQ EETPPAGKEECKLHEGMNYVV LTCIPGAIKQYLACSRYSKTPGP RDSCWEVQSDNQCWWWLDSG AHGLVTSFKGVMMTVEATTM AAVF
23799	54167	A	23937	3	718	PASTISCSVTRSRRAVSRLSARP GKVSAVMASLASGPYLTHQQK VLRLYKRALRHLESWCVQRDK YRYFACLMRARFEEHKNEQDM AKATQLLKEAEEE\FWYRQHPQ P\YIFPDSPWGHPPYERY\DCYK VP\EWCLDDWHPSEK\AMYP\D YFAKREQWKKLRRESWEREV\ KQL\QEET\PPGGSF*LEALPPGP KRKVILPPLWW\YIVTRP\RERP MLERERPHLSCLQVKYVTEHG
23800	54168	A	23938	269	488	TDGVIFIGLSWSPRRCGLGIQRD AERIFFALDQASCGFTIHPHIDA AETPRGLT\MHLCRRCQRGQSQ AEKLP
23801	54169	A	23939	1	1560	MVHLGAPVMALNLQGKHLCD STASSLLPRRRESNSDDTARED ARQKRPANTDMRTQELQTRET GQGTARETEVATPLSGPSAGDS PPAASEMSCGQLVLALLLLFFL LVWNTGTKSGSGRVARLAQLA HDCDGGLALGLCYAVLDQRSV VQATPQAPKPGPVQPLTVQGL QPVHVAQESSGNEITARRQSAR SRPRGDRTAPSRRVTRRPKHAP ERAPIQQGNIVTVRAPTARKKW RPAVGTPTGAHPVCTAKGTGG RPTPTQAHTRYTERDPIRNSAEL TGSRPCTGRERSGVEACKAAV HNLL\AQTGSSGLIINYPLDD\Q DAIAVEAACTNVPALFLDVSDQ TPINSIIFSHEDDVWRTPLVAPT NLNTRSSQPARHHRAGAVRRH HMTVARSATAHARLRRHAKPQ GRERIKPSGAREGSEPLGGESGI RTPRGRERDPNPSGAKAGSEPG RIPETLPRCKGETEAKCWARGN FHTAQGSWPRGGRSRWEPLEA PALSQQAHGGELPLPAAARSHR
23802	54170	B	23940	98	229	

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23803	54171	A	23941	1	256	
23804	54172	A	23942	289	433	VLWSCAAEDFDWLVYRPIGSA LSCRLIGPWAIGMWETGFP*VL WSCAAEDFDWLVYRPIGSALSC RLIGPWAIGMWETGFPLLSSVS LS
23805	54173	A	23943	450	1260	LCACVVGGEKRSGPRIGCAGA GKDPFWRAVGVAQKAAAVVA CGAASPYRNRADVSVSDHSQS RGPGGLSLSGGTVCDMGKKTK RTADSSSSEDEEEYVVEKVLDR RVVKGQVEYLLKWKGFSEEHN TWEPEKNL\DCPELISEFMKKY KKMKEGGN\NKVREKSESSKR KSNFSDSAEDIKCKKKREQSND IARGFERGLEPEKIIGATDSCGD LMFLMKWKDTDEADLVLAKE ANVKCPQIVIAFYEERLTWHAF\ PEDAENKEKETAKS
23806	54174	A	23944	3	267	AMVGGGGVGGGLLENANPLIY QRSGERPVTAGEEDEQVPDSID AREIFDLIRS*AWPLTPQPAYW YPGPSSCQGCYRCFLESLTMRN
23807	54175	A	23945	1	942	
23808	54176	A	23946	3	470	AMVGGGGVGGGLLENANPLIY QRSGERPVTAGEEDEQVPDSID AREIFDIRRCWARAGSGGLRW GEQ*YRAAGGAASQQGVPGRG F*VGKGAESLFLHFPQ\LIRFLN DP\EHSLTLEELNVVEQVRVQV SDPESTVAVAFTPTISHWSMGT
23809	54177	A	23947	2	604	ARSHRISGGGSAMVGGGGVGG GLLENANPLIYQRFGE\RPVTAG EEDEQVPDSIDAREVF\DLIRSH QMTPEHP\LTLEELNVV\EQVR\ VQVSDP\ESTVAVGFPKPTHSGT CRHGPPLIGLS\IKVK\LLRSLPS AFSRWDVAHLLPGDPLPQEHA VEQATLQIKEAGWATALGRTH HLLEVVN\QCLSSPAPGTWAFV
23810	54178	A	23948	1	1002	

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23811	54179	A	23949	89	2587	STSRDRRLSKRSRTTMAAQPRG GDYRGSFLLSILLGTPWEAWAG RILYSVSEETDKGSFVGDIAKDL GLEPRELAERGVRIISRGRTQLF ALNQRSGSLVTAGRIDREEICA QSARCLVNFNILMEDKMNLYPI DVEIIDINDNVPRFLTEEINVKI MENTAPGVRFPLSEAGDPDVG TNSLQSYQLSPNRHFSLAVQSG DDETKYPELVLERVLDREEERV HHLVLTASDGGDPPRSSTAHIQ VTVVDVNDHTPVFSLPQYQVT VPENVPVGTRLLTVHAIDLDEG VNGEVTYSFRKITPKLPKMFHL NSLTGEISTLEGLDYEETAFYE MEVQAQDGPGSLTKAKVLITV LDVNDNAPEVTMTSLSSSIPED TPLGTVIALFYLQDRDSGKNGE VTCTIPENLPFKLEKSIDNYYRL K\TTKNLDRETLSLYNITLKATD GGTPPLSRETHIFMQVADTNDN PPTFPHSSYSVYIAENNPRGASI FLVTAQDHDSEDNAQITYSLAE DTIQGAPVSSYVSINSDTGVLY ALQSFDYEQLRELQLRVTAHDS GDPPLSSNMSLSLFVLDQNDNP PEILYPALPTDGSTGMELAPRSA EPGYLVTKVVAVDKDSGQNA WLSYLLLKASEPGLFAVGLYTG EVRTARALLDRDALKQSLVVA VQDHGQPPLSATVTLTVAVAD SIPEVLADLGSLEPSDGPYNYDL
23812	54180	B	23950	165	335	
23813	54181	A	23951	217	859	GSAMAQQRALPQSKETLLQSY NKRLKDDIKSIMDNFTEIIKTAK IEDETQVSRAT\QGEQDNYEMH VRAANIVRAGESLMKLVSDLK QFLIL\NDFPSVNEAIDQRNQQL RTLQEECDRKLITLRDEISIDLY ELEEEYYSSSPGPSLVSQQLSEQ QLLSSAWTAWPKVTLSSLAPGP QYSVNGPAAIIAHPGTCASAGIS SSLLPEPVLLVPVF
23814	54182	A	23952	1	1263	

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23815	54183	A	23953	70	2530	PGVSRLVSKLRRARGMGSGAG ELGRAERLPELFLFLLTLFCPAL CEQIRYRIPEEMPKGSVVGNLA TDLGFSVQELPTRKLRVSSEKP YFTVSAESAELLVSSRLYREEIC GKKPACALEFEAVAENPLNFY HVNVEIEDINDHTPKFTQNSFEL QISESAQPGTRFILGSAHDADIG SNTLQNYQLSPSDHFSLINKEKS DGSKYPEMVLKTPLDREKQKS YHLTLTALDFGAPPLSSTAQIH VLVTDANDNAPVFSQDVYRVS LSENVYPGTTVLQVTATDQDE GVNAEITFSFSEASQITQFDLNS NTGEITVLNTLDFEEVKEYSIVL EARDGGGMIAQCTVEVEVIDE NDNAPEVIFQSLPNLIMEDAEL GTHIALLKVRDKDSRHNGEVT CKLEGDVPFKILTSSRNTYKLV TDAVLDREQNPEYNITVTATDR GKPPLSSSSSITLHIGDVNDNAP VFSQSSYIVHVAENNPPGASISQ VRASDPDLGPNGQVSYCIMAS DLEQRELSSYVSISAESGVVFA QRAFDHEQLRAFELTLQARDQ GSPALSANVSLRVLVDDRNDN APRVLYPALGPDGSALFDMVP HAAEPGYLVTKVVAVDADSGH NAWLSYHVLQASEPGLFSLGLR TGEVRTARALGDRDAVRQRLL VAVRDGGQPPLSATATLHLVF ADSLQEVLPDITDRPDPSDLQA
23816	54184	C	23954	75	149	
23817	54185	A	23955	442	618	CQRLRSWVSQPFSFSFFPSFPTF* NILCLFVYLEVEFPSCCPGWSN NWAKSSGKALEAN
23818	54186	A	23956	1	245	

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23819	54187	A	23957	30	1079	APCASFLTPLAAASVGKVWLG LRGAAPMASVLSYESLVHAVA GAVGSVTAMT\VVFPLDTASIF DFSVDF\KRKSKTTHMVVLEIIK EEGLLAPYRGWFPVISSLCCSNF VYFYTFNSLKALWVKGQHSTT GKDLVVGFVAGVVNVLLTTPL WVVNTRLKLQGAQFRNEDIVP TNYKGIIDAFHQIIRDEGISALW NGTFPSLLLVFNPAIQFMFYEGL KRQLLTFAFQLSSLDVFIIGAVA KAIATTVTYPLQTVPLFPQFGR HRLNPENRTLGSLRNILYLLLQI FRTPSEREPFYTSVTLSVLSSVA YPMMPLSNITSAYRIGVLEKGG GSGKSDNSDDDDDNDDGGV
23820	54188	A	23958	1375	2451	VPRVPFAINVLTHSRQRYRRNL RFYADDPTIRV/GGPTYHWVRE\ AEEERVVDNRMHDRFCELRTA AGHPVEGGRPLVIKGITHPAET ALQRFKFLMYQVVASDLDGTL LSPDHTLSPYAKETLKLLTARGI NFVFATGRHHVDVGQIRDNLEI KSYMITSNGARVHDLDGNLIFA HNLDRDIASDLFGVVNDNPDIIT NVYRDDEWFMNRHRPEEMRFF KEAVFQYALYEPGLLEPEGETK ALLTPGKLKNFLVEKMRTLGT AACPPYHIAFVIGGTSAETNLKT VKLASAHYYDELPTEGNEHGQ GSAMSSWNRNCWKRPRNSVLA RSLAVNTSRTTFALSVCHVTAH PARSAWASPVR
23821	54189	B	23959	1	1386	
23822	54190	A	23960	1375	1609	VPRVPFAINVLTHSRQRYRRNL RFYADDPTIRV/GGPTYHWVRE S\EEERVVDNRMHDRFCELRTA AGHPVEGGRPLVIK
23823	54191	A	23961	433	741	
23824	54192	A	23962	12	224	
23825	54193	A	23963	3	2053	

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23826	54194	A	23964	1	2408	MGGADIAGPRREHNAKHPTVG LGSAAQTTCLPGPKQKGDPTRH QPVDKRNDVGPRQHFWCWRV EIHKEKRMKTGPLNESELEWLD DILTKYNTDHAILDVAELDGLL TAVLSSPQEIEPEQWLVAVWG GADYVPRWASEKEMTRFMNL AFQHMADTAERLNEFPEQFEPL FGLREVDGSELTIVVPPGGRTA TNALSCGSLFGEETSPRGPSADS TSQSIGGGSPHDCAKGIALVAA NGGDIRDYEGVDRSAKPQLPMI AINTTAGTASEMTRFCIITDEAR HIKMAIVDKHVTPLLSVNDSSL MIGMPKSLTAATGMDALTHAI EAYVSIAATPITDACALKAVTM IAGISTFFASSRMALMQASAPSA SFLPVTFTPIAAAQSRRRAAAT GYRDRWLCHGDVLLQICANTQ DTVIHALRDIIKHNSCPDDCSVQ HDAVIDDGCDFIDYLGGSETVV ALNTPRADDYHPVMVLCAKTD KAHRNVIHTSKLCFITLTPEISQ RSHGKSSKRVFSCFPVFLLLKH RRIVAQKYAELAYDLFHLGFD VLIIDHRGQGRSGRLLADPHLG HVNRFNDYVDDLAAFWQQEV QPGPWRKRYILAHSMGGAISTL FLQRHPGVCD\AIALTAPMFGIV IRMPSFMARQILNWAEAHPRFR DGYAIGTGRWRALPFAINVLTH SRQRYRRNLRFYADDPTIRVGG
23827	54195	B	23965	1	3357	
23828	54196	A	23966	14682	14931	EIGPGPRPLPSPLP*ATSTSVLAA SGRPERTR\HAGIKIVLEDIFTL WRQVETKVRAKIRKMKVTTKV NRHDKINGKRKTAKEQSPLLQE SLFATGDVSHNLLRALDVGLLA NLSALAELDISNNKISTLEEGIF ANLFNLSEINLSGNPFECDCGL AWLPRWAEEQQVRV/AAARGS HVCWAWLPGWPASAWHPLAG QWLW*GVCRLPP*QQLRHRGS SVLFSCPRRPA/CSQRPAAPSAS PPARASQPSPSRA

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23829	54197	A	23967	1	714	MVKLSIVLTPRFLSHDQGQLTK ELQQHVKSVTCPCEYLRKVINT LADHRHRGTDFGGSPWLLIITV FLRSYKFAISLCTSYLCVSFLKTI FPSQNGHDGSTDVQQRARRSN RRRQEGIKIVLEDIFTLWRQVET KVRAKICKMKVTTKVNRHDKI NGKRKTAKEHLRKLSMKEREH GEKERQVSEAEENGKLDMKEI HTY/MITPSARKPLCNRVRMAA AEHRHSSGLPYWPYLTAETL
23830	54198	A	23968	111	216	ALLFPISTWSTPLGTQQAPQCV* PTPMPMRPVPS
23831	54199	A	23969	1	4710	
23832	54200	A	23970	3544	3723	RSHRSPPRCPPSRAPAPRRSAAA PPRR*PPRAPAAPRPGPP/CMAR PPPARPTAGSRVPPL
23833	54201	A	23971	3	1119	EFGTSHRHRGTDFGGSPWLLIIT VFLRSYKFAISLCTTYLWVINTL ADHRHRGTDFGGSPWLLIITVF LRSYKFAISLCTTYLC\VSFLKTI FPSQNGHDGSTDVQQRARRSN CRRQEGIKIVL\EDIFTLWRQVE TKVRAKIRKMKVTTK\ATRLTK IKERRKTAQDHWRKLSMKERE HREEERQVSEAEENGKLDMKEI HTYMEMFQRAQALR\RRAED\Y YRCKITPSARKPLCNRVRMAAA EHRHSSGLPYWPYLTAETLKNR MGHQPPPPTQQHSIIDNSLSLKT PPECLLTPLPPSALPSADDNLKT PAECLLYPLPPSADDNLKTPPEC LLTPLPPSAPPSADDNLKTPPKC VCSLPFHPQRMIISRN
23834	54202	A	23972	1	1149	

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23835	54203	A	23973	93	1165	HRRSAAEAPAAAVMPFPFGKS HKSPADIVKNLKESMAVLEKQ DISDKKAEKATEEVSKNLVAM KEILYGTNEKDPQTEAGAQLAQ ELYNSGLLITLVADLQLIDFEGK KDVAQIFNNILRRQIGT\RTPTV EYICTQ\QNI\LFMLLKGYESP\EI ALN\CGIMLRECIRHEPLGKIIL WSEQFYDFFRYVEMSTFDIASD A\FATFKGLLTRHKLLSAEFLEQ HYDRFFSEYEKLLHSENYVTKR QSLKLLGELLLDRHNFTIMTKY ISKPV\NLK\LMMNLLRDKSRNI QFEAFHVFKA\FVANPNKTQPIL DILLKNQAKLIEFLSKFQNDRTE DEQFNDEKTYLVKQIRDLKRPA QQEA
23836	54204	A	23974	3	158	
23837	54205	A	23975	3	1071	GVRASGRAVPRAVFAGMKRPC EETTSESDMDETIDVGSENNYS GQSTSS\VIRLNSPTTTSQIMAR KKRRGIIEKR\RRDRINNSLSELR RLVPTAFEKQGSAKLEKAEILQ MTVDHLKMLQATGGKGYFD\A HALAMDFMSIGF\RECLTEAAR YLSSVEGLDSSDPLRVRLVSHL STCATQREAAAMTSSMAHHHH PLHPHHWAAAFHHLPAALLQP NGLHASESTPCRLSTTSEVPPAH GSALLTATFAHADSALRMP\ST GSVAPCVPLLSTSLLSLSATV\H AAAATATAAAHSFPLSFAGAFP MLPPNAAAAVAAATAISPPLSV SATSSPQQTSSGTNNKPYRPWG TEVGAF

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23838	54206	A	23976	1	1416	MPGNLTRKESSSPLTDRHCHTS SQFSHRFNAISPFPPAELGCDHV ASAAADPLGVPGVATQWAGGL SAALAAPRRPHSCRRLQVLGAL GILKSAGRVNFRCFGPLSIRGKP KTPLWEQEKPKLQTGSAGSQQ KRVMLKPSRGADRVLGRGSQR PAETDRETTDLRQRKRMKEGK ERTLRAARGETRRSNGNLARQ TVPEGCRSQTQALQVVRNART PPCIPNLDRPPEACSSGSTGGM MPLRVAPSPVASGESSHLSSGR GDRGLVRCKVEELRFQPVAFPE FIPPPTSPRADSESGDWCCTVLA NPSKTGSGGWEQRKTEC\PQGR TQNPQQRGS/RNLVLLTAGQES TPRRSQLTRSPAAERRTEEQGE DRKNRALGCNLFPRVPRHARD SQRALRASTQAPKKSTFAFPGI HSGAVCSKRRICGVQGEPFPLPF ASQCSSCLKILPSPGPTKELTSY LLHSGCGFLDKLRV
23839	54207	A	23977	3	139	
23840	54208	A	23978	141	734	GSQLRRPAFGVRVALEESKGLI RKDSCRGRACAGANACARRRR PPTMSGAAWRGTPLALVRSSRT RGVWAWQWSATRSPSDSCFPG VARDKEDGEPKTKHLREEEEE GEKHRELRLRNYVPEDEDLKK RRVPQAKPVAVEEKVKEQLEA A\SPEPVIEEVDLANLAPRKPDW DLKRDVAKKLEKLKKRTQRAI GRLDP
23841	54209	A	23979	3	585	GTVGGVCGPRRSSSASPQEQDQ DRRKDWGHVELLEVLQARALF TAVPLSEEDRATVLKAVHKVK PTFSLPLQLPPPVNTSKLLRDVY AKDGRVSYPKLHLPLKTLQCLF EKQLHVELASRMCVVSVEKPT LPSKEVTHARKT\LKTLRDQWE KALCRELRETKNRLERQVYEG RFSLYPFLCLLDECEVVRMLLQ

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23842	54210	A	23980	1	3778	MRRRGPVGWPGAACVMSALC WGRGAAGLKRALRPCGRPGLP GKEGTAGGVCGPRRSSSASPQE QDQDRRKDWGHVELLEVLQA RVRQLQAESVSEVVVNRVDVA RLPECGSGDGSLQPPRKVQMG AKDATPVPCGRWAKILEKDKR TQQMRMQRLKAKLQMPFQSG EFKALTRRLQVEPRLLSKQ\MG GCLEDCTRQAPESPWEEQLARL LQEAPGKLSLDVEQAPSGQHSQ AQLSGQQQRLLAFFKCCLLTDQ
23843	54211	A	23981	101	805	HMYTSMKPSSQPRSWISTPHPK ACSSLSFPLSLDNWMNINLREVI CTSRDGDKFWRMPECYIRGSTI KYLRIPDEIIDMVKEEVVAKPR GRGGLQQQKQQKGRGMGGAG RVGSPLSSG\VPGAGRQPHVAS LLLGVALAALPRRLPNLPGPPS CPLAMNRGPGRGAPRHGTQPSS QCASWRSSGHIKSPPQAPVSPM RGNGGAHLSRPLATTLGTLRGS IQSQGRPPPPEMMNWH
23844	54212	A	23982	133	1069	RIAWGQDRSCLQGGPFATYVP GLILCSLQGWYGVQAGQDLQG LPRSQGWARRPGGKLITCSPSP QDGDKFWRMPECYIRGSTIKYL RIPDEIIDMVKEE\VVAKGR\GR EGPCQQAESQQK/GVRGMGGA\ GRCVFGGRGRGMGSPITG\RCH PDKKPGRQAGQTVSAHPDRLL RPLLARVGDFRSTVSERNLLQK GRGRPPRGEPPFRVLVTPSLFKV KAPFFLPKNRQILRVRKCLLCCF FGFCETGPSQKLGWNPLERVLC LKAIFSSPFASGFSRASHFPRRG LFLHFLGSLSEASNQTGRFLILK
23845	54213	A	23983	1	326	PVSLECYTVPPEDNLALLQLYF RTLVTGA/LRPRWCPVLYAVTL WPHVNSFIFSQRPRIVDIDGKM GTLSCIQPFNRCLARRRTLCPNG RQETKEQKACLPGSRLFELF
23846	54214	A	23984	2	341	

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23847	54215	A	23985	114	712	DLISALMIWFHVIVIHTPYVCIYI PTLPLSTSFPLSQLPVSLECYTV PPEDNLALLQLYFRTLVTGALR PRWCPVLYAVAVAHVNSFIFSQ DPQSSVSYISIFRGRKGASN*AA SGPAGEEVSVKQGQWWVPAL GSVPPLPVLLL\DEVKAARRSM LQKTWLLADEGLRQHLLHYKL PNSTLPEGFELYSQMPPLRQHY
23848	54216	A	23986	357	2771	FESSCPPVGSPVGAGPTPSLYKV PCATAMKLLRVLASAGRNIAA RLLSSFDLRSRLCRIIAEAPQEL ALPPEEAEMLSTEALRLWAVA ASYGQGGYLYRELYPVLMRAL QVVPRELSTHPPQPLSMQRIASL LTLLTQLTLAAGSTPAETISDSA EASLSATPSLVTWTQVSGLQPL VEPCLRQTLKLLSRPEMWRAV GPVPAACLLFLGAYYQAWSQQ PSSCPEDWLQDMERLSEELLLP LLSQPTLGSLWDSLRHCSLLCN PLSCVPALEAPPSLVSLGCSGGC PRLSLAGSASPFPFLTALLSLLN TLAQIHKGLCGQLAAILAAPGL QNYFLQCVAPGAAPHLTPFSA WALRHEYHLQYLALALAQKA AALQPLPATHAALYHGMALAL LSRLLPGSEYLTHELLLSCVFRL EFLPERTSGGPEAADFSDQLSL GSSRVPRCGQGT\LLAQACQDL PSIRNCYLTHCSPARASLLASQA LHRGELQRVPTLLLPMPTEPLL PTDWPFLPLIRLYHRASNTPSG\ LSPTDTMG\TAM\RVLQWVLVL ESWRPQALWAVPPAARLARLM CVFLVDSELFRESPVQHLV\AAL LAQLCQPQVLPNLNLDCGLRG LTSFPDLYANFLDHYEAVSFGD HLFGAMVLLPLQRRFSVTLRLA LFGEHVGALRALSLPLTQLPVS LECYTVPPEDNLALLQLYFRTL
23849	54217	A	23987	291	454	KAETGSLPYTLCKNQFKMD*RL TC*T*NHKNPRRKPR*YHSGHR HGQRLHDENT
23850	54218	A	23988	1	613	

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23851	54219	A	23989	807	1345	RCEERLLPLNLAVIALPSGLER WSFFAVYNGHPGSQVAKYCCE HLLDHIADNQ/DFTGSAGAPSLE NVKNGIRTG/CPEPEVHDTERSE EDDHFIILACDSIWDVMGNEEL CDFVRSRLEVTDDPEKVYNEIV DTCLHKGSQDNMCVIF\LWFPN APKVSPEAAKKEAELGKYRLN SILSDQ
23852	54220	A	23990	344	636	SSLSLLDIWVGSKSLLL*IVPQ*T YVCMCLYSSMIYSPLGIYPVMG WLGQMVFLVLDPSGIATLTST MVELVYSPTNSVKVFLFLRILSS TCCFLTF
23853	54221	A	23991	1	2793	
23854	54222	A	23992	18	409	SSVVEFVDPRVAPALLPQLPLES SSHGSVLPTMAVCLDKGHKMT KNMSKPRHSCRRGRLTKH\KFM WDMIREVCGFAPYERHAMVLL KVSKDKRALKFIKKRVGTHIRT KRRQEELSNVPAIMRKADAKK D
23855	54223	A	23993	1	609	MHPRGPPPPAQEESHTDESPGID HQSLARRAGRVGRTGGFSQLL AQTNTSMLSSSPASCTSPSPDGE NPCKKVHWASGRRRTSSTDSES KSHPDSSKIPRSRRPSRLTVKYD RGQLQRWLEMEQWVDAQVQE LFQDQATPSEPEIDLEALMDLST EEQKTQLEAILGNCP\RPTEAFIS ELLSQLKETPETQPASEISLRDH
23856	54224	A	23994	1	204	
23857	54225	A	23995	1	418	MWNRLCNWVTSIGWKSLEGSE EDRKSSQWGTLPSGAVRRGPPS SRSKNGRSNSSLHPVPGKATGT QLEPMRAVMGDESCKATGTEL LHALGAHPLHRLLKQHSHMMF QKVQVEPLRK\EPHHWQRL*PF SSE*NHGPSR
23858	54226	A	23996	104	253	

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23859	54227	A	23997	666	1436	WRPCFWLQAKKEAPAP\PKAK AKVKAL\KAKKAVLKDVHSHK KKKD\RKSPTFRG\PKTLCTR\KP PKCLQKTAPRKNKLDHCAITKF PLTTKSTTKKIEDNNTLVFIVDV KANKHQFKQAVKKLYDTDVA KNITKRWDVTSIITSCYIHLRLA SRLALEDLLAGLMNCLKGTFW NEESGERVETRPESRFKQQSKLI YTIKNPGRKKYGAEEKRAFWC HTDLLLHDHDEQVNHFSSPSST FTKCKRRKPFLLREFVWIK
23860	54228	A	23998	2	301	
23861	54229	A	23999	1	242	MGMVRKQALERTEWALVCRQ AWSSRMGYSTTVSPTQCQYTC SRGLLDSQLQLYKCTQALPEIH SLGHVCPSLITVKYSHYVLAAA TLFIWDNNESLRTGLLSVSTCK SGTRDFMRISGMVSLTSEVDNV EVFHYFPLHIQGKKFWAVGAI MTIFVISIYYEPGAHWHHMWK LLKVYSLESQKREEDISKRLPNF LKSSRRPWEDLILMLRKSPEMS KEYRASPLSLSAALRSKDRQSR HRCVTSTFHIREVRCCKSQGLP LCMHETAAHICP*TEGQQKGSG GLLYIP*TSPEIFSASESDPPMAC
23862	54230	A	24000	2	948	CGTPTVVPGTGTSRRVRTATVE PTWKCRAAQQPPPPP/PPLWVK LPPPDTSTKPELQLEELDADSS WMPLHGSCPTGKLAVDARSSL FTEPAFPYWKKMKHTFQNILS WSKFTNLTYSVTQLWLLVVMA QTSYPHSLVGRKQVILHSSCLY SLDNKTSLAGDDHDDDDHDDN DSSPAEKGPPPITKSLDKADEQS HLRLAVLELGFYKPVNLLLVA MTGCLLQLMMKKEQCGTHGG EGSTLEGSRPDVPQDLFSPTLGF YGSTSLSADLGENVILKLYLPSF PLQESEPSAEHGENLWALYVGF EERRSEASLAKAP
23863	54231	A	24001	265	513	
23864	54232	A	24002	513	796	TGTAWTPPPPPLTTGAPCTPPPR CTARGRT/PGDSHLGGGPAATA GGPRTSPMSSGGPSAPGMRPPA SSPKRNTTSLLNSGLEPTFSFRIT FGFM

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23865	54233	A	24003	1268	2097	TPELTGAISLSTLGDPSPFRQPSS AQMGHLLSTSLSTPPTTSNSETT QPAFATVTPSSSSVLPGLPQTSF SGMGPSAELMASTSPKQQLPQF SAAFGHQLSSHSGIPKDLQPSHS SIAPPTGFTVTGVKLQTFAVSVT VLKATCLELFVPPGGFVVSLAS GVKLQTVTPLHFSGNHPSAFYY YRLSFEMDKGKKRQFGVEKEK CGSLGGFVMLGNEEMIRRAVT LIAWTKIPFLGIREAKNPGSENI RLATILEAP\PPSWELWEQGPPG APYYQP
23866	54234	A	24004	3	1163	GEVTSWNRGRGLRIWRYFLFGP VQKTMRLLLSRLTYCWLEQDG RVSWRLGLEIGSLPTPVPVRLCP ANRSPPMVCGTTGRSSSNSSTE KRMCTCSSRAALHFLKGPEGG TLMEEIRALIKEPPESSLTPSTRG GHSEKAPSKNHQAATVNTTTLS RISHISHTHLLIHCTGKEQHEPY EDAATRSRPEADLSRHERLTCR HLDLGLPDMQNRQCVPGSQGL RPVGGLEGPRHWCLVRSSRLG VLPRRPQGCEDDAGGLQRQDC GQWRELVQLPTPP/VCPGGASP HPKPLPDLPDPPGSSRCFCLLPG TCPAAPPAGSPSPCSQSPGCLPP VPTPSVLECCTQVLLEDSKPQS HRNSAPHLQPGIWSHIPGSHPW CLVLAAEGSTSSV

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23867	54235	A	24005	1	2502	MEARVERAVQKRQVLFLCVFL GMSWAGAEPLRYFVAEETERG TFLTNLAKDLGLGVGELRARG TRIVSDQNMQILLLSSLTGDLLL NEKLDREELCGPREPCVLPFQL LLEKPFQIFRAELWVRDINDHA SVFLDREISLKILESTTPGAAFLL ESAQDSDVGTNSLSNYTISPNA YFHINVHDSGEGNIYPELVLNQ VLDREEIPEFSLTLTALDGGSPP RSGTALVRILVLDVNDNAPDFV RSLYKVQVPENSPVGSMVVSV SARDLDTGSNGEIAYAFSYATE RILKTFQINPTSGSLHLKAQLDY EAIQTYTLTIQAKDGGGLSGKC TVVVDVTDINDNRPELLLSSLT SPIAENSPETVVAVFRIRDRDSG NNGKTVCSIQDDLPFILKPSVEN FYTLVTEKPLDRERNTEYNITIT VTDLGTPRLKTEHNITVLVSDV NDNAPAFTQTSYTLFVRENNSP ALPIGSVSATDRDSGTNAQVIY SLLPSQDPHLPLASLVSINADNG HLFALSPWTTMPLRAFEFRNNS PALHIGSVSTAETNIQVTYSLLP PRNPHLPLASLVSINTDNGHLF ALRSLDYEALQEFEFRVGASDR GSTALSSEALVRVLVLDANDSS LFVLFPLQNGSAPCTELMPRA\A AEPGYLVTKNAWLS*QLLKAT EPGLFGVWAHN/GTDRLLSERD TAKHRLMVLVKDNGEPPRSAT

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23868	54236	A	24006	1	1960	MEARVERAVQKRQVLFLCVFL GMSWAGAEPLRYFVAEETERG TFLTNLAKDLGLGVGELRARG TRIVSDQNMQILLLSSLTGDLLL NEKLDREELCGPREPCVLPFQL LLEKPFQIFRAELWVRDINDHA SVFLDREISLKILESTTPGAAFLL ESAQDSDVGTNSLSNYTISPNA YFHINVHDSGEGNIYPELVLNQ VLDREEIPEFSLTLTALDGGSPP RSGTALVRILVLDVNDNAPDFV RSLYKVQVPENSPVGSMVVSV SARDLDTGSNGEIAYAFSYATE RILKTFQINPTSGSLHLKAQLDY EAIQTYTLTIQAKDGGGLSGKC TVVVDVTDINDNRPELLLSSLT SPIAENSPETVVAVFRIRDRDSG NNGKTVCSIQDDLPFILKPSVEN FYTLVTEKPLDRERNTEYNITIT VTDLGTPRLKTEHNITVLVSDV NDNAPAFTQTSYTLFVRENNSP ALPIGSVSATDRDSGTNAQVIY SLLPSQDPHLPLASLVSINADNG HLFALSPWTTMPLRAFEFRNNS PALHIGSVSTAETNIQVTYSLLP PRNPHLPLASLVSINTDNGHLF ALRSLDYEALQEFEFRVGASDR GSTALSSEALVRVLVLDANDSS LFVLFPLQNGSAPCTELMPRA\A
23869	54237	A	24007	1	966	MGHHLMIDKLVALGGLYYAIQ RHYATKCSVLKNDQILVIGLFM IQNVIYRKHFANPLSALFLQQGI ELFAAIAEIHITTVAERNHAITQI RLEAQTIFDSLKEWHNAIRKSL DYEALQAFEFRVGATDRGFPAL SSEALVRVLVLDANDNSPFVLY PLQNGSAPCTELVPRAAEPGYL VTKVVAVDGDSGQNAWLSYQ LLKATEPGLFGVWAHNGEVRT ARLLSERDVAKHRLVVLVKDN GEPPRSATATLQVLLVDGFSQP YLPLPRAAPAQAQADSLTVYL VVALASVSSLFLFSVLLFVAVR\ LCRRSRAAPVGRCSVL

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23870	54238	A	24008	1	2673	MEVMGNMGSKILITGITSTKRK VALLAKKRERKIISQRKDVTDS RAKRQSEEKSIGKETVVIGIGLI SKDSAAAICESRWRLSESHFER LIQRRMEARVERAVQKRQVLF LCVFLGMSWAGAEPLRYFVAE ETERGTFLTNLAKDLGLGVGEL RARGTRIVSDQNMQILLLSSLT GDLLLNEKLDREELCGPREPCV LPFQLLLEKPFQIFRAELWVRDI NDHAPVFLDREISLKILESTTPG AAFLLESAQDSDVGTNSLSNYT ISPNAYFHINVHDSGEGNIYPEL VLNQVLDREEIPEFSLTLTALDG GSPPRSGTALVRILVLDVNDNA PDFVRSLYKVQVPENSPVGSM VVSVSARDLDTGSNGEIAYAFS YATERILKTFQINPTSGSLHLKA QLDYEAIQTYTLTIQAKDGGGL SGKCTVVVDVTDINDNRPELLL SSLTSPIAENSPETVVAVFRIRD RDSGNNGKTVCSIQDDVPFILK PSVENFYTLVTEKPLDRERNTE YNITITVTDLGTPRLKTEHNITV LVSDVNDNAPAFTQTSYTLFVR ENNSPALPIGSVSATDRDSGTN AQVIYSLLPSQDPHLPLASLVSI NADNGHLFALRSLDYEALQAF EFRVGATDRGSPALSSEALVRV LVLDANDNL\PFVLYPLQNGSA PCTELVPRAAEPGYLVTKVVA VDGDSGQNAWLSYQLLKATEP
23871	54239	B	24009	1	993	
23872	54240	B	24010	1	4056	
23873	54241	B	24011	1	906	
23874	54242	B	24012	1	4318	
23875	54243	B	24013	41	1935	
23876	54244	A	24014	3	328	GWQSGPVLGGLCGTAGQSCGD GDGIWWAQAAQAGDPAHLRL LTHGQPSSVPEAPVRAHQPALP QPRSAAARECGR/AGRSTTNSL RKRVASESYMIVAPPMPSSWSS SG
23877	54245	A	24015	114	567	VKKPHSAEWVPLWGLQPGWR QPFRCNSGSEKELRRPVSNSQEI LSPVTMRKPAVSVCCDLTLREA APPFQRHERTYTGEKPYKCKQC GKAFSGFCYTQILEKAQTGKQP YE/AHERTHWKQNHDCTQFGK AFSFSSSLCIHEKIHTGEKLYE

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23878	54246	A	24016	170	491	PAQHQRGLWQSPTHQALTLML SVHREDWKPVLTINSIIYGLQYL FLESKNRWLGLERLGFCPSGLIT PPTCTGHRSP/NPEDPLNKEAAE VLQNNRRLFEQNVQRSMR
23879	54247	A	24017	1	1062	
23880	54248	A	24018	2	700	RRPTRPGGGSGGGGGRMIKLFS LKQQKKEEESAGGTKGSSKKA SAAQLR\IQKDINELNLPKTCDIS FSRSQTTLLNFK\LVICPDEGFY KSGKFVFSFK\VGQGYPHDPPK VKCETMVYHPNIDLEGNV\CLN ILRGDWEASPLRLNSIIYGLQY\ LFL\EPNPEDP\LNKEAAEV\LQN NRR/VCFEQNVQRSMRGGLHPA PPTFERCLKIGLAHTHPPPRPQA LASPAKYLLGAMG
23881	54249	A	24019	302	884	PMAPLSSQQPTLFPNTLTQAQQ VQLTKGLRKWMVQHGGDGW VVEENRTTVPGAPSQTCFVTSF/ EVNAPAIQSWCCKKQVLDLEE EGLWPELLDSGRIEICVSDWWG ARHDSGCMYRLLVQLLDANQT VLDKFSAVPDPIPQWEQQCLPF TFTHVFFQHSRWGVRFCVFSEH RGPGTHSSGAGPLLSPCEQLQC
23882	54250	A	24020	274	866	SSLLNLPSSWDYGWVSYEQAN CKGEQFVFEKGEYAHWDWWT SSQRTDFSSLR/RPSKVDSQEPK V\YLYENPNFTGKKMEIIDDD\V PSFHA\HGYQEKVSSVWVRSG MWVG\YKYPGYRGLQYLLKKG DYKDSSNF\GARHPQV\QSVRCI HDMQGHQCGAFHPLGTQEEEE AGQKEQMEQVPFWLARGDICE LSGKKSVI
23883	54251	A	24021	179	374	AASIGRSMTEKAHAGPRPGRN* ADAPSSSDTLFPPDALLSNQAG RLACWLFSYGPQTKNDFHIFK
23884	54252	A	24022	1	141	

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23885	54253	A	24023	1	506	PHSPLWKTLCSPSSGVCCGFVT LFCNDRFACLFQLTPPPSPAWM TAAASLLASLLPALPPLNLQDA KFVEERRKQLQNYLRTVMNKV IQMVPEFAASPKKETLIQLMPFF VMGLQVGMYGLFHFGVMMDQ PQPSLTRADESPCDRVLSPCAA HRKQRDCCLSWKAEPE*FLVK* KTLCSPSSGVCCGFVTLFCNDR FACLFQLTPPPSPAWMTAAASL LASLLPALPPLNLQDAKFVEER RKQLQNYLRTVMNKVIQMVPE FAASPKKETLIQLMPFFVMGLQ VGMYGLFHFGVMMDQPQPSLT RADESPCDRVLSPCAAHRKQR DCCLSWKAEPE
23886	54254	A	24024	1	396	
23887	54255	A	24025	1	1176	MVPGDLSQTSEDQSLSDFEISN RALINVWIPSVFLRGKAANAFH VYQQSIAGVSGIARKRALIPFGK STFSYVCITNIKLTDALPSWDYT CHFNLPKAQKPGEPTKCILTME WLALLQGDPGSWIQKEFIVGKR GGKMDNILWDQRDVQPPGLRP HQLLHSGGGPLISFRNGGPILV WELRRKGASGKEIVGSRYFRES DEVLVWKNPKTLQKEDEEVNS THPMHTYPCTHCQVFCVTAEII NIYLQACIVLEMSMLPPGERPLF LLRLTTVLEVTVFDSQWSRPYH VSADPSAWKHHHHYHHHHY QLSSSSPTITIINHPSPS/LSHASPS P/CHPSPSPAVHHHHQPSITITSR PSPSPAVHHHHQPSITIIIRPSSITI INHPSQASSIHHHHQPSIPFIVSH
23888	54256	A	24026	1349	2125	
23889	54257	A	24027	670	972	KTDEWNIYRRYTEFRSLHHKLQ NKYPQVRAYNFPPKKAIGNKD AKFVEERRKQLQNYLRSVMNK VIQMVPPSSLPAPKKETLIQ\LM PLLRSTSTPPRRAL
23890	54258	A	24028	1	699	

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23891	54259	A	24029	221	864	VDCPRSFSAVVVWQGRFWLLS FIPGGFLGMTLFFASGMNWTVT LLGFLAGNLEVEPSDTIENVKA KIQDKEG/IPPDQQRLIFAGKQL EDGGTLSDYNIQKESTLHLVLR LRGGMKIFVKTLTGKTITLEVE PSDTIENVKAKIQDEEGIPPDQQ RLIFAGKKLEDGRTLSEAIFLDV GLLLSCRTVSSCGAFILGWSVVI LIPVISTRDDTSTTK
23892	54260	A	24030	2	864	PSFRLAWPEGRLALLGELVCVP VVGRGMENGRILVSADRSGGHI CLKTLT\GKTIT\LEVEPSDTIEN VKAKIQDKEG\IPPDQQRLIFAG KQLEDG\RTLSDYNIQKEST\LH LVL\RLRG\GMQIFP*RP*PAKTI TLEV\EPSSHHRKF*RARFQGKE GIP\PDQQRLIF\AGKQL\EDGRT LSDYNIQKESTLHLVLRLRGGM QIFVKTLTGKTITLEVEPSDTIEN VKAKIQDKEGIPPDQQRLIFAG KQLEDGRTLSDYNIQKE\STLHL VLRLRGGC*FFSHGIRSAQ
23893	54261	A	24031	1	124	
23894	54262	A	24032	97	296	
23895	54263	A	24033	71	269	AAGYRPCPRHPGARRTAATRR CHPSPAVARPAGCSGPP*CYAL SPDPARTRRGDPQTPPCRLPRA G
23896	54264	A	24034	206	667	STRLGLPKCWDYRREPPRPAKS SFLTAQACEAQKTGSATRRKD CFLQPTFWLLPFLVLEKGAPSA CRGKRYVRAVWLSLSTGAILQP YPKLQVSNWL*CARDQEMPEG CL*QSCQTLSLLVLPPKEKKDV *EISPWTPAPPEHQYTVRTFQSP
23897	54265	A	24035	3	190	GTFKNDLILLISKSYY*APLPSD FSHSDTSS*KPSKSLKTYPSPPFF SAKTSLLQCPRNILY
23898	54266	A	24036	197	474	SPLSHRGASELLSSLHLRSSCSS PKMAETPEAGFQIVHSASPQPG TAPGNPWAAGAGG*HCEPGQL AGPYRAASFFGQAWPPHPRAK LGVSR
23899	54267	A	24037	164	323	GQEIKTILANMVIPRLY*KYKKI SWAWWHAPVVPATWEAEAGE LLEPGRQRLQ

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23900	54268	A	24038	582	1166	HCEPGQLAGHLGQPLSSGRLGH LMASHKLSNNYYRTRDGRRES VPPSIIMWSQKALVSG\KPAERV YGDANHTVGNMCASRLGGYL GFSIRIVVFIWYLGLSVVVNML VGRQCDWQGLVYGQPELLVFS GNMPGEVARGKHRNEKAPLSM RPASQCRVFCVLKGCSERSRHK EQTPDTTIFKNCNTHCEGPWLH
23901	54269	A	24039	1214	3878	
23902	54270	B	24040	62	1242	
23903	54271	A	24041	74	408	
23904	54272	A	24042	790	1877	DEIVDPGSMKWSYKSQLNYKT KRPSVFVTALTHRPDILILGTLE SGHSRNLTCSVPWACKQGTPP MISWIGASVSSPGPTTARSSVLT \LLPQSPQDHGTS\LTCQCT\LPG TGVTTTSTVRLDEAYPA\WNLT MTVFQGEGTASTTLRNGSALSV LEGQSLHLVCAVDSNPPARLS WTWGSLTLSPSQSSNLGVLELP RVHVKDEGEFTCRAQNPLGSQ HISLSLSLQNEYTGKMRPISGV MLGAFGGAGATALGFLSFCIIF VGVRSCRKKTARPTMG\VGDT GMEDT\NAVRGSA\SQGTPELN PRQKEQAPQNHGSANALANPP RPEEGEIQYASLSFHKARPQYP QEQEAIGYEYSEINIPK
23905	54273	A	24043	183	1176	VHQLVFPRQHQRHSVFPKANSS WIHQLFPQ\QHSYGPSAVSAGQ HQLMVHSLFPQATPAHASISLV FRQGTHQLHRVHQRRIPSAQHQ RHRLHQRRLPSAQHQRHRDSIS VCFPFRAHTRPHCDSIQRQHQL MRSIGLFSSGKTDPTVTLLKEA AAEHEICLCSRHPVNLRETKAH LGNAAHAVFPRGNQKKPEMCP YLPTHKLVVPTPPLIPLEAALRN IAHSRSIPPPKKFSPTPDTSDDYL LVFNSFPYSKLTTPKTGQGENL GSTRPIPCNGPPTRGPHNGAKY PGDVSHPVGVGTLWANRLLTG QYEENGKSFFLLICTIATFQVNA
23906	54274	C	24044	178	342	
23907	54275	C	24045	86	283	
23908	54276	C	24046	91	177	
23909	54277	C	24047	11	169	
23910	54278	C	24048	209	673	
23911	54279	C	24049	164	208	

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23912	54280	A	24050	182	255	DAESRRSWQPLPEPLELRP\RLSD
23913	54281	A	24051	146	456	LKNHKRSEKPCPTLTDDIPPQKKCKWPVLALSADITL*KSFSWLILAQKAPPLSTL*PPLLPAREQMSFD\LIFLYLPKSYKVAPPLSSFTESLFGLSPPAPR
23914	54282	C	24052	90	215	
23915	54283	B	24053	1	1059	
23916	54284	C	24054	129	215	
23917	54285	C	24055	19	347	
23918	54286	C	24056	228	260	
23919	54287	B	24057	406	602	
23920	54288	C	24058	7	375	
23921	54289	A	24059	322	400	FLLSRVPSV*DPTENQTVQLTWEWLP
23922	54290	A	24060	818	1078	ILDVFSYTMKIEPSPLRSYPISPHYNL*QLPP*LDP*ESGYKTPLSALLLTFLLYISSFASHKVSSSSVDPLPTCAYLPIGQAHVH
23923	54291	C	24061	1	411	
23924	54292	A	24062	1	861	
23925	54293	A	24063	425	484	
23926	54294	A	24064	1844	2097	HSAGTKLRLVNFLLTLRRLVNSVMRLKKSFMMVQRMVSIPKVWSISLGFLLSFVPSVWDPT/ENRTVQLT*HPLPEPLELGPRLSD
23927	54295	A	24065	729	807	LFSCSCPPKPPRP*LTAEKGGLCIFL
23928	54296	B	24066	1	1317	
23929	54297	B	24067	509	810	
23930	54298	A	24068	1	385	MDLPSTVRVTRSSASVMVQGGSEAIRQRQSSAAKPRRSGKESKSLGPEFQGLWEWLPEIYFSQFRRLGNPKSRHQQIQCLMGACFVVTERLSFQDSLDLAEPRHSYPLQVKRLDLPTVLETETDLEKLDPFTTIPSPVETLQCLFVSLRIKSRVP*FWISQPPEL*EINFWQPLPEPLELWPKAL
23931	54299	B	24069	1	774	
23932	54300	A	24070	350	640	SLQGCLSDNSPTFQRCQTTQGRLPWSFTLSGKSHFSGGVARACYTCQKSGHWA\RNASSPGFLLSRVPSVSDPTENRTVQLTWQPLPEPLELWPKAL
23933	54301	B	24071	85	331	
23934	54302	B	24072	1	1844	
23935	54303	B	24073	1	1169	

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23936	54304	A	24074	63	220	NLTGNIWNREWYSHFDFDLLD PVGFSGSIAKMPKRKLFKCHSV *GHWRSKSE
23937	54305	B	24075	497	898	
23938	54306	A	24076	3	678	GGGFSDRDRTIALQPGQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGEKFYFIPKAMG AMEGSGQRRTLPDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLRE/KD PPTTSGPQSNQPRKH/LTNFKSG A/CYTCRKSGHWAKECPLPGFL LSRVPSVWDPTEN/RTVQLTWQ PLPEPLELWPRLSD
23939	54307	B	24077	522	873	
23940	54308	B	24078	329	530	
23941	54309	C	24079	147	439	
23942	54310	A	24080	3	3889	
23943	54311	A	24081	2	394	
23944	54312	A	24082	1	197	
23945	54313	A	24083	1	205	CLRAGPHALYLLC/NIPEFTFL\S RADF\ARSQLVDLLTDP\FQ\QEL EELLQVGAVTLILRILPCLPCLP
23946	54314	A	24084	134	182	SCFIPSSQPVAGTERSRFLGPQY FQTPHNPSGPGLGNQLMR*AF
23947	54315	A	24085	257	481	
23948	54316	A	24086	415	630	
23949	54317	A	24087	123	340	
23950	54318	B	24088	49	270	
23951	54319	A	24089	1	900	RSRVRREVVALRRGLACIPSLG VWRFPSVGVLAVSDRWCLAVS DRWCLARATLSCFGCAMPMYQ TRRQENDLRTASIAV*RRKQQN DH*KQRRWQNIQRKGPKRYIVI AGNSQSHQPMIFSMLRKLPKVT CRDVLPEIRAICIEEIGCWMQSY STSFLTDSYLKYIGWTLHDKHR EVRVKCVKALKGLYGNRDLTA RLELFTGRFKDWMVSMIVDRE YSVAVEAVRLLILILKNMEGVL MDVDCESVYPIV*ASN*GLASA VGEFLYWKLFYPECEIRTMGGR EQRQSPGAQRTFFQLLL

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23952	54320	A	24090	1	812	MARTPGAELAVAKYPKKGSQA VHRHSRKQSEPPANDIFNAAKA AKSDMQHREVRVKCVKALKG LYGNRDLTARLELFTGRFKDW M\VSMIMDREYSVAVEAVRLLI LILKNMEGVLMDVDCESVYPIV LFYPECEIRTMGGREQRQSPGA QRTFFQLLLSFFVESKLHDHAA YLVDNLWDCAGTQLKDWEGL TSLLLEKDQSTCHMEPGPGTFH LLGESPGISAIVQGAIEKSGERSS PPPKRIGSMKEGPMVLPLALDT QCWFPVEVPLD
23953	54321	A	24091	152	1209	MPLKNVQNITHFPLEKELALPL LIFSPLHWCVSGYLSLPLPNPKP HFSNPLLLQVILPALTLVYFSIL WTLT\HISKSDASPGECGS*MG* WEQRNLCPSILPLQSPLCPTEAA VEFEGTRMVAFCELC\QSCLSD VDTEIP/ESR*VLAQSGRKKAEY PCPPFPRRN*QCHYLPWETFCPF KHPFFSPLQAFVLLSDLLLIFSP QMIVGGRDFLRPLVFFPE\ATLQ \SELASFLMDHVFIQPGRPGQW CSDSIPGAQ*GLGLGCSSKI*GR KLKSVIPFCLPCEPGDSQEDHLQ IERLHQRRRLLAGFCKLLLYGV LEMDAASDVFKHYNKVHQGPS LGFTKPLVMPRFSAATV
23954	54322	A	24092	37	625	SLMLLTPFHFPPEECPPPIPTAH HLLPFLLSTWELFLQQLQEVVV KHAEPAVLEAGAHAL\YLLCNP EFTFFSRADFARSQL/V*DLLTD\ RFQQ\ELEELLQGRELGAGTMG DTPNKGWGGGCKTGGMWDL MSSGGKCYCGIFFSFSILPSQIED EVYNLGSHSETPLCLLQVSGFP PLPHPVFTGVCGVGSLCSFPV
23955	54323	A	24093	2	198	PNDRSRVTREMSAPSRSLGRFL SVGVWHAPPSLALVPPCRCTRL KTYHGRGAPLRVELPTCMYRL SNVQGRSGGPAPGVGHLQSLV DEWLDSYKQDQ\DAGFL\ELVN FFI*S\CGM*RNSGDYPLTAPGL SWKKFQGSFCEFVGTLVCRCQ YILLHDDFPMDNLISLLTGFSDS QVCAF\RHTSTLAAMKLMTSLV RVALQLSLHQDINQRQYEAER NKGPGQRAPERLESLLEKHKEL H*YQAKNLSRARCASTCGASH
23956	54324	B	24094	211	3841	

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23957	54325	A	24095	1	1798	MSLLAFKIILVGFEGSKARVQT DLFYRSLVLFLLLQICFPLSCFG NWKGEEGGMQRWVLGKNEKI ASPHRLPAPTARFAVSLQLNLRI LGAFQFGPVLFVLWRPLDRDN ASPQSEFLNSCGITAYLVGKRE GGVERGGGGRSSERCRTRLSFS PRHSHVFSTSRFCKILKKSPGAN GGRCRARGGGLHGARAANPPT PIAEPARLPACLSRAEPEPQAAE PAPPPVGVVRSRPLSHRRHPVV CPAAPIRLINKRLAHSARPAGIC CVSRSGLSALAAAGTASMFQLP ILNFSPQQVAGVCETLEESGDV ERLGRFLWSLPVAPAACEALN KNESVLRARAIVAFHGGNYREL YHILENHKFTKESHAKLQALW LEAHYQEAEKLRGRPLGPVDK YRVRKKFPLPRTIWDGEQKTHC FKERTRHLLREWYLQDPYPNPS KKRELAQATGLTPTQVGNWFK NRRQRDRAAAAKNRSQTSPWA EAFRFPECGSRLAKHFAEEPGLI PQAQMLLTILFAFRSGRPDPTRS REHLLRRKPQADAPLEM\LQQQ VLSQGSGRALRAEGDGTPEVL GVATSPAASLSSKAATSAISITS
23958	54326	A	24096	3	1034	GLHGARAANPPTPIAEPARLPA CLSRAEPEPQAAEPAPPPVGVV RSRPLSHRRHPVVCPAAPIRLIN KRLAHSARPAGICCVSRSGLSA LAAAGTASMFQLPILNFSPQQV AGVCETLEESGDVERLGRFLWS LPVAPAACEALNKNESVLRAR AIVAFHGGNYRELYHILENHKF TKESHAKLQALWLEAHYQEAE KLRGRPLGPVDKYRVRKKFPLP RTIWDGEQKTHCFKERTRHLLR EWYLQDPYPNPSKKRELAQAT GLTPTQVGNWFKNRRQRDRAA AAK\NRLQQQVLSQGSGRALR AEGDGTPEVLGVATSPAASLSS KAATSAISITSSDSECDI

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23959	54327	A	24097	3	1024	GTRVGVAWRSVRLLLGPGAGL RGGVVLKVSPSPCRGGRRVPVR AEGARGRGPINKVPGASSGAA VGAARLTAPLLAKAMASKLLR AVIL\GPPGLGKGAPVCQRIAQN FGLQ\HLS\SGHFLRENIKA\STE VGEMAKQVYREKVFLVPDHVI TRLMMSELENRRGQHWLL\DG FPRTFGQAEALDK\ICEVDLVIR LNISFETLKDGLN\RRWIHP\PSG \RVYNL\DFNPPHVHGIDDVTGE PLVQQEDDKP\EAVAA\RLRQY KDVAKPVIELYKS\RGVLHQFS GTET\NKIWPYVYTLFSNKITPI QSKESILTLAQWEEPGRCGSFIP IVWCSNWCCCPNLEA
23960	54328	A	24098	2	178	
23961	54329	A	24099	96	340	FGALTRIG\DLPWEINPLSSCSLL PEKDPPMTSGPQTDQPKEHLTN FKSAARRSSRTSSHRNLLHVLEI WQLDQGMPAARDS
23962	54330	A	24100	3	155	
23963	54331	A	24101	1	162	
23964	54332	A	24102	1	1032	
23965	54333	A	24103	167	476	TAMLLTQSLFGGLFTPTHMKFG AVTQIG\DLPWEINPLSSCSLLR EKDPPTTSGPQTHQPKEHLTNF KSDHHGCRASGNSHSGRMLLIF SPSRGLYACSCVKT
23966	54334	A	24104	371	772	
23967	54335	A	24105	146	312	QKRSIPNSSPIP*SHSLLANCTK/ DHHFLNGSKSFQPQLLSCKFS* GQHLFQGALCT
23968	54336	A	24106	76	441	
23969	54337	A	24107	1	1284	
23970	54338	A	24108	150	371	EESRAAGIPWPSGQISGTCSKL\ CGRRFWRNAWPLRFRHLEVLV CWRCGCGLSHSGGKELQLFSII VHLEGEVN
23971	54339	A	24109	280	351	
23972	54340	A	24110	1	483	
23973	54341	A	24111	129	363	FGVVTQIG\DLPWEINPLSSCSL LCEKDPPTTSGPTKKHLTNFKS SKRPLFTLFSNLPHYPSTSFSFQS WRYTSISPFS
23974	54342	A	24112	2	111	
23975	54343	A	24113	3	808	

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23976	54344	A	24114	497	815	TALLLTQILFGGLFIWTRVKFG ALTWIG\DLPWEINPLSSCSLLH EKDPPTTSGPQTDQPKKHLTNF KSACFERIKACYHSPATAWPFK AYKLSLQFPHFTCPKTR
23977	54345	A	24115	1	753	
23978	54346	A	24116	1	513	
23979	54347	A	24117	625	701	IHVAHKLAVVMPGCKRGCLSL FYFQLIWSHKGWVRSGEASHR EMAGLLLLCSS*PPSPCETLPRS EPSLCDSRSAESRTKTSNLSCIP ASLQQVCGPREFIWSGNHCHPF LPITRCYGCLCYHYCMENSIL
23980	54348	A	24118	458	605	VVEEGIEDKRVYRLGTTGWIGK TIWLVRRRS*TNL*DLSGFWTG KMGEL
23981	54349	A	24119	566	769	IKEKGGLFSFSASNLWKQVTSS FLCSPLPLSLLKSSKLLANRDKY RMCGPVPANGNRTQQ*SKHVR
23982	54350	A	24120	345	664	GEIAASQEPAGGFSGSSAQPCPL PWTGPPTTQAPGH/CNSAPSSRD NASSNGGRRQRVPTVPGGGLIL QREHILLPLGPALRAAGKEPAT AATIPESPGGDSDDSRT

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23983	54351	A	24121	2	2204	IDMIFTPGPPSTPKHKKSQKGSA FTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFVKVERQVQDMG KKLDFLVDMHMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTIICNYSETGPPEPPYSF HQVTIDKVSPYGFFAHDPVNLP RGGPSSGKVQATPPSSATTYVE RPTVLPILTLLDSRVSCHSQADL QGPYSDRISPRQRRSITRDSDTP LSLMSVNHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDTDTDPFTPSGSMPLSST GDGISDSTVPLFLSSEILQKQVG QSITSMLGFLSRGPSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFSLLSVTSYS SFAFHKFSVAVYNISNLKTVDP AKFPTRYCYCLNNRTNDLSDFT ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFICVMTGKSGR NLSDFWEIEEKYPIINYTFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIG\DLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARPTFLGQGQVPLNPF SFTLSGKSCFPRRQEPPNRLFPH PNLLSLCPNPLFLCPNPFSTFLE GKNHHPHPFSVSQVFSLGLPPS LWEHSPMAHRLRVQPRQQPPDI HKQVISLQSGHSLLVKSQSWSQ DPIKFQLPHHHKNTASVCINPSV
23984	54352	A	24122	2102	2529	ETTMSFIFSLLYPFRMHLSFLIVS PALRSISRRALAAFPRGRSLDLQ PAMPEPPTPS/CGLLCVPS\PPMS AAPCSKVPQSHLFAFMSCNTAK VCSFTAEASETTSPPGGTNNSR RATLRAVTLTRRSATLTRRSAA SHRSSTV
23985	54353	A	24123	299	567	TAMLLTQSLFGGLFTQTRMKF GAVTQI\ADLPWEINPLSSCSLL HEKDPPTSSGPQTDQPKEHLTN FKSGETKEMHFIRGPKTPAPVM
23986	54354	A	24124	684	822	KVKRQSYSQNTFYYPICSRH*IK LQKLNSGPQTPQQDLINLAIKV

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23987	54355	A	24125	1163	1826	TVLLLTQSLFGGLFIWTRMKFG AVTR/IRGDLPWEINPLSSCSLL HEKDPPTTSGPQTNQPKELLTN FKSVPTPSVAESFQSSFSTDPSD PSSPPQAAPRQAKPGPNSSSASA PRPYNPFITSPPHTWSGLQFHSA TSPPPPAQQFPLKKVAQVKGTV KWLKTDAARSPQKPTGTITDAL DNSHSGGPIMDRPLLVKSPKQF LRLLVFSKTFISLTILNLQE
23988	54356	A	24126	636	922	TATLLTQSLFGGLFTRTRMKFG AVTRIG\DLPWEINPLSSCSLLRE KDPPTTSGPQTHQPKEHLTNFK SDKGDMFYPWTQNSSAGHGLG RQPSLGV
23989	54357	A	24127	728	1013	MKFGAVTRI/RGDLPWEINPLSS CVLC/CREKDPPTTSGPQTDQPK EHLTNFKSGKRPAFYSLLQPPSL SLNLFLLSILAPHFNLSLLLISIPF IFW
23990	54358	B	24128	1	3993	
23991	54359	B	24129	105	420	
23992	54360	B	24130	45	2866	
23993	54361	B	24131	1	1680	
23994	54362	A	24132	1257	1403	
23995	54363	A	24133	1	2130	
23996	54364	A	24134	1	725	
23997	54365	A	24135	2825	4123	RAADGVITLEDNDPCVKKDSSR FPYEDRLDLVLKGTADIPRLTV HRGSEYIISRATFPCYFIKEQSVI NHCYTEIDLKIFRQYLAPALGV THRFVGTEPFCRVTAQYNQDM RYWLETPTISAPPIELVEIERLRY QEMPIYASRVMFIFRPDNTALP RNDTPQMVKLFMDRFQVVKDI GVIELKVVEDQRTRAVMIKFRA FVKEGAVIVIRFDNKEVAFAQM SGNLTVPRSTSDYKARDIFFQY RFLTRISTGHGVANNHQIRLRL ELAGIVPLNQLNALLLKVYPLS KLCNSPKKCQLESVFRLTQWV VKKPISNRQSGLGGIVLPGLFRV LSPGNLSPIKGTVILPNEVQPGF LGNLVGPI/RGWIGLS*IYLPHGF TG*QNSAGLADH*RASASPERA GVYPIHNERCAHRASRYY*KW HPDSVAADHLLG

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23998	54366	A	24136	137	1199	ISSGGPRELGLKMIIVPGSQLSQ LPPGLDSTEFAAIVGNLLDNAF EASLRSDEGNKIVELFLSDEGD DVVIEVADQGCGVPESLRDKIF EQGVSTRADEPGEHGIGLYLIA SYVTRCGGGITLEDNDPCAPLT LLIVEDETPLAEMHAEYIRHIPG FSQILLAGNLAQARMMIERFKP GLILLDNYLPDGRGINLLHELV QAHYPGDVVFTTAASDMETVS EAVRCGVFDYLIKPIAYERLGQ TLTGFP\QRKHMLKSIESATQKQ IDEMFNAYARGEPKDELPTGID PLTLNAVRKLFKEPGVQHTAET VAQALTISRTTARRYLEYCASR HLIIAEIVHGKVGRPQRIYHSG
23999	54367	A	24137	2	243	RPGRGLGQRGIWEPAA\LLDSV AQQQGAWLPHVADFRWRVDV AISTSALARSLQPSVLMQLKLS DGSADLEKRCERRLQD
24000	54368	A	24138	1	1483	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPDSDLRYLQSC EWGDTGIFLKWSCIPAEKGLQT SGAWVEAADIPLLPGSPRRLSP QAGSRGGQGPKHGQQCLKMP GPRAPGLQGGSNRDP/AP/GPAV ERAPAAALSSTTIWMPMSLCP WRPVLAACTSMTVRGRSTMYL PTTTGNAGCTWPKASLATRWL SSPMGRQARSLMLGAQVTLSW DRSMPWRRRGRSSGRNLSTI

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24001	54369	A	24139	727	1498	GICIWDRPPGLADQRRSHSHGW WGELATPLPWHH/HLSDSHSG\ RVSFLGAQLPPEVAAMARLLG DLDRSTFRKLL\KFVVSSLQGED CREAAAAVLGSAPTCRR\AAGC \LLAGMHTLLQQALRLPPTSLK PDTFRDPAPGALHPPRPGRGL\G QRGIWE\PSGPSFDSVAQQARV AWLPHVA\DFR\WRVDVTIST\S AL\ARSLQ\PSVLM\QLKAFQNG SSIPAFEVPPQPKF\QEL\RYSVA\ LV\LKEMADLEKK\CE\RNLQD
24002	54370	A	24140	1	312	
24003	54371	A	24141	2	524	
24004	54372	A	24142	144	494	AGSCPFAAGPGPLGSGRCFVLIR FILI\QNRAGKTRLAKW\YMQFD DDEKQKLI\EEVHAVVTVRDAK HTNFVGVSGTFKIILPPLCWPLL LASVWMFNDNKPGLYLGGPFH NFRGRS
24005	54373	A	24143	1	428	
24006	54374	A	24144	108	422	
24007	54375	A	24145	3	387	
24008	54376	A	24146	3	337	TRLMLLDRSGQGKVYGLVGR* RFQQMDVLEGLNLLITI*RNRN KLRVYYLTWLRIKIMDNDPKLE KKHDWTTAGYMEGCGHYRVG KYERIKFLVIALKSSAEVYAWA PKPY
24009	54377	A	24147	1	340	ERTRMNKQHNSTLAKSRPGNT GPEPLMPQASPGPPGPLSQTPP MHRPVEPQEGPHKSLVAHRVP LKPYAAPVPRS\QSLQDQPTRN LAAFPASHDPDPAIPAPTATPSA RGAV
24010	54378	A	24148	335	869	ATPTLILSQKSHFWPQPLSSVLK LTSGPEISLQSSPSPICRMKKRR LSPLASGLES*VKSGEWCEVLS RAPLFP/HNPSQAAP/EWEMQG TRPSIPHPLGLAGLPTQLQQGRL WGYRNPASPFRTRVAARDCAG KQVRTGPDARLEGSRPGVRAG LGWGRGYSERVQTCAKSSVSPS
24011	54379	B	24149	158	5640	
24012	54380	A	24150	1	1854	

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24013	54381	A	24151	1	1510	MPCGKQGNLQVPGSKVLPGLG EGCKEMWLRKVIYGGEVWGK SPEPEFPSLVNLCQSWKINNLM STVHSDEAGMLSYFLFEELMRC DKDSMPDGNLSEEEKLFLSYFP LHKFELEQNIKELNTLADQVDT THELLTKTSLVASSSGAVSGVM NILGLALAPVTAGGSLMLSATG TGLGAAAAITNIVTNVLENRSN SAARDKASRLGPLTTSHEAFGG INWSEIEAAGFCVNKWVKAIQG IKDLHAYQMAKSNSGFMAMV KNFVAKRHIPFWTARGVQRAF EGTTLAMTNGAWVMGAAGAG FLLMKDMSSFLQSWKHLE\DG ARTETAEELRALAKE\LEQELD RLTQHHRHLPQKASQTCSSSRG RAVRGSRVVKPEGCLATSQPH QHQQERGDRPREDTDNEKRGG EKWSDFGSVLKGEPTGFVHGL DLWCEGKKSQDNGGLWPEQL AGWSCWHLKWTGGSRSGLPVP VLDAACTGTLSPDLTSWRYHPS SIPLPKQPLQHGF
24014	54382	A	24152	3	515	VGTQAGAAPGPVQFLSSAWVA L\HETELPPLTAREAKQIRRE\IS R\SSKWVDMLGDWEKYKSSRK LIDRAYKGMPMNIRGPMWSVL LNTEEMKLKNPGR\YQVRSARA QPTGQAVSGAQVSSWRERQDH PGELGVKIMKEKGKRSSEHIQQ MDLDVSGTLRRHIFFRDRYGT
24015	54383	A	24153	1	1317	
24016	54384	A	24154	1640	4841	TITGSSPLAGGHHSTCRGRMDM VENADSLQAQERKDILMKYDK GHRAGLPEDKGPEPVGINSSIDR FGILHETELPPVTAREAKKIRRE MTRTSKWMEMLGEWETYKHS SKLIDRVYKGIPMNIRGPVWSV LLNIQEIKLKNPGRYQIMKERG KRSSEHIHHIDLDVRTTLRNHV FFRDRYGAKQRELFYILLAYSE YNPEVGYCRDLSHITALFLLYL PEEDAFWALVQLLASERHSLPG FHSPNGGTVQGLQD
24017	54385	A	24155	1640	4056	

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24018	54386	A	24156	479	3902	GQVDEDVSVKMDTVPGVNLSC ILNEMRDQDKKLVEKSYKDAK GCFFSMGEPSLIDPCLEVCYGT QLAQLQGLIRSMEQQLCELCCD AEHQDHEHQVLLDVKTRLEQEI ATYSRLLEVEDAQQGPIVMRA MTSECHWCLAPIRSPDCVCVLR QLHTRSGIHKRFCGLKGFLPER HNPGQLIHQNQSGCCSRMYPFD RKLGISVALNIPGGRSYRDLWC LTAVHIHIPGIDHHRLFTLGRM DMVENADSLQAQERKD
24019	54387	A	24157	780	983	QHQSLIGHKYQRSHRSL*AEPE* LECHQPDLAEPADGPPLTTRYG IVNAEMGLEQLLPKGPSLKEAK
24020	54388	A	24158	773	2016	DWPTLRENRKEPTLKYWGLVP LISGMPTWFFFFLSACGNLIPSG GIRVPMENML/RVFRAVEEHCP WFPEKGTLSVEQWDSVGAKFQ ELVPTGNYVPITVWGDWALLL QFSESGDPLPLPQLSSPTGPSLS DQPLPSPTPPPPDDVENSISNSG DFGLTLPPGDLILFPEEPLLAAS AAPNRTALGHIYANSSLFKPLQ HLPLESANGSGAKLQFTYNSAG PSPSSAAPRPPVVSVPQPVTLPS TQAASLYPSSHMDTSNHQCTSA SSAPPMPLSHTLIPSDETTCNVF NYPLKKPTGRELREAKNKGSQP KVHEKTNPGNIRCISTEERPHEN KGFNHLLEWLAELKTTIHLLDC WFIAKDVNREQPDGRDAGDKR LCVKFLREIAANTYKTEVGAAK VMEILLHSHGATTTIAN
24021	54389	A	24159	365	675	
24022	54390	A	24160	1	1191	

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24023	54391	A	24161	363	1434	QQGVCSGEKGGHWAPRQVGV YLLPGRVGCVSSRVSPSFPGDG LDSGLARRGSAVSALASGLVEE PMLGPPFHPTPRFKAVSAKSKE DLVSQGFTEFTIEDFHNTFMDLI EQVEKQTSVADMLASFNDQST SDYLVVYLRLLTSG\YLQRESQ VLRALHRRVDGTVQRSSAKQE VEPMCKESDHHSHHCAGPGPS ACPSRVGVHGTAARAAPPIRTS F/H*GVPSPKVYLLYRPG\HYDI LYKLGLGSSPLGCPGCPLLARA LGHCYRGFSVVVNGPISPPSSCH MTPPPCFIKGGAGGEPCVRVPA LLPAWLLCLLPPPPRWVPLLFT YLLLSFPNRSRFEGPGLLEAPPA SLGSASFPS
24024	54392	A	24162	2	888	VFRSRHQGCLKMAAEEPQQQN QYPLGSDSEGVNCLAYDEAIM AQQDRIQQEIAVQNPLVSERLE LSVLYKEYAEDDNIYQQKIQ\D LHKKYFVHPQDQGLTGTCFYS GFRDSPTWEGTCWIDSKELQRF QGLVS/SQRSKGKTLVSQGLSL EFHNFEGFSTTTFI/VDLIEQVEK ADLCRRPCLASFNDQSTSD\YL VVYLRLLT/SRAYLQRESKFFEH FI\EGGRTVKE\FCQQE\VEPMW QGEATTSTSLALAQALSVSIQV EYMDRGEGGTTNPHIFPEGSEP KVYLLYRPGHYDILYK
24025	54393	A	24163	3	819	EGATMAAPPQPVTHLIFDMDG LLLDTERLYSVVFQDI\CHRYD KKYSWDVKSLVMGKKALEAA QIIIDVLQLPMSKEELVEESQTK LKEVFPTAALMPGAEKLIIHLR KHGIPFALATSSGSASFDMKTS RHKEFFSLFSHIVLGDDPEVQH GKPDPDIFLACAKRFSPPPAME KCLVFEDAPNGVEAALAAGMQ VVMVPDGNLSRDLTTKATLVL NSLQDFQPELFGLPSYELEGRA SVFRPQPTLMVHTAGGKGKEIS NSSIPTCAVILAS
24026	54394	B	24164	115	594	
24027	54395	A	24165	4	160	SIIFPAIPVSLK*IKPNCPEPPPDH LLQAAWGCVSLGQGLSYSALN TLLYFT

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24028	54396	A	24166	88	2280	VPLYDRMGGETGLLIPSPFRSL HAATDAHSCKNRHSLTGKTDS LWQQDTKLQTRPKATQGKGES GGCGPHRPLLLLRTKSTPESKS AHDPPVAPAQAGASGCGRGAA QKGFGAKAAVDGQGRDRTPG VPAAGPPTSSGRGDRGPSSSRR TRSQTPESPTGRPGSRQFQAAPP PSHHSRPAHAPFPGFQMYRGPL YSSSPAPATPNTSAYESPRFCST SYISSSPRFCPTSYICSSPRFCSTS YICSSPRFCSTSY
24029	54397	A	24167	2	352	WRTLIVLGMSCLGSYPK*MHLT HLIHCS*EARSLVTLHIIPLTICG EPRNIIKLVGCP*IQWKK**KKI MNSRILSPSFRSRY*TSNLLGLP *LRGLSPVERELKLWTNRHKLL
24030	54398	A	24168	2	252	NKSSVFATSCSLDPISIMSLM*W TSVISCRSKK*SRSLRIRL*HKA KELIYPLPVRESMWGYCQLLS MSMPIMHAGTGEMTTG
24031	54399	A	24169	1505	1680	RTSSLVTL*TLHLEPAGT*VLTP GSTTGITVSGTVLFLILLSCFLSS TPFRLKLACLS
24032	54400	A	24170	681	932	
24033	54401	A	24171	1740	1950	HHHHLLQMSWSAGMQAWHW PSFYNVVTGKTLA/LPNLIALQH IPLSPAGVIAKRPAPIALPNSCA ALLSSQ
24034	54402	A	24172	1	652	GKLTEARTRCCMQLTSDRHRH TALNHTTCSHHCNSGVMAGRL GPITVLSGD\GPKGMRALTMW HTLARPTGDLEAPRHGRPRRIT ATQPDHAPPATSRNRAAHP\HN HTP/PHPQTAH/PTATHSHLTYR TPRPTPATRTPL/HPHSHQQYPY Q/PTQRSPYLHPPPAPPHISLHPS TTRATVNAPDTRPTIYARESVPF GRLLNLGRQRGMELANILQVH GP
24035	54403	A	24173	267	400	RFLHCGNLAGLLVGFLSFKLGE YEGLGPLAALTAGKGLFFLPLE SRLRLHRRPKPRSPASFG*VSRH THAIHFN
24036	54404	A	24174	422	452	
24037	54405	B	24175	131	1047	
24038	54406	A	24176	2	199	LGLR/CARLEARARPPWATVRE KLWLFGHPTHMRCSWRGLFQD DLGLQKPLSGGSSSAYRGCENL NS

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24039	54407	A	24177	440	1746	RNLQCVFQGRIKEGIPVLALS/L RPSP/RVLHTATKQKNSCQHLE EDVD\QTKWRTDTPSMDKILME EVKLEEQLKEAVEEDKQALAD TEGSEQSSQKLVEEGNMYSIQG FCKDSLEVADVLEKATQCVPEE EIKDNNPHLKNLCETLTMSEEL SQMVDCCRLPQDVSVLGVALH WVTPQMLCVPVNEDIPEVSDT VLKAITAPPRVPIGRTSGDVTGT GVRRRRVSSAMSQHRAFRDVT VTVQCLELGCFLLRVELASQFL KRPRSPESNEKVPEIEVTVEASA KMSHPTLYDATRSPWGMFQSQ SVLLSCAHHSLLRGATLDRCGS IDESEEWYGMDTFECTGVGVSI RRATEPERSSGSAAALDSHRSM HPIVNHACEGSTLRCPYENLMP DALSLSPILSSRSGDASPQAEILP VVGPFRMRRCLTVDPPGLDVT
24040	54408	A	24178	391	656	

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24041	54409	A	24179	1	2150	MEDSTSPKQEKENQEELGETRR PWEGKTAASPQYSEPESSEPLE AKQGPETGRQSRSSRPWSPQSR AKTPLGGPAGPETSSPAPVSPRE PSSSPSPLAPARQDLAAPPQSDR TTSVIPEAGTPYPDPLEQSSDKR ESTPHHTSQSEGNTFQQSQQPK PHLCGRRDVSYNNAKQKELRF DVFQEEDSNSDYDLQQPAPGGS EVAPSMLEITIQNAKAYLLKTSS NSGFNLYDHLSNMLTKILNERP ENAVDIFENISQDVKMAHFSKK FDALQNENELLPTYEIAEKQKA LFLQGHLEGVDQELEDEIAENA LPNVMESAFYFEQAGVGLGTD ETYRIFLALKQLTDTHPIQRCRF WGKILGLEMNYIVAEVEFREGE DEEEVEEEDVAEERDNGESEAH EDEEDELPKSFYKAPQAIPKEES RTGANKYVYFVCNEPGRPWVK LPPVIPAQIVIARKIKKFFTGRLD APIISYPPFPGNESNYLRAQIARI SAGTHVSPLGFYQFGEEEGEEE EEAEGGRNSFEENPDFEGIQVID LVESLSNWVHHVQHILSQGRC NWFNSIQKNEEEEEEEDEEKDD SDYIEQEVGLPLLTPISEDLEIQN IPPWTTRLSSNLIPQYAIAVLQS NLWPGAYAFSNGKKFENFYIG WGHKYSPDNYTPPVP\PPVYHE YPSVPEMAEMDDPSVEEEQAF RAAQEAVLLAAENEESEEDEDE
24042	54410	B	24180	1	489	
24043	54411	A	24181	39	423	RSPTPDAASRSQCSSRRRRGVS KEVFVSMARTKADWPANRTG G*STPRKPTGPTKSPLRKSAP/A PTGGGERNPHRLQGLVTVAAP* NLDGYQKVHSNFLIRKLSLPSV WVREIASGLLKQNLRFQERQ
24044	54412	A	24182	3	384	
24045	54413	A	24183	1	434	MLQNVTPARAEWQRKTALQG VEDPVPARPPISSPEDLLRSGEC STAPTQRQVPQPVHE/SHRPTQ DSPGARRKPTSERGHTEQRAAP DREARPATRGWGLRPGGQWLG GSEHAAAAPGPSDHPRGRCRH HTILQRPRLLSGKTES

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24046	54414	A	24184	15	286	LPSRGAWLGTCSPPCLSLPPPP WAPVRPEPPR*APPPAPRRPVPS TTQGSLGPHCFYEL*HSPRRSA ASLLKPARPRAHQEERTTPDAP P*EL*HSP*RSAASLLKPARPRA HQEERTTPDAPP
24047	54415	A	24185	2	214	CLSLPPPPWDPVRPEPPQ*VPSP APQHPVPSTTQGLRSVGARRGT GRQLHLQSRCGIHWVKPAGLL SLGL
24048	54416	A	24186	308	311	LPSHGAGLGTCSPPCLSLPAAP WAP/RVARASPTSAAPTPQHPV PSTTQGPLGSPSTLRKL*SFALC NKSCCCSLFGSTLPL*AVTLTA KVCSFTPKA\ARP
24049	54417	A	24187	1	669	MMNEGSGISLSGCDLGTALQLL SQAIVECLKLFQMLNRSTILGSG GQQPSSHSSTKLRPDSGAQLAS PSGSCTGAAGGAACQSRTVCSH SSALGWSMGLGAVEQGVVLV GEAQAAQEPMEGVGGSGMAG CRSRALPHGKAAKARRAIEHST GGLALLGDPVHSPQPLARVLSP SLPRASRAGW/PAPSAGPPSPHP PGTPAGPQAPHAAPVPARASPS TPPCKL
24050	54418	A	24188	157	395	RCSSCQREMTPYGK*NVQKRL KTTKNGSM*LKSHILSTPEQ\PA SPTSS/PPLLQPAAPAPPLMPRPS PPPGISVA*YPGM
24051	54419	A	24189	2	287	CLSLPPPPWAPVRPKPPR*ATPP APRRPVPSTTQGLRSAGARRGT GRQLHLQPLCGIHWVKPAGLLS LVGTWRTFMSSSGIVNTPISTLC LAQGL
24052	54420	A	24190	500	724	
24053	54421	B	24191	1	2154	
24054	54422	A	24192	688	1215	SRLAPALLSPWVVDGTGRCGA VGGAHWGGLGRTGAHGGGGR LRHGGLRVPSPAPREGS*GPPR YRAQRWWAGT/DWRTQYTLRS CWPGTLPSK*REMTPYGK*NV QKRLKTTKNGSM*LKSHILSTP EQ\PASPTSS/PPLLQPAAPAPPL MPRPSPPPGISVA*YPGMPWTC PFYWQ

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24055	54423	A	24193	308	1131	VLQLLRRRTWSCSLRAWSWDL IVPPGGLVVSLASGVKLQTFAV SVTALKEARLDLFVPPGGLVVS LASGVKLQTFAVSVTAHKSSV DPKNSGAQLASPSGSRTETAGG AACQSRAVRSHSSALGWSMGL GAIEQGAALVRGGSGRTG\PME WVGGSGMAGCRSRALPRGKA AKAQREIEHSAGGPALLGDSVH PPQPLARVLSPPLPGASRACWL LRVRGPPSPRPPGTPAGPQAPH AAPVPARASPSTPPLVHLTNDV LRVKVKWAFFFTLHK
24056	54424	A	24194	192	818	SWCLSRAVVGDSMTSEVIED\E KQF\YSKA\KTYWKQIPPTVDR HAWGEGPNKTGTSCALDCGAG IGRITKRLLLPLFREVDMVDITE DFLVQAKTYLGEEGKRVRNYF CCGLQDFTP\EPDSYDV1W\IQW VIGHLT\DQHLA/ESFLRPCKGQ ASAPNGIIVIK\DNIA\QEGVILD D\VDSSVCRDLDVVRRII\CSAG LSLLAEERQENLPD
24057	54425	A	24195	1	233	FFFFETESRCVARLECSGAISAH CNLCLPGASNSPASASQ/CSWD YRCVPSRLANFLYFSTDGISPC WPRMVSNLLTS
24058	54426	A	24196	240	476	LLPQYRRVLLIYSGIQLLPGLGL RRRMCPGIYSFLLDFLVYLRRG VYSIL*W*FVFVVLVPWFSAPS GHLRSSLCCLF
24059	54427	A	24197	288	677	NLPEDVVPDDKPHQPLLRAV\C LFVISKDLFLESPFESPIWRMYP NSTVHIQRLELALLC/CHCPRAL PASAHSCHSLERGLPICKE**CM PCSEYTIASQRPAGGAPAILPEC DSRRRTTQATSEPGSHI
24060	54428	A	24198	99	399	LLCHGFEHPPLAQRSLLLPIV*S LLLSTRQSHSPSSFVPLLARSCG SWVSPAEAAEPQILQKGKCSCL IVPLEALCQRGTRLSLWLPLTFF PSFQLWPV
24061	54429	A	24199	1	586	LSFFKVFSFFAIGSNILFSSEKFII TDHLKPSSPTCQSHSLSSFVPLL ARVAFRWGFGVDVLSFVSFPSN SQDPQLQVCGVCWRSTPDRLP GYHQRGSGGCRTADIIEPQMLR LIVRLEVLSQRSTRPQRCQ\SA\L LGGASQLGCC/GVRDLLEEAVC PFSDL/KLHAGKTTTLFKAVRQ/ SHLSLQRLLLSFVCLCPT

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24062	54430	A	24200	1	822	
24063	54431	A	24201	1428	1801	RSAGIDPE*FFSG/PRRIHTASCL PSQRSSNRACSSSVTRIVSILSRF IGIITPMNRNPRFWRNSTSWTR MNRQTSVNRFTTTLMSFTAAA SRVSVMTVKTSDTCSSRRRSQL VKYHLSISTQVL
24064	54432	B	24202	1	2040	
24065	54433	A	24203	176	564	AWEPKWYSTTATRTHFWEMRS RSIMSTTKAFSTSNSASDSLEEP SSRKTRSSSLLQ*KSCNGGSEM SSTYRVVGLTGASLSASALNSLI DSRSNR*V/FSRNTLANITRRNQ LKMLPAPDPDGFSSGSPFQ
24066	54434	A	24204	1	774	
24067	54435	A	24205	1	1807	MPLRAFNPVSSFRWARGMTIV AALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGEK QAIIAGMAADALGYVLLAFAT RGWMAFPIMILLASGGIGMPAL QAMLSRQPNFDHWTADRHGD LCRLGEHMERVGMDCRRRPIPC LPPRVASRCMEPGHLDLNGSRR HLANGFTTPRIGANQFLRRTVN AQTNPWQNISIASAISSSRTRRIS GSVGSWPRSGNAEVSALHHYV PDLHRRMLLATLWNTYICINEA LALTLSDFSLVPPHPYRQLFTLT TFHNRACSSSVTRIVSILSRFIGII TPMNRNPPYTEASVTKQEKTAL NMARFIRSQTLTLLEKLNELDA DEQADICESLHDHADELYRSCL ARFGDDGNSYDHDYAKLACLQ VEGRGGGTFAHELLAVEYAGW ISPAFRLKVMHWLMNRMLDAR NRDRYKQWKQDFFHDSYNRQS AGHILSQCANLAATTSEYFIHKP HRLIAAETGYSQSTVVRAFREA VNKGILSVEIVIGDHRERRADL YRFTPSFLVFAQQAKNALIESKS KI\SSAATKVRLLAPISPTSPMG KIGLATSGS
24068	54436	A	24206	291	851	
24069	54437	A	24207	2	694	
24070	54438	A	24208	2	331	HLSTIEPEDYNLLFRRVSLKLSV WLPTWQSKSNGWSKKCLWMH LKSNPLNALLPPAGF*SATMPK CSAWAKTISSPGCVITEF*SQPV NAGTSPNKNTYLVGISPLKKP
24071	54439	A	24209	1	4455	

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24072	54440	A	24210	698	1088	LTSKFIAAVCMRRISLCGKGSA QNTDSGIAATPCSCVSD*QNSTS SRIRM*PWMCPCPMKRKSAT*N ITLRC*RAAPPISSRVRK*/MSM Y/NHLQSAECGGHRPFPVPQEE SILLLLHLIANRSSACHSIR
24073	54441	A	24211	1	1902	
24074	54442	A	24212	1	2898	
24075	54443	A	24213	1	2604	
24076	54444	B	24214	1	1254	
24077	54445	A	24215	1	2946	
24078	54446	A	24216	698	1285	RFWRNSTSWTRMNRQTSVNRF TTTLMSFTAAASRVSVMTETA MTMITPSLHACRSKAVAAALLP MNCSLWSTQAG/CSP/DVSAEG KPDIYRLSNRKITTCYSAES/LL KLSVWLPTWQSKSNGWSKKCL WMHLKSNSLNALLPPAGF*SAT MPKCSAWAKTISSPGCVITEF*S QPVNAGTSPNKNTYLVGISPLK KP
24079	54447	A	24217	1	1986	
24080	54448	A	24218	1	2262	
24081	54449	B	24219	1	1014	
24082	54450	A	24220	1	1155	
24083	54451	A	24221	5	386	
24084	54452	A	24222	1922	2146	SSSAGISCWSSSPTPGSIPSRVGS AAA*GWTTSRSSTGSANPSASR KPAAAIRASMPPNCRSGEARWP LWSGSL
24085	54453	A	24223	1091	1435	
24086	54454	A	24224	1	2919	
24087	54455	A	24225	1324	1502	
24088	54456	A	24226	1	2901	
24089	54457	A	24227	5	253	
24090	54458	A	24228	1227	3031	

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24091	54459	A	24229	1	1940	MNRQTSVNRFTTTLMSFTAAA SRVSVMTVKTSDTCSSRRRSQL VCKRMPGADKPVEGRGGGTFA HELLAVEYAGWISPAFRLKVN QTFiDYRTGRLQPAIPQSLPEAL RLAADLAEQKQRLEQKMLMD APKVEFAERVATASGVLIGNYA KVLGLGQNYLFTWLRDNGILIA TGERRNVPKQEYISRGYFTLKE TVIDTSNGSRISFTTRITGKDVV RTTSIVMLAKVTFLSCITMSDFT FSGYELACFVTHSGLSRSAGHIL SQCANLAATTSEYFIHKPHRLIA AETGYSQSTVVRAFREAVNKGI LSVEIVIGDHRERRANLYRFTPS F\LAFAQQAKNALIESKLKISSA ATKVKAVLAKTLALFNFLSTPP CQNDTPSPCQDDVAIKNKKSQ VKKTKRSVSGGAGTTSLKKLTS WIAKAKAKADNLRLSKKRTQK HEFKQKVEAAARKYAYLKNKR SPDIGGISNFDNLPHCMTVNEA LNAVLAKNKDNEQWGAVAGA YIADITDGEDRARHFGLMSACF GVGMVAGPVAGGLLGAISLHA PFLAAAVLNGLNLLLGCFLMQ ESHKGERRGELLKIVVLPGDHV GQEITAEAIKVLKAISDVRSNV KFDFENHLIGGAAIDLQGGGGK PRCVSKSLMLHCTR
24092	54460	A	24230	1	1230	
24093	54461	A	24231	1	799	MKPRTYTVSVTAVKDGVSGVC SFRCSDVSRVSSFQWVRGLADF RSEAADLHNSGAQLASPIGSRT GATSGAPCQSRTHAPALLSLW AVDGTGRHGAGGSTRRQGSGG TQEPMVAGKAQAWRAAGFSG SGDGVGVSILVPWGGTCIGSFR QANSWISGGAFSDAGCDSDRL GKDWNSLEGSEEERKMWESLE LPRDLKSSEDRKMWESLELPRD LLNGFDQNAD\TICTMKSRLRW SQMEMKNLLGTGVNVTLVML* QRDWRHLLLV
24094	54462	A	24232	416	775	
24095	54463	A	24233	548	882	PGGHQYPPCHLEEKETDLPLLY TAVEEKGLSYSIIPGSLVEKPLT STNSSGTPIQSNITSL*IPLAGIMS MAASQN*AI*WPLAPTMQSFTC TT*RLS*SHRRSWWHRGCT
24096	54464	A	24234	144	570	

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24097	54465	A	24235	254	1117	LSRMKLRTLVVSVTVLKDVVS GVCSFRYSDVSGVSSFQWVRG LADFRSEAADLRGLKLQTFVVS VTPHKGSVDPKSDQQRDLLQR VKEQNFRNVKGDPAALAHEDD VNGTESGAPRKHGDRELDDVV ITNPHIEAILENKDWIEDASGLM SHCIAILKICHTLTEKLVAMTM GSGAKMKTSAIVSDMIVVAKW NSPRVDDVVKSMYPPLDPKLL DTGTTTLLLSV\SHLVLVTRNA CHL\TG\GLDWI\DQSLS\AAEEH LEVLREAAL\ASEPDKGLPGPEG FLQEQSAI
24098	54466	A	24236	472	844	RTDGVLVWMSFLFVSFPSNSQD PQLQVCWSLLEVHSRPCLPGYQ QWRLLCPHEITGESMSKLHIIQK YTSSCCLFKSS\SERGSSTPCPSW LGSGEGLSTLHATDFSFSAPMA QRGKSSLVSLE
24099	54467	A	24237	206	456	
24100	54468	A	24238	50	392	LGLLPFFHRCPTQRGGI*RGSLA TAALLSCGGLCPVGS\SRHLCL\ PVRGKRPTQASVMGDALPPTK LECPRSASGCCAGSDNFKPVDL SLLSSMGLGSTELDHLAPWLQP PFQG
24101	54469	A	24239	1	204	SFSVQFCSLVGDPLG*SSCDPLE EKRCSGFWNIQPFCAGFSPSLW DYLSLVFDVDDLQMRSLSGCPF
24102	54470	A	24240	1	375	MCNAQVLEYMGKSSSLLTSDL QLVRDALRSLRNSFSGHDPQHH TIDSLEQGISSLMERLHVMETQ KKQERKPPLVIPRQT/WVWSGP PANSNRPAAEGPDC*KEN*RDA LRSLRNSFSGHDPQHHTIDSLEQ GISSLMERLHVMETQKKQERKP PLVIPRQTGSGVDLQQTPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL
24103	54471	A	24241	1	674	MVVYACSPSYLEAEVGGSLSLE VEATNPKNSSKKFLDLISEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFKYFGI YLTKEEERLKPSRKKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTPPLVIPRQ T/WVWSGPPANSNRPAAEGPDC QKEN*QTERNSINIKKKDIHTKT PLCI

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24104	54472	A	24242	1676	1768	
24105	54473	A	24243	270	471	PSREYQDANPWLKWIKYSVRT LNKSDCYASGYK*ACLLCSVYS HGKAAGECTLSAGSKNGLAEVI KK
24106	54474	A	24244	23	200	AQMKAHGRSRSS*RC\DEEHWR ACRAQEPPCSQSQRERSKRTCR QGTVASKVKCHSEAR
24107	54475	A	24245	3	270	ASTSHVPQPICGLDDLAIRHSAV RLNRERVHSTAVLP*EYTKQRR QGHL*PDPYKKEGAATNEDAL LLRWERGRGARLHIPGCKAPQL
24108	54476	A	24246	135	275	
24109	54477	A	24247	365	583	
24110	54478	A	24248	2906	3114	
24111	54479	A	24249	108	405	NLHTPYRPQSLGQGEPLDDYV NTQGAS/LFSVTKKELGAGSIEE CAAKCEEDKEFTCRYFHCRCTF LSIPQVTSSFLCFPLPLPLLKSSK LLANRDKYRM
24112	54480	A	24250	1	386	
24113	54481	A	24251	1	808	MSYSQCVSDPKAHGILPGYHC WLFRDQGLLKSQHVINPAKAST GFFLQDTLMVLEIKTTIRNYYK HLYAHELERLEEMDKFLDTYT LRRLSQEVIDSPNRPIMSSKIESV KGYTHQQFCHKSTLNKGDRVI DNLTCPPYCCVWFPLAGTGPHI LYLSRLVSNLELFKRGKGRGEQ RKEEVTCGMLRKSLVTSDLPEP GGVTSEGCETAKVTACSSLWE LCHREVLTPYCPKDTCRKWLE TPVRRSCPVRRSRISTCLRKKFG HILAEQLSCA*RCL**FL/YGCFY FQDHECVLKEESSTSFGRINHV LTLKEPLVPE
24114	54482	A	24252	833	1245	ANMFPAFAAVAAGAATEAAA AAAAAPAPLAPARRAAAAARG PPLPRLP/WSCAEVMYHPQPYG ASQYLPNPMAATTCPTAYY/RA GAPTWPAGESPDGQPAGGGGE GHREYRSGARRRPAGTRGAED ALGSAGASLSRKP.

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24115	54483	A	24253	145	766	TGCIREKFHLPEGSLLIVSSRKH LQRLAFQAKVSSMMLPLQGAQ MLQMLEKSLR\KSLPRNPLKVY GT\VFHINHG\NPFNLKAVV\DK W\PDFN\TVVV\CPQ\EQDMDRW TLDHYTIT\YQIYSKDPQNCQEF LGSPELINWKQHLQIQSSQPSLN EAIQNLAAIKSFKVKQ\TQRILY MGRLETAK\ELTPFLAGNQRILS P\SGWAKPKAM
24116	54484	A	24254	215	550	VGFRSCLVMSGRGKGGKGLGK GGAKRHRKVLRDNIQGITKPAI RRLARRGGVKRISGLIYEETRG VLKVFLENVIRDAVT\YTEHAK RKTVTAMDVVYAL\KRQGRTL
24117	54485	A	24255	3	292	TLLNLAAAHCSGPCLLWFQLSF RSPSTSAVGRCRRPSADFHPSRS SRVSAVLLIQ/QRCPLPILIQLKA CHCSCTAKWLGSSPKPETFFEII HPSPS
24118	54486	A	24256	1	789	
24119	54487	A	24257	3	256	TLLNLATALSSGPCLLRLELSFH SPSTTAVCCRHRPAADFPPFGR VSSLLLIQ/QRCPLPLLIGLKACQ CSCAAKCCVRPNRAEQ
24120	54488	A	24258	3	212	
24121	54489	A	24259	2	491	
24122	54490	A	24260	20	272	
24123	54491	A	24261	160	876	
24124	54492	A	24262	623	796	GANSWNLTGTLAVKAGTVENP I*VFATHVESAGPR*LDPRTGSL AVRTKGRHWDQGA
24125	54493	A	24263	242	659	TSNSPPQTRPHVCHGPRQYLLQ LSSRDLEFLVQIAVRSCLCPGLR IRSPVFAVASTSTFGTLRGKVV KDFGFVFPPPWGQPCLCPVEER ALSCQGPVVDSRCPRCGHEGM AYHTQQMRSADEGQTVFYT\C TNCKFQEK
24126	54494	A	24264	66	238	
24127	54495	A	24265	2	278	
24128	54496	A	24266	168	565	TENFRALSTGEKGFGYKSSCFH RIIPGFMCQGGDFIRHNGTGGK SIYGEKFDDENFILKHTGPGML SMANAGPNTNGSQFLICTAKTE WLDGKLVVFGKVNGMNIVEA MECFVSRNGKTGQKITIA\DCG
24129	54497	B	24267	20	88	
24130	54498	C	24268	183	254	

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24131	54499	A	24269	412	590	KSGLATQG/GRRRGWVFLAPQ KGGEGVETQREGVGVLAPSPE KRDLPLRVKDQGRRPCVV
24132	54500	A	24270	550	852	
24133	54501	A	24271	207	381	
24134	54502	A	24272	412	589	KSGLATQG/GRRRGWVFLAPQ KGGEGVETQREGVGVLAPSPE KRDLPLRVKDQGRRPCVV
24135	54503	A	24273	191	235	
24136	54504	A	24274	95	375	AEKIWEGVSQRALGQSSRGSGS GCQMNPLSGRPQVVCFFTAHM LTKKREEGASMLNMPCFQ*KE EMIQANLGPIADSSHCLGIEGPP WAPLTP
24137	54505	A	24275	144	293	WQVPLFWQPFPEPLELWPKAL* LTPSQIFSD*RLKTDAARSPRKP PAPR
24138	54506	C	24276	1	909	
24139	54507	A	24277	1	1744	MGCLGTQRAPRAFLLLPLPLHF AQLSNLTQLQAAASLSMVTHR SSGGGGERGATAAGTEQGGAC LAASLLRGLWDAGEVTPIRVRV RPYDPFTLAPLHEHSEAQCVAS PSLTVTKEKSLLPKSLLAGSREV ARSRALCHGQARPPPRPQVTQQ RTQLQGQRILQWRPATEGPHSP RRGSDSAKGTHPPTTGTCPPRR RQGAGYSRYNSGESRRRLGRQ QDLVARSDEQRDPAPATRRED KMIEELQPFGEHRPRRSPSQGC DTLFQALWFLASPSFQRGGQLQ VLALCKAAAGPGAPQAASTAG TREHGYAWKLGDTRNHRALK RKSQTWLRRFPAGCPDVCSAL ADLRAFMGLRGEEVCADWSM GGHGSGECRRGTGGQRAVVPK SPVQEKGKEPLSLLQYFMVDEK ERFLRITSEHEDNDNSNNSSNHS SINETKETCFIHEPKTPAPVTDW EGSLPLVFNHCRDASLIIHSCFK GVRPHRDACLG/RFTLSGK/FPL SWGRGKYPSTPSPSPLAASPTFL GQGQELVTSARNLTTRPRNAC GPGFLLSHVPSVRDPTGNRTVQ LTWQPLPEPLELWPKAL
24140	54508	A	24278	2	120	QSSAAKPRTSGKGSVREPWAR VPGALGVAAR*AEQSDFQ

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24141	54509	A	24279	1135	1483	ILTMTGSLSCTPSNAVIEKV*VC CSSLSTG*SKV/QVASNTSLCDG ED*GVVIQKKVKLWVFCIFYVL VQSYYS*R*SQIETVRNGCSHW GRFQDIALITGHCKIWTLIVFIQ YFNV
24142	54510	A	24280	1	860	ATTGGTNLRDDIMRLDDTVHV VIATPGRILDLIKKGVAKVDHV QMIVLDEADKLLSQDFVQIMED IILTLPKNRQILLYSATFPLSVQK FMNSHLQKPYEINLMEELTLKG VTQYYAYVTERQKVHCLNTLF SRLQINQSIIFCNSSQRVELLAK KISQLGYSCFYIHAKMRQEHRN RVFHDFRNGLCRNLVCTDLFTR GIDIQAVNVVINFDFPKLAETYL HRIGRSGRFGHLGLAINLITYDD RFNLKSIEAQL*TEIKPIPSNIDK SLYVAEYHSEPVEDEKP
24143	54511	A	24281	848	1218	PMQRKSMLKISVS/PVSVQKFM NSHLQKPYEINLMEELTLKGVT QYYACITELQKLAETYLHRIGR SGRFGHPGLAINLITYDDHFNL KSIEEQLGTEIKPIPSNIDKSLCG AEYHSEPVEDEKP
24144	54512	A	24282	241	477	
24145	54513	A	24283	38	208	MTAGAPPPPPPFET\PEGV*GNP TCSGG*EDASGSTRSQRHPVGL PVSCALRACHLK
24146	54514	A	24284	794	1455	AQQGGTSKKRRFPQDGQQRAG LACSRPPGPGGCGFQAPAGERY PNIKPHPTSVAPLVLCICYLM/P MLPWAWSYWRGARRPSRHPG AFPCSVAHQCPSAARSPTLRQE DPEKGSQASSFPTGPSPQSMVD RCLKGPQLDVSRKQLSLPQTGL RPVLVNQLSKKPTGYPQTQIQW VLMRDTGKDTDTEEKEGHAK MEAEIGVMYPQEHLEPPESGRA KGEIPL
24147	54515	A	24285	90	354	QSPGVHQLSRFVS*SYSERP*SL LVSTRYHTRALH**HYADSIQ* ARSSKHTGLIGCTVP*RGFPRTH SFYSRKREPRRQTSSFRGIL
24148	54516	A	24286	236	520	TACFLTHVAIKWVMHSSIPSSN GGGIYMIGLKAQVSYMRKWLK SPWSPLLLSPSLHRWPHGKFPM IS*QRKRRLGPGSQMVLHDMQ APPKSGQL

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24149	54517	A	24287	16	278	FAQAMKPHLVQQLQLESPLG* AYDNPLSFSKIHLSDLHKPVL*L GDSNDVLGTLESMSAQSQCPV VPEMSDHLPFPMHSYPGKRPEV
24150	54518	A	24288	74	168	LGKCLFLHSCP*APPEAICLQLP LLSSPNGP
24151	54519	C	24289	92	564	
24152	54520	A	24290	1	876	
24153	54521	A	24291	71	282	PLVTQVVFRLFPTNSSLDLLQ/S PSP/GSGPHSNWQPFGSLDKWA GVKHPNEECAASKIQTGPPCVV PLPWL
24154	54522	A	24292	81	1054	PRLFSDCFPPTAAWTCCRAFSC SGPHSNWQPFGSLDKWAGVKH PNEECAASKIQTGPPCVVPLPW L*EEPNAAIYPSPVSPVCFLLLA HWIQSA*CHQCNGPVWYLVEV KSNQVLSK*HYDTKPES*YTPY GQEWRKGHLPSQWPHTRYQE MY*FAQAMKPHLV*QLQLQSP LG*AYNNPLSFSKIHLPSPHGSH SEPCL*GPTRTLV*L*L*KQTGM LAVAPEENQHYLAWQLPQGRP SLLPQAVQGLSPQTKVERLMA ASVGEGMLPILGMEKLF/PSGK KD*SGFTSSVSPASSGSSHTSPF QVAGSHSFPINAFTLTVDTW
24155	54523	A	24293	5	88	
24156	54524	A	24294	779	1041	PPLSSPSGP/DEQSD/LWWQQSIP LHQETVKVLH*MGPVPCATQL DKIHQQGFSDPYRGAVLLASG WCPKRPEIPEEGATTHLCCFPAS
24157	54525	A	24295	248	3714	
24158	54526	A	24296	4177	7804	TFQESRFEQGFQKAIFILELVDA EDPPDEEEEEASSIFSSSFHFLFP SSSSCFSFSSSSSSLLLRSPGDKD MPTAGMPSLLQSSSESPQSYPE GEDSQSPLQIPQSSPESDDTLYP LQSPQSRSEGEDSSDPLQRPPEG KDSQSPLQIPQSSPEGDDTQSPL QNSQSSPEGKDSLSPLEISQSPPE GEDVQSPLQNPASSFFSSALLSI FQSSPESIQSPFEGFPQSVLQIPV SAASSSTLVSIFQSSPESTQSP
24159	54527	A	24297	145	219	

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24160	54528	A	24298	191	1075	QPKVSRHCQTSPGSYLYSLQSG RWTTGKPLQQTKSVYLRSFHH HHFQNHRHYLHHHHLYHHHH YHPHPSHHHLHCY\SQHHHHH HHHHHHHEHHLCRHQKSTQVE YSVFAERENDLGLNGTGDEAL HDNGTTERVSGPPAGYLYRAD YAIGLQPFMPRLGRRTPGAGGP HSRAPELAYLQKLITSPATLPFV YLETGGWSPRDAHRVDNFDM GPRENMGSVWEKSFLFTRNPSK SSYIADKNLIYLYASECIGRQSQ KARASKSGVQAEHPYITGAIKD DTRAIVKTRDLANRLK
24161	54529	A	24299	155	381	LICTSFKILSRLFCPSSL*SSSSQG ACISKLLSVLTYAHLYFALEKE VLTFLSRAIVSSSTLLTHGVAHS LTLFH
24162	54530	A	24300	1052	1338	TGWDGPPANCSSPMEGDSNVH CSCVCCCSCFGLLL/CAIHCCCA PPGCSACGAATLLYSAPLGSSA YGIALLSPFHHVRMMLSTKQEV GLHQTLNLP
24163	54531	A	24301	1	723	MLNVQALVVMVMCFMWASL WAPGGHPSAGNISSWVSGLVSF PEWSSWELVVSVVGWAGKLW LHESLLTLNLSCGLLVVLVALV FDEWHPWSGHVAEACSTGYWS TGGIWFHEIAAP*DCSSSPAME QSWMEND\DELIEVGFRRLVIT NFSELKEDVRTHLKEAKNLEKR LDEWLTRINSIEKTLNDLMELK TMARELRDACTSFSSQFDQVEE RVSVIEDQMNEMKREEKFREK RVKRNEQSLQEI
24164	54532	C	24302	295	430	

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24165	54533	A	24303	811	1947	QTERNSININRNGHQHQNPICRS PSSKTKGSIKPQRSGRNQSRKA ENSKNQSTSSPPKDCSSSLAMK QSWMENDFDELTGAGFRRLVI TDFSELKEDVQTHHKEAKNLE KKIRQM\VTRINSVEKSLKDLM ELKTMARELCDACTSFSSRFDQ VEERVSVIEDQMNEMKRKEKF REKRVKRNEQSLQVIWDYVKR P\NLRLIGIPESDEENGTKLENTL QDIIQENFPNIARQAN\VQIQEIQ RTPQRYSSRRATPRHIIVRFTKV EMKEK\MLRAARQKGRVTHKG KPIRLTADLSAETVQARREWGP IFNILKGKNFQPRISYPAKLSFIS EGEIKYFTDKQMLKDFVTTRPA LQELLKEALNMERNNWYQPLQ
24166	54534	A	24304	1	2394	
24167	54535	A	24305	1902	2413	
24168	54536	A	24306	2	610	WAPPAIHIRCMPEAYNFPRKPL SLIPSAIQSNELIIMNGNRALNIQ LLKRYQCTLDIRYKQTSMLNC YEGTVITPSHIQYPCLSDSYGLY DIGIRNTDFLKGELSMNIRPLHD RVIVKRKEVETKSAGGIVLTGS AAAKSTRGEVLAVGNGRILEN GEVKPLDVKVGDIVIFNDGY\G VKSEKIDYEEVLIMSESDILAIV
24169	54537	A	24307	1	801	
24170	54538	A	24308	1268	1579	TAIWSPSKSALYAAQTSGCSWI ALPSISTGSNAWIPRRCRVGARF SSTGCSRITSSRISQTTASSRSTIF FAALMVVARPRSSSLP*MNGLN SSSAIFFGRPH
24171	54539	A	24309	583	796	IHICDIRFSATPAGGEFWQYIAS RQSIFHAIVETGHALIQPSSVPG LTPAMKAVATTSH*TVESCFRS ASR
24172	54540	A	24310	1	313	MPNVDVVGEMVNTMSASRSY QANVEVLNTEKAMSIAVTTTDP TNTGVSTTSSSSLTG\SNAADLQ SSFLTLLVAQLKNQDPTNPMEN NELTSQLAQISTTLRAY
24173	54541	A	24311	54	323	SASAQVSALSIHSAAFQNEYLSP CPN*RLV\SAFTNSSRQSG*PEK SVSQTPVITASAFT*YADIAASV RNKILRPGTNVFGDTIGFRVQ
24174	54542	A	24312	816	866	
24175	54543	B	24313	1	985	
24176	54544	A	24314	1828	2505	
24177	54545	A	24315	1	1938	

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24178	54546	A	24316	4201	4668	
24179	54547	A	24317	269	503	
24180	54548	B	24318	1	1702	
24181	54549	A	24319	829	1584	
24182	54550	A	24320	1238	1926	IQAAYNRIAPSSSPKFPRACGKP CLGERGRIRGPGPSFGLINRPST PDPTITGVSTT/SSSSLTGSNAAD VQS/SFLTLLVAQLKNQDPTNP/ MENNELTSQLAQISTVS/GIEKL NTTLGSISGQI/DNSQSLQASNLI GHGVM/IPGTTVLAGTGSEEGA V/TTTTPFGVE\WDGTL/TDGST APNGSYNVAIS/ASNGGTQLVA QPLQFALAAERFCALSPGAPYR YDTWVRQWVASP
24183	54551	A	24321	487	1509	FYLQGLRQQPQVRQPLNIGVTA QGVNAAACHPHIAEQQLDHRH RTNVLRTNGVLRPAEGIQERGS FIVSTGFCDVFADFQERVFWRT TDVFNHIWRVAGNVLFQQVPH AARMLQRGIAFGEAVFVQFISP GGFIVLAFFRVVAGEQAIFKAVI LTHDQAGGGIGFGVFAVEFFIV QQVQQYA*QESNVSTGTNRGIV VSYRRRTRKARIDHNQLRAVV NFGFHRPAEPDRVSAHHHDEV GVLDVDPVVGHRKTFFDIWHD DQFIDQRVRRFSGDNRRLQDRE QVGLQSANNSPIDKSLFRGINQF QLYAAFTAQDVNIDIFKTRQQF FAVIGQTTGVQYGK
24184	54552	A	24322	377	749	
24185	54553	A	24323	140	298	
24186	54554	A	24324	342	1094	MGAPWLHRPRRALQRWRLGS GFSCGSGLGLQENNGGRPVMV LALSTLPRRPTRCGCEFYCLIKP GFRLGMKSVKMEIRGLWAGGE DKIAVPAEPRSAGPERTLSDLH NESIF/ITGGGSGLGLALVERF/IE EGAQVATLELSAAKV/ASLR/Q RFGEHILAVEGN/VTCYADYQR AVDQILT/RSGK/LVNTPAETLE TGFHELFNVNVLGYLLGAKAC APALIASEGSMIFTLSNAAWYP\ GGGGPLYTASKHAATGR
24187	54555	A	24325	1	1785	
24188	54556	A	24326	2	1760	
24189	54557	A	24327	2437	2679	TFQYIGQPHGDEFPHVAPVKHG DKLGEGKNHHDKSRHLFHRFN H*MR*IRLTSNCAGSDAISQRD NKEKKNDQWHDTFNKG

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24190	54558	A	24328	3	415	
24191	54559	A	24329	1	1932	
24192	54560	A	24330	1932	2117	RAISLGRTAAGYLNSDVAQRA ASGADPAGDFVVWH**IRKNLS GGARYAIPHLYQHLAWHP
24193	54561	A	24331	1	1017	MRYREPPARGVEPNELHACRSE DKLSEDAFDDQCTGANPRYPLI SELKQILLDTYYGRDYVEDRLS FLLAVATLNGERLDGEMSEGK LVMPFRHVSDAFEQTRETIGVR GNNAINDMVRQRLLN\RFTSEQ AEGNAIYRLTPLGIGITDYYIRQ REFSTLRLSMQLSIVAGELKRA ADAAEEGGDEFHWHRNVYAPL KYSVAEIFDSIDLTQRLMDEQQ QQVKDDIAQLLNKDWRAAISS CELLLSETSGTLRELQDTLEAA GDKLQANLLRIQDATMTHDDL HFVDRLVFDLQSKLDRIISWGQ QSIDLWIGYDRHVHKFIRTGID MDKKPRPSRRCL
24194	54562	A	24332	5	220	GLSWLNYC*ASTLTISLRCATR AVPLTRIRCRPRLLPSRRERTAL PCIYVKIAVTLLTATCASCVRR WIPA
24195	54563	A	24333	3	180	
24196	54564	A	24334	229	564	PGFKPRHSSWQRLPSLGHLPLY GSSVFTLLNLATAHSSGPCLLQ LELSFHSPSTTAVCRRHRPTADF HPSESGRVSHVLLIQ/QRCPLLL WIRLKACHCSCTAKCPGSSQLS
24197	54565	A	24335	148	404	
24198	54566	A	24336	213	1306	SCEHSVAHGRGIMDLSLLKALS EADAIASSEQEVRQIL\LEEADR LQKEVRVDGLGSVLIRLNESTG PKVMICAHMDEVGFMVRSISRE GAIDVLPVGNVRMAARQLQPV RITTREECKIPGLLDGDRQGND VSAMRVDIGARSYDEVMQAGI RPGDRVTFDTTFQVLPHQRVM GKAFDDRLGCYLLVTQLRELH DAELPAEVWLVASSSEEVGLR GGQTS\TRAVSPDVAIVLDTAC WAKNFDYGAANHRQIGNGPM LVLSDKSLIAPPKLTAWVETVA AEIGVPLQADMFSNGGTDGGA VHLTGTGVPTVVMGPATRHGH CAASIADCRDILHMQQLLSAFI HKSNELGGVLRLRIQICRDGNE
24199	54567	B	24337	1	1075	

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24200	54568	A	24338	438	1462	QIVQCLDVPSYTFIWFAVLDPIY GDSVSTGLVVAIISIIVNAITIPIG LYLLNPSSGADGKKNSNLSALI SAAKEPVVWAPVLATILVLVG VKIPAAWDPTFNLIAKANSGVA VFAAGLTLAAHKFEFSAEIAYN TFLKLILMPLALLLVGMACHLN SEHLQMI\TLASALPPAFSLKLIY CAA/ARLMCYTRTGTTSLAITLT ETVTQKLTGSRPRISSYGRNLM WPLAWYKDNGKPHLCSQLETT RIHSTAAQGRSSGSLRRGLGAS PFYRQHDQARSEGQIPITRIPMG LAQRAPKGRAQPRGLTAPFTN GALGQPQGRGTSKQASQTRPR ASAWPHTPT
24201	54569	A	24339	30	177	GSGYQRCHNNAASDRLRSYRK QPAER/WLAPPIDSITSPPASRRA LILLY
24202	54570	A	24340	3350	3430	
24203	54571	A	24341	425	824	SISGSENACFNAT\NHSGRYSQY GACLTSSSCRKGQLARRGLSYQ SPHAPADPAFPAARRSPVFCLS DDGGHKSPRDMSPDKPSRHPD QVALTRRIPSPPAVALPSVVKR TVHEGQGDDDESNPSPLSPDVH
24204	54572	B	24342	1	2118	
24205	54573	A	24343	1	888	
24206	54574	A	24344	730	1101	
24207	54575	B	24345	1	1992	
24208	54576	A	24346	880	1103	TMMRRLISRQPVLPLQKCFSVLI SNPWRVFGGTGGGNQER/CRY AEESVAETRLCP*CRLYAEYDP GSGCAGLSL
24209	54577	A	24347	1	952	MITLRKLPLAVAVAAGVMSAQ AMAVDFHGYARSGIGWTGSGG EQQCFQTTGAQSKYRLGNECE TYAELKLGQEVWKEGDKSFYF DTNVAYSVAQQNDWEATDPAF REANVQGKNLIEWLPGSTIWA GKRFYQRHDVHMIDFYYWDIS GPGAGLENIDVGFGKLSLAATR SSEAGGSSSFASNHIYDYS/NEN AND/VFDVRLARWDSPGGPLTG FPPSALACTSGVSGQKGVPGPP EAQVTFATPKKPGKEACSSIQV LNRGYRPPTFSYNTGVRRSARD YYPRRQRSISTNSPSRRWKGKL NSRRCSTGNRPLVGAVS

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24210	54578	A	24348	805	1274	ASFATTRPVTKLAMRVAIFDSV VGQRYWGSAASPEHSRFAVLW ILASIFR/DRIASLRVQATVKS*K MS*AWYWQGCFRNWKSSPA*Y QFFSPARSASSHFAGEPVSLHSP IALGYRSSESSSCHTSTASLSVH RDYAHLHGLRFDHSSSRRRLCY C
24211	54579	A	24349	275	490	
24212	54580	A	24350	1	696	
24213	54581	A	24351	1	735	MFTPDYRSVSRVLGSGPGYASR MNQPDVMPDIPGKRFYQRHDV HMIDFYYWDISGPGAGLENIDV GFGKLSLAATRSSEAGGSSSFA SNNIYDYTNETANDVFDVRLA QMEINPGGTLELGVDYGRANL RDNYRLGKGLSQGSGVAFDNE KFAYNINNNGHMLRILDHGAIS MGDNWDMMYVGMYQDIHWD NDHG\TK\WWT\AGIRP\MFKWT PIMNTGMKF/GYE/NVESQGPG QNIRTIYLAKP*QPDVMPDIPGK RFYQRHDVHMIDFYYWDISGP GAGLENIDVGFGKLSLAATRSS EAGGSSSFASNNIYDYTNETAN DVFDVRLAQMEINPGGTLELG VDYGRANLRDNYRLGKGLSQG SGVAFDNEKFAYNINNNGHML RILDHGAISMGDNWDMMYVG MYQDIHWDNDHGHQVGGPAG IRPDVQVDAHHEHRDEIRYEKL NPRARDKTFVQFTSQNPDRC
24214	54582	A	24352	1	3414	MIVQPLAIIGSHFDSIAAGNLAR PIAVYGRNEITAIFASLKTMQQ ALRGTVSDVRKGSQEMHIGIAE IVAGNNDLSSRTEQQAASLAQT AASMEQLTATVGQNADNARQ ASELAKNAATTAQAGGVQVST MTHTMQEIATSSQKIGDIISVID GIAFQTNILALNAAVEAARAGE QGRGFAVVAGEVRNLASRSAQ AAKEIKGLIEESVNRVQQGSKL VNNAAATMIDIVSSVTRVNDIM GEIASASEEQQRGIE
24215	54583	A	24353	1	2493	

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24216	54584	A	24354	1	1201	MQPALLIVLNKVRQEARRRAR ACRIRRASGIVQFGKVRRQLAA VELRQRQTPERFVLLRGTRQQA TGQRIVKTEQRVIIITQRSFRRPG EGRRINDHFRFPAHLPSIRPIGK HQTPFGISGHHFNFFTVAIGDDI AQLDRIGANQSVLKGFNKFVV QYATDSMTSQGKGLSQGSGVA FDNEKFAYNI/SFNGHMLRILDH G\INWDNDNGTKWWTVGIRPM YKWTPIMSTVMEIGYDNVESQ RTGDKNNQYKITLAQQWQAG DSIWSRPAIRVFATYAKWDEK WRYDYTGNADNNANFGKAVP ADFNGGSFG\RGDSDEWTFGAQ MEIWGLSRASGTLVTRAWRYK TTPTRHCLLMNHYAGEAAMR WKNYLKSTQKVQLQNFANWP KYSLSTLFHFPFSKSC
24217	54585	A	24355	188	406	FIRSFDPSFVPSVLDRFFVLSTVF HSSSIFLVVIDRPSCVGEPSLF*V GGSCPTNSLYRCSGLAWYLMR SMD
24218	54586	A	24356	1	1798	
24219	54587	B	24357	1465	7841	
24220	54588	A	24358	174	3762	TLNDAMRREKCLARINRTAKS GVVMPKLVTWMNNQRVGELT KLANGAHTFKYAPEWLASRYA RPLSLSLPLQRGNITSDAVFNFF DNLLPDRTIVRDRIVKRYHAKS RQPFDLLSEIGRDSVGAVTLIPE DETQHHYESLTITDEGEFVVFV GPSGCGKSTLLRMIAGLETITTG DLFIGEKRMNDTPPAERGVGM VFQSYALYPHLSVAENMSFGH ATGLAQHKEVAEVLPSRRICWI ANRKRSPVVSVSVWRL
24221	54589	A	24359	364	845	RPLLDHGSSPRLNFLRFWYVVH AHTLMRMTEGWAGFDILRPYR WRRVIAFVVAFYFRHLIALLVV QMHFKLVKGNVDVVFTAQLID STVQLIDSTTTVTQFTHIQTQLM IQRAGTKCRKEDFRHWFVHHP WVL/MSPPSVTLYALFPDRSHR PRRDGSPDA
24222	54590	A	24360	781	1275	

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24223	54591	A	24361	1	1185	MDKFDANRRKLLALGGVALG AAILPTPAFATLSTPRPRILTLNN LHTGESIKAEFFDGRGYIQEELA KLNHFFRDYRANKIKSIDPGLF DQLYRLQGLLGTRKPSCGYVT TAPAARSYRLTSKFIAVGQKAL SSLNIIHIAAPHLEALIIGESDTK NFASHDHAILIYKLEPTTGMLR TRAYIGQHMPLYCSAMGKIYM AFGHPDYVKSYWESHQHEIQPL TRNTITELPAMFDELAHIRESGR TMDREENELGVSCIAVPVFDIH GRVPYAVSISLSTSRLKQ/PRQH RFRLRERQPAGGTPPAGTNSVT GGASLHHARCQRRK*KPYRPER A/ESFLPARGKICWP*AGTLTVC IMASASRLISGCTPDSTCWSTA HAPICRRRGRAINRCHCSS
24224	54592	A	24362	1	801	
24225	54593	A	24363	1523	1950	LLPA/AQKRRVDFLRATDFNAL MPGVVEIDGKNIYTQIIDLTTRE AVVNRPEVHRRYIDIQFLAWGE EKIGIAIDTGNNKVSESLLEQRN IIFYHDSEHESFIEMIPGSYAIFFP QDVHRPGCIMQTASEIRKIVVK VALTALN
24226	54594	A	24364	281	997	LTFARLKGITRKIGRLQSRRRKR CKAMGVDVNRVYSLDELVRG NDILFSATGVTGGELVNGIQQT ANGVRTQTLLIGGADQTPMAT LTEDDVLEQLDAQDNLF\SFMK TAHTILLQGIRQFLPSLFVDNDE EIVEYAVKPLLAQSGQIDDIDV ALRLIYALGKMDKWLYADITH FSQFWHYLNEQDETPGFADDM TWDFISNVNSITRNAMLYDALK AMKFADFSVWSEARFSGMVKT

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24227	54595	A	24365	263	1410	AMISRRRFLQATAATIATSSGFG YMHY/CLNSDAIALGIEQRPDLI LLGGDYVLFDMSLNSSAYSDV LSPLAECAPTFACFGNHDRPVG TEKNHLIGETLKSAVITGMLNQ ATVIAYANRPFELVGTGDLWS GQCKSASASETNLSRLVLAHNS CSKEVMRDEPCDLMLGSHTHR WQLSVPMAGEPFCHVADERYV LGLNAFCERHIYTIPRGGKRIPQ TFAADLPGKGITVNPVQSTITEE TFQTLLVSRALEKLGYTVNKPS EVDYNVGYTSLASGDATFTAV NWTPLHDNMYEAAGGDKKFY REGVFVNGAAQGYLIDKKTAD QYKITNIRQLEDPEIAKLVDTNG DGKADLTGCNPGLGFEGAINH QLGAYELTNTVTHN
24228	54596	B	24366	1	2872	
24229	54597	B	24367	1	1704	
24230	54598	B	24368	1	1470	
24231	54599	B	24369	1	2301	
24232	54600	B	24370	1	900	
24233	54601	B	24371	26	856	
24234	54602	B	24372	1	1743	
24235	54603	B	24373	1	1410	
24236	54604	B	24374	1	957	
24237	54605	B	24375	1	2742	
24238	54606	B	24376	755	1816	
24239	54607	B	24377	1	1968	
24240	54608	B	24378	926	6441	

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24241	54609	A	24379	1	1739	MTWTHEAVNRREPLRGCEPNW DVDVKPAGCMISRRNELPYTLG LRIDMLVDLGTPASLMGQSSVY NTTDRHSTHRMDGLEQLMQQA DFAADIAVVAPWDNWSPTAGR FGLIRLLDEQTAPYAWYTSPMH LMDEKCSCHRQRPVIGLNQPQ YQSGTIEVDNVSFAYRDDYLVL KNINLSVPSRNFVALVGHTGSG KSTLASLLMGYYPLTEGEIRLD GRPLSSLSHSALRQGVAMVQQ DPVVLADTFLANVTLGRDISEE RVWQALETVQLAELARSMSDG IYTPLGEQGNNLSVGQKQLLAL ARVLVETPQILILDEATASIDSG TEQAIQHALRRDCSPLIDHCDA DTILVLHRGQAVEQGTHQQLL AAQGRYWQMYQLQLAGEELA ASVQPLPNSDRRGSMKLVTVII KPFKLEDVREALSSIGIQGLTVT EVKGFGRQKGHAELYRGAEYS VNFLPKAAYTGKIGDG/KIFVAE LQRVIRIRTGEADEAALYLWHT ATERDGPFRNFTAGAFRASLPH PARHGRRPILAAPFMPVNPSRLP PRRRHLASGRSLRFNCCTAGDE TCSARSGERRSLVF
24242	54610	A	24380	547	684	

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24243	54611	A	24381	1	2208	MLLVSASVNAMSISGQAGKEY TNIGVGFGTETTGLALSGNWTH NDDDGDVAGVGLGLNLPLGPL MATVGGKGVYTNPNYGDEGY AAAVGGGLQWKIGNSFRLFGE YYYSPDSLSSGIQSYEEANAGA RYTICVQVFVVVMLIRNQLFTP VNTAIDGFATNYAIMPAYAVG EGVATHGLQFELMRTTGGNTQ HVFHHPLPLFAMWRYAAEMFP YQQMCQFVRYHFFNKSFTVFQ QQNGIEANFIAFQPGRSGGGSA LGRNVFGFRYQPQCQQDKQYV QSRIHPEGVGVTQRVEHGQERC ANDHVQSSGTELMQEGVMSAS LKNQQGFSLPEVMLAMVLMV MIVTALSGFQRTLMNSLASRNQ YQQLWRHGWQQTQLRAISPPA NWQSGAAMLRVYHSNRLDVL EALMEFIVERERLDDPFEPEMIL VQSTGMAQWLQMTLSQKFGIA ANIDFPLPASFIWDMFVRVLPEI PKESAFNKQSMSWKLMTLLPQ LLEREDFTLLRHYLTDDSDKRK LFQLSSKAADLFDQYLVYRPD WLAQWETGHLVEGLGEAQAW QAPLWKALVEYTHQLGQPRW HRANLYQRFIETLESATTCPPG YLRASLYAAIQHALASVREHTT LVVIAHRLSTIVDADTILVLHRG QAVEQGTHQQLLAAQGRYWQ MYQLQLAGEELAASKGHAELY
24244	54612	A	24382	2	729	DCSPLIDHCDADTILVLHRGQA VEQGTHQQLLAAQGRYWQMY QLQLAGEELAASVQPLPNSDRR GSMKLVTVIIKPFKLEDVREAL SSIGIQGLTVTEVKGFGRQKGH AELYRGAEYSVNFLPKAAYTG KIGDG/KIFVAELQRVIRIRTGEA DEAALYLWHTATERDGPFRNF TAGAFRASLPHPARHGRRPILA APFMPVNPSRLPPRRRHLASGR SLRFNCCTAGDETCSARSGERR
24245	54613	A	24383	683	1161	RTGHCH/SAFSFSTVLTSCSLSRF SFLAHRLQYLLRVAEPLPNSDR RGSMKLVTVIIKPFKLEDVREA LSSIGIQGLTVTEVKGFGRQKG HAELYRGAEYSVNFLPKVKIDV AIADDQLDEVIDIVSKAAYTGKI GDGKIFVAELQRVIRIRTGEADE

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24246	54614	A	24384	631	1149	FFGIKEQVITANNANSNRNKTD RCCRNWLEDHADNHCHKHSEV MPCLRRHTVGDRDKKHDTHH HQWGQ*FPYIIFWLVSPLIAISRS KVSTHGLRQRDFILLREASQSF RFVLRVYDVADHIAGKFTVHD LQFIGYHGGQAQLVAQVFSKES KAAGGNRHFPAQRFQLEHQLR
24247	54615	A	24385	833	1264	
24248	54616	A	24386	1	1632	
24249	54617	A	24387	2078	2371	
24250	54618	A	24388	1	159	
24251	54619	A	24389	530	811	RPGTGTAAQVLNRRIKISRST*L TVVMGYWSIIPSVSLLKWDRR KSPKCSSALRVNISNTLLSTARR RKRYLIVIPALLVVRRCRPRGPS ACG
24252	54620	A	24390	1806	2115	AAFQEIELAFQDPQCVGLLTAP MLMPLFLDQLILQCFFW/W/TN LERA*TSFSALFIDLQPPGYRTT TSKHKVSSSLIKGHVLLDHSFH DLNTQLWISTNAFRFGN
24253	54621	A	24391	1476	1751	ALLLVSFASQRFISA/TVGNQNA GVDLLNLTLLVGGIFVLNNAGN FAVFTGDTSITGRIIQFHRQQTN ATLRFSITQTLECFDRDQRHVA VEH
24254	54622	A	24392	606	4519	EEVVRAISAKRNEPEWMLEFRL NAYRAWLEMEEPHWLKAHYD KLNYQDYSYYSAPSCGNCDDT CASEPGAVQQTGANAFLSKEV EAAFEQLGVPVREGKEVAVDAI FDSVSVATTYREKLAEQGIIFCS FGEAIHDHPELVRKYLGTVVPG NDNFFAALNAAVASDGTFIYVP KGVRCPMELSTYFRINAEKTGQ FERTILVADEDSYAAKRLTDYP HQLSGGERQRVMIAMALLTRP ELLIADEPTTALDVSVQ
24255	54623	A	24393	129	256	

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24256	54624	A	24394	1	1082	MAMSKVKSITRESWILSTFPEW GSWLNEEIEQEQVAPGTFAMW WLGCTGIWLKSEGGTNVCVDF WCGTGKQSHGNPLMKQGHQM QRMAGVKKLQPNLRTTPFVLD PFAIRQIDAVLATHDHNDHIDV NVAAAVMQNCADDVPFIGPKT CVDSWIGWGVPKERCIVVKPG DVVQVTALEIHAPDAFDRTAPI TWLADQKRRRTVKGRTTRPCN RSVTVRPRRRDAVIGRFYRHQS ITQKGLLLMVMPGCAFPLWIDS ELNLTFIDALFEGVSGITTTGAT VIDDVSSLPRAYLYYRSQLNFIG GLGVIVLAVAVLPLLGIGGAKL YQSEMP/AAI*G*QTHSPPGRYV TDTVDNLFFIRCRT
24257	54625	A	24395	49	281	ASDHRYLCSQSVPLRGIPACYL LQAPLTRWR/RIPPSRRICAAIDS AISRSPQRWLTAVCCGTVNFTN TCLLPDGVCA
24258	54626	A	24396	737	1419	CIWRMYSHRLVAWRRCVKRR/ RYLTRFAKTRGVAIVMVGHVT KDGSLAGPKVLEHCIDCSVLLD GDADSRFRTLRSHKNRFGAVN ELGVFAMTEQGLREVSNPRGR GKRKFISPKKTPALAKFRRNLL PPKVPGNGTSVRFRHSRICWMN PLPGAAWNCILTLKKPISPGVQ VFPESFTPARLEAFAGRSQACL VPAQNILHQKSQAWLFDFPEQE KELRELSAWMAGA
24259	54627	A	24397	526	1693	STTGIRSIAMSNPILSWRRVRA\ LCVKETRQIVRDPSSWLIAVVIP LLLLFIFGYGINLDSSKLRVGIFL EQRSEAALDF\THTMTGSPYIDA TISDNRQELIAKMQAGKIRGLV VIPVDFAEQMERANATAPIQVI TDGSEPNTANFVQGYVEGIWQI WQMQRAEDNGQTFEPLIDVQT RYWFNPAAISQHFIIPGAVTIIM TVIGAILTSLVVAREWERGTME ALLSTEITRT\ELLLCKLIP\YYF\ LGMLAM\LLCM\LVSVFILGVP YRGSVLILFFISSLFLLSTLGMG LLISTITRNQFNAAQVALNAAF LPSIMLSGFIFQIDSMPAVIRAVT YIIPARYFVSTLQSLFLAGNIPV VLVVNVLFLIASAVMFIGLTWL KTKRRLD

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24260	54628	A	24398	655	915	IAVNVTLAFNGGKQLR*STSLL CCQEGLAFAVNLRQHFRVQTIS FFFLPVLRFWRPGIQQAKKCHP APRTAKGIPQQVIRAMRLLFK
24261	54629	A	24399	549	827	
24262	54630	A	24400	472	626	WRFFRPRKDNIRRTLFADGHQI AAQPGLNLSCTRTIF*IKRINTFP GRWRK
24263	54631	A	24401	333	617	SDQSETDYRFADGERHLENQPH AGQTGRGGAGPGCTLYQRFAQ LCEVSEVERSGCRTLSAQHVEQ NLPAAICGGDDADGAVVHLWT TA*RTRIGTLRSGPKMNDSAISII TATDSGWKILLHMLS
24264	54632	A	24402	74	265	
24265	54633	A	24403	1	1005	
24266	54634	A	24404	1068	1185	SVAIRQASTGNRCQCLCPACA WA*VNADVK*SARVSRL
24267	54635	A	24405	1	2292	
24268	54636	A	24406	720	2496	RRAGYRKAADAMTTIVPEKLS REVGSHFHALDRTTAVHRQPVI SATTTVHEFLRCHQFPLVVCDG GRMTPRAMFLFSSAHILMPLNY HNSHINTLFPVAGTLMVEPTES ESKVELDRFIDAMLAIRAEIDQ VKAGVWPLEDNPLVNAPHIQS ELVAEWAHPYSREVAVFPAAL VTGGSRGIGRATALLLAQEGYT VAVNYQQNLHAAQEVMNLITQ AGGKAFVLQADISDENQVVAM FTAIDQHDEPLAALVNNAGILF TQCTVENLTAERINRVLSTNVT GYFLCCREAVKRMALKNGGSG GAIVNVSSVASRLGSPGEYVDY AASKGAIDTLTTGLSLEVAAQG IRVNCVRPGFIYTEMHASGGEA\ GRVDRVKSNIPMQRGGQAEEF AVQTFPVWRVAQHCAVRPFRQ RIGQLRDIFHLKGDQFTNPRKT GVTPQPPCSTYPDPSPPPVPAAG HIDRPALAPTFTPPIMCSKATVK PLSPSPPGTPDPASVLPFREQRA AVHRLRTVVTRHLLALRRDPF ANRHRQQDQRNGGFHHRQRHL HTGKTRSLHHHQFAALRQHPK TKQRRKQSRHREEDLHIFRHAQ
24269	54637	C	24407	49	186	
24270	54638	A	24408	470	811	
24271	54639	A	24409	1	1006	
24272	54640	B	24410	1	2793	

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24273	54641	A	24411	463	1258	CCRSSWCNSDSETGLQIVASYF EDRNGDS\LALRPEGTAGCVRA GIEHGLLYNQEQRLWYIGPMFR HERPQKGRYRQFHQLGCEVFG LQGPDIDAELIMLTARW\WRAL GISEHVTLELNSIGSLEARANYR DALVAFLEQHKEKLDEDCKRR MYTNPLRVLDSKNPEVQALLN DAPALGDYLDEESREHFAGLC KLLESAGIAYTVNQRLLNYRLS ANLIENNLSLFDGEGIYRFYHPK PTKNAERENRQCRNDLFFRCGF
24274	54642	A	24412	221	832	TMAENQSTVENAKEKLDRWLK DGITTPGGKLPSERELGELLGIK RMTLRQALLNLEAESKIFRKDR KGWFVTHPRFNYSPELSASFQR AAIEQGREPF\WGFTEKNRTSDI PETLAPLIAVTPSTELYRITGWG ALEGHKVFYHETYINPEVAPGF IEQLENHSFSAVWEKCYQKEPV VKKLIFKPVRMPGDISKYLGGS AGMP
24275	54643	A	24413	158	481	
24276	54644	A	24414	2201	2350	
24277	54645	A	24415	621	1830	AGWKRGGAGEPDQGLQA\EME VLENLQELKDLNQRQAHAESKI FRKDRKGWFVTQPRFNYSPELS ASFQRAAIEQGREPSWGFTEKN RTSDIPETLAPLIAVTPSTELYRI TGWGALEGHKVFYHETYINPE VAPGFIEQLENHSFSAVWEKCY QKETVVKKLIFKPVRMPGDISK YLGGSAGMPAILIEKHRADQQG NIVQIDIEYWRFEAVDLIINLCF MVTINNARKILQRVDTLPLYLH AYAFHLNMRLERVLPADLLDIA SENNLRGVKIHVLDGERFSLGN MDDKELSAFGDKARRLNLDIHI ETSASDKASIDEAVAIALKTGA SSVRFYPRYESNLRDVLSIIAND IAYVRETYQDSRLTFNIEWGKS SCCSPYVHPWAKLAAIYYRLQP HINDAF
24278	54646	A	24416	83	502	
24279	54647	A	24417	15	95	
24280	54648	A	24418	500	786	LTQRFGTVPLLLQ\AYLYSAFFF TPEFLRPAPPLFSAAVLPEQRQR AQGIGGLVIRPTVELHQALQLF FGHQPKIQSLHALLRGSTGFQA SFRLPL

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24281	54649	A	24419	1	2914	MYYSHASCVADQYACGMHRT PSRTGRPRIHAPRQARLKPQVK VASKKRNARDKMQPPNEQQKT RAHACTPSSRFRAVVRTLTCPV VANVTRIFPRYFSNTRVLRRRR KQARGTWWRLRHLHLYVQPH KHTSYYIYRLYRVTYVMSAQV VDTGIYEFTTRKHDIGTIELPNS EIRYHGNPAMSRPRKTPTPPNSP ASERATGPTTLLPPIRQRRYAA RHTSTIAYTNSTSDIFEAPYNKA APIMRYTSVYCSLFSP
24282	54650	A	24420	2	420	CPYPENRWRGKILARPLLFRAA *ASRFAGAGMPGRLIPTVRPRN SNSGRLVSASRCAKESLTVTTC TPLPGSAVREASN
24283	54651	A	24421	212	497	
24284	54652	A	24422	1	1149	
24285	54653	A	24423	535	589	
24286	54654	A	24424	1	1458	MFDPETLRTFIAVAETGSFSKA AERLCKTTATISYRIKLLEENTG VALFFRTTRSVTLTAVGEHLLS QARDWLSWLESMPERAATVW MFVPTPLSVASGLQRIGRAGHQ VGGVSKGLFFPRTRRDLVDSAV IVECMFAGRLENLTPPHNPLDV LAQQTVAAAAMDALQVDEWY SRVRRAAPWKDLPRRVFDATL DMLSGRYPSGDFSAFRPKLVW NRETGILTARPAAFAADSDIAD GQTQRFDFSILQSMAHDLSQTA WR/GIQYDAEKSLWHNVE\NRQ LDAQFFHMGMGFRRRVRMFSV DPATHLAREIHFRPELFKYNDA GVDTKQLEGQSDLGFAGFRVF KAPELARRDVVSFLGASYFRAV DDTYQYGLSARGLAIDTYTDSK EEFPDFTAFWFDTVKPGATTFT VYALLDSASITGAYKFTIHCEKS QVIMDVENHLYARKDIKQLGIA PMTSMFMPRKNASRLSKRCYDI RERDGREERK
24287	54655	A	24425	157	650	PIRASTCLFKPLITQCFRQFGSE GVNDHLLGILLIDPARAQIEYLF IINTPHRRAVAAFHIICIDFQLRF RIHFRQFAHQQIVVGHLTIRFDG VLRDVDQTVKYRAAFVADDSF VQLSAVTKTFIVFQPGTGITHLV FHRHRQAQ*PFKVPFSRRLRNGI HTHC
24288	54656	A	24426	269	2024	

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24289	54657	A	24427	1	3548	MPRSNYFSERCKGEIFLKFENM QRTGSFKIRGAFNKLSSLTDAE KRKGVVACSAGNHAQGVSLSC AMLGIDGKVVMPKGAPKSKVA ATCDYSAEVVLHGDNFNDTIA KVSEIVEMEARIFIPPYDDPKVI AGQGTIGLEIMEDLYDVDNVIV PIGGGGLIAGIAVAIKSINPTIRVI GVQSENVHGMAASFHSGEITTH RTTGTLADGCDVSRPGNLTYEI VRELVDDIVLVSEDEIRNSMIAL IQRNKVVTEGA
24290	54658	B	24428	1	2691	
24291	54659	A	24429	2174	3315	NLPKPDWARSAPHPASANYKS NTRRLPFAREQ/QDQHTLLAGT LFIAKILIPMQIAQSAAYRRRCP DAQLHFLPLQLAPRGHRYKRV CQVRYPPIIALIPVVFRLMNDAN GLSQPADAGLAHHEMRNFLDF ASSNVAASRRRCVAALPCATG KGRQANEQAENKCSKDPQTHR TDNKETKTPPARPTTTTQPHTK EEEPLSTPTQTKHPPTHVTGTGP HPTPASGQTEKHERKRPTQQKS NARQNSKDKRTPNKSKTTKPN RGYNQHPAGEPTMSTHEKVKP HQQNRKIQAPPKRQKTDHRHT HNTHPHPPHRAASTTTQAAPPP RRATRSGTSATAHNNTEPHGTR HTQPGDHKRAEEHDRTADEPT PPEHTLPSHTQLGP
24292	54660	A	24430	1	2925	
24293	54661	A	24431	341	689	RPLAFRQRCTFYWR\PGSANCR LV*GASGTDPRLYSPCAAAADD CGRRQNAGRRRRATSGD*SPHR RWENALLFDSRHRHCPRRAKN AGGEYRQRGIAGSDLQQRFTA AEKDHSRS

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24294	54662	A	24432	1	1931	MGTLLGTLTVLTLVAEELPAET DVAADPAASPTCTAVNQTIGRA IVAADFFIIFQLWQNTVRQLVT HFKPHGQSEMSDTPELINRARY LTYLYCRQPAKAIRELSEQELA WKKQATHEYQVLVTRCKQTL HQVEPLREIEPGRKRLVFDENL RPKQNPIPHLLDTCWPLTVDEH ANRSSIGNNNISFVVNRAVVTN VLNTMRTACNSQATIQIYNADI ARDFGTRGIFSINSGFSTVIRGG VVTVDLSAGAAIGDSALAFVID DGLVAVNLDTDGLRIGDGHGA LVIHRCAVAGDINTVTAAADM DLEDPRIISARFGVPRTQVRTW VALYEKHGEKGLIPKPKGVSAD PECVLGRESCDRAAHVPYQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK AAEIPRSTFYYHLKALSKPDKY ADVKKRISEIYHENRARYGYRR VTLSLHREGKQINHKAVQRLM GPSHLKQRLRSSDTALTEERDF KATRPNEKWVTDVTEFAVNGR KLYLSPVIDLFNNEVISYSLSER PVMNMRRSRPGVGYFYALTPV YLANRLQALLGVEQ/HHPDGEL FLTGYVADGGYHS
24295	54663	A	24433	3	158	
24296	54664	A	24434	1	3432	

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24297	54665	A	24435	1298	2649	TFITRPTSNGTSIFKLMNRRRLE GGNVATLR/RLTIGMIFQDHHL LMDRTVYDNVAIPLIIAGASGD DIRRRVSAALDKVGLLDKAKN FPIQLSGGEQQRVGIARAVVNK PAVLLADEPTGNLDDALSEGIL RLFEEFNRVGVTVLMATHDINL ISRRSYRMLTLSDGHLHGGFGG RLDRFRKSVGGSGDGGRNAPK RAKSSPKPVNRKTNVFNEQVR YAFHGALQDLKSKPFATFLTV MVIAISLTLPSVCYMVYKNVNQ AATQYYPSPQITVYLQKTLDDD AAAGDPDRPSLQLRWRVIPGFS IAVAIYFLNESLGRPLMITGYSA ECSLLAWPVRSGLRKAPMKTFP LQSLTIIEAQQKQFALVDSICRH FPGSEFLTGGDLGLTPATELKPR RLPSGVEQVLADAFHAQAAAL VQGAGTGAIRAGLAALLKPGQ RLLVHDAPVYPTTR
24298	54666	A	24436	546	707	
24299	54667	A	24437	428	1464	RNSRSLAEISRLRGQTRSGLPM LLNLQSMGAS/WYLSPVIDLFN NEVISYSLSERPVMNMDHHLL MDRTVYDNVAIPLIIAGASGDD IRRRVSAALDKVGLLDKAKNFP IQLSGACWHCRAVVNKPAVLL ADEPTGNLDDALSEGILRLFEEF NRVGVTVLMATHDINLISRRSY RMLTLSDGHLHGGFGGRLDRF RKSVGGSGDGGRNAPKRAKSS PKPVNRKTNVFNEQVRYAFHG ALQDLKSKPFATFLTVMVIAISL TLPTSCYMVYNIAKSERISDIST QLNAFPGCEVAVSDAPSGQLIV VVEAEDSETLIQTIESVRNVEGV LAVSLVYHQQEEQGEETP
24300	54668	A	24438	1	429	
24301	54669	A	24439	307	424	
24302	54670	A	24440	300	468	
24303	54671	A	24441	946	1558	KGCVSIPFFSFSWAVMSNLTYL QGYPEQLLSQVRTLINEQRLGD VLAKRYPGTHDYATDKALWQ YTQDLKNQFLRNAPPINKVMY DNKIHVLKNALGLHTAVSRVQ GGKLKAKVE\IRVATVFRNAPE PFLRMIVVHELAHLKEKEHNK AFYQLCCHMEPQYHQLEFDTR LCNRIRLNGHDHFRRRYALFRV NTGRTASPVIQP

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24304	54672	A	24442	1	774	
24305	54673	A	24443	1	452	MELKKLMEHISIIPDYRQAWKV EHKLSDILLLTICAVISGAEGWE DIEDFGETHPDFLKQYGDFENG IPVHDTIARVVSCICPAKFHESFI NWMLDYHSSDDKD/DHRN*W KNTPAFL*QESP*GSDSCH*CVL NNAQSGHRTDQDG*EIQ
24306	54674	A	24444	486	572	
24307	54675	A	24445	1	683	MHSLVIGQIKTDKKSNEITAIPE LLNMLDIKGKIIKTDAMGCQKD IAEKIQKQGGAVMNLQRFDDST LIRIFALHELHRLKEHGLTRGAL LDYHSRYKLVFL\AHPQPESRK LGPF\VADIHQWQNLDDYSPQY RQRVVVLLSHPANARDHTNVL MHVQGYFRPHIDSTERQQLRAL IDSYRRGEQPLLAPLMRIKHYM ALYPDAWLSGQRYFELWPRVI NLRHSGVL
24308	54676	A	24446	896	1066	WRLSPSSR*LMPKVPRIQAYFT T*YCS*VIQRSPC*FHCYSRSIPW AWGAGKQSLT
24309	54677	A	24447	1	3660	
24310	54678	A	24448	1	1530	
24311	54679	A	24449	1	1890	
24312	54680	A	24450	746	1872	KHWRGSLISLSTPARFNGGPFW GANQGGDPKGRGGSQRALFRR KNNRGGETVSGAEDACIVNNN AAAVLLMLAATASGKEVVVSR GELVEIGGAFRIPDVMRQAGCT LHEVGTTNRTHANDYRQAVNE NTALLMKVHTSNYSIQGFTKAI DEAELVALGKELDVPVVTDLG SGSLVDLSQYGLPKEP\MPHELI AAGVSLVSFSGDKLLGGPQAGI IVGKKEMIARLQSHPLKRALRA DKMTLAALEATLRLYLHPEALS EKLPTLRLLTRSAEVIQIQAQRL QDPLAAHYGAEFAVQVMPCLS QIGSGSLPVDRLPSAALTYTPH DGRGSQLESLADRWRELPVPVI GRIYDERLWLDLRCLEDEQRFL
24313	54681	A	24451	1358	1419	

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24314	54682	A	24452	1	1568	MKGRNIDAQEIQKRYGMVGDP VIIGVVLGLIFGLAAGEGFKGC ASLMITVAAIMVLFPRMIRLIVE GLLPISDGARKFFQKYFKGREV YIGLDTAVTLGHPTTIAVGLLLI PIMLILASILPGNKVLPLADLPV APFFICMATVIHRGDLVRTLISG VIVMITVLLIATQFAPYFTEMAL KGGFSFAGESAQISALSVGNMF GWSISELMSLGIIGRVVAVGIVA SVVLFLRVLSMSWLKEVIGTEK AVIAMCHLRALPGDPSFDAQLG MNWVIDKAWDDLMALQNGG VDAVMFSNEFSLPYLTKVRPET TAAMARIIGQLMSDIRIPFGVNV LWDPVASFDLAMATGAKFIREI FTGAYASDFGVWDTNVGETIR HQHRIGAGEVKTLFNIVPEAAV YLGNRDICSIAKSTVFNNHPDA LCVSGLTAGTRTDSALLKRVKE TVPDTIVVLANTGVCLENVEEQ LSIADGCVTATTFKKDGVFANF VDQARSNNPSAIPAAFVKSIDG DRYQINPNRHGVNDG
24315	54683	B	24453	1	3352	
24316	54684	B	24454	60	2284	
24317	54685	B	24455	1	2475	
24318	54686	B	24456	1	2890	
24319	54687	A	24457	1065	1139	
24320	54688	A	24458	282	615	
24321	54689	A	24459	2657	2919	
24322	54690	A	24460	1	835	
24323	54691	A	24461	167	338	
24324	54692	A	24462	834	1515	LRWCSMPCCRWSKDRAAPSPA YSRLSSHVIIAGYVGGGVARG\ HSWVFVALTLVLTAVLFSLAGL LNGVFAKTFDDISLVPTFVLTPL TYLGGVFYSLTLLPPFWQGLSH LNPIVYMISGFRYGFPWLNHNR PGVAVDINRLLLPRKQEKLGIK LDKDQLIAGVQDAFADKSKLS DQEIEQTLQAFEARVKSSAQAK MEKDAADNEAKGKEYREKFR QIPSVSSCQKQ
24325	54693	A	24463	3	557	
24326	54694	A	24464	255	693	
24327	54695	A	24465	3	242	QKAPVLANQRQPRRPTGALLLE /SLPLVAESSDG*EPMTNATEPH SRPLP

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24328	54696	A	24466	1	2636	MKNIIRTPETHPLTWRLRDDKQ PVWLDEYRSKNGYEGARKALT GLSPDEIVNQVKDAGLKGRGG AGFSTGRKWILMPKDESMNIRY LLCNADEMEPGTYKDRLLMEQ LPHLLVEGMLISAFALKAYRGY IFLRGEYIEAAVNLRRAIAETTE AGLLGKNIMGTGFDFELFVHTG AGRYICGEETPPLLKPQTGVWQ RHSCWKLQELAMNDRDFMRY SRQILLDDIALDGQQKLLDSQV LIIGLGGLGTPAALYLA
24329	54697	A	24467	506	673	
24330	54698	C	24468	1	3411	
24331	54699	A	24469	2455	2694	
24332	54700	A	24470	1	1081	MGGLRDPWLHKLRSLWGLCR YGHKEQYDHIRIELNLAPGDTT LVPTGLAIHIADPSLAAMMLPR SGLGHKHGIVLGNLVGLIDSDY QGQLMISVWNRGQDSFTIQPGE RIAQMIFVPVVQAEFNLVEDFD ATDRGEGGFGHSGRVFCNMAE KQTAKRNRREEILQSLALMLES SDGSQRITTAKLAASVGVSEAA LYRHFPSKTRMFDSLIEFIEDSLI TRINLILKDEKDTTARLRLIVLL LLGFGERNPGLTRILTGHALMF EQDRLQGRINQLFERIEAQLRQ VLREKRMREGEGYTTDETLLA SQILAFCEGMLSRFVRSEFKYRP TDDFDARWPLIAA\SCSNMTPD
24333	54701	A	24471	93	475	RCKCADAATRGKSRRDLPDVQ NSARQYG/WI/GCATHARSG*HI VEAVQSG/TPPQPLRPRGTSRKV STDRYWRAASQLPAQYQDLTSI YDVYTVPDRVAKRAFKSPPDD GPVMWRMGHQPHLIPRNVLAQ
24334	54702	A	24472	254	1150	RFLTCRYGPGMAEDMQSLVGG TVTRSG*LSVVVNNNGE/LLAK ELSVQVGIRPEYLDRLLHAFSG GQRQRIAIARALSSQPDVIVLDE PTSALDISVQAQILNLLVTLQEN HGLTYVLISHNVSVIRHMSDRV AVMYLGQIVELGDAQQEIAQA LRRTPAPMVYIGNLGRELSLPA ANLKLESKLAIMEQYVGKKVID AVIVGPKVDVSAVKERIVIQEV LEASDIPYRHDRQLLHNALEKA LQALGGLEVIQLYRRDSNLVPG QLLKTSEMGKTRLYAADSRLIA AKGSPIQPTLDSLK

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24335	54703	A	24473	1874	2927	KEDQVKGGMVCPKKLLCQGTR *RGGVVGGISQASVTSVIGYSA SCQPTPAIMQLHL/ANAASRRL QPDRNRPNPGWHRPPIHAFTTP GLVSVSFLGYPCSTPTCLPFSES SVGESVNLWPQSNENLRRTLV GEGNLLLTFIGNGKHEIIASIFFA FSEGISAQSHWQPRYISPASVCT LVTEIDIKANKITFSIFDENAGA WLPPFCKAVVPGWVYKPNLGH EIACVDHWLMPNRLIENLCDIM LPIWVLTKFNDCCAGCVPCCVII VDDALHGAPKRMCCCITRGMR LLKLSVHAATRSTLQQASHGH CAWSAPGWLDTSGMDGDRLW WTLHEVLRDLCTSHGNIVESAR
24336	54704	B	24474	1	672	
24337	54705	B	24475	1	2496	
24338	54706	A	24476	3260	3363	RPDSGGP*RQRRYLRCADHRRR AVRNQQQLTACA
24339	54707	A	24477	112	224	
24340	54708	A	24478	1614	2326	CTYSRKCRPDKRSASGNFALSS LKSSPLTKNRRYWKVSPTHLLL SKRPKISLNAYFGACSLVRPVL AAASDWTLQGAWSPTRAKALP ICESWRIPYADSLSSLAASCDAV FVHSSTASHFDVVSTLLNAGVH ICVDKPLAENLRDAERLVEG\M REWREERGQGVVHKPIPGWQS TLEQRGFVGCARHFIECVQNQT VPQTAGEQAVLAQRIVDKICSS FNVVRVAPLGDPIQSKPVV
24341	54709	A	24479	19	885	
24342	54710	B	24480	1	1704	
24343	54711	A	24481	974	1156	

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24344	54712	A	24482	162	1602	HRRKRARGTPKATTTRKPARTI ETLSPLLAILAFAPKLAICTRSPL L/DDMTPFTQCTNAYSHSGIRNP TAISSAAYPRRITGY/KLGPTGE ERTVYGIYGISESNLAECEKGV KSAVALTPALQPIDGVAVSYID AAVALGNTINEMDKYYTQENY KDDAFAKGKTLHQTFLKNLEA FEPVAESYHAAIQEINDKRQLA ELKNIEEREGKTFHYYSLAVMI SAKQINNLISQDKFDAEAAMKK VSELETLVAQAKEADKGGMNF SFINSAGQYQLEAKKYVRRIRD KVPYSDWDKEQLQDANSSWM VEDSFPRALREYNEMLMTRIGG GAGDQDMVNDFSYSPQLVGRG WFNDQVATGCTRDSTFNQQQV ALSVNAYYVVNRFGKIDWKPM YAEADKLLAKPNMRFKSDKLV GDLSIGDQQMVEIAKVLSYESK VIIMDEPTDALTDTEAESLFRVI REMKSQAPRYCLYLPPHENNL
24345	54713	B	24483	1	1263	
24346	54714	B	24484	148	894	
24347	54715	B	24485	1	1071	
24348	54716	B	24486	168	1088	
24349	54717	B	24487	1	1236	
24350	54718	B	24488	1	849	
24351	54719	B	24489	1	1548	
24352	54720	B	24490	1	1372	
24353	54721	B	24491	1	2469	
24354	54722	B	24492	1	1917	
24355	54723	B	24493	1	1159	
24356	54724	B	24494	1	2294	
24357	54725	B	24495	217	2476	
24358	54726	A	24496	477	916	SLPECEDRVQYRRSLFADPSYR YGLARHGDPRRAGRLRDV*PL HE*YRHWHDQS/RLLIASVLPQ VWHGACNAMTSSCIARQVS*N TALIIRMRKGDLSAVMSSQTGL INIVRRGLLLSCFRLTAMKISTV SPFRPQMPSIVRSVWC
24359	54727	A	24497	1136	1317	
24360	54728	A	24498	3	317	
24361	54729	A	24499	1	1245	

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24362	54730	A	24500	85	1293	ITVATTQHQAGLTLRRAGIRQP DMAVQRDHLPFRVAGVIRHIM LMLHSQRRTGLLITAKNRLLFF QRRSVPKFHSKLNQAYCLIAAT DCPRRLLLICRYPHHFLHQLIIL AIGIGSAVFEPHQIIGVSRCCPR HLGVERVLFLFLNDFIEQVIIRC HVVCQSAPAAANIQYAHPWF* LQFFTNHFELRLLGRFQIIGIFPV SAGILHEGIKHAAEQVITQIVML FADYPGTFFTL/RD*RDERRQY AACL*NDGGVGSRDLRVRLC* KTYPVGHIPTSHPYN/CSPNPKE PSCRTRLKKSGFFTRISAGAEPL MAIPARLSNSLACGARDSAAKE VLLWFRFVLLLKQTLLNWTTK NVTSLWRTLGSPVGVKEVRAW TIPV/VSNRAAGSGQNPY*F*KR
24363	54731	A	24501	2794	3531	SPRDSPTFWTKGGPGGSRGKAL RLVVGTDFHQAADNIPDHMMY KSIRFNIYHHIRTVTRDINMHNV APRGSGLALHRTERGEIILAQQ ALRSPMHPFSVQRFVKMGYPFT QYRRAQPMIVDDVAITASRGA KSGMKIIRYSFNPTHSDVTR*IRI YAQGPRRVFAQRGCFEMHNLP GTVYPCVSTPGAEDGDGFVRH LGERLFQLLLHTADFVLPLPAVI LTGGVLNAQRNFINRRLLPYVE
24364	54732	A	24502	1	1767	
24365	54733	A	24503	1	1275	SNPTAIGGRPRRPYQAEDRSLD FVDTALNRKILKDSIFHALQTIM VGIKDFLRLTQVFFDLATRIPRH LYHPVDITTHYGRFCRHRRHHF QLLQLCFRFLFCLFRHLRRVDF ALQGFVFVRRVVHFTEFFLNSF HLLVQIVLTLGFLHLLFNAVAN AFLNLQQIDFRFHHCHQIFQTFV NVGHLQNRHRKIGIVIFRSDVL EHPHRNNTIKLVVQVTIILQQN GDIQAFTAFLSHFLLFGRNGDA HHAYVIIRCHVVCQSAPAAANI QYAHPWF*LQFFTNHFELRLLG RFQIIGIFPVSAGILHEGIKHAAE QVITQIVMLFADYPGTFFTLQIE ETSAGNTQRVFEMMGELVLET RLRSPAGFTQWIPHQGCRWSCL PVPRGTLALLSPWVVDGTGRR GAGGGTPQGGSSCTGAHGGGG
24366	54734	A	24504	1	2052	

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24367	54735	A	24505	1	1060	MNARQQVAALRVPGVEKATIV YRRSLQEMPAWREEYEEALHD GFRFLNNPERFDADGTLTLRVM SLGEPDEKGRRRPVETNETVTL LVDSLITAIGEQQDTEALNAMG VPLDKNGWPDVDHNGETRLTD VFMIGDVQRGPSSIVAAVGTAR RATDAILSRENIRSHQNDKYWN NVNPAEIYQRKGDISITLVNSDD RDAFVAQEAARCLECNYVCSK CV\DVCPNRANVSIAVPGFQNR FQTLH\LEA\YCNECGNCAQFCP WNGKPYKDKITVFSLAQDFDN SSNPGFLVEDCRWVPHRGLYH RLYREPTWRSEWPRRHICPEGS TFPERHCDHLSANNSRNKLLPL QKPGFIN
24368	54736	A	24506	1316	2678	
24369	54737	A	24507	2172	5242	IYFSERLPALCTPDAHYREPCQ YNCTRLDYDSALNIRELKKVAL EKGWDEYKQRWHKPAGSGSR HPVAVIGAGPAGLAAGYFLAR AGHPVTLFEREANAGGVVKNI VPQFRIPAELIQHDIDFVAAHGV KFEYGCSPDLTIEQLKNQGFHY VLIATGTDKNSGVKLAGDNQN VWKSLPFLREYNKGTALKLGK HVVVVGAGNTAMDCARAALR VPGVEKATIVYRRSLQEMPAW REEYEEALHDGVEFRFLNNPE
24370	54738	A	24508	192	484	RGLVHRGRYRWRQKWSAGSP ARHPV/SQSTTDTPATHALSTKII SPIPNAPISALARTTATRL*RSM NQPPVKRPTVIPRVKPA*ISEPE VGPIILGP
24371	54739	A	24509	1	1713	
24372	54740	A	24510	1	651	
24373	54741	A	24511	3	783	PVLSKTPLTAKAIDAAQPQDKP YKLTDSLTPGLFLLVHPNGSKY WRFRYWLNKREFLQAIGVYPLI TLKEARRRATESRSLIANGINPV EQARKEKAIDALNMAAGFKKV AEDWFATRVGGWSESYAKQV RSALEKDVYPVLGKRSIVDITA RDVLALLQKKERTAPEQARNV\ AGASVRSSSLPLSPNWGGWLA RAAFPHHITIAARMTKHPPCW WCTILACRQASLAVRGSTHYSL ELLIRRHILSLLRSPICASPLTV

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24374	54742	A	24512	746	2387	WTALPARLKQIRSGRKLPLTVM PALRETDTFDTFMESSWYYAR YTCPQYKEGMLDSEAANYWLP VDIYIGGIEHAIMHLLYFRFFHK LMRDASMTNPSSVPRAGGPAL LFENPKGYSMPVLCNLFGTPKR VAMGMGQEDVSALREVGKLL AFLKEPEPPKGFRDLFDKLPQF KQVLNMPTKRLRGAPCQQKIV SGDDVDLNRIPIMTCWPEDAAP LITWGLTVTRGPHKERQNLGIY RQQLIGKNKLIMRWLSHRGG\A LDYQEWCAAHPGERFP\VSVAL GAVPATILGAVTPVP\DTLSEYA FAGLLRGTKTEVVKCISNDLEV PASAEIVLEGYIEQGETAPEGPY GDHTGYYNEVDSFPVFTVTHIT QREDAIYHSTYTGRPPDEPAVL GVALNEVFVPILQKQFPEIVDFY LPPEGCSYRLAVVTIKKQYAGH AKRVMMGVWSFLRQFMYTKF VIVCDDDVNARDWNDVIWAIT TRMDPARDTVLVENTPIDYLDF ASPVSGLGSKMGLDATNKWPG ETQREWGRPIKKDPDVVAHIDA
24375	54743	A	24513	576	878	NLGSVWHYFRRSPEPATHHDA ANLERSPAA*RLSGARYRILAV *ADQSQTGSGDGSPDLQTGRV GDEARHRKRGLHVPQPRSEPPV GARGFPYRFATRWR
24376	54744	A	24514	2	878	
24377	54745	A	24515	1	735	
24378	54746	A	24516	1	1992	
24379	54747	A	24517	721	1239	

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24380	54748	A	24518	1	1954	RQLNGVQLAFRESFHTVTRVTE QHAAGAVAIHQHRNQLLTGAL GIFAVAVCCLQQRLDILLADHL AEHVQFVIAQFVTCQQHGNGV RNRTIIFLLFNELRKIVETVRVQ QTQTGEVAFHPQLFRGRVVYG PDLNARRGNGVINCSTLEDPQF GLILFVYTIGIQVGPGFFASLRV SGLRLNLFAVLIVIIGGLVTAIL HKLFDIPLPVVLGIFSGAVTNTP ALGAGQQILRDLGTPMEMVDQ MGMSYAMAYPFGICGILFTMW MLRVIFRVNVETEAQQHESSRT NGGALIKTINIRVENPNLHDLAI KDVPILNGDKIICSRLKREETLK VPSPDTIIQLGDLLHLDSRGSPL DTQDIDLQINSSVEKQFGDAIRT TILDVLARYNVRGVQLNVDDK GALDCILRARLEALLARASGLP MISASLQQRKTRTRRSMLFVPG ANAAMVNNSFIYPADALMFDL EDSVALREKDTARRMVYHALQ HPLYRDIETIVRVNALDSEWGV NDLEAVVRGGADVVRLTKTDT AQDVLDIEK\EILRIEKACGREP GSTGLLAAIESPLGITRAVEIAH ASERLIGIALGAEDYVRNLRTE RSPEGTELLSARCPIWQAARSA GIQAFDTVYSDANNEAGFL/QE
24381	54749	A	24519	5121	5492	
24382	54750	A	24520	2520	3525	
24383	54751	A	24521	1	1263	MAINSPLNIAAQPGKTRLRKSL KLWQVVMMGLAYLTPMTVFD TFGIVSGISDGHVPASYLLALAG VLFTAISYGKLVRQFPEAGSAY TYAQKSINPHVGFMVGWSSLL DCLLAVVIIAAIYVGFSLAGFHV YIGMLFVPGANAAMVSNSFIYP ADALMFDLEDSVALREKDTAR RMVYHALQHPLYRDIETIVRVN ALDSEWGVNDLEAVVRGGAD VVRLPKTDTAQDVLDIEKEILRI EKACGREPGSTGLLAAIESPLGI TRAVEIAHASERLIGIALGAEDY VRNLRTERSPEGTELLFARCSIL QAARSAGIQAFDTVYSDANNE AGFLQEAAHIKQLGFDGKSLIN PRQIDLLHNLYAPTQKEVDHAR RVVEAAEAAAREG\LGVVSLN GKMVDGPVIDRARLVLSRAELS
24384	54752	B	24522	62	405	

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24385	54753	A	24523	891	3240	RYRKSPGSWR/CMSCILTSWITT MFPI*RLGQWC*NPCVTMAL/L APIDVHLMVKPVDRIVPDFAAA GASIITFHPEASEHVDRTLQLIK ENGCKAGLVFNPATPLSYLDY VMDKLDVILLMSVNPGFGGQS FIPQTLDKLREVRRRIDESGFDI RLEVDGGVKVNNIGEIAAAGA DMFVAGSAIFDQPDYKKVIDE MRSELAKFEDIRGVAFDLDGTL VDSAPGLAAAVDMALYALELP VAGEERVITWIGNGADVLMER ALTWARQERATQRKTMGKPPV DDDIPAEEQVRILRKLFDRYYG EVAEEGTFLFPHVADTLGALQA KGLPLGLVTNKPTPFVAPLLEA LDIAKYFSVVIGGDDVQNKKPH PDPLLLVAERMGIAPQQMLFVG DSRNDIQAAKAAGLDAQARRK NAGYYYYLRLAKRQMRAGVA EALRDDLLAAKLNVKLVNAGD YKFKQIASEKLLIVVTSTQGEGE PPEEAVALHKFLFSKKAPKLEN TAFAVFSLGDSSYEFFCQSGKD FDSKLAELGGERLLDRVDADV EYQAAASEWRARVVDALKSRA PVAAPSQSVATGAVNEIHTSPY SKDAPLVAWRLPNVEGRARAG GASSFLADRVEEEGEVRVFIEH NDNFRLPANPETPVIMIGPGTGI APFRAFMQQRAADEAPGKNWL FFGNPHFTEDFLYQVEWQRYV
24386	54754	A	24524	950	2124	MSLISSVIAATWLHVKSYRLSC GFYACQSLVLVS/IFPTLSCLFA AEQLLIWSASAFITKVLLVPLIM TYAARNIPQNIPEKALFGPAMM ALLAALIVLLCAFVVQPVKLPM ATGLKPALAVALGHFLLGLLCI VSQRNILRQIFGYCLMENGSHL VLALLAWRAPELVEIGIATDAIF AVIVMVLLARKIWRTHGTLDL TPLLFSLLCFACRKRRLSATRTV TVLHSLGITLLLILALWVVQTA ADAGEIFAAGLWLHIDGLGGLF LAILGVIGFLTGIYSIGYMRHEV AHGELSPVTLCDYYGFFHLFLF TMLLVVTSNNLIVMWAAIEAT TLSSAFLVGIYGQRSSLEAAWK YIIICTVRVAFGLFGTVLVYANA ASVMPQAEMAIFWSE

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24387	54755	A	24525	1	757	RWRLPGVPPFNGFFSKFPLFAP GFALSVEYWILLPAMILLMIESV ASFAWFIRWFGRVVPGKPSEAV ADAAPLPGSMRLVLIVLIVMSLI SSVIAATWLHVKSYRLSCGFYA CQSLVLVSIFATLSCLFAAEQLL IWSASAFITKVLLVPLIMTYAAR NIPQN\IPEKALFGPAMMALLA ALIVLLCAFVVQPVKLPMATGL KPAL/AGLATDAIFAVIVMVLL ARH\IWRTHGTLDVNNLHALK GIMSCSYSS
24388	54756	A	24526	249	3943	
24389	54757	A	24527	1	1278	
24390	54758	B	24528	48	144	
24391	54759	B	24529	27	239	
24392	54760	A	24530	1	551	
24393	54761	A	24531	3	258	MLFDEPTSALYPEMIN*VLDVM VELANEGMTMMVVTHEMGFA RKEANRVIFMDEGKIVEYSPKD AFFDDPKSDRAKDFLAKILH
24394	54762	A	24532	2	979	
24395	54763	A	24533	1	4116	
24396	54764	A	24534	1	1195	MLIAEGLMTAKNITVITNSLPA AFALSENKDITLVVCGGTVRHK TRSMHGSIAERSLQDINADLMF VGADGIDAVNGITTFNEGYSIS GAMVTAANKVIAVLDSSKFNR RGFNQVLPIEKIDIIITDDAVSEV DKLALQKTRDTSLVYVLSLADF FRTASTIGERDGTQVEMILFAGF VYLVISLSASLLVLTDCSTEVK KGEVVVVCGPSGSGKSTLIKTV NGLEPVQQGEITVDGIVVNDKK TDLAKLRSRVGMVFQHFELFPH LSIIENLTLAQVKVLKRDKAPA REKALKLLER/VSGFFAHANKF\ PAQLSGGQQQRVAIARALCMD PIAMLFDEPTSALDPEMINEVLD VMVELANEGMTMMVVTHEM GFARKVANRKHTTRSTIALQSL ATCT
24397	54765	A	24535	383	962	TDNDRPGLGTDMKKASAIVTN VAVVLSGRYRRERASGEWAAL SFLRPHTLTVFVIPHIQWDDPQ MSRP\SGRHLFRCRTVQRKHAL QVVEKFRPFFPSDRYRYGAPGD YAQSFGGQIDDVVKAIQTPSKF RRFLRVSFD*IRLPILHSGKSPLR RMPNLMRRHSHTARHYPALGT RGPQPTDRQERPAVASGQ

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24398	54766	A	24536	1477	2387	
24399	54767	A	24537	1	1560	
24400	54768	A	24538	305	718	
24401	54769	A	24539	1	2161	MNDVDRVGGKNASLGEMITNL SGMGVSVPNGFATTADAFNQF LDQSGVNQRIYELLDKTDIDDV TQLAKAGAQIRQWIIDTPFQPEL ENAIREAYAQLSADDENASFAV RSSATAEDMPDASFAACTLVPG QNLSTSNKDVIELPDNQYDLDK MVNIYPVTPGLIDQLRAKPIMS QANPELEQQIANYEYRIGIGDV LMVTVWDHPELTTPAGQYRSA SDTGNWVNADGAIFYPYIGRLK VAGKTLTQVRNEITARLDSVIE SPQVDVSVAAFR\SQKAYV\TA EVSKSGQQPITNIPLTIMDAINA AGGLTADADWRNVVLTQNGV KTKVNLYALMQRGDLRQNKLL HPGDILFIPRNDDLKVFVMGEV GKQSTLKMDRSGMTLAEALGN AEGMNQDVADATGIFVIRATQ NKQNGKIANIYQLNAKDASAM ILGTEFQLEPYDIVYVTTAPLAR WNRVISLLKKLERLTSIAITLPGI IDTENGIVHRMPFYEDVKEMPL GEALEQHTGVPGEAKGLVGAP PGARDVIQVVSIPNVGRAVIPN GHLLPQGSSSLVEIAHTQGGPL MGKRCYCGNHGCLETIASVDSI LELAQLRLNQSMSSMLHGQPL TVDSLCQAALRGDLLAKDIITG VGAHVGRILAIMVNLFNPQKILI GSPLSKAADILFPVISDSIRQQA LPAYSQHISVESTQFSNQGTMA
24402	54770	C	24540	1	1389	
24403	54771	A	24541	405	576	CEMGAPPWPGCWLS\LFDVDG RFVLAWMLFQGSYLAGALGDQ PVHIHLGQLLALWRPL

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24404	54772	A	24542	1	1127	MARTLAHELIDFGEIKRGLLGIK GTEMSADIAKAFNLDVQRGAF VSEVLPGSGSAKAGVKAGDIIT SLNGKPLNSFAELRSRIATTEPG TKVKLGLLRNGKPLEVEVTLDT STSSSASAEMITPALEGATLSDG QLKDGGKGIKIDEVVKGSPAAQ AGLQKDDVIIGVNRDRVNSIAE MRKVLAAKPAIIALQIFPVDHR GAIGGQTTDIPPDPSGINHDRC MKGLSFAGEMVTYTNTAHRRA FTNQPRDFMSVAWLGKGIAILP SVGEVRSPVAGRIASLFATLHAI GIESDDGVEILIHVGIDTVKLDG QIFSAHVNGEAGLKRVVKKEH AD/VQRHAESV*RRGQAQGTD GIRRQDNRVQPGCERCTHQLLR
24405	54773	A	24543	95	599	QIMRMLNGSSTPNTSLPTPQAF DRSLPINATSARPSSTSTRHSAE SSISRDCVSNVS/HSGG*TGGIK G*CHAHPADLTACHEADSRGSP SHAVAAVALHVID/GWYLGDQ TAAYATGSAVSCPSSGNQFSRP SAAGRFSAVSAPQGAQRHPGR ARRRPRRRRTAGGCRR
24406	54774	A	24544	640	890	LANAQLGSNEISIFQCFAAIQRFI KLHRDASVINHPLAE/TRK*YPV SVYHLRHPPAIIR*PAIRDNA**I LPVTPGYSCSRHQ
24407	54775	A	24545	3	257	ETDIFICDSREFFHHFAKASVHI* PVVSIANFAIQSGKILALGAENI ATTSDRRAQRQKAVCKAHDAS SVSFRTLSVRPTNDCP
24408	54776	A	24546	332	1047	RTRPYCPGMGNEPMTGWMAA AVVTLMIRMCFSVYTMLSESC QRMVIVGYGRCFADRQNLMVC LRSMPNVFTGSCARMRCCLSEN LLYRHRNGHIQAEWP*KKAISD VKQYRTSCWERWNAASATIFR/ LSPVEWLTDNGSCYRANETRQ FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDYISIMPKPDGLT AAKNLAEAFEHYNEWHPHSAL GYRSPREYLRQRACNGLSDNR CLEI
24409	54777	A	24547	1200	1544	LTGVADGNVDKPCYKFARLW YWIYPAFPPIRRVKVAYREYRP PTTPRVRQVRDLTFCHRPAIPDR MHRY*SSHRALPGCWSKVPAQ KSSRTVSGTD*VDLLSPRAQRA PSPLQG

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24410	54778	A	24548	263	625	
24411	54779	A	24549	742	851	VSAQQRVILNKIAVLNRK*RYG CWRLWICPYISRHLLSLNPLQA RCRRYSRGER
24412	54780	A	24550	1	532	MKTLLIIDANLGTRLYGEDPAG AAARKAKLEIIDNPNDAEMAIV LGDSIPNDSALNGKNVWLGDIS RAVAHPELFLSERKGHAKPYTA PVAATAPVGASGPKRVVAVTA CPTGVAHTFMALKPLKPKRKN VAGIPDTGQYCETVQTSCW/AA VETPLRQRSSVVSSGVADG*WF MLPG
24413	54781	B	24551	1	888	
24414	54782	A	24552	1	2283	
24415	54783	A	24553	992	1662	KKAISDGALTGSSSAVITERDC VSRSRWTAVIVRHCTGRSLPAA STVKQYRTSCWERWNAASATI FR/LSPVEWLTDNGSCYRANET RQFARMLGLEPKNTAVRSPESN GIAESFVKTIKRDYISIMPKPDG LTAAKNLAEAFEHYNEWHPHS ALGYRSPREYLRHGLVSFISSLQ KFINDFAFEDGLFSGYDAEKRQ YEKSSWNYQLDENGYAKRDET LTHPRC
24416	54784	A	24554	1	2262	
24417	54785	A	24555	158	410	
24418	54786	B	24556	1	2607	
24419	54787	A	24557	715	1016	KSAAVPRSGASSQSDSAHFAQP EYAAFSRFPRGSFRHPRAA*YF GRLNHHVRSERGINP*YHRFNL HWRYVADAISADGAFRTVSGG GGRRSGAGRVDWQ
24420	54788	A	24558	652	1214	RTDHCVSRSRWTAVIVRHCTG RSLPAASTVKQYRTSCWDRWN AASATIFR/LSPVEWLTDNGSCY RANETRQFARMLGLEPKNTAV RSPESNGIAESFVKTIKRDYISIM PKPDGLTAAKNLAEAFEHYNE WHPPSALGYRSPREYLGQRACT GHAIGSGPSSAFFGAPVRRVSRT SVTAKACPRGLL
24421	54789	A	24559	647	1976	
24422	54790	A	24560	289	574	ETPASSPTLRTSIPSISWMTRGSL RRVMLLCPFPSESGTVSEKAWP EWSSFSSSPPSCRTSASSPPSHLR /NIDVSPKHVVFATIPRNYTMSF LPR
24423	54791	A	24561	816	1375	

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24424	54792	A	24562	1	3993	MSQKLKVVTIGGGSSYTPELLE GFIKRYHELPVSELWLVDVEGG KPKLDIIFDLCQRMIDNAGVPM KLYKTLDRREALKDADFVTTQ LRVGQLPARELDERIPLSHGYL GQETNGAGGLFKGLRTIPVIFDI VKDVEELCPNAWVINFTNPAG MVTEAVYRHTGFKRFIGVCNIS IGMKILKTRTLDTTGSTSTGDTL LTQSLLMELSALCRVEVEEGLA LVALIGNDLSKACGVGKEVFG VLEPFNIRMICYGA
24425	54793	A	24563	1136	3608	KKAISDGALTGSSSAVITERDC VSRSRWTAVIVRHCTGRSLPAA STVKQYRTSCWERWNAASATI FR/LSPVEWLTDNGSCYRANET RQFARMLGLEPKNTAVRSPESN GIAESFVKTIKRDYISIMPKPDG LTAAKNLAEAFEHYNEWHPHS ALGYRSPREYLRQRACNGLSD NRCLEIYGQIQLGTGELNITTGV VVTARDTHIALNFQKRRTTGLA TQSRQRCQNRRRVMGKIVIYRD AIRFTTQLQTATSINKRTQRVSG ICRRYTNMASRCNRHQAIVHIM FAYQRPFHFAHFFAIQQNFPFGS IGGQLFRLPVTLLTHQLLLAPA AHRHGLFQVDVIFRPDNTALPR NDTHQMVELFLDRFQVVKDIG VIELKVVEDQRTRAVMNKFRA FVEKGAVILIRFDKKKDIFLQYR FHTRISTGHGVANNHQIRLRLE LAGIVPLNQLNPLPLNSVPMINI MNGGENADNNVDIQEFMIQPV GAKTVKEAIRMGSEVFHHLAK VLKAKGMNTAVGDEGGYAPN LGSNAEALAVIAEAVKAAGYE LGKDITLAMDCAASEFYKDGK YVLAGEGNKAFTSEEFTHFLEE LTKQYPIVSIEDGLDESDWDGF AYQTKVLGDKIQLVGDDLFVT NTKILKEGIEKGIANSILIKFKAQ HAGLLHMYTCAMLGVGGQCW RYCMSQAFKEDRFAQDQRVAV
24426	54794	B	24564	83	2851	
24427	54795	B	24565	1	1578	
24428	54796	A	24566	574	753	
24429	54797	A	24567	1	2112	
24430	54798	B	24568	27	969	
24431	54799	A	24569	1	1773	

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24432	54800	A	24570	822	984	PSALCGCHSL*CSNASARFFAA VNPSGAFGCRADHPDGELFLTG YVADGGYHS
24433	54801	A	24571	1	4287	
24434	54802	A	24572	1	2384	
24435	54803	A	24573	3	3682	ACSARPSEAELLELIDTLNADN TIDGILVQLPLPAGIDNVKVLER IHPDKDVDGFHPYNVGRLCQR APRLRPCTPRGIVTLLERYNIDT FGLNAVVIGASNIVGRPMSMEL LLAGCTTTVTHRFTKNLRHHVE NADLLIVAVGKPGFIPGDWIKE GAIVIDVGINRLENGKVVGDVV FEDAAKRASYITPVPGGVGPMT VATLIENTLQAMSNMATFSLGK HPHVELCDLLKLEGWSESGAQ AKIAIAEGQVKVD
24436	54804	A	24574	1	1382	MLRGVNVLADAVKVTLGPKG RNVVLDKSFGAPTITKDGVSVA REIELEDKFENMGAQMVKEVA SKANDAAGDGTTTATVLAQAII TEGLKAVAAGMNPMDLKRAS RSRKGYGPARIRQELNQKGISR EATEKAMRECDIDWCA**RF*S DKHHHRT*RQ/PTRHRYPDESV PGSHNHRSAHALSSAQGYILLP RAVLSGWRFENVHPTPGYPAG SGSVFVPPPMTSRRLPAPDNFA APHRYRVLKTGLLSPGCHVRN ADTL
24437	54805	A	24575	466	1215	
24438	54806	A	24576	1104	1923	LAIPMKDFITEAWLRANHTLSE GAEIHLPADSRLTPSARELLESR HLRIKFIDEQGRLFVDDEQQQP QPVHGLTSSDEHPQACCELCRQ PVAKK\PDTLTHLSAEKMVAKS DPRLGFRAVLDSTIALAVWLQI ELAEPWQPWLADIRSRLGNIMR ADALGEPLGCQAIVGLSDEDLH RLSHQPLRYLDHDHLVPEASHG RDAALLNLLRTKVRET\ETVAA Q\VFITRSF\EVLRP\DILQALNRL SSTVYVMMILSVTKQPLTVKQI QQRLGETQ
24439	54807	A	24577	243	644	HAGSVCPSLYRCQRTAKRSGFY LLLKRLWSFSGNI*IHSGQQNPG RNQQLGLPRSRKGESSRAHPSC QRRPQVWPHPLAGSRPPRPWA ACARLGPIAPARQIPERWPGQV PVLADAHVLPCLAGSLRPALYD F

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24440	54808	A	24578	237	454	RSRLPEGVPVCWCNHSVR*RDC RFPVGKLHRLWL/LALPGVRLIF RASTKRITGYINARSASIASASA RNRLV
24441	54809	A	24579	377	1155	KAYSFATMKSLAISCRWQNA*S HVSTFVMVRW/LKGVQFRNHEI IGDIVPLAKRYAEEGADELVFY DITASSDGRVYPTLITRLADRFG VQCIVVGIDTWYDARNLKDISV VGLLGAQVPSVRAGMPQSRRQ TEGAQGMVRNEEGGSLRLSHH QACKATHTQQWTLEVTAQSSY NLFPEQWVKLFWGIRQGDLPL AFSQKLSRQTFQQQQTQTPRPI VGQAPKDLQTGTGTPQTHAVH SGDHAAGEQSCKSCKAPIYPLT AQFSLETRSFWGSEWGYSTHG ELRRRDKGRRRFY
24442	54810	A	24580	1107	1458	RTFWWTTCNSLAPCAGGYPST GAALPVSRKLPGRGLLLSGWG EHNARYRAGTFLWALFCAAAV AYWRRC\WGQYGMWFLRIRRG TLGDGTIRRVFVGSLWAAVVIV EIGVEHIGVFKA
24443	54811	A	24581	171	352	PPAPPAESDGLPAHTTRARTTA DDLRNKRRQHVGC*YRTRGSP RPNRTWWRVCRYRSPHR
24444	54812	A	24582	5	226	
24445	54813	A	24583	476	1939	RPESQHNTAKPAMKVLEQARR FLGIRWLSAPASLAN/PVILLVV GNILNIVLDVWLVMGLHMNVQ GAALATVIAEYATLLIGLLMVR KILKLRGISGEMLKTAWRGNFR RLLALNRDIMLRSLLLQLCFGAI TVLGARLGSDIIAVNAVLMTLL TFTAYALDGFAYAVEAHSGQA YGARDGSQLLDVWRAACRQSG IVALLFSVVYLLAGEHIIALLTS LTQIQQLADRYLIWQVILPVVG VWCYLLDGMFIGATRATEMRN SMAVAAAGFALTLLTLPWLGN HALWLALTVFLALRGLSLAAI WRRHWRNGRPGTGCLNTKGS QQQHRHDSTTQHIHLQLLVIRV KTTTTNNSQQTPQYPCQQYHT DSRQHRQQNRMVCQRIPHALPS PRFRQISRGSTAKVPCAKARAF LRVKSDPTLITRLADRFGVQCIV VGIDTWYDAETGKYHVNQYTG DESRTRVTQWETLDWVQEVQK RGAGEIVLAYVSE

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24446	54814	A	24584	1	50	
24447	54815	A	24585	354	456	HLFSEACCSPGVLRELCRPF*SP GTDRNLVMHGH
24448	54816	A	24586	494	835	ITWLPGFRPPFQGSEQFCLAGVP GATGGSESVLHTRNSYKMLEV RREVAALISALKVSAKCRNCGS SHALTEP/ASSPCWRETSTRPTG APAPTIPPPAASPSPGPMCVQPH GED
24449	54817	A	24587	3	726	
24450	54818	A	24588	1	1635	
24451	54819	A	24589	1614	2454	RTTHAPASTPNTGTMLCRPYPC CWRRKTP\IIFRATPQWFVSMD QKGLRAQSLKEIKGVQWIPDW GQARIESMVANRPDWCISRQRT WGVPMSLFVHKDTEELHPRTL ELMEEVAKRVEVDGIQAWWD LDAKEILGDEADQYVKVPDTL DVWFDSGSTHSSVVDVRPEFA GHAADMYLEGSDQHRGWFMS SLMISTAMKGKAPYRQVLTHG FTVDGQGRKMSKSIGNTVSPQD VMNKLGADILRLWVASNDYTG EIAGSDENLKRACHYNACSISL ARRRH
24452	54820	A	24590	362	517	TKSLISSMSSISSPPVVLICRNSS PEV**RKI*LGTELEFVIMVIAVS AWP
24453	54821	A	24591	250	930	
24454	54822	A	24592	1388	1912	VCPAAMTGFAGSPFCTAVVTFP DITPLLWILMC*LAILMAESEPK AISPPTISVVP*YAAESLLRVRIP VPSFVTSPLPLILCVIAQLRSVE MVSRPLLITEASPRFFCSLTLSA LPVSMLNCPTKRLLSPSNSTSVL AVALTIPFPLMLLRSSPVTFFSV NRPSWAIFPLPNP
24455	54823	B	24593	1	6018	
24456	54824	A	24594	510	1003	VALQADQKHKHERPLPPPIPTM FQLAQPGVQLHAKPVYQVP/V MMQATEPTGI*VRIPVLSISTNA PSITSIWPLFVRKISVLTLASVV AASHAASSPRQCAIRCKIWGRW AGSLRRDDGFGVRSRGSRYGA SVSISNFSAGINGKSSRSSSPRRS SQTQPVMPI

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24457	54825	A	24595	197	4314	RASTELSLRCCAPSLQ/ALLHFL YLACFTWMLLEGLHLFLTVRN LKVANYTSTGRFKKRFMYPVG YGIPAVIIAVSAIVGPQNYGTFT HCWLKLDKGFIWSFMGPVAVII LINLVFYFQVLWILRSKLSSLNK EVSTIQDTRVMTFKAISQLFILG CSWGLGFFMVEEVGKTIGSIIA YSFTIINTLQGVLLFVVHCLLNR QINSLLLTWTLWILRQRLSSVN AEVSTLKDTRLLTFKAFAQLFIL GCSWVLGIF
24458	54826	A	24596	1409	1573	
24459	54827	A	24597	1283	1563	
24460	54828	A	24598	281	839	CVPTTDLVVQSQI*PRWRNWPR CSCSHVSMKAASSPERTFTYCS GIYWLISGSGIGVSVPLLISIGES VINLAVRPVIAHAIRVAITTRQT TRVAVTVVVALPVFRAVEHHV FQHLTQTRTGFRWHQFFFNRRQ REQSFTQGEGQRWANFQNGKV VNHQLAQRLRRLIIGRVRFENQ RFVVFDHLA
24461	54829	B	24599	1	5652	
24462	54830	A	24600	559	1665	RVERKATIEMKSQRTTSDSWLII LAKQTGIIRAAKKGKKTFILHD GPPYANGSIHIGHSVNKILKDII VKSKGLSGYDSPYVPGWDCHG LPIELKVEQEYGKPGEKFTAAE FRAKCREYAATQVDGQRKDFI RLGVLGDWSHPYLTMDFKTEA NIIRALGKIIGNGHLHKGAKPV HWCVDCRSALAEAEVEYY\DK TSPSIDV/AHPFMGFDVPAILGD HVTLDAGTGAVHTAPGHGPDD YVIGQKYGLETANPVGPDGTY LPGTYPTLDGVNVFKANDIVVA LLQEKGALLHVEKMQHSYPCC WRHKTPIIFRATPQWFVSMDQK GCDIGFHASSNGKRRADDSTDN HVRRLCARQRGQPHPHQFQRT

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24463	54831	A	24601	1	1190	MTDFRESDTMSLFDKKHLVSP ADALPGRNTPMPVATLHAVNG HSMTNVPDGMEIAIFAMGCFW GVERLFWQLPGVYSTAAGYTG GYTPNPTYREVCSGDTGHAEA VRIVYDPSVISYEQLLRKYRCV AVALLGYFKCKPILLNPSYKSM QDDLAFIARFHFKDLKFRRFSL KADQKSRIYERVLSIAGVNSWK DKQHQPRLVEHLLVCAESWVA PRALFDAAIEYLAHQKIAIPAYL VAFLVLGPLVLSLIPSQMLPSLT WSSITYSIVVIVEAGYQYHSRLR RFGRVEVNEQIEYLIHNPIRTRA RAVNFVDNNNRLQAPRILRQDS WWITRPLPGLTWAIIGSPGILPQ VVKSARVMKQAVAYLEPFIEA SKEQGKTNGKMVIATVKGDVH DIGKNIVGVVLQCNNYEIVDLG VMVPAEKILR*KLGGTPRTL*R SNRVPGPPEDRHSCLFGCV/YW FLVP*CCLSSLRRCCRR*RGQAS RIQ*LLSSKLAISTIL/GLRRFGR VEVNEQIEYLIHNPIR/IARQGG QLC**QQSASGPTDITAGFMVD HQTFTGADVGDNRVARNPATG GQIGARHETGGGLPRTVY*SQQ RAGQNQRQDGDRHREGRRPRH

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24464	54832	A	24602	1	1591	MGILVSPLLAPLIGGLLDTMWN WRACYLFLLVLCAGVTFSMAR WMPETRPVDAPRTRLLTSYKTL FGNSGFNCYLLMLIGGLAGIAA FEACSGVLMGAVLGLSSMTVSI LFILPIPAAFFGAWFAGRPNKRF STLMWQSVICCLLAGLLMWIP DWFGVMNVWTLLVPAALFFFG AGMLFPLATSGAMEPFPFLAGT AGALVGGLQNIGSGVLASLSA MLPQTGQGSLGLLMTLMGLLI VLCWLPLARGYRLSSWTSTTAS EDIDCEEGDGEGNETHGLQLAV EPEGLQPNYMGRGKIRFRDTCL LFCTQSRGSQWGFARTELVALL PPFLSGAADYRAGLALWLARG ADCDVDERHRADRQSNLARSS GGFIALAAGAKSDRRLRELNQS LQKELARNQHLAERLLETEESV RRDVARELHDDIGQTITAIRTQ AGIVQRLAADNASVKQSGQLIE QLSLGVYDAVRRLLGRLRPRQ LDDLTLEQAIRSLMREMELEGR GIVSHLEW\QSMNQR*AKTSA* RCFVSARKG
24465	54833	A	24603	1	1752	
24466	54834	A	24604	1	699	
24467	54835	A	24605	965	5516	
24468	54836	A	24606	84	3760	
24469	54837	A	24607	27	278	

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24470	54838	A	24608	311	2529	REWGSTRRCERRISLSRNIARW RTIWRITRPCRRCVFRFIASTLR LHLHLIMNDLPLEEYPCVRDLV PGRFLKFL/HRDPKGTTLVLASD LPGRIPVDPRSIIVMLFLAVRWL QRQLAGQELLETRATRILNGER GSNVLGTIYEWPPRTSSALDTL LREIQNAREQHSRLDTLIRSYA AQDVKTGLNNRLFFDNQLATL LEDQEKVGTHGIVMMIRLPDFN MLSDTWGHSQVEEQFFTLTNL LSTFMMRYPGALLARYHRSDF AALLPHRTLKEAESIAVFRALS RLPDLWHRSIGTLTEALPQTDK RQEQIAVALTSYSGLYGLGYGS KEIQLTYSGTAGDLISPGLSAIH GRCILNTLVFIVKLRWMENTLH RFGTHHGCSAVRSSHLDSGSPR RSSWHMARARNHIHVLEENMA LLMEQAIANEGLFYRLLYLQRS LTAASSLDDMLMRFHRWARDL GLAELLVVLPEAKAVGSVAMS MLGSDADWGVVLFTSRDASHY QQGQGTQLLHEIALMLPELLER WIERGWEQQVWRYGFLRYVAF LTGWSAQNELKANPAKGVSAP KAPRHLPKNIDVDDMNRLLDID INDPLAVRDLMYGAGLRLSELV GLDIKHLDLESGEVWVMGKGS KERRLPIGRNAVAWIEHWLDL RDLFGSERERRQHAGTNVLQT ADQRASRARQEGERLHRAAGR
24471	54839	A	24609	1	1749	
24472	54840	A	24610	1	2911	MNIDAKILNKILANRIQQHIKKL IHHNQVSFIPGMQGWFNIHKSM KVIQHINRTKDKNYMIISIDAEK AFDKIQQPFMLKTLKKLVAGM MAVAAPDDPPPPSVSSSKPSTV APPGRISPSGRALCTSLPSALSSS SKFSLLRIFQVPAKLGMVAVAA AAGVNAMLRKVAVAAASKPH VEIRQDGDQFYIKTSTTVRTTEI NFKVGEGFEEETVDGRKCRVR PQSHYSVPVSPLGAHGPLLLEE PVSPFAACGAPS
24473	54841	A	24611	249	609	QIEVCVRIKPKAGTVLAYS*RSR QERPPAPGMTSLSLAAVSSDNP VSGDEHIRLARASGRFGIGRVA QPKRIQRRSSTPRAATDLGNPG HRPCTVRKSALLVVSVCRRHSS RSLRFRSC

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24474	54842	A	24612	942	1121	
24475	54843	A	24613	1010	1658	EISSSKRSRTVCKRRAPMFSVDS FTCHAASAMRLIPESVNSIFTPS VAISALYCTVIEAFGSVRIRSKS LVVSACSSTRIG\DDLAVPGSGQ TVSQSGTRQKR*TECGQF*PSR VWWKRCNLLPAAAGHAERLH EKHPDRKTRRVRLVWLAGPPT RLLGTMGAGTLVLGACCLPWP REGAHNVATAACGGWRARCD LRFRLSCKLGLSRQFFGWNA
24476	54844	A	24614	1	1995	
24477	54845	A	24615	1	2853	
24478	54846	A	24616	1	1755	
24479	54847	A	24617	2942	3454	SVPDWLMCTAFLSLSRINSPRL LKAELLLTSSIPVLLPSLLLPRFQ VPSLFATAVPVSAAPLIIAPSV*L LKTPPADIIRPVTLPLLLNTPAFC TILLMVPVLFTNELSAPAFMVIC AVISPALLRIPPLTSTLFVITPAF LMTAPLSSFTKLLMMPPLVFSR RPLDTVI
24480	54848	A	24618	1	2959	MKRYRPREILPWKVPPGNYTPK IFKIKGTGHNPMSAIENFDAHTP MMQQYLRLKAQHPEILLFYRM GDFYELFYDDAKRASQLLDISL TKRGASAGEPIPMAGIPYHAVE NYLAKLVNQGESVAICEQIGDP ATSKGCCRSGNRNGGRKIVAVS LKKVSGAAKPCGHFRSTRYRV AYSTIINNKAGIWSAFEGVSAT RPNPTPRASPAVRTLSRGTPEPR KISTDADNLAQGSLKERLPAWL WGKKENSKWEVLD
24481	54849	A	24619	441	1425	
24482	54850	A	24620	1	2574	
24483	54851	B	24621	1	1725	
24484	54852	A	24622	160	390	
24485	54853	A	24623	892	1183	
24486	54854	A	24624	1	2493	
24487	54855	A	24625	435	829	ASDVLVSEGCR/YRGASALTST SVICINTDKALRKIIRLPLNGLR KPLNAMTPLPGITWPLCITTEKE DLSISDRLSTCIVKFSHPEPEMS VRKFVPPAILLCSVCLRFSCPTR HQKAPAKWILKSCSAWMR
24488	54856	A	24626	763	1863	
24489	54857	A	24627	1423	1712	

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24490	54858	A	24628	1	2792	MTYLSAQDHELIQVVQNGHLQ MCGKSETGNEASPVKCIVLQVL RGLQYLHRNFIIHSQEQTIPDPSI SDQQETPLLAGDMAQRGRRGG FYYVTAYIYVDKKAPVHMRTA AQGLITLCCQGFGSLLGYRLGG VMMEKMFAYQEPVNGLTFNW SGMWTFGAVMIAIIAVLFMIFF RESDNEITAIKVMEDSMSSATT LTTPQEQVDSLIMQIAEENGLE VLDQLSQLPEGASAVGESSVRS QEDQLSRSFICLMAMM
24491	54859	C	24629	213	345	
24492	54860	A	24630	1	474	MHQTTAKTPHTSYPNNYEEHN RRANRSKNYDRIRHTTIILKRTN PAQTITNLLKSRFNRYNYVQPR SCRSIFIHIPGERDLNLCIAPNPP AIFPTSIGYLGPDLNNLPTYAPFI TTNLTGPAPTTTHPVGNLGTTG NPEPGGCGILIVWCCVNWACL WDSVVAAPREPYMPAGLLRHR RHYRHRREDLIAVPAARQTDE NRRPALCHEYAVGHRKIKTNV EHTEPYILPLITHSQPLNRGAFF CPGVRFLVVSVLDFEKRL**RR WRRSPAGI*GSRGAATTLSQRQ AQLTQHQTIRIPHPPGSGLPVVP KFPTGCVVVGAGPVRFVVING
24493	54861	A	24631	1	924	
24494	54862	B	24632	177	468	
24495	54863	B	24633	592	883	

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24496	54864	A	24634	1	1926	MATAKANQEIQEWLGKYGTAR VKLNVDKDFSLKDSSLEMLYPI YDTPTNMLFTQGAIHRTDDRTQ SNIGFGWRHFSGNDWMAAVIT FIDHDLSRSHTRIGVGAEYWRD YLKLSANGYIRASGWKKSPDIE DYQERPANGWDIRAEGYLPAW PQLGASLMYEQYYGDEVGLFG KDKRQKDPHAISAEHSPEFRSE ALKLVNASVLLPQPVNSACMN HNSTTGAVNSKISRRLLNVNW RCLPRLHVSNASWQNGMKSWL SSKRPRHTSEAPEMKYVFIEKH QAEFSIKAMCRVLRVARSGWY TWCQRRTRINIAVVRRADGSRT SFVYTSYLAKVNEEWKNNVGT GSTVKWPIGLGGKGNDGIAAF VQRLPGAIGYVEYAYAKQNNL AYTKLISA*NEVCLY*KTSG*V QHQSNVPR/RSGWPAAAGIRGV SGGQG*TLL*YAAQMAPELPSS TPATWRK*TKSGKTTLV/HGST VKWPIGLGGKGNDGIAAFVQR LPGAIGYVEYAYAKQNNLAYT KLISADGKPVSPTEENFANAAK GADWSKTFAQDLTNQKGEDA WPITSTTFILIHKDQKKPEQGTE VLKFFDWAYKTGAKQANDLD YASLPDSVVEQVRAAWKTNIK DSSVNFDMANVFFRVTPGNFL VNREASHQRRVFAVRAGVDFI YRASSDGLRRCRDRRTRFKRIN
24497	54865	A	24635	1387	1639	ESKPLNLGRGSGFLLTRALSAQ PLWQSPDQHLTPQAGLRSRL*A QRQA*QKTASRVV*PKPLWAL VKATSEDISVVL*ESACQC
24498	54866	A	24636	1570	2516	IEVAMSIVVKNNIHWVGQRDW EVRDFHGTEYKTLRGSSYNSYF IREEKNVLIDTVDHKFSREFVQ NLRNEIDLADIDYIVINHAEEDH AGALTELMAQIPDTPIYCTANAI DSINGHHHHPEWNFNVVKTGD TLDIGNGKQLIFVETPMLHWPD SMMTYLTGDAVLFNYDAFGQH YCDEHLFNDEVDQTELFEQCQ RYYANILTPFSRLVTPKITEILGF NLPVDMIATSHGVVWRDNPTQ IVELYLKWAADYQEDRITIFYD TMVNNTPMMADAIAQGIA\ETG PRLAGENFNV\ARNDKHEDPDL LSFRSERGA

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24499	54867	A	24637	24	363	
24500	54868	A	24638	2	366	RATPRHIIVRFTKVEMKEKMLR AAREKGRVTLKGKPIRLTADLS AETLQARREW*QNLSAFACL*R ILFLLHL*SLVWLDMKCWVENS FL*EC*ILAPTLFWLVGFLPRDP LLV*WASL*G*PDLSLWLPLAF FPSFQLW*I*QLCVLELL
24501	54869	A	24639	232	292	
24502	54870	A	24640	4	911	
24503	54871	A	24641	2795	3226	SWWISFLMCCWIWFASILLRIFA SMFIKDIGLKFPFLVVSLPGFGI RMMLAS*NELGRIPSFSIGWNSF RRNGTSSSLYLW*NSAVNPSGP GLFLVGKLLVIASISEPVIGLFTD STSSWFSLGRVYVSRNLSISSRF SSLFA
24504	54872	A	24642	1	3285	
24505	54873	A	24643	1	4368	
24506	54874	A	24644	200	335	YALLNKDSSPWYPFSVPVLASN TRYLWPLSST**GSLSVWLSPD V
24507	54875	A	24645	174	263	
24508	54876	A	24646	1244	1354	

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24509	54877	A	24647	194	2481	GMFRMNLMEPLTQCINAGHEM TKAIAIAQFNDDSPEARKITRR WRIGEAADLVGVSSQAIRDAEK AGRLPHPDMEIRGRVEQRVGY TIEQINHMRDVFGTRLRRAEDV FPPVIGVAAHKGGVYKTSVSVH LAQDLALKGLRVLLVEGNDPQ GTASMYHGWVPDLHIHAEDTL LPFYLGEKDDVTYAIKPTCWPG LDIIPSCLALHRIETELMGKFDE GKLPTDPHLMLRLAIETVAHDY DVIVI\DSAPNLGIGTINVVCAA DVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMV\IKNVVRETNEVGKAA PMVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAFTDKEELLKQQASNLHEQK KAGVIFEAEEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMVLNLDSPQSFSPGAGDHA NSPQSSSPSTGVHINSPQLSSLS AGVHTISPQSSNPSVGVTALSHP DLVWVFTLTAHSRPVLVWVFT
24510	54878	A	24648	1361	1694	
24511	54879	A	24649	1	3852	MKLMETLNHCINAGHEMTKAV AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHRAQ DLALKGLRVLLVEGNAPQGTA SVYHGWVPDLHIHAEAALLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALPRIEPELMGK/FDEGRS FMPGPP/HHHPLGRSSQ*QVSNS LDRAAKGN*KPLCHC

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24512	54880	A	24650	1	1720	MEKLLLENDSLSKDVSRLETVF VPPEKHEKEIIALKSNIVELKKQ LSELKKKCGEDQEKIHALTSEN TNLKKMMSNQYVPVKTHEEV KMTLNDTLAKTNRELLDVKKK FEDINQEFVKIKDKNEILKRNLE NTQNQIKAEYISLAEHEAKMSS LSQSMRKVQDSNAEILANYRK GQEEIVTLHAEIKAQKKELDTIQ ECIKIMKRAPVIPKHTLNTQPVE DTSLSTPAAPMVDSLIARVGVM ARGNAITLPVCGRDVKFTLEVL RGDSVEKTSRVWSGNERDQEL LTEDALDDLIPSFLLTGQQTPAF GRRVSGVIEIADGSRRRKAAAL TESDYRVLVGELDDEQMAALS RLGNDYRPTSAYERGQRYATR PQNEFAGNISAMADAENISRKII TRCINTAKLPKSVVALFSHPGE LSARSVIDSAPNLGIGTINVVCA ADVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEPDVRILL TKYTNINASQSP\WMREKFGMA WESMVLKNVVRETDEVGKGQI RMRADFV\QAIDQRSSTGAWRN ALSIWEPVCNEIFDRLIKPRSEIT
24513	54881	A	24651	1094	2271	APFHRPHTKQSLQEQTDVVSIN EFLKQMAF*AQKLKE/WRTSAA SDITPAGFCSCRAIKDAEKPGRL PHPD\MEFRDRVDQ\RVVSPFGQ II\HMRNVFGPRLPRAKDVFPPV IGVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGN\DP\QGT ASMVSREGDPALHI\YQEAPFLP FYLGEKDDVTYAIKPTCCPGLN IIPSCLALPRIETELMGKFDEGK LPTDPHLMLRLAIETVAHAHDY DVIVIDSAPNLGIGTINVVCAAD V\LIVLTPVE\MFDYTSARQFFD MLRDLLKNA\DLKGFEPEVRIL LTKYSNSNGSQFP\WMEEQIRD AWGSMVLKNVVRETG\EVGKG \QIRMRT\VFEQAIDQRSSTDTSL STPAAPMVDSLIARVGVMASR
24514	54882	A	24652	1	1415	

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24515	54883	A	24653	3008	8165	ILIPFFIGLQNRFTQFRLSETKEIT NPYAMRLYESLFQSSKTNGSGI VSLKIDWIIERYQLPQSYQRMP DFRRRFLQVCVNEINSRTPMRL SYIEKKKGRQTTHIAIRDAEKA GRLPHPDMEIRGRVEQRVGYTI EQINHMRDVFGTRLRRAEDVFP PVIGVAAHKGGVYKTSVSVHL AQDLALKGLRVLLVEGNDPQG TA\SMYHEWVQNLHIHAEDTLL PFYLGKKDDVTYAIKPTCWPGL DIIPSCLALHRI
24516	54884	A	24654	1	848	
24517	54885	A	24655	2354	3640	NVICNQELVYSSRHQFAPGATV LYKGDKMVLNLDRSRVPTEYR YGVFLNVLLPATKYFQLHDPSL RNMELNYSLASEDLVLKGLRV LLVEGNDPQGTASMYHGWVP DLHIHAEDTLLPFYLGEKDDVT YAIKPTCWPGLDIIPSCLALHRI ETHLMGKFDEGKLPTDPHLML RLAIETVAHDYDVIVIDSAPNL GIGTINVVCAADVLIVPTPVE\L FDYASARQFFHMLRPLLKNVD LKGFEPDVRILLTKYSNSNGSQ SPWMEEQIRDAWGSMVLKNV KEFAGNISALADAENISRKIITR CINTAKLPKSVVVFFLTPVNYL PGDALQKAFTDKEELLKQQAS NLHEQKKAGVIFEAEEVITLLTS VLKTSSASRTSLSSRHQFAPGA TVLYKGDKMVLNLDRSRVPTE CIEKIEAILKELEKPAP
24518	54886	A	24656	667	870	QIVSSEPKYTDFLSKIPFEQRVR DVQRNGDHTEGAVR*LSIAFFS ALLKLLAFFTEEVRAAAVVRFV
24519	54887	B	24657	1	1086	
24520	54888	A	24658	2	250	WRTKSLDIPPLIYPNGIVKNILR HLSQLLNVPITRPFSWILRPF*RP *RKISTSFIRPLFTFLPA**MLIRS SVWQ*KTVSW

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24521	54889	A	24659	1	1608	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLLYMTYRKPDGS GIVSLKIDWIIERYQLPQSYQRM PDFRRRFLQCINAGHEMTKAIAI AQFNDDSPEARKITRRWRIGEA ADLLGVSSQAIRDAEKAGPLPH PDMENRGRVEQRGGYTIEPNN HMRDGVGTRWRRAEDVF\PPLI G\VAGHKGGR\YKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLPD LVKNRDLKGVEPDMRKQRHR KAKDLLAQDPTAMTTDELLKE ATRCPICTAYLEKPMSLECECV FCLSCTNSLQKEPQGEGVLCPF CLEASQKNNIRLNRQLGRLVSH IKELEPKLKKILKMNFKDAEVP RFSSPKPCSSFFSTCYLSKNCSN HPCYSPYPGSGWG
24522	54890	A	24660	1	1128	
24523	54891	A	24661	1035	1208	SLIDRIEALGIFRFAAV*GSAAY HGV*YERRRTFLCMLFGYFLSR RLESLLLPEVQS
24524	54892	A	24662	1	1316	MEIRGRVEQRVGYTIEQINHMR DVFGTRLRRAEDVFPPVIGVAA HKGGVYKTSVSVHLAQDLALK GLRVLLVEGNDPQGTASMYHG WVPDLHIHAEDTLLPFYLGEKD DVTYAIKPTCWPGLDIIPSCLAL HRIETELMGKFDEGKLPTDPHL MLRLAIETVAHDYDVIVIDSAP NLGIGTINVALQNFQRYTGIQH VHRIGMAERMWCDRNRERHT VSSSGGNRLPNPGPDRSDLALK GLRVLLVEGNDPQGTASMYHG WVPDLHIHAEDTLLPFYLGEKD DVTYAIKPTCWPGLDIIPSCLAL HRIETELMGKFDEGKLPTDPHL MLRLAIETVAHDYDVIVIDSAP NLVFRICFVIWAQERIDIKGFEP DVRILLTKYSNSNGSQSPWMEE QIRHAWGSMVLKN/VVRETDE VGKDTGVRSKSIWCHRNSRWE

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24525	54893	A	24663	504	1254	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHPARQPEHDIAFGKC SSSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWVPDLHI HAEDTLLPFY\DPHLMLRLAIET VAHDYDVIVIDSAPNLGIGTINV VCAADVLIVPTPAELFDYTSAL QFFDMLRDLLKNVDLKGFEPD VRILVVRVSQRMVVAGCIIAFID KLLNVLICFPFSVKNRFVIFHSV DFECVIRF
24526	54894	A	24664	1	3216	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPG FGDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRL/VKRAPTC WPGLDIIPSC\LALPRIETELMGK FDEGKLPTDPHLMLRLAIETVA HDYDVIVIDSAPNLG
24527	54895	A	24665	1	419	MSSSDKDFDFSVANMVNFFAP VFPMGKYYTQADKVLIPLAIQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE/ VGCRR*KRL*IFSLVYQTCAQSI QRALQCTYQPISHSLLYRVTEP VYAVSA
24528	54896	A	24666	1	2598	

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24529	54897	A	24667	1	2027	MRGHREKAAACKPRTRASEGT TPASTFILDFQPPNCNYTSGDNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWYLFTDSRGSKMTIDGINSN DIYMLGYVSNSLTGPYKPLNKT GLVLQMGLDPNDVTFTYSHFA VPQAKGILCEEDNYTAGDNHM MRAPHCEEDRAHKFVVFDANA GTESGHQGESSLFNRACGGGGT FFFSKESQKLQQSAKKRDCINA GHEMTKAIAIAQFNDDSPEARK ITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQ RVGYTIEQINHMRDVFGTRLKR AEDVFPPVIGVAAHKGGVYKT SVSVHLAQDLALKGSLLLPKND FLFKLGLEGHLPLGKIHSPPTGA DVARGSSGLPKSELFLPERNTQ ELQQDSEEGPLALQVLQSNLM DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQNNDGIC EIHVAKYVEIFGLTSAEASKDIR QALKSFAGKLVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQRAL QCTYQPISHSLLYRVTEPVYAV
24530	54898	A	24668	1	989	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDRNRERHTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSVMAETAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPE/V GCRR*KRL*IFSLVYQTCAQSIQ RALQCTYQPISHSLLYRVTEPV

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24531	54899	A	24669	350	1203	LLTARLTWVSARLMSDFADFG TTIKQDFRLLGQTSVDRLLQLS QGQAVKGNQLLPVSLVKRKTT LAPNTQTASPRALADSLMQLA RQD/LALKGLRVLLVEGNDPQG TASMYHGWVPDLHIHAEDTLL PFYLGEKDDVTYAIKPTCWPGL DIIPSCLALHRIETELMGKFDEG KLPTDPHLMLRLAIETVAHDYD VIVIDSAPNLGIGTINVVCAADV LIVPTPAELFDYTSALQFFDMLR DLLKNVDLKGFEPDVRILLTKY SNSNGSQSPWMEEQIRDAEGSR
24532	54900	A	24670	1	936	
24533	54901	A	24671	1070	1324	LGTPGGCSRMTCALVPLIPNDD TPTRRTRPLLGQGVFSVRS*TVP ADQSTSGDGDSTCNVRGSCPCR IAITILITPATPAAACV
24534	54902	A	24672	1	1212	
24535	54903	A	24673	2373	3381	FKRGQYGQLLRPRFHHGQILYA RRQGADAAGDSGIW/HGIWTEP MTM*KKDER*PSPTQAS*DNW KSIRGSCWQALSITRN/CKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR KPDGSGIVSLKIDWIIERYQLPQ SYQRMPDFRRRFLQHIFVLRER PETVLIDLIQRTKDAVRELDNL QYRKMKKLLFQEAHNGPAVEA QEEEEDD
24536	54904	A	24674	31	811	RRGLLGTRLRLSEDVFPPVLGV AAHKGGVDKTSVSVHLAQDLA LKGLRVLLVEGNDPQGTASMY HGWVPELHIHAEDTLLPFYLGE KDDVTYAIKPTCWPGLDIIPSCL ALHRIETELMGKFDEGKLPTDP HLMLRLAIETVAHDYDVIVIDS APNLGIGTINVVCAADVLIVPTP AELFDYTSALQFFDMLRDLLKN VDLKGFEPDVRILLTKYSNSNG SQSPWMEEQIRDAWG\SMVLK NVVAFQNLEFLFILLRIWL
24537	54905	A	24675	1004	1105	

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24538	54906	A	24676	1	1139	MEKKITGYTTVDISQWHRKEHF EAFQSVAQCTYNQTVQLDIKK KLKTVKKNKHKFYPAFIHILAR LMNAHPEFRMAMKDVAEYNG YHVVFALAGSPKDADDTSIYM FYQKVGDNSIDSWKNAGRVFK DSDKFDANDPILKDQTQEWSGS ATFTSDGKIRLFYTDYSGKHYG KQSLTTAQVNVSKSDDTLKING VEDHKTIFDGDGKTYQNVQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTASSIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPE/VGCRR*KRL*IFSLVYQT CAQSIQRALQCTYQPISHSLLYR VTEPVYAVSA
24539	54907	A	24677	1	930	
24540	54908	A	24678	1	2486	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DKWPLANADGTVAEYNGYNV VDKFDANDPILKDQTQEWSGS ATFTCDGKIRLFYTDYSGKHYG KQSLTTAQVNVLKSDDTLKING VEDHKAIFDGDGKTYQNVQQL IDEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTNFFRKESQK LQQSAKKRDAELANGALGIIEL NNDYTLKKVMKPLITSNTVTDE IERANVFKMNGKWYLFTDSRG SKMTIDGINSNDIYMLGYVSNS LTGPYKPLNKTGLVLQMGLDP NDVTFTYSHFAVPQAKGNNVV ITSYMTNRGFFEDKKATFAPSF LMNIKGNKTSVVKNSILEQGQL TWLQVAKRAGLGGGQSGRTVL RERLPNYKNFKGTIQELGQNQY AVSGEIFVVDRNTVEITELPVRT WTQVYKEQVLEPMLNGTDKTP ALISDYKEYHTDTTVKFVVKM TEEKLAQAEAAGLHKVFKLQT TLTCNSMVLFDHMGCLKKYET VQDILKEFFDLRLSYYGLRKEW LVGMLGAESTKLNNQARFILEK IQGKITIENRSKKDLIQMLVQRG YESDPVKAWKEAQEKCDNLKT CHTSHGSVMAETAVINHKKRK

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24541	54909	A	24679	5	253	SAPKVWRGLRQQGAGISVLP*V CAQP/VQVAKAPELILNFDLPK KYFDKL/R/DTHFFSPHTGKFPT VKILMAPFANSASRGVALC
24542	54910	A	24680	334	842	PDKEGNEIWVDMYTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFSIFSNMDLADTVMFLVG GHKIFVFHCHTELRMSIHQAGK NVNKGRIKLVLIFLYGL*/QRP* YPAERSGYRYIEQLTEMPQNVL YDAIGIYQRWYIQ
24543	54911	A	24681	676	1169	DNLKTCHTSHGSVMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPE/VGCRR*KRL*IFSLVYQTC AQSIQRALQCTYQPISHSLLYRV TEPVYAVSA
24544	54912	A	24682	1	783	
24545	54913	A	24683	1	1884	
24546	54914	A	24684	1	1131	
24547	54915	A	24685	1	2856	
24548	54916	A	24686	528	725	
24549	54917	A	24687	1	898	
24550	54918	A	24688	1879	2343	
24551	54919	A	24689	1	1254	
24552	54920	A	24690	1	1113	
24553	54921	B	24691	1	1156	
24554	54922	B	24692	1	1980	
24555	54923	B	24693	1	1932	
24556	54924	A	24694	1	663	
24557	54925	A	24695	1123	1764	
24558	54926	A	24696	2	1772	
24559	54927	A	24697	1	1040	MELKTKARELREECRSLRSRCN QLEERVSAMEDEMNEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLARQANVQIQE IQRTPQRYSSGRETPRHIIVRFT KVEMKEKMLRAAERKCDNLK TCHTSHGSVMAETAVINHKKR KNSPRIVQSNDLTEAAYSLSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDEKSYEQPSKDIRQALKS FAGKEVVFYRPE/VGCRR*KRL *IFSLVYQTCAQSIQRALQCTYQ PISHSLLYRVTEPVYAVSA

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24560	54928	A	24698	1683	4289	RVFKDSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTIFDGDGKTYQN VQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWHSK ILVSGTHRARTEVEVTDPIHQQ RMGCCFTVGAGEICEKPTGCFF TPLPNCNCQWTGSAILDRRSHS HPHSPASGSWVKVVTGSYQLT HSPGIGLRDFADFGTPHQTGFSP AGANQRGPLVATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AVSATQLMHFKILVSRAHRART ELEVTDPGSSAENGLLFPVVLL LRKARKTLMPPHSTCFIKRSAP TQSTAGKTRPRVLKDSDKFDA NDPILKDQTQEWSGSAPFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNYT SGDNHTLRDPHYVEDKGHKYL VFEANTGTENGYQGEESLFNKS VLRRRHELLPDFADFGPTIKQD FRLLGQTSVDRLLQLSQGQAV KGNQLLPVSLVKRKTTLAPNTQ TASPRALADSLMQLARQVSRLE
24561	54929	B	24699	1	2034	
24562	54930	A	24700	1	1038	
24563	54931	A	24701	1	1149	
24564	54932	A	24702	2	823	WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQCDNLKTCHTSHGSVMAET AVINHKKRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEK/ML*IFSL VYQTCAQSIQRALQCTYQPISH SLLYRVTEPGYAVSA
24565	54933	B	24703	1	1206	
24566	54934	A	24704	2	1037	
24567	54935	B	24705	1	1389	

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24568	54936	A	24706	1	602	MGTGDFICISMTGGAPWGFRLQ GGKEQKQPLQVAKWANLKPGP PSHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPE/VGCR R*KRL*IFSLVYQTCAQSIQRAL QCTYQPISHSLLYRVTEPVYAV
24569	54937	A	24707	1	774	
24570	54938	A	24708	1479	1947	
24571	54939	A	24709	1	696	
24572	54940	A	24710	1	1773	
24573	54941	A	24711	1	1509	
24574	54942	A	24712	1	891	
24575	54943	A	24713	156	242	VAGRGIGYRLSPNKGL*TWSAL CKPIAE
24576	54944	A	24714	1441	1866	
24577	54945	A	24715	1	1098	
24578	54946	A	24716	1	1989	
24579	54947	B	24717	126	848	
24580	54948	B	24718	58	688	
24581	54949	A	24719	1	542	
24582	54950	A	24720	1	675	
24583	54951	A	24721	1	1209	MKMPEKHDLLAAILAAKEQGI GAILAFAMAYLRGRYNGVLEA RSLKSRCQQSHALAEGSRGGPP VTGRFKSTFTADSWNRYSLPSL TGGGNILHSRTHRRTVSRLLGR RWQELLRDVFGTRLRRAEDVF PPVIGVAAHKGGVYKTSVSVH LAQDLALKGLRVLLVEGNDPQ GTASMYHGWVPDLHIHAEDTL LPFYLGEKDDVTYAIKPTCWPA LDIIPSCLALHRIETELMGKFDE GKLPTDPHLMLRLAIETVAHDY DVIVIDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEPDVRILLT/ KYSNSNGSQSPWMEEQ\IRDAW GSMGLKNV/VRETDEIG\KGQIR MRTVFETAMDKRLLTGAWEK AFFFLEPGFEEKSNR

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24584	54952	A	24722	1	743	MIGMELPGLEGTELEGCHEREV VYDRVRVFEKRGEARHVEARS PGGGSEKRGWGGARHQRMCR KGADNGGAGRARRVARLRQL ASRAIGRRKGAVLYQTPVINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTL WREASKDIRQALKSFAGKEVV FYRPE/VGCRR*KRL*IFSLVYQ TCAQSIQRALQCTYQPISHSLLY RVTEPVYAVSA
24585	54953	A	24723	1157	1471	
24586	54954	A	24724	1	824	MEENERDLEINMINMSKELKVE NIKKHIGMLEKDEIEIIVTKSILI EIEIPTQCLRNLNTLHLAASAGN HMSNTACWYGCEDFTSVSTFA HQGVGSWDAYEPAASLLLSCD NLKTCHTSHGSVMAETAVINH KKRKNSPRIVQSNDLTEAAYSL SRDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVANYAEIYGLTS AEASKDIRQALKSFAGKEVVFY RPE/VGCRR*KRL*IFSLVYQTC AQSIQRALQCTYQPISHSLLYRV TEPVYAVSA
24587	54955	A	24725	996	1169	SLIDRIEALGIFRFAAV*GSAAY HGV*YERRRTFLCMLFGYFLSR RLESLLLPEVQS

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24588	54956	A	24726	3	1743	DSPE\ARKITRRWRIGEAADLV GVSSQAIRDAEKAGRLPHPDME IRGRVEQRVGYTIEQINHMRDV FGTRLRRAEDVFPPVIGVAAHK GNDPQGTASMYHGWVPDLHIH AEDTLLPFYLGEKDDVTYAIKP TCWPGLDIIPSCLALHRIETELM GKFDEAQPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEPDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTDTSLSTP AAPMVDSLIARVGVMARGNAI TLPVCGRDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTPAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG KYFLRWLMRKIFHIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQQASNLHE QKKAGVIFEAEEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMVLNLDRSRVPTECIEKI EAILKELEKPAP
24589	54957	A	24727	1	1623	
24590	54958	A	24728	1	1863	
24591	54959	A	24729	1	2622	
24592	54960	A	24730	1	1338	

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24593	54961	A	24731	1	1823	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEVYTK VFALDVAARHRCDNLKTCHTS HGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPE/VGCRR *KRL*IFSLVYQTCAQSIQRALQ CTYQPISHSLLYRVTEPVYAVS
24594	54962	A	24732	1476	2221	

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24595	54963	A	24733	1	815	MRVGRKAVGAIWWSSKQELFQ QLFLRTELEDIGPGIVKRELGRE GSKDTGSSDDWEQLPDWKTKR VGNERDQELLIEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLVGEL DDEQMAALSRLGNDYRPTSAY ERGQRYASRLQNEFAGNISALA DAENISRKIITRCINTAKLPKSV VALFSHPGELSARSGDALQKAF TDKEELLKQQASNLHEQKKAG VIFEAEEVITLLTSVLKTVQSKN LSHFTWICHAETAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKHWVTISP QTSAYERGQRYASRCKNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQQASNLHE QKKAGVIFEAEEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMVLNLDRSRVPTECKRK LRPF*SGQRTDTAYVFDPGRDY

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24596	54964	A	24734	2	1249	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQLAISGRI LFLPMLNSINKLAAPSQPCTEPF FRRDPTLHPKSEVRLPPKVTTIT VISNPILITPQEKSVAQCTYNQT VQLDITAFLKTVKKNKHKFYPA FIHILARLMNAHPEFRMAMKD GELVIWDSVHPCYTVFHEQTET FSSLWSEYHDDFRQFLHIYSQD VACYGENLAYFPKGFIENMFFV SANPWVSFTSFDLNVANMDNF FAPVFTMGKYYTQGDKVLMPL AIQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLPIDWIIERYQLPQSYQRM PDFRRRFLQVCVNEINSRTPMR LSYIEKKKGRQTTHIIRISDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDERGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAMRLY ESLCQYHLCGTLRNSRFCEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPE/VGCRR*K RL*IFSLVYQTCAQSIQRALQCT

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24597	54965	A	24735	1	2286	MLTLILLDLQFMAQLAGYQMS FNSTKSKQTKNNFAVGYRTGD FQLHTNVNDGAEFGGSVYQKV CEELDALINLAWTSSTSCTRFG LAAKFQLKPIAFISTKVNHWLT GVSYTPPLEAGVKLNLSALCDN LKTCHTSHGSVMAETAVINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAMRLY EIPVVSIRKPGMGSGIVSLKIDW IIERYQLPQSYQRMPDFRRRFLQ CINAGHEMTKAIAIAQFNDDSP EARKITRRWRIGEAADLLGVSS QAIRDAEKAGPLPHPDMENRG RVEQRGGYTIEPNNHMRDGVG TRWRRAEDVF\PPLIG\VAGHKG GR\YKTSVSVHLAQDLALKGLR VLLVEGNDPQGTASMYHGWV PDLHIHAEDTLLPFYLGEKDDV TYAIKPTCWPGLDIIPSCLALHR IETELMGKFDEGKLPTDPHLML RLAIETVAHDYDVIVIDSAPNL GIGTINVVCAADVLIVPTPAELF DYTSALQFFDMLPDLVKNRDL KGVEPDVFIRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSVPVTPHTF

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24598	54966	A	24736	1	1400	MDAKMHSGGTAPPGTLSQRQP SSNSKTNGSKLNPLKDTLLSTPS CPEGELVNAARRSNGSGNAITL PVWGRDVKFTLEVLRGDSVEK TSRVWSGNERDQELLTEDALD DLIPSFLLTGQQTPAFGRRVSGV IEIADGSRRRKAAALTESDYRV LVGELDDEQMAALSRLGNDYR PTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQQASNLHE QKKAGCDNLKTCHTSHGSVMA ETAVINHKKRKNSPRIVQSNDL TEAAYSLSRDQKRMLYLFVDQI RKSDGTLQEHDGICEIHVAKYA EIFGLTSAEASKDIRQALKSFAG KEVVFYRPEEDAGDEKSYEQPS KDIRQALKSFAGKEVVFYRPE/ VGCRR*KRL*IFSLVYQTCAQSI QRALQCTYQPISHSLLYRVTEP
24599	54967	A	24737	1	1628	MLHITNDQGNASQNHNAMPPY SCKNGHNLKTVDGGMDAVNG EHFYTAGLSQGPLKGSFLLFFNI LILVCPPIFRVSGNEVFIRDKLM ERRNRRTGRTEKARIWEVTDRT VRTWIGEAVAPLLLTCDNLKTC HTSHGSVMAETAVINHKKRKF SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THICDNLKTCHTSHGSVMAETA VINHKKRKNSPRIVQSNDLTEA AYSLSRDQKRMLYLFVDQIRKS DGTLQEHDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPE/VGCRR*KRL*IFSLV YQTCAQSIQRALQCTYQPISHSL LYRVTEPVYTISAY

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24600	54968	A	24738	1295	1675	SVTSCLKVTSVCLTSGRRFLQIR ISDGTLQEHDGICEIHVAKYAEI FGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYLI PFFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIAWVIERYQLPQSYQRMPDF RRRFLQVSDFLMAPYRNIDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLCQY RKPDGSGIVSLKIDWIIERYQLP QSYQRMPDFRRRFLQVCVNEIN SRTPMRLSYIEKKKGRQTTHIE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDERGYESFPWFIKRAHSP SRGLYSVHINPYLIPFFIGLQNRF TQFRLSETKEITNPYAMRLYQS LCQYRKPDGSGIVSLKIDWIIER YQLPQSYQRMPDFRRRFLQIRK SDGTLQEHDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEEGYESFPWF IKRAHSPSRGLYSVHINPYLIPFF IGLQNRFTQFRLSETKEITNPYA MRLYESLCQYRKPDGSCIVSLK IDWIIERYQLPPRYQRMPDFRRR FLRVWVQEINSRTPMPPLLPWE
24601	54969	A	24739	1	1986	

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24602	54970	A	24740	1	398	MVDSLIARVGVMARGNAITLP VCGRDVKFTLQVLRGDSVEKT SRVPPGNERDQEMLTEDALDD LIPSFLLTGQQTPAFGRRVSGVI HTADGSRRRKAAALTEKFCIVD NPPGEIRKRACLFIPTHALNLNR FEDICYAHQLPDGGLLSARVGV MARGNPILSPVCGRNVKFTLKV LRGDSVENPSRVWSGNERAQE LLTEHALDDLTLSFLLTGQQTP AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGELDDEQMAA LSRLGNDYRPTSPYERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSHPGE LSARSGNERDQELLTEDALDDL IPSFLLTGQQTPAFGRRVSGVIH TADGSRRRKAA/DTYRKILYR** PPGGD*KKSVPFYSNTCAQSQP
24603	54971	A	24741	1450	3699	RNPLQIPKQQQNEKYQVPQFDQ STIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNSIDS WKNAGRVFKDSDKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHYGKQSLTTAQIFQ MITVFITSLCNTTSSHICLHISWV TTMHGAMPHPGHIPTAPASLPA KVKGSGKVCWLAFPLSELTPPS ALQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQHFIDEGN YTCGDNHTLRDPHYVEDKGHK YLVFEANTGTENGYQGEESLFN KAYYGGGTNFFRKESQKLQQS AKKRDAELANGALGIIELNNDY TLKKVMKPLITSNTVTDEIERA NVFKMNGKWYLFTDSRGSKM TIDVPQAKSTNVVITSYMTNRG FFEPEGSKGSITAAVMAKGLSV ASGNSTPERRRATANENVQPRA IRDAEKAGRLPHPDMEIRGRVE QRVGYTIEQINHMRDVFGTRLR RAEDVFPPVIGVAAHKGGVYK TSVSVHLAQDLALKGLRVLLV EGNDPQGTASMYHGWVPDLHI HAEDTLLPFYLGEKDDVTYAIK PTCWPGLDIIPSCLALHRIETEL MRKFDEGNLPTDPHLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAEQLDISSS RQFFD\ILRDLLKNVDLKGFEPD

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24604	54972	A	24742	1	3899	MVDSLIAPVGVMARGNAITLPV RATNVKFTLEELRGDSVEKTSR VWSEKKDRGGQEAEVSGEGSS QTKSLQKRQHSNGSDFTARGF HTGQALVRSKGTYWNPTGLGL SHGTEDPNLIGEELDAGEWDK NTRKELAVLNVRRDFADFGTTI KQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQFWVFEGGLRVLVR ERVTTPKGT\ASMYQGW\VPD
24605	54973	A	24743	268	2617	RMFRMKLMETL\SQCINAGHE MTKAIAIAQFNDDSPEARKITR RWRIGEAADLVGVSSQAIRDAE KAGRLPHPDMEISGR\VKHGVG YTIEQIYL\TRDVFGTRLPRAED\ VFPPVIGVAAHKGGVYKTSVSV HLAQDLALKGLRVLLVEGNDP QGTASMYHGWVPDLHIHAEDT LLPFYLGEKDDVTYAIKPTCWP G\LDIIPSCLALHRIETELMGKFD EGKLPTDPHLMLRLAIETVAHD YDVIVIDSAPNLGIGTINVVCAA DVLIVPTPAELFDYTSALQFFD MLRDLLKTVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMVLKNVVRETDEVGKGQI RMRTVFEQAIDQRSSTDTSLSTP AAPMVDSLIARVGVMARGNAI TLPVCGRDVKFTLEVLRGDSVE KTSRVWSGNERDQELLTEDAL DDLIPSFLLTGQQTPAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQQASNLHE QKKAGVIFEAEEVITLLTSVLKT SSASRTSLSSRHQFAPGATVLY KGDKMALNLDRSRVPAYIIRSY IRCGRKGFASAGVGGCRGWLN YAASEQIVLRVHHMRCEIPHRC

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24606	54974	A	24744	1	2624	MTPQKRGYLCKAGARNLDVLL EGCEIFLLIPMGMRSESGVSDA DTVSAPRKKHSLEQGIFRAQVE ASKPSSVPACIVVGNVSGYQFP PGTSYGPDSESELGYREKFMSF VGTMNEAGNPPFSANYSKAKK PKPRMFSLIERMSPSPRVGSQSV QSSCFRDIPFEQDQMFPHPSLVL RSKEQQPLLTQSIGVNSARKAM AKRRRHRRRRRVSGVLPIA\VG VPS*SVHLPKVLSCSGASWI*QS CISRLGRLSPTRLMNVA\GNDP QGTASMYHGWVQILHIHAEDT LL/PFY/LGEKDDVTYAIKPTCW PGLDIIPSCLALHRIETELMGKF DEGKLPTDPHLMLRLAIETVAH DYDVIVIDSAPNLGIGTINVVCA ADVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WASMV*K\NNVRNANEVGKDT LKGFYSLKERPLGNHFLGPNNR PFGKIMKHKTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAFTDKEELLKQQASNLHEQK KAGGFCRFRNHHQTGFSPAGA NQRGPLAATLSGPGGEGQSAV ARLTGEKKNHPGAQYANRLSP
24607	54975	A	24745	1	385	MWQAISRLLSEQLGEGEIELRN ELPGGEVHAAWHLRYAGHDFF VKCDERELLPGFTAEADQLELL SRSKTVTVPK\AFILGQQIARLH QWSDHAVLKIVTTGVL*GAYV GAPSIWKCPERITLPGYHQ
24608	54976	A	24746	1	1209	

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24609	54977	A	24747	1	857	MHACRSELLGEGEIELRNELPG GEVHAAWHLRYAGHDFFVKC DERELLPGFTAEADQLELLSRS KTVNRALKVWA\VGADRELTV FLV\MDYLPPRPLDAHSAFILGQ QIARLHQWSDQPQFGLDFDNA LSTTPQPNTWQRRWSTFFAEQR IGWQLELAAEKGIAFGNIDAIVE HIQQRLASHQPQPSLLHGDLWS GNCALGPDGPYIFDPACYWGD RECDLAMLPLHTEQPPQIYDGY QSVSPLPADFLERQPVYQLYTL LNRARLFGGQHLVIAQQSLDRL
24610	54978	A	24748	1	2094	
24611	54979	A	24749	1	1209	MVREDLYTYYSCNTSREQQQL ENPMESPLCSKEINQGGVFMLA GKASDTLLAGGTMNNLGGEDS DTIVENGSIYRLGTDGLQLYSS GKTQNLSVNVGGRAEVHAGTL ENAVIQGGTVILLSPTSADENFV VEEDRAPVELTGSVALLDGAS MIIGYGAELQQSTITVQQGAPP VKLRFALYGRPGFTKCGWMLG YKPAHDKTLLRITRGHDFACYQ RTTQLARQRGLKVCSHLIVGLP GEGQAECLQTLERVVETGVDGI KLHPLHIVKGSIMAKAWEAGR LNGIELEDYTLTAGEMIRHTPPE VIYHRISASARRPTLLAPLWCE NRWTGMVELDRYLNEHGVQG SALGRPWLPPTENSLMKQIRLL AQYYVDLMMKLGLVRFSMLL A\WPSSFLPLWYKWR
24612	54980	A	24750	200	310	
24613	54981	A	24751	1	4398	MCIPVPPIATGDRHFIAVAHIHQ NSRRSPVDSDESSTRSAVAAHP ATRDFNVRALYTVTSSVSPTKP PLPATFRQGRYRPAEPCVGSIG VIPQSSCVLANGSTGAQSAFGDI IRAGPPSAGLVPVAQATVIETFL RYQTINERDFWAARNRLLKQP YGSRILRFTEAYAIAERAAQSV LRISLADAFNVDGPRPAEDSIFR LLRMPGSAVQRPDRRHNRRCQ YRPAMAFPAGSKANKQRQYNG GRQFYRKRICWL

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24614	54982	A	24752	939	2169	RPASPPARDGARWSTGLHSSYS AMRCRNASTCAEDSQLS/DPLA R/PSVASGPYRVTSWKLGQNIV YCRVKDYWPATLTVNRGRWN FDTIRSDYYLDDNVAFEAFKAG AFDLRMENDAK\NWATRYT/G DRRVREAITLAFDFEWMNKAL FYNAWSRTNSYFQNTEYAARN SPPPPEL\VLLPPIKKVLPSEVFP\ QIYQPPVSKGDGYDRDNLLKA DKLLNEAGWVLKGQQRVNAT TGQPLSFELLLPASSNSQWVLPF QHSLQRLGINMDIRKVDNSQIT NRMRSRDYDMMPRVWRAMP WPSSDLQISWSSEYINSTYNAP GVQSPVIDSLINQIIAAQGNKEK FLPLGRALDRVLTWNYYMLPM WYMAEDRLAWWDKFSQPAVR PIYSLGIDTWWYDVNKTAKLPS ASKQGE
24615	54983	A	24753	3	450	
24616	54984	A	24754	2	203	PLPDAARYLRRQCQKPARVHDI FAAMHTAHRSRPDRPSLPDDAF SSLRL*FFQPEHYPRQYQHRHL CS*ERYQHQALSRTRFRSG*PTP SVPETSTGSRYFCGNAHSAPKP PRPPITTGRRVFFTTPLILPTRAL PASISTPASL
24617	54985	A	24755	1016	1219	
24618	54986	A	24756	1695	2021	PDTFSMLPATRFLPPLQFPDLQH PEAAQYAHWLPASGCFLFLPPP GSGTVFLLPYPSPRLCRSTSETP LPAITR*HFPVTDRVQK*ITRRR KPRHKPFYPDDLQRDAR
24619	54987	A	24757	1671	1911	
24620	54988	A	24758	513	1104	CWRNCARCERNLVFRCQYGIY WCDNAANRSCRTKRDQPRLVE W*KSACSHHR*LH\PCGHCRQF MNELNSGLDLRIHLPGREAHAL RDYLPDAFGPKDLEIKTLLMDE QDHGYALTGDALSQAAIAAAN RSHMPYSKSPSGVALECKDGRI\ LVAATLKTPH/INPTQICGQPWS MHRRALTSKFGAHGDRRTSAG FRRN
24621	54989	A	24759	131	759	
24622	54990	A	24760	662	889	LPIKCRAARGVPARCLRWTRW ALRRILPPLRNRSRAASRWRAS PGARK*WMPSLQAVWAAPMR VTRLPAWLRWKC

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24623	54991	A	24761	1	1518	MQRRDGDIALIYRSKIGPRTSIT FTARRANPVQRIAARILLRDHLI CRMSCTAARHANTFDLIQGSG ADNFAAIYGGANDRITRADAA VAGAGNWHRFGISNGKLSPRSI TRTSSPARAMTKMPYNPQASG GSNLAVSNPELDKLIAARVAAL RAANPDASASVPVELVTASASY PRSLMRCNRILSPGSARGQMIIT ALFIYAGNPIACVAALEVLKVF EQENLLQKANDLGQKLKDGLL AISFWRAKWLKIFVVCGAEIFV EYVLKNKVIWLLCFANIFLYVV RIGIDQWSTVYAFQELKLSKAV AIQGFTLFEAGALVGTLLWGW LSDLANGRRGLVACIALALIIAT LVIPFHMVFHPNEQYAYCVNEL NSSVDVWELKDPHGNIECVQT LDMMPENFSDTRWAADIHITPD GR\HLYACDRTASLITVFSVSED GSVLSKEGFQPTETQPRGFNVD HSGKYLIAAGQKSHHISVYEIV GEQGLLHEKGRYAVGQGP\MW
24624	54992	A	24762	3	486	ACRRALKD\AGVEADEVLEVV MVGGSTRVPLVRERVGEFFGRP PLTSIDPDKVVAIGAAIQADILV GNKPDSEMLLLDVIPLSLGLET MGGLVEKVIPRNTTIPVARAQD FTTFKDGQTAMSAGGAHIRVTF QVDADGLLSVTAMEKSTGVEA SIQVKPSYG
24625	54993	B	24763	1	2469	
24626	54994	A	24764	1255	1761	ESFQVRTHGTGEPVNKTRTSQA VSHHNQSCQVDQCVPCAVIAG NVFPRHNVQGQH*RNCQQTNR SSINDFTKLSNTRPISVHSLGIKQ SRPDRHAKASPVVTAVKACEQ VIAAVNQIADDHQPDRTKQRN AIVVADDLPDLFPVHFFGVDHQ QHNHRDKKQPGEDLLCC
24627	54995	A	24765	1	3141	
24628	54996	B	24766	1	3969	

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24629	54997	A	24767	643	2082	GAHAMDKHFSTTPAEKNLPVL LALIGIWYNNFFDKNDALVMV DDFPRRSGLSWKIVVVPHEYW VGGSTRVPLVRERVGEFFGRPP LTSIDPDKVVAIGAAIQADILVG NKPDSEMLLLDVIPLSLGLETM GGLVEKVIPRNTTIPVARAQDF TTFKDGQTAMSIHVMQGEREL VQDCRSLARFA\CVVFRRYRL/A GAHIRVTFQVDADGLLSVTAM EKSTGVEASIQVKPSYGLTDSEI ASMIKDSMSYAEQDVKARMLA EQKPGQQEAKLALKTFHWQQA IADKRVIGAGITGVTAGTDHRA DVTEVASDFRVQTTNADSALF HVRSAQQHIHQLLHFTTHLLCQ LAGLDHVVFQQIATNPADQVQ AVGFTRTGKDLCHFHGGFTHA EELHKAGVEAGKVTGQAKVEQ MRVQAFYLQQNGADHLRTFW HLNTHRVFHRRGVGGAVGKA ADPAHTVREEGHFVITHTGFRQ FFHAAMDVEQ
24630	54998	A	24768	1	502	

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24631	54999	A	24769	1	2345	MFMIGALVLALVMTLITFMVL RRIVIRPLQHAAQRIEKIASGDL TMNDEPAGRNEIGRLSRHLQQ MQHSLGMTVGTVRQGAEEIYR GTSEISAGNADLSSRTEEQAAAI EQTAASMEQLTATVKQNADNA HHASKLAQEASIKASEGGQTVN GVVKTMGAMSTSSKKISEITGR HQQGIRTPVTAVKGRCPGPLDE GDTDTAYYALRDIFALTPNRKR LAIPVSTDNPGKPCKDPSLSKD VSNRVPQRVPCYDSPRSSSVNG NRLPGKDFHDDERSMGRSGSY VLALAYPPKIALSDADSVTVNV AGWQGEISREQFNELIAPLVKR TLLACRRALKD\AGVEADEVLE VVMVGGSTRVPLVRERVGEFF GRPPLTSIDPDKVVAIGAAIQAD ILVGNKPDSEMLLLDVIPLSLGL ETMGGLVEKVIPRNTTIPVARA QDFTTFKDGQTAMSIHVMQGE RELVQDCRSLARFACVVFRRYR LAGPVDLFLRPWEVDISRRTSL DSPLPVQVLEASPKGHYTQLVV QPLGWYNEPLTVVMHGDDAP QRGERLFVGLQHARLYNGDER ASRDPGFLMARFVTCRPDKTRK LRIRQHHVWIEIVSTLEQTIGNT PLVKLQRMGPDNGSEVWLKLE GNNPAGSVKDRAALSMIVEAE KRGEIKPGDVLIEATSGNTGIAL AMIAALKSYRMKLLMPDNMSQ
24632	55000	A	24770	313	676	DCQPRSSAFTKPDATTAGHYLA GSGGRMTQLAIGKPASLGAHLE REGGENFTFFSLNADGEKL/CVF DANGQ/EHRYDLPGHSGDIWH/ G/YLPDARPALRMVSRH/GP/WQ PAGGMLTPAVVMILPRK
24633	55001	A	24771	1760	2053	FRVHGKNAFSH*IKPAAMLLPS SPVTRSVKPTQCGSAPSKRPNL TLLPSITLMPPLPVTDLKLGCIA PCSSDCFSFITFSISCATRLSVNW LPAAGQ
24634	55002	A	24772	296	732	
24635	55003	A	24773	606	695	
24636	55004	A	24774	1520	1737	PVHGLCGTRRDAGS\PAIYPFHS LML/RFWLR/TCTVPGWPLDDS SLAGEAFSAFTTDAAVWSLISA TAMLAVQAG
24637	55005	A	24775	1	1049	

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24638	55006	A	24776	248	933	RTTMRAVSRPKYCSRERWL/HY DFTVARFDENASCGTFAATSAV VLIFSHCLRLLCRVVVLVTRVN FQFTEHSTTQRAFWQHAFNRDF NHTLRTASNHLFKGRLFDTTDV AGVVIVHFVSTLVAGYSNFVSV QNDDVITGIYVRSVFRFVLTAQ ATSQFSSQTAQSFTGRVNNIPV AFYGFWFSCAKYYRHGARWCS NGRKIDQRHTHCFFCPCIRTDFA VEIGKEEFIT
24639	55007	A	24777	219	3441	DCQPRSSAFTKPDATTAGHYLA GHSGDIWHGYLPDARPGLRYG YRVHGPWQPAEGHRFNPAK\LL IDPCARQIDGEFKDNPLLHAGH NEPDYRDNAAIAPKCVVVVDH YDWEDDAPPRTPWGSTIIYEAH VKGLTYLHPEIPVEIRGTYKAL GHPVMINYLKQLGITALELLPV AQFASEPRLQRMGLSNYWGYN PVAMFALHPAYACSPETALDEF RDAIKALHKAGIEVILDIVLNHS AELDLDGPLFSLRGI
24640	55008	A	24778	454	586	
24641	55009	B	24779	130	1557	
24642	55010	B	24780	92	2808	
24643	55011	A	24781	2	1051	WRLRPITPLWRWQKIFFPDA/R YGIRFRNLETGNWYPELLDNVE PSFVWANDSWIFYYVRKHPIFI DLTTEELAASSYHESWVLEDRII KDGSYNIDQGVGVRAISGEKTG FAYADQISLLALEQSAQAARTI VRDSGDGKVQTLGAVEHSPLY TSGRSGWQSMSREEKLDILRRV DKVAREADKRVQEVTASLSGV YELILVAATDGTLAADVRPLGK VLLVGQSPNAELSARAKQIAM GVDGANEVYNEIRQGQPIGLGE ASNDTWITTKVRSQLLTSDLVK SSNVKVTTENGEVFLMGLVTE REAKAAADIASRVSGVKRVNR TLFLGYAVMFSELILAPVTPSNS
24644	55012	B	24782	1	2079	

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24645	55013	A	24783	1	3214	MGAEKQLIPDGCGVSYIPSSGP LDKWRALLFIQPDYRADPVYR QIITITDLRILYDYTENFVLPLSH DEVVHGKKSILDRMPGDAWQK FANLRAYYGWMWAFPGKKLL FMGNEFAQGREWNHDASLDW HLLEGGDNWHHGVQRLVRDL NLTYRHHKAMHELDFDPYGFE WLVVDDKERSVLIFVRRDKEG NEIIVASNFTPVPRHDYRFGINQ PGKWREILNTDSMHYHGSNAG NGGTVHSDEIASHGRQHSLSL
24646	55014	A	24784	1	1079	MKQIKELQRLLGKKTWKMNSS KKPLNMDGPKVDSARALIGRG WGTHKFYRCDCIKPTIKTNTSS RGNEKNPDGSHNNIHNSWFRL LTSQNMCKVPESPAILVDVGQS AETVQSVLTVKVEHPILRIAVA GYACQRQSCLLAMRHPQYAIN SSKVVKPCSTARQPFQKAYAYP PVVRAFPAINVGISGNKLTNDR RYGRTSNKAWGSGDGHTLSEC GWAPLAAGDNVGKVSYQTLG YYQRILGYIFYPIAW/VMGVPSS EALQVGSIMA/TKLVSNEFVAM MDLQK/IASTLSPRAEGIISVFL/ VSFANFSSIGIIAAAAECRDWFG ILAAQTLAVRAALRVVQAERD CVLSMEQHQCARGRQR
24647	55015	A	24785	121	258	LTEPRHYCRSIQFFGLTNMGQN CYQLS*E*FIGTLNHIRRIPQPLS
24648	55016	A	24786	1	470	WGSGDGHTLSECGWAPLAAG DNVGKVSYQTLGYYQRILGYIF YPIAW/VMGVPSSEALQVGSIM A/TKLVSNEFVAMMDLQK/IAS TLSPRAEGIISVFL/VSFANFSSIG IIAAAAECRDWFGILAAQTLAV RAALRVVQAERDCVLSMEQHQ CARGRQR
24649	55017	A	24787	1324	1539	GWCGCEVPFKITDGLACLLQSP QGHQTFCFT*HNLGLQPFWIPM CLCSVNVFKTRLILTQVEEGCR AVSMTQ
24650	55018	A	24788	71	403	RTTFIFDLSSGWPFILWQVLSPN *RCLQVGLFAQIPTGRMGCLHR FLTCRMGVCTDSSPAGWAVTLI RMSPIFPASSKSTLSAALLNTSC LHSRDLEPPGAFRSGGPVLL

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24651	55019	A	24789	309	1653	SVLMDESDIYRNNRERFFCVFL LVGVPARGACLGGGGGCGLCV RYLRSAGWGCGRRFPCVGDN WSAILAHIGKPEELDTSARNAG ALTRRREIRDAATLLRLGLAYG PGGMSLREVTAWAQLHDVATL SDVALLKRLPKCRHWFGILAG QTLAHIRVLPVIIRAIGFLLSKV NGMGKLESFNAVSSLILGQSEN FIAYKDILGKISRNRMYTMAAT AMSTVSMSIVGAYMTMLEPKY VVAALVLNMFSTFIVLSLINPYR VDASEENIQMSNLFEGQSFFEM LGEYILAGFKVAIIVAAMLIGFI ALIAALNALFATVTGWFGYSIS FQGILGYIFYPIAWVMGVPSSE ALQVGSIMATKLVSNEFVAMM DLQKIASTLSPCAEGIISVLLDSF ANFSSIGIIARAVKGLNEEQGNE GSRFGLKLVYRSTLVS\VLSASI AALVLSDHT
24652	55020	A	24790	754	957	
24653	55021	B	24791	75	3707	
24654	55022	B	24792	75	264	
24655	55023	B	24793	344	461	
24656	55024	A	24794	1	2203	
24657	55025	A	24795	20	198	
24658	55026	A	24796	1239	1409	RGPPTPFFHVWEWQQRPLSVW EADHV*RRDEGACPRMVARAR NCRPKLLELRAESQ
24659	55027	A	24797	1325	1564	
24660	55028	A	24798	323	694	TGYARQKPVPALGWWTNVSAS TAPPIILPSITGSRLAVIKWLTVS AGKLSALLCASCQKGGGAKWR MAMANGITNKLAIQCSPPHSTI EKFTSQSQHVLA*GVSAVRSM VSSG*GRRPLPALG
24661	55029	A	24799	4708	4878	
24662	55030	A	24800	20	199	
24663	55031	A	24801	743	1186	

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24664	55032	A	24802	1394	2651	KLMTCRHEGSLGDDPGINGQL WDVNRIDVTAHEGTWERWTV RADEPQAFHIEGVMFQIRNVNG AMPFPEDRGWKDTVWVDGQV ELLVYFGQPSWAHFPFYFNSQT LFSWPQYWAACFGPAPFLPMS REEMDQLGWDSCDIILVTGDA YVDHPSFGMAICGRMLEAQGF RVGIIAQPDWSSKDDFMRLGKP NLFFGVTAGNMDSMINRYTAD RRLRHDDAYTPDNVAGKRPDR ATLVYTQRCKEAWKDVPVILG GIEASLRRTAHYDYWSDTVRRS VLVDSKADMLMFGNGERPLVE VAHRLAMGEPISEIRDVRNTAII VKEALPGWSGVDSTRLDTPGKI DPIPHPYGEDLPCADNKPVAPK KQEAKAVTVQPPRPKPWEKTY VLLPSFEKVKGDKVLYAHASRI LHHETNP\AVPAH

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24665	55033	A	24803	1	2126	MQEKQVLAAYVQPSSEGQSRS RRARRVSQCHQHSAAAASLAR TAASATADSAHPPCPRSAARAG ATMHVKKYLLKGLHRLQKGPG YTYKELLVWYCDNTNTHGPKR IICEGPKKKAMWFLLTLLFAAL VCWQWGIFIRTYLSWEVSVSLS VGFKTMDFPAVTICNASPFKYS KIKHLLKDLDELMEAVLERILA PELSHANATRNLSFSIVNPTP\L VLIDERNPHHPMVLDLFGDNH NGLTSSSASEKICNAHGCKMA MRLCSLNRTQCTFRNFTSATQA LTEWYILQATNIFAQVPQQELV EMSYPGEQMILACLFGAEPCNY RNFTSIFYPHYGNCYIFNWGMT EKALPSANPGTEFGLKLILDIGQ EDYVPFLASTAGVRLMLHEQR SYPFIRDEGIYPMSGTETSIGVL VDKLQRMGEPYSPCTVNGSEV PVQNFYSDYNTTYSIQACLRSC FQDHMIRNCNCGHYLYPLPRG EKYCNNRDFPDWAHCYSDLQ MSVAQRETCIGMCKESCNDTQ YKMTISMADWPSEASEDWIFH VLSQERDQSTNITLSRKGIVKLN IFFQEFNYRTIEESAANNIVWLL SNLGGQFGFWMGGSVLCLIEFG EIIIDFVWITIIKLVALAKSLRQR RAQASYAGPPPTVAELVEAHT NFGFQP\DTAPRSPNIGP\YPGEQ ALPNPG/TPAPPNYDSWRLQPL
24666	55034	A	24804	905	1051	
24667	55035	A	24805	1	1257	
24668	55036	A	24806	1	3116	MPIITLPDGSQRSFDHPVSVAEV AQSIGAGLAKATLAGKVDGRLI ITPKDEEGLEIIRHSCAHLVGHA VKQLYPTAKMVIGPVIEEGFYY DIFFERPFTPEDMAAIQQRMRE LIDKDYDVIKKMTPRAEVIELF KLQAAPDRRHAGREGHGLYFH EEYVDMCRGPHVPNTRFLKAF QLTKISGAYWRGDSKNEQLQRI YGTAWADKKQLAAYIQRIEEA EKRDHRRIGKQLDLFHLQEEAP GMVFWHPNGWSVYQ
24669	55037	A	24807	1924	2790	
24670	55038	A	24808	1	1185	

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24671	55039	A	24809	823	5990	MARPVPLWSSWGLRTSYLPKP LSVNPSRNDGSA/FAGTHPLGV TRGTLAGPAFVRLSLVFLLRRV LAGSSLLPLLMG*QK/PEVLLPD GASEHDYSLRPSDVKRLQNAD LVVWVGPEMEAFMQETGKQIT RSEVSPLCRRVAFNKFNRDPQP RYDWGRLTVLYSGSSLSGGRY VVIIRECHCQLSKPLRLEQNEIR SLLPEASEPIDQAAQEDEAIPQD ELDDKIAGEAGVHEYVVSTGD TLSSILNQYGIDMGD
24672	55040	A	24810	2305	2550	
24673	55041	A	24811	665	844	ISFNNEVISYRLSGKNQ*LNLG* EIWLESGAFKKALSPQKHPGLE PSVCTPTPTLVPDR
24674	55042	A	24812	1	2031	
24675	55043	A	24813	106	912	HFETVIDQRDFHPVFSHKGIRAT PEGNEEKGQRVADVTEQCGRC RCQPPAATLTQAVKNVHVEDL PQRVGHETGGGDTGDKQVEVG ECAESHTLDALGLRCPEPVMM VRKTVRNMQPGETLLIIADDPA TTRDIPGFCTFMEHELVAKETD GLPYRYLIRKGG**GLIGFDAAF SPHPNPLPRGARGPIALNVAIGL PYLLRNNLNAFAVTSTVAPVSA STASHNPVIQRGDEEDPFQPQR NSDVLADIGVSGACQFNHLHQ AAQVVMG

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24676	55044	A	24814	1	1495	MQKLTLTYAETRRLYGKEVYH RPSRFIGELPEECVEEVRLRATV SRPVSHQRMGTPMVENDSGYK LGQRVRHAKFGEGTIVNMEGS GIAALCHCRVLIATAALMDPDD AVELSVTTMMFALCNTRNPRV AWDTAPCVPATTAASMAKRAP DMSQSAAPEAGSQKPPRLSCGE SLHPLPATKRAYNYCRPVGRIR HLCRIRQSMPDATLSRLIRPTTV ADPPDKALAPHPAVFTRGDSKF LSHKPARSPAIRYLLASVWGPV GMMAMMLAMTGFVVATRKLR RRFGFKSCKNGVLYRISSSSITT SPASPIATCRPVLPCWMRMDPM LDMMGMQMLMEKYGDQAMA GMDHSQMMGHMFLGHKVIRA NHVGDWGTQFGMLFRIAVETF KEDWEAVWDQLDDLNLEGKIV A*GRDPAAFHIDNGAFTKLSVA YALAELVAAVVLDHRRTHPLM ADRAAYRGAQAHLFHTLFRQL ADKARRAMVNLFTIQTAGFRV GQRQFLH
24677	55045	A	24815	3	707	GCTLGPVKSFSLRVAWLSWPQ YFYIIERACSPCCGPLAPGEAPH VNLFHSTHSENKKQPHNSPYHN DIQPTLNYLPTNQKKQTQQEQS HNITKQGSQLHDVTQVPYQAY RSAIVVGLIRRDSVASGIDCRM RRERLIRPTGRASDNTEFTGTQ NMQNITHSWFVQVMIKATTDA WLKGWA*AQRRQPDATPG*RR YRTISRQFPATSVLYPAQPAHA FTGKYTVYCHRLGQILP
24678	55046	A	24816	2	1340	
24679	55047	A	24817	1	2457	

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24680	55048	A	24818	41	1053	QRNQQAHLSF/QHSRDIYDNQV HLVRNCNLEMPDQEFIVLYGPS DCGKSTTLRMIAGLEEISGGDL LIDGKRMNDVPAKARNIAMVF QNYALYPHMTVYDNMAFGLK MQKIAKEVIDERVNWAAQILG LREYLKRKPGALSGGQRQRVA LGRAIVREAGVFLMDEPLSNLD AKLRVQMRAEISKLHQKLNTT MIYVTHDQTEAMTMATRIVIM KDGIVQQVGAPKTVYNQPANM FVSGFIGSPAMNFIRGTIDGDKF VTETLKLTIPEEKLAVLKTQEV CPDHTLDALGLRCPEPV/HDGA QNRAQYAAWRNVADYRRRSG HYPRYSWVLYLYGTRTGC
24681	55049	A	24819	3	131	
24682	55050	A	24820	247	492	
24683	55051	A	24821	2	241	YFFQKSSKTVIGGRRLCSVFRY QFSIVLATC*GTFFPSR*STILS* VTQSATSSGREGRSSSRSLNGRF MFSIASMMSW
24684	55052	A	24822	1	1143	

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24685	55053	A	24823	242	2151	FSRQHVVKMKHCCKNVVILMP EPVAEPALNGLRLNLRIVSIVMF NFASYLTIGLPLAVLPGYVHDV MGFSAFWAGLVISLQYFATLLS RPHAGRYADSLGPKKIVVFGLC GCFLSGLGYLTAGLTAVCLSSA VILCRGVQLHPVSDLRIPRGEK AGRNRSVDGCCEKAMSVIIVG GGMAGATLALAISRLSHGALPV HLIEATAPESHAHPGFDGRAIAL AAGTCQQLARIGVWQSLADCA TAITTVHVVELHNVGQRLFA\L LRKAPGVTLHCPDRVANVART QSHVEVTLESGETLTGRVLVAA DGTHSALATACGVDWQQEPYE QLAVIANVATSVAHEGRAFERF TQHGPLAMLPMSDGRCSLVWC HPLERREEVLSWSDEKFCRELQ SAFGWRLGKITHAGKRSAYPL ALTHAARSITHRTVLIQSERLNH KALEKRTLTVWDNSFLIYRQSD VSEIRLASLFASFSIRKSKQQAR KHTNRRSKDKEKRTRQKRKTT SRQRRRRQRMVRVGDEQIAGC HCLYSTGSPNRQLREAGIELSDF VRGNEKARERMKAQYSIAGMT SGVVVGTDHAAEAITGFFTKYG DGGTDINPLYRLNKRQGKQLL AALACPEHLYKKAPTADLEDD
24686	55054	A	24824	2	91	
24687	55055	B	24825	1	2346	
24688	55056	A	24826	1	1713	
24689	55057	A	24827	1	918	
24690	55058	A	24828	415	816	
24691	55059	A	24829	72	296	FCSATFGRPSDQYQNGE*LRWR GLGSFACQSPAHENPQWKFVL ARRGFARGTAEAHPSQYRHWC KIHRLNPGLR
24692	55060	A	24830	1	620	

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24693	55061	A	24831	1625	2460	GVVNPRQGRVLSMLPAMLLYL LFFLIQTSLKSNGGKGKLDPTL WMWTVNLIYLALAIVLNLWDT VPVRRLRASFSRKGARIPFVGC RETCELPQIELVKMMLGRELDT HALQRAGRTLLSDKPVAAFKN YGKKGTIAPFDLEVRPGEIVGL AGLLGSGRTETAEVIFGIKPADS GTALIKGKPQNLRSPHQASVLG IGFCPEDRKTDGIIAAASVRENII LALQAQRG\CYVPFPAKNSKRL PNALSASLAFAHLQLNNRLNFS PAAISKKCCFYVGY
24694	55062	A	24832	1	2034	
24695	55063	A	24833	3839	3970	
24696	55064	B	24834	694	765	
24697	55065	A	24835	1778	1982	
24698	55066	A	24836	1	268	MTCRLLTRLPGQAGVGKRVSG VPDELSPLFSVGSRYLQGGVGL VSPTSGANVGLPVISTNNLVKE CR\DGKWKMTEKGCLNMFHFK
24699	55067	A	24837	568	713	
24700	55068	A	24838	217	1910	AFTFQESVMAFSQAVSGLNAA ATNLDVIGNNIANSATYGFKSG TASFADMFAGSKVGLGVKVAG ITQDFTDGTTTNTGRGLDVAIS QNGFFRLVDSNGSVFYSRNGQF KLDENRNLVNMQGLQLTGYPA TGTPPTIQQGANPTNISIPNTLM AAKTTTTASMQINLNSSDPLPT VTPFSASNADSYNKKGSVTVFD SQGNAHDMSVYFVKTGDNNW QVYTQDSSDPNSIAKTATTLEF NANGTLVDGAM/ANNIATGAIN /GLSFLNSMQQNTGANNIVATT QNGYKPGDLVSYQINDDGTVV GNYSNEQTQLLGQIVLANFAN NEGLASEGDNV\WSATQSSGVA LLGTAGTGNFGTLTN/GSIESGI AFLVNVPLNPKLKRVNVAGAR WHPYGWPAFAERACLIEPEGD RRTHHRPNNQRTYSRKTQRQG GHKTRQDNWEQKGDGGPRPEP TDPHQHDANRPTVATKKRRKS TQSQRNHRNPKGTHPTEEHGT AGTTKPPDTPQTDNWTHKGSL REGKANRKRNPLRGAEVAGGG KQRAKAERQTQRGERREDVDE GEEDRSKKTEK
24701	55069	A	24839	500	653	

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24702	55070	A	24840	445	849	GSPGTAGTEVAVVLKIGGVHD KVIGHYRCSTTNTGRVLDVAI/S QNGFFRLVDSNGSVFY/SRNGQ FKLDENRNPATGTPPT/IQQGAN PTNISIPNTLMQRKPTAGQIVLA NFANHEGLASEATTSGLRRNLL AWRCM
24703	55071	A	24841	1	453	MKQMDTRGKVINCAFAVSAAF ALGDHLGFAAANMNAMIFPMI VGKLIGGVTAIGVAMMLVPRY EFIKREISWQSPVFFTPVDKQGG LKEAELKTLILEQYHAAGIEPES VDSGAIIITGESAKTRNAR*TGR FKRSGTENL\KLEQYHAAGIEPE SVDSGAIIITGESAKTRNARPTV MALSQSLGDFVVASAGPHLE
24704	55072	A	24842	370	670	YSSNIMLRVLSRKALILVPSSSP VKARKPAMLARRGWRSLSRW AILSLPGPGR*TGRFKRSGTENL \KLEQYHAAGIEPESVDSGAIIIT GESAKTRNARPAGMALSQSLG DFVVARAGPHLESVNAGYRTRI RNHGHSWFPGEIGIRSQFPHTLR TGSINGKAWGA
24705	55073	A	24843	1	1623	
24706	55074	B	24844	1	4986	
24707	55075	B	24845	65	726	
24708	55076	A	24846	4107	4460	FMSTCGYGGGLSRFPARCLSYQ PLRSWRETVAASG*RRTGSARA NCFCFSGLTRDFSIWRPETK*SA QTFVVGTWRCGGMGR*IAAVL SRYSTVESGVSSTHHRLPLQPDI PSGRRL
24709	55077	A	24847	624	895	PLVPAYKQSQRQKPHDYLNRC RKSL*QNSTTLHAKNSQ*IRY* WD/SISE**ELSMTNPQPISY*MG KNWKHSL*KLAQDRDALSHRS YST
24710	55078	A	24848	1434	1594	
24711	55079	A	24849	1294	1488	PAGKQTQQQRQQFANDGRGEI WRKLIKPNPRRQKS*CSTDPRQ KSTLISQREAVIRRFSEAGNFH
24712	55080	A	24850	595	879	RRCSTTNIIKKIQQDKKGNRKA VHRSRFVHGRPITLLFFQLSGRI QSHRLPGRAALFAGIPAACDQS PSLRQPISSEWSDGR*HRRIFRS* SEEF

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24713	55081	A	24851	1009	1478	YSLSVSVWAGATVMESPVWM PIASKFSIEQTMMQLSFLSRTTSI SYSFQPISDSSISNSLVGERSRPR AQISSNSSRL*AIPPPLPPMVKD GRIMHGKPTSAATASASSIVCAI PERAVSRPIFFIATSKRRRSSALS IASAVAPIMVTPNSSNTP
24714	55082	A	24852	48	209	GLFQVGYAENCRDNNHSFSLH SVVIGSSSERVVAKK*PDADHF SASFVPVILK
24715	55083	A	24853	1358	3194	PTASFAATLAIGKPVAFDASAE ERDTRGFISITIRRPFFGFTANVT RLETERGGICSRSVPWEVVSKI AWAEAPDPPGVTILGLKTQHAT /VSERVTSRFTRSHYRQFDLDQ AFSAKIFDRYLNLLDYSHKRKT ELGDEAAFSAKLDVFYDLYNL AQKRRFERYQYALSVLEKPMD FTGNDTYNLDRSKAPWPKNEA ELNALWDNVFSLAMTAFAREI DPHTNYLSPRNTEQFNTEMSLS LEGIGAVLQMDDDYTVINSMV AGGPAAKSKAISVGDKIVGVG QTGKPMVDVIGWRLDDVVALI KGPKGSKVRLEILPAGKGTKTR TVTLTRERIRLEDRAVKMSVKT VGKEKVGVLDIPGFYVGLTDD VKVQLQKLEKQNVSSVIIDLRS NGGGALTEAVSLSGLFIPAGPIV QVRDNNGKVREDSDTDGQVFY KGPLVVLVDRFSASASEIFARD VVVGLCICLSSLDVWLCGLFCR CSVDAERTKRQGKKGEESRKR RRKGYELSYLLFGWSAVVLLF VSDAEQHRASRHGGNACQQHP DVRHDEADGYPRQSHQLRLRR FRCFRPGRPLRLRRCQHERHDL PDDCRQVDRRRNGDWRGDDA
24716	55084	A	24854	100	671	
24717	55085	A	24855	852	1335	YFCFWTYPLLFPVCMDRKAGK HG\APAGDLYVQVQFNSHPIFE REGNTLYCEVPINFAMAALGGE IEVPTLDGRVKLKVPGETQTGK LFRMRGKGVKSVRGGAQGDLL CRVVVETPVGLNERQKQLLQE LQESFGGPTGEHNSPRSKSFFD GVKKFFDDLTR
24718	55086	A	24856	326	471	PLQTHPAPQQRGHPIYQHGQTV S*SCRRRGWSSISRPVIHHADAQ LMP

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24719	55087	A	24857	1095	1283	SCRRRGWSSISRPVIHHADAQL MP*PQIVYQHLKPPGIYRQQDR L*IPD*RPVLTIQDVRGP
24720	55088	A	24858	1	1159	
24721	55089	A	24859	1744	3019	KISPRRPQET/CFQKSTNIAREKT LEQEFSVQLFEKIGRRMCLTRE GKKLLPHIYELTRVMDTLREAA KKESDPDGELRVVSGETLLSYR MPQVLQRFRQRAPKVRLSLQSL NCYVIRDALLNDEADVGVFYR VGNDDALNRRELGEQSLVLVA SPQIADVDFTEPGRHNACSFIIN EPQCVFRQIFESTLRQRRITVEN TIELISIESIKRCVAANIGVSYLP RFAVAKELECGELIELPFGEQSQ TITAMCAHHAGKAVSPAMHTFI HALYSCRMRRERLIRATRSCQF NILHEPRRADKRSASGSLRLQE FNYQDKPCMEIRIRTYEKTPIR MDKGLTNFGSRWILPELAHKE KDEETQQRRKSKRDSRREETDT KKKTRDKATKREKDKEIEEMA SISITSRCEDKLENFSSMKYYTEI
24722	55090	A	24860	321	575	SYRRYVFPAQ*NRHLQFAVKPP APVIVHPTLVDSEHHHSLHDKR RQHRPHHSVAHHGSRNSSATA TINALLGRVAQNAATRGTR
24723	55091	A	24861	935	1637	PQPPPPLRREGAGLEKELGGRR VRVKGSGCQPWICGKVPVFIPV ITEQESFQELI/RRTTTACESLGK EYEILMIDDGSSDNSAHMLVEA SQAENSHIVSILLNRNYGQHSAI MAGFSHVTGDLIITLDADLQNP PEEIPRLVAKADEGYDVVGTVR QNRQDSWFRKTASKMINRLIQR TTGKAMGDYGCM/LRAYRRHI VDAMLHCHERSTFIPILANIFAR RAIEIPVHHAEHS
24724	55092	A	24862	1020	1229	

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24725	55093	A	24863	98	1242	MDKFRVQGPTKLQGEVTISGA KNAALPNLFAALLAEEPVEIQN VPKLKDVDTSMKLLSQLGAKV ERNGSVHIDARDVNVFCAPYD LVKTMRASIWALGPLVARFGQ GQVSLPGGCTIGAHIVMDKVSV GATVTIMCAAILTEGATIIEVFY FLPLAIGKFNELYPNIKVRIL\EQ GTNNCM\ESVLCN\ESDFG\INM\ NNVTNSSI\DFTPL\VQRRPFVL\ ACRRDHPLAKKQLVEWQELVG YKMIGVRSSSGNRLLIEQQLAD KPWKLDWFYEVRHLSTSLGLV EAGLGISALPGLAMPHAPYSSII GIPLVEPVIRRTLGIIRRKDAVLS PAAERFFTLLSDFCPGVPSEDNI FESPASQQHEYIGSRQCFLMPSE TTGTMHV
24726	55094	A	24864	1	833	MAELGKRSSVAVSWIGKVKTT AQMVALAWLLWRPPIWVEYA GIALFFVAAVLTLWSMLQYLTL RVQICLISDRFGVIFSKRSKVVK NIVDSSRQEYLEEFYARYNVELI RAPEGFFYLRPRSTTLIPRSVLS ELDMMVGKILCYLYLSPERLA NEGIFTQQELYDELLTLADEAK LLKLVNNRSTGSDVDRQKLQE KVRSSLNRLRRLGMVWFMGH DSSKFRITESVFRFGADVRAGD DPREAQRRLIRDGD/AMPIENHL QLNDETEENQPDSGEEE
24727	55095	A	24865	819	1428	SPRGISRGGCRCQPISGDG\RIFA GILHGLDNELPLQEEVEGNGLE QEGLPFPIRQSDALDLCFSDILV SPNMYIDDGMKRDWPVMKQC ALQRRWRILPDHYGTEPAEKRP GFAPHYCFSYALLVHMMAQQC DLEVGDFVWTGGDTHLYSNH MDQTHLQLSREPRPLPKLIIKRK PESIFDYRFEDFEIEGYDPHPGIK
24728	55096	A	24866	2	1445	
24729	55097	A	24867	1	1785	

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24730	55098	A	24868	3	654	VRFFKGRGSSWHMV\SQWDYV ADRFGTADLLPFTISDMDFATA PCIIEALNQRLMHGVFGYSRWK NDEFLAAIAHWFSTQHYTAIDS QTVVYGPSVIYMVSELIRQWSE TGEGVVIHTPAYDAFYKAIEGN QRTVMPVALEKQADGWFCDM GKLEAVLAKPECKIMLLCSPQN PTGKVWTCDELEIMADLCERH GVRVISDEIHMDMVWGEQPHIS LE
24731	55099	A	24869	955	1278	TLTPDFL*QGHFFRFAGIAYQIV KQTTVGTTVEITLRRYVVDGNR IPPRQDRQGDAFFGFATHTQQW HQVFKRQRDIQIVTANTATTVT QQAGFTIETRTPLRPHQQQ
24732	55100	A	24870	1	1707	
24733	55101	A	24871	1	3615	
24734	55102	A	24872	1	1931	MLLLREHTDTRHDHPRTPTRAT RRRRHTEKKRRKKKRPATHVL MTATLIPVSRLLATDQPQLFHE SASKPAPHLVSSLGCHCGDASC SGRAVADAMQFKTVFPVFVAA AMNPEHMAESGHRITRPEFPDY RELFRESDIKSAVVDSICQCNTP FNYLFRCFELQCLSRHGHSAYG VMQRRHSPMQETRIASLPLQRY RWHEDSVRNRWFSVMVGPSVR VNEWFSAYAMAGMAYSRVST FSGDYLRQPLVSGFHEA
24735	55103	A	24873	1281	2234	ISTNSILRIFSGFRKLMEV/TRLR DTPILTFMNKLDR/DIRDPMELL DEVENELK/IGCAPITWPIGCGK LFK/GVYHLYKDETYLIQEVRIV KGLNNP/DLDAAVGEDLAQQL RDE/LELVKGASNEFDKELF/LA GEITPVFFGTALGNF/GVDHML DG\FMAGDRSHVEEAY/PGDIL G\QGEMMKFTGIPNF/APELFRR IRLKDPLKQK/QLLKGLVQLSEE GAVQV/FRPISNNDLIVGAVGV LQFDVVVARLKSEYNVEAVYE SVNVATARWVECADAKKFEEF KRKNESQLALDGGDNLAYIATS MVNLRLAQERYPGRQFHQTRE

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24736	55104	A	24874	2	760	AKFEEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIFVA NIESKDPQQI/DRIQALAGWIAE Q\IGADVNHATRAGLLSKCDLM TNMVFEFTDTQGVMGMHYAR HDGEAEDVAVALNEQYQPRFA GDDLPSNPVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRIIVEKNLNLDLQTLT EEAVRLYGDKLTNANVVDDVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPTRPADFDDWHA
24737	55105	A	24875	2	391	
24738	55106	A	24876	2	1785	WLLYRAHVKGE/STEALLPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLLLGDKVIPATIL GIQSDRVIRGHRFMGEPEFTIDN ADQYPEILRDSGKVIADYEERK AKIKADAEEAARKIGGNADLSE TLLEEVASLVEWPVVL/TAKF/E EKF/LAISRTALVPYSADNMYQ LVNDVQSYPQFLPGCTGSRILES TPGQMTAAVDVSKAGISKTFTT RNQLTSNQSILMNLVDGPFKKL IGGWKFTPLSQEACRIEFHLDFE FTNKLIELAFGRVFKELAANMV QAFTVRAKEVYSASMRYIYVIV YISYRPPNLLDSHIIGFSSITTHC AVTSHHYNSCDMTMTIHSYVT PYISVRVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDDTRHIHTI ESRCRVCGAHDSRDAERLDRF AQTADEIRIADRGFSSRPECIRS LAFGEADYIVRVHWRGLRWLT AEGMRFDMMGFLRGLDCALIS KTRLLSENRRKGRVVQAETLE AAGHVLLLTSLPEDEYSAEQVA DCYRLRWQIELAFKRLKSLLHL DALRAKEPELAKVGIFANLLAA FLIDDIIQPSLDFPPRSAGSEKKN
24739	55107	A	24877	1	2022	
24740	55108	A	24878	2344	2523	
24741	55109	A	24879	82	732	

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24742	55110	A	24880	828	2184	SGCILPPESLRLWASVARRPRTP NQPRQPGPKIGGISPAGSALALA CGKRTVLFASLCTRTGGSQLGE \PALVLLADQMLALDDQYTFLQ RIPRSPYGLAFGPVPHLHYLHQ MRLLDIAPIAFRAMSLAFPVNY LDAVRTGSICSNCNQRSNDSAM GISMNVSTLMRVRAIWVYAAY MERVLDNLLNNALRYCHSTVE TSLLLSGNRATLIVEDDGPGIAP ENREHIFEPFVRLDPSRDRSTGG CGLGLAIVHSIARGNWATSDHR SLTGTQPYARIVVFLVRLIFAFR VTQLTLQISFVRFVVVQNAFPG CPLGIGIDVHFYYAVAYGVFDF LSSRTGTTVFFDDLNTPDFDRC FAFMQAVGKGYTDAYLPIVER RKAMAYGERERNFQLYRRGRY VEFNLPSELAATVYQSDPNFAT GCFRLYTSCNTFNMHKAATML VRAEFSQGYQHQV
24743	55111	A	24881	679	1628	PDADAKRVDITLCLAFGCDAQF IEITFTRLPEVRIHHLQSPASALS SCNHLLIRITQFNADITIGHHLP VNRRVVTVLRDMRHHGDIVHP GVRRGVEHYAAMDPGIVKEIM EVRLLFLAVFVGNHHSRRDSLP VQFVVHTNGDTYTFPGNNIRRD IGFKWRIAALMLHHFLIIDPHFA VMSDRIETQHDTLACPNFRYKD FALIPERCRII/SEYLDRRTDRLK WCYAAFQQGDQSQASNPMYA KAPV*VRWVHGYKALSEKGHL VYQRLYQIFQHAEYQTGTNDA EISTKLCLFSSSLLLLSSSSLQHSI PPNACL
24744	55112	A	24882	1	1515	
24745	55113	A	24883	1954	2859	
24746	55114	A	24884	121	393	SLARWIICNTSEELAANIKRLGD VTVRLNAFHAHGVYGEAQSM GERHAGRR*AVG*CVKGARGE PVDISGAQL/RGCGVNALSGLR FGTDL

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24747	55115	A	24885	1	3706	MDLGANGWQTFRYVVLPNLSS ALLAGGMLAFALSFDEIIVTTFT AEQVDAAVRAADAAFAEWGQ TTPKVRAECLLKLADVIEENGQ VFAELESSNNTAFARASSNGDL PTKADLQAQLDSLNKQKDLSA QDKLVQQDLTDTLATLDKIDRI KEETVQLRQKVAEAPEKMRQA TAALTALSDVDNDEETRKILST LSLRQLETRVAQALDDLQNAQ NDLASYNSQLVSLQTQPERVQ NAMYNASQQLQQIRSRLDG
24748	55116	A	24886	2842	5034	NVRLSPAMRCRWRRGSPMPAM FEVGVKTRIIQRSREVILMADHS KFDAVEPHAVATLSCIKTIISDS GLPETIAQRYQRAGSSLPEAQP DREIEKRGPAIAQAFDAEGKPS KASEGWARGCGITVDQAERLT TDKGEWLLYRAHVKGESTEAL LPNMVATSLAKLPIPKLMRWG ASDVHFV\WPVHTVTLL\LGDK VIPATILGIQSDRVIRGHRFMGE PEFTIDNADQYPEILRERGKVIA DYEERKAKIKADAEEAARKIGG NADLSESLLEEVASLVEWPVVL TAKFEEKFLAVPAEALVYTMK GDQKYFPVYANDGKLLPNFIFV ANIESKDPQQIISGNEKVVRPRL ADAEFFFNTDRKKRLEDNLPRL QTVLFQQQLGTLRDKTDRIQAL AGWIAEQSGTDAGDQTGYSDE RWVPDAHSEAPSPVSDMLSAL LLLTLVLAGMVRMAARLLMA KPPQAVNRGDIGWLTTSPMVIL LVMMLAMGTHIPQPVIRIPGGR FHYSPHQGRTDLPAQRSTWHD FCLQAPHLFRRNTVNVNSSSNR GEAILAALKTQFPGAVLDEERQ TPEQVTITVKINLLPDVVQYLY YQHDGWLPVLFGNDERTLNGH YAVYYALSMEGAEKCWIVVK ALVDADSREFPSVTPRVPAAV WGEREIRDMYGLIPVGLPDQRR LVLPDDWPEDMHPLRKDAMD
24749	55117	A	24887	49	531	
24750	55118	A	24888	1619	1968	
24751	55119	A	24889	1	553	
24752	55120	A	24890	744	970	LAVISEASNQKRGDPVDHAD*I AVANMLLNQFQQSYTPMLHDL IVRYDGDIHQQKSFGVQLPGKL RIVKLIQPVE

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24753	55121	A	24891	52	455	
24754	55122	A	24892	2988	3614	PVSVLTQKRLSPATSHRSTCRVI LNQAYVTPSKCWPDVEEISFNF FHSEDVVRHPVVARIVNAYEA WEEAEQKTMTPANQHAGGLV QCDKMLLQRRSREVIELSEQNA AQMRHVRGADMAMIFQEPMT SLNPVFTVGEQIAESIRLHQNAS REEAMVEAKRMLDQVRIPEAQ TILSRYPHQLSGGMRQRVMIA MALSCRPAVLIADEPTTALDVT IQAQILQLIKVLQKEMSMGVIFI THDMGVVAEIADRVLVMYQG EAVETGTVEQIFHAPQHPYTRA LLAAVPQLGAMKGLDYPRRFP LISLEHPAKQAPPIEQKTVVDGE PVLRVRNLVTRFPLRSGLLNRV TREVHAVEKVSFDLWPGETLSL VGESGSGKSTTGRALLRLVESQ GGEIIFNGQRIDTLSPGKLQALR RDIQFIFQDPYASLDPRQTIGDSI IEPLRVHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEFSGG QRQRICIARALALNPKVIIADEA VSALDVSIRGQIINLLLDLQRDF GIAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVFENPQH PYTRK\LLAEDPVAEPSRQRPQR VLLSDDLPSNIHLRGEEAVVALI KPGAQIGR\PQSWT
24755	55123	A	24893	134	595	IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIP PAPVANDTLVAEVSDAPQAND PTFNNEDLA*FAVLSTPTAILISC PGRWGPAAGSECGVRGAHAHR ELALRAFSCCCFSSNAISIPN
24756	55124	A	24894	708	1444	TDAPGDEEASLQRAAQAGVGK IIVPATEAENFARVLALAENYQ PLYAALGLHPGMLEKHSDVSL EQLQQALERRPAKVVAVGEIGL DLFGDDPQFERQQWLLDEQLIL V\KRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERFVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP
24757	55125	A	24895	1460	1777	

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24758	55126	A	24896	381	482	IPGPQSPQSSPDLGWLQC*NP*R LLWKAPRSDK
24759	55127	A	24897	977	1144	
24760	55128	A	24898	2	280	CTFALRDEYPRMLNVDNKGLR DHIELQPLAV/DASYPGGDFRK NAVYVPMW*SAHCEPEGRFAE TGSRRYGEDFASTAPGFRRAAT RKRVRRKR
24761	55129	B	24899	1	1665	
24762	55130	A	24900	296	495	
24763	55131	A	24901	1	5352	
24764	55132	A	24902	187	280	AVDTGLADHRD\EPNMVARLP LSFTASLSIS
24765	55133	A	24903	1775	1981	HIWQNSLIVLFRGCRSAHAKVH RWKN*LPLNLAPLLPRSGSSAPI RPPPSAQARQPMKSTYGVDRR HS
24766	55134	A	24904	760	1473	
24767	55135	A	24905	1	2124	MNRMSGGYWQLFAESGETCR ARELEQCLEDFYDQRKESVRW HLDLHTAIRGSLHPQFGVLPQR DIPWDEKFLTWLGAAGLEALV FHQEPGGTFTHFSARHFGALAC TLELGKALPFGQNDLRQFAVTA SAIAALLSGESVGIVRTPPLRYR VVSQITRHSPSFEMHMASDTLN FMPFEKGTLLAQDGEERFTVTH DVEVAKNAITEIKTQFEKEKLA QDRIKRNQ/LDANIQRLNYSLDI ANAAGIKKPVYSN\DGIERKLEI EKAVTDVAELNGELRNRQYLV EQLTKAHVNDVNFTPFKYQLSP SLPVKKDGPGKAIIVILSALIGG MLYCRVCIKRNADSPEVFSGFS DPNVVLIAAVFIIGDGLVRTGV ATVMGTWLVKVAGNSEIKML VLLMLTVAGLGAFMSSTGVVA IFIPVVLSVAMRMQTSPSRLMM PLSFAGLISGMMTLVATPPNLV VNSELLREGYHGFSFFSVTPIGL VVLVLGILYMLVMRFMLKGDT QTPQREGWTRRTFRDLIREYRL TGRARRLAIRPGSPMIGQRLDD LKLRERYGANVIGVERWRRFR RVIVNVNGVSEFRARDVSLIAM SAADVDLRQFCSERLLEPDGIA RFSLIPESELIGESVREIGLRTRY GLNVVGLTRTGVALDGSLADE PLLLGDISWLWALESDRYAAM LGRSRSLTYRRGDEHCRASRSP

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24768	55136	A	24906	834	993	EEIEVARLRDQKSAEGGIQNRE YWPGRSGHR*SPHAPIIGTQFLQ ALFQTWDQFVFALSACGRRHP TDGRRQNPAVSGHSVAARQPA HSQTDEASG
24769	55137	A	24907	3519	5161	
24770	55138	A	24908	374	1891	KWKLKRPDSNIDHRRVPNLET WFSRHDKTRPTSKNPSDYQAG DIVSWRLDNGLAHIGVVSDGFA RDGTPLVIHNIGAGAQEEDVLF NWRMRQCQHNQHNTATFNGP RILAEQPPGKEYAANGNGQLYP MSSLNIKQGSDAHFPDYPLASP SNNEIDLLNLISVLWRAKKTVM AVVFAFACAGLLISFILPQKWTS AAVVTPPEPVQWQELEKSFTKL RVLDLDIKIDRTEAFNLFIKKFQ SVSLLEEYLRSSPYVMDQLKEA KIDELDLHRAIVALSEKMKAVD DNASKKKDEPSLYTSWTLSFTA PTSEEAQTVLSGYIDYISTLVVK ESLENVRNKLEIKTQFEKEKLA QDRIKTKNQLDANIQRLNYSLD IANAAGIKKPVYSNGQAVKDD PDFSISLGADGIERKLEIEKAVT DVAELNGELRNRQYLV\EPITK AHVNDVNFTPFKYQLSPSLPVK KDGPGKAIIVILSALIGGMVAC GGVLLRYAMASRKQDAMMAD
24771	55139	A	24909	1111	1895	PLVNFSNSSHPVSNPSIQLSSITL PLVENESRARA\VKDQMDAIDH QTGVRPLVFYSIVLPEIRAIILQS EGFCQDIVQALVAPLQQEMKL DPTPIAHRTHGLNPNNLNKYDA RIAAIDYTLAHDDGISLRNLDQ AQVILLGVSRCGKTPTSLYLAM QFGIRAANYPFIADDMDNLVLP ASLKPLQHKLFGLTIDPERLAAI REERRENSRYASLRQCRMEVA EVEALYRKNQIPWINSTNYSVE EIATKILDIMGLSRRMY
24772	55140	A	24910	77	434	EKKRGREDKPGTMATFPPATSA PQQPPGPEDEDSSLDESDLYSL AHSYLGPLIMPMPTSPLTPALV TGGGGRKGRTKREAAANTNRP SPGGHR/ERKLVTKLQNSERKK RGARRLRQSWR
24773	55141	A	24911	31	295	

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24774	55142	A	24912	75	426	EKKRGREDKPGTMATFPPATSA PQ\QPPGPGGRDSQPWMDLDLL /YSLAHSYLG\GGGRKGHTKRE TAANTQPPQPLAGHERKTVDP KLQ\NSERKKRGARALRQELEM RRRPWTLTPSQ
24775	55143	A	24913	1	1107	
24776	55144	A	24914	1	1468	
24777	55145	A	24915	1	2463	
24778	55146	A	24916	1	603	
24779	55147	A	24917	118	1087	IRSKKMTTQTVSGRRYFTKAW LMEQKSLIALLVLIAIVSTLSPN FFTINNLFNILQQTSVNAIMAVG MTLVILTSGIDLS/VAASIVGIEV NALVAVAAALALGAAIGAVTG VIVAKGRVQAFIATLVMMLLL RGVTMVYTNGSPVNTGFTENA DLFGWFGIGRPLGVPTPVWIMG IVFLAAWYMLHHTRLGRYIYA LGGNEAATRFSGINVNKIKIIVY SLCGQLASLAGIIKVARLSSAQ HTAGTGYELDAIAAVVLADDR QSGGDFAGGAGRQQKAVITTT GHLEYEHEKTGYPGFRCCAKR HRQCECDGKRHHRAGGLHA
24780	55148	A	24918	1	1286	MHEREPGLRAALAGQLEFRVG LGLGVWTLRLMELLRQRLELV VYTASDGQEYEMVSRLNWVN YLVLEDVHIILPDQMRGITGCY ATHPHERRLHAGTVHRQNIVN NPPDCVPRDAGEAEVAPDPSLA SLQLQTPELPGLISCHNSIQVSN EARLFELLICQWRDFRKRVIAA KSMQGRELEGGQRGQDKATNP FRVLALKGSGDPDPHGAGRQG SDLLLHPVSDAQVLQHFFQRRA LLSSPWDYHDVVGLCAQEPCG YIMELFIIKHQCSLAQTAGSLAP EQKKELEMTVRYYISSADLTAE KFATAIRN/HWHVENKLHWRL DV*RQFDKHCSTADSTRILASF VRHVNAALDVRVVFASGSETT HGDGARRYLRCVDVDWRRRT AVAQADKSARACHFHYAGYH HHEHFADPVSVGAKYHTVFST

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24781	55149	A	24919	417	861	AKGPCPDRNHSSDDKDVIAIDG KTLRHSYDKSRR\RGAIHVISAF STMHSLVIGQIKTDEKSNEITAI PELLNMLDIKGKIITTDAMGCQ KDIAEKIQKQGVIFSLCPASIIDD KKVTDLAVAVQGTLKTGSGGI LPPGGALKKISEKL
24782	55150	A	24920	3	1767	HISIIPDYR*AWKVEHKLSGILL LTIFAVISGAESWKDIEDFGKTH LDFWKQYGDFENGIPVHDTIAR VVSCISPAKFHE\CFINWMRDCH SSNDKDVIAIDGKTLRHSYDKS RRRGAIHVISAFSTMHSLVIGQI KTDKKSNEITAIPELLNMLDIKG KIITTDAMGCQKDIAEKIQKQG GDYLFAVKQRNGAVENRAKTQ TRIAFGDHFFRRQVSQRIRLFCH RLATQFAARLRMFIATGQPMN GLRLLLFIVNKQAALLVNKLDA QMAAFQQLPGRGRQATVRRE MDLCAFAERMGLPVSRPGDIQE FHAGCRTKFDAGAFRDKHHVA CFGDHGLAFVANMQLPFQHHV DFVVVQGPREECVLPLHKTGG HAAAVVSGHKISQAHAMRLCA VETTKLDATGINHFDAAFAGHR FESSVDCACSATVSFITFPSVCD RFGNWLRSGRCSHAARKNEITL TNTRRSLRPKRNTERHDMQTR ATVIAAGEKLLPYAETLMSTW QAARKEVAHTSRHNEFSIGASA SLWDMVMTSAGAVVTTVVVA VRPSSFYILCSHKKKRTLHTKR EKTVDRRKEYETRAKRSETDT

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24783	55151	A	24921	110	1282	SNTPYIIKENKMELKKLMGHISI IPDYRQAWKMEHKLSDILLLTI CAVISGAEGWEDIQDFGETHLD FLKQYGDFENGIPVHDTIARVV SCISPAKFHECFINWMRDCHSS DDKDVIAIDGKTLRHSYDKST/ RRRGAIH\VNNAFSTMHSLVIG QIKTDKKSNEITAIPELLNMLDI KGKIITTDAMGCQKDIAEKIQK QGGDYLFAVKGNQGRLNKAFE EKFPLKELNNPEHDSYAMSEKS HGREEIRLHIVCDVPDELIDFTF EWKGLKKLCVAVSFRSIIAEQK KEPEMTVRYYISSA\DLTAEKFA TAIRNHWHVENKLHWRLDVV MNEDDCKIRRGNAAELFSGIRH IAINILTNDKVFKAGLRRKMRK AAMDRNYLASVLAGSGLS
24784	55152	B	24922	258	507	
24785	55153	A	24923	1	3060	MTEIEENMLLPISGQELPIRWLA QHGSEKPVTHVSRDGLQALHIA RAEELPAVTALAVSHKTSLLDP LEIRELHKLVRDTDKVFPNPGN SNLGLITAFFEAYLNADYTDRG LLTKEWMKGNRVSHITRTASG ANACGGNLTDRGDSFVHDLTS MARYVATGVLARSMGLVIYSFI QHTLTLEEYREITAFLFREFTHA AAARYTGEQETLPLSPQWILRQ CKEVASLCDGDTFSGEQLNLM LQQREWREGFLAER
24786	55154	B	24924	56	967	
24787	55155	B	24925	1	1776	
24788	55156	A	24926	1	864	
24789	55157	A	24927	424	513	
24790	55158	A	24928	1	5049	
24791	55159	B	24929	1	939	
24792	55160	A	24930	1	1837	

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24793	55161	A	24931	1	2249	MLPDIARFLPRLANDQIEEFTW YVNHFTYSNAIKIFCYQMFLAS TQARASGAPLQRLFRAIGGNA WERPFRMVFCSAAFSEESSPFR ETNYEPQLFLGFATDYRFAGW TLRDVEMGYNHDSNGRSDPTS RSWNRLYTRLMAENGNWLVE VKPWYVVGNTDDNPDITKYM GYYQLKIGYHLGDAVLSAKGQ YNWNTGYGGAELGLSYPITKH VRLYTQVYSGYGESLIDYNFNQ TRVGVGAIGVNVAQAEVLNLE SGAKQVLQETFGYQQFRPGQE EIIDTVLSGRDCLVVMPTGGGK SLCYQIPALLLNGLTVVVSPLNS LKEKSANPFEFTFAAFAHAFHW VIQAIGMINTPADGSTHKQART SWLPYSSLPVLSVSTQDEKAKK KMRFMQRSKDSLAKWLSAILP VVIVGLVGLFAVTVIRDYGRAS EADRQALLEKGNVLIRALESGS RVGMGMRMHHVQQQALLEEM AGQPGVLWFAVTDAQGIIILHS DPDKVGRALYSPDEMQKLKPE ENSRWRLLGKTETTPALEVYRL FQPMSAPWRHGMHNMPRCNG KAVPQVDAQQAIFIAVDASDLV ATQSGEKRNTLIILYALATVLL ASVLSFFWYRRYLRSRQLLQDE MKRKEKLVALGHLAA/GVAHE IRNPLSSIKGLAKYFAERAPAGG EAHQLAQHVQIRRFHAHHPAS

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24794	55162	A	24932	261	2115	TLVFCWHAKLLSHGVFMDIISV ALKRHSTKAFDASKKLTPEQAE QIKTLLQYSPSSTNSQPWHFIVA STEEGKARVAKSAAGNYVFNE RKMLDASHVVVFCAKTAMDD VWLKLVVDQEDADGRFATPEA KAANDKGRKFFADMHRKDLH DDAEWMAKQVYLNVGNFLLG VAALGLDAVPIEGFDAAILDAE FGLKEKGYTSLVVVPVEDLAGI EIDHTTSMVMIFGIIFLTAVVVH IILHWVVLRTFEKRAIASSRLWL QIITQNKLFHRLAFTLQGIIVNIQ AVFWLQKGTEAADILTTCAQL WIMMYALLSVFSLLDVILILGQ\ KFPA\AFQLPLKG\IFQGIKLMGP ILVGILMISLLIGQSPAILISGLGA MAAVLMLVFKDPILGL\VAGIQ LSANDMLKLGDWLEMPKYGA DGAVIDIGLPTVKVRNWDNTIT TIPTWSLVSDSFKNWSGMSASG GRRIKRSISIDVTSIRFLDEDEM QRLNKAHLLKPYLTSRHQEINE WNRQQGSRESVI\NLRRMP\NIG \TFCAYLNK\YLGTH\PRIRKDM TLMVRQLAPGDNGLPFEIYAFT NTVVWLEYESIQADIFDHIFAIV EEFGLRLHQSPTGNDIRSLAGA FKQ
24795	55163	A	24933	1	757	
24796	55164	A	24934	8	343	
24797	55165	A	24935	1423	1761	
24798	55166	A	24936	1	851	MKGDTKVINYLNKLLGNELVA INQYFLHARMFKNWGLKRLND VEYHESIDEMKHADRYIERILFL EGLPNLQDLGKLNIGEDVEEML RSDLALELDGAKNLREAIGYAD SVHDYVSRDMMIEILRDEEGHI DWLETELDLIQKMGLQNYLQA QIREEGKSIYQEQTTAMKRPDY RTLQALDAVIRERGF/EARGTK AVHYTISRLTAH*ATGKYVRAA AVGAYRTAAPDGTRAKTAGTA APGGVAGRRVAGR*TNRFDSA AAFTGGQRRQSGDVVASCTGS CVG

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24799	55167	A	24937	1645	2009	PVFIQFVEGMCGTANEPACLLV NQSPAIYFPGKIAAIWQNPRHV ESGSM*TL/IDSD*VSPTECLSPR HHYMPFEEAARGYEIFEKREEE CRKVILVPGAQSAEAAQKAVS GLVNAMPGGTI
24800	55168	A	24938	1	3936	
24801	55169	A	24939	1	2240	MRSPMTRNSRNGKHDYKPPPR KRRQPPHDHTAPNSTPARNQRG RPHRPNRQAGQREQRANNPTP NTPSPPPTNDPAEPHQTRHDSR QPHNTPPAYAELVAAALLTTDT NVTRRRLRYMQPDTKLCHSAG KSIYQEQTTAMKRPDYRTLQAL DAVIRERGFERAAQKLCITQSA VSQRIKQLENMFGQPLLVEDET RTQERLRRGEVVGAVSIQHQAL PSCLVDKLGALDYLFVSSKPFA EKYFPNGVTRSALLKAPVVAFD HLDDMHQAFLQQNFDLPPGSV PCHIVNSSEAFVQLARQGTTCC MIPHLQIEKELASGELIDLTPGL FQRRMLYWHRFAPESRMMRK VTDALLDYGHKADDIILRITAT AICGSDLHLYRGKIPQVKHGDI FGHEFMGEVVETGKDVKNLQK GDRVVIPFVIACGDCFFCRLQQ YAACENTNAGKGAALNKKQIP APAALFGYSHLYGGVPGGQAE YVRVPKGNVGPFKVPPLLSDD KALFLSDILPTAWQAAKNAQIQ QGSSVAVYGAGPVGLLTIACAR LLGAEQIFVVDHHPYRLHFAAD RYGAIPINFDEDSDPAQSIIEQTA GHRGVDAVID\AVGFEAKGSTT ETVLTNLKLEGSSGKALRQCIA AVKRCGIVSVPGVYAGFIHGFL FGDAFDKGLSFKMGQTHVHA WLGELLPLIEKGLLKPEEIVTHY
24802	55170	A	24940	687	792	TPTLTRPLRHPVAYRATLK*NR PAKVSQLCCTNA
24803	55171	A	24941	3	510	AGDMVWLCVRTQISY*IPRTHP AVGIPRERPLRGADTPQRGASH RIRGEGKRK*KRWALLCCPGCN I*RHFCHHN*ERYFW\IYWVEST GAVKHLQNTGHWLNAGALPV RRPRKSVTGSIARQ\VSVPISAR ALLACPCGQCAGYATQFVMKS ITQRFNVACRTRMYAVG
24804	55172	A	24942	189	563	

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24805	55173	A	24943	1224	1772	GSPSVSLATSSCSIKVQNPGISR VVAGSSAIISNVSPGCILRTVLR TIITGSGQRRPSASSVWSGHTSC VFRTANFSSGMVNLSVSVTNLS PSIVPRIKFIAGDPINPETNIFAG WL/VNGFRRTYLLNNPVFHNH NPRRHGHRFGLIVGHVDHGGV QFLMQLADLCAHLHAQLGIKV
24806	55174	A	24944	1541	3675	LEIIKRKISMRRNWMHSHTRY WRFLDFPTLRGGRWMR*SGEK LNPISTPLRANCLALAQRATRL APMSFTWGMPTSQPDCAVPGR RALPPELLCLQRSSQSRFAGTAI T
24807	55175	B	24945	1	1497	
24808	55176	A	24946	650	739	
24809	55177	A	24947	4447	4804	RQNDRYSGRERHEITPLCW*IPR IAWALWLRSLRRGPQEKSLHN RVARTISWPYQARHPCRTLLGG HGFFLHIVLSQLPCLSYPLSSFA GLLARSSMFLKLAARFLCCRRS YAASPLSI
24810	55178	A	24948	1	3774	
24811	55179	A	24949	431	949	NYAIYHQNHGVNISPGLGKTHN YRQQHCGITYYWRDLMPANK NYKQRWITPGSASFYRSSHKAL IRLLATRLPAFPWGRRSAWRWP VRY*IRVPSSGSYHLEISMRWVI FPQPKALTPSNLHWKTA*LWS* KTLSFVCWIATVLPARFWKLTD PWLAILPCANIYWQASAPD
24812	55180	A	24950	337	648	

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24813	55181	A	24951	1	1430	MFTYPHSKFRVNRFVGQVLLIE FSILLDGGRTGLGHSLSVWCISG DCSSFLQGKPTSLPLRKPSAIICS DSLSGSADLLRNHNFVCTAADT FTTDITPEAGDARLIGIAQTVRH LEDPMRAWKSIHKSCEILDPIHR APVKENTHPARKINISDPAAGA VARIRYEGVLSVCRASASAYVS RSRTITVACWYVSNTGVTGATI GVKRQHRHARLFSGDGAPGFG TGKRDIRQLRRLVRIQIQRTFFA AVLHVPTPWSRAIDAAALLTVI DVKVLTACACQACRTLALRVA QVIDRCSNPGDIMSSVARRYWF ISRWSAKRDCAVSYDQDPGQA QRSCRSCLVAVDRGLWLSAYC RSLMTQTLLPDDVPRILPNASSP SRLRCL\HIWVITACWICANSSG FIARNL/GLCGWEKRLVKDLTRI QDTGRAKEILGATATLEFR\R*T PTLTRPLRHPVAYRATLK*NRP AKVSQLCCTNA
24814	55182	B	24952	1	1295	
24815	55183	A	24953	3151	3207	LQWLID*WCL**TFDLRFA
24816	55184	A	24954	2740	3917	NGRSVWAVKLELFRVKPLDIPQ QRVGQQHVLLKAFNRRLAMQF IQLIATDVTEILPLHVVEDGTDS LYCLALSHLRCGRLSLRWRREL PRGLGVNVSWCYPFKAQGQCA AEITDKAGQREIFGFARVKENA GYVIYECYQPDDGDKLIRELPF SSLIFARQWFVVGELLQHLPPE DRITPIVGMLQGVVEKGGELRV EVADTNESKELLKFCRKFTVPL RAALRDAGVLANYETPKRPVV HVFFIAPGCCYTGYSYSNNNSP FYMGIPRLKFPADAPSRSTLKLE EAFHVFIPADEWDERLANGMW AVDLGACPGGWTFQLVKRNM WVYSVDHGSMVQ/SLWITTGT CWGTRFHSARGQKFPEVLQGS QTLPAATDPPGMQWLASGVLE
24817	55185	A	24955	1	519	
24818	55186	A	24956	510	731	

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24819	55187	A	24957	1	1055	MRLCPEKTTKAKRVKAVLAWS KEEPWLSEWSEEVLEMGYKKL GDFSTAGAILETEIRPSPASAFTL DSQPPESNNLSEAKYAPNNIESI AKYFAPKSPMFSESPSGTALDS FNRNERRRWPLWPNKSGFGSD LTLSKIGISSPDIALERLYEQAR KLSGKFRALSELDESARSGVLK VLCAFAYQDYSRSAASTRKCD CCDGGGFTEAQVFTNKVSYPW GKPPYWSKMSRAVRPSDWESW TQAREVVRVKCKPCNGKGVIS NSCRCHGKGKVLAKHESDRRG VPVMKACDRCGGRGYARLKFS SV\MRALILLRRLKKTAAYEQL QPLFEELVAECHKQESMADSIL SKVTR
24820	55188	A	24958	361	725	
24821	55189	A	24959	1100	1738	WQRSTLPLLFESAMQTGVNAG NPVAW*KSAGYGHIKLYDAKN RL\LVQSTALWASQLVQYLSTF FRKNLKRPSEFVTLADEIEHVN AYLQIEKARFQSRLQVNIAIPQE LSQQQLPAFTLQPIVENAIKHGT SQLLDTGRVAISARREGQHLML EIEDNAGLYQPVTNASGLGMN LVDKRLRERFGDDYGISVACEP DSYTRITLRLPWRDEA
24822	55190	A	24960	1	2043	
24823	55191	A	24961	2164	2487	KLKRIARHNFHGIRDLHLFQQV NRFSSGFPTTYWLMMADHVHH LKTYSTCRIEGGHRFLKDHRHS CAAPLTKLFFPRVKNIFSQQGN LPPMYAITARR*QTHNQHCGD

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24824	55192	A	24962	128	2574	QVVVVMAMVAKVVIDIVVVV GVEMIRVKVVAIVVEVVVVEV VVVMVAWWW****WW*/DMG EARWWWEYGVWEVEPEIILNA PQQYLLAGIGDTLAKWYEAVV LAPQPETLPLTVRLGINNAQAIR DVLLNSSEQALSDQQNQQLTQS FCDVVDAIIAGGGMVGGLGDR FTRVAAAHAVHNGLTVLPQTE KFLHGTKVAYGILVQSALLGQ DDVLAQLTGAYQRFHLPTTLA ELEVDINNQAEIDKVIAHTLRPV ESIHYLPVTLTPDTLRAAFKKYS QSCFVIRLGGDFIHQLAENHIVI FVNNHNGTRCQTFQWAISNCH TVSLQKFSVRKFLSDLFAIGGR RGVRPPTEAPGHQKSDNQAHV SVSFDGLDLVFFVVNQWAGVV FCFDLFSRKRGRFSVWRNKGFG RYCQRLANFRDRQAFQLLNQIH FTRCKQVDNGGTEFKATHFLAF QQCHRTVVFPGRPAIKTRVERL DRYRNRMEKSNGQANLRVHG GTWEKLVLQLDSAGMVNRVSS VGAPLREPIPTEGKGAKEDTWG NLSSNDPLLEAFGGQFGIAISMH QTLATRGGKRNARPTTRPRFHR GTNPRGIAPHIGTANARYSTGH CPVALPFGLRGPPLARENVATA TKGHESASRETEVVAVAKLTSR VLLICDATHALPIQVLRNDIRVI AAGNGCTDDLQLEHLPANTDIR
24825	55193	A	24963	117	335	PGLAPATRRSTPGRFNADAGAD *RRAAGTGAGRAKRRGVGIHR CLADPFLADCRNAGLRGAALC GTAAASGK

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24826	55194	A	24964	208	1903	YLAIKTFRCLHDFFTDEQLSRA VWIYGKRAIAAAQTKLPPAFGL PGAKHILFRGHCSESDVQQLAA ESGDDRSVVIGVGGGALLDTA KALARRLGLPFVAVPTIAATCA AWTPLSVWYNDAGQALHYEIF DDANFMVLVDPEIILNAPQQYL LAGIGDTLAKWYEAVVLAPQP ETLPLTVRLGINNAQAIRDVLL NSSEQALSDQQNQQLTQSFCDV GDAIIAGGGMVWGLGDRFTRV EAAHAGPNGLTGLPQTEKFLH GTKVAYGILV\QSALLGQDDVL AQLTGAYQRFHLPTTLAELEVD INNQAEIDKVIAHTLRPVESIHY LPVTLTPDTLRAAFKKLIQGLIS AEQLAQALAEQNGVAWESIDA WQIPSSLIAEMPASVALHYAVL PLRLENDELIVGSEDGIDPVSLA ALTRKVGRKVRYVIVLRGQIVT GLRHWYARRRGHDPRAMLYN AVQHQWLTEQQAGEIWRQYVP HQFLFAEILTTLGHINRSAINVL LLRHERSSLPLGKFLVTEGVISQ ETLDRVLTIQRELQVSMQSLLL KAGLNTEQVAQLESENEGE
24827	55195	B	24965	31	205	
24828	55196	B	24966	69	402	
24829	55197	B	24967	1	721	
24830	55198	A	24968	1	1703	
24831	55199	A	24969	2853	2889	LIIGLDLPAVSAIFQRALRFTHV GIADGGAYVVQR/HRPDEPRRR CCSE
24832	55200	A	24970	297	473	
24833	55201	A	24971	1179	2148	CQVLRPRTKRLNVLFLHRMQH QWRQRELVHNMCFVIACAKRK RAPFVQAAEEV\RPGQHDDEFP LAIWQTGSGTQSNMNMNEVLA NRASELLGGVRGMERKVHPND DVNKSQSSNDVFPTAMHVAAL LALRKQLIPQLKTLTQTLNEKS RAFADIVKIGRTHLQDATPLTL GQEISGWPASRSGTGSWRYSGG YWTKYPSGVCASRSKMNWYST RASDGGHASDAVRTAQAADRE LRAPVRDELNASITSKTRLAEST SLAEWVKASPHDDDKPILLPGE WEVNTRRERQKQGIPLDAGSW QAICDAARQIGMPEETLQAFCQ Q

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24834	55202	A	24972	166	365	NPFSNSPWETYPVAFTIPLALFM GIYLRYLRPGRIGEVSVIGLV/SP DFRHYLWRLGGRKSDLGTVL
24835	55203	A	24973	83	362	KPPCFLQASVTCWLRLPFASMII LPPCACS*ST*ESIRPAVVGPREP EGITFRRFGRTRVVNRMIFDVL RHLFTVIHPLFQFGVTYITTDDN
24836	55204	A	24974	584	853	
24837	55205	A	24975	1	3017	MSQDPFQEREAEKYANPIPSRE FILEHLTKREKPASRDELAVEL HIEGEEQLEGYAPVLAPESGILI MRPTLTMPALTKFVDGTGPVW TGNLFPFLFITIACGAVSGFHALI SSGTTPKMLANEGQACFIGYGG MLMESFVAIMALVSACIIDPGV YFAMNSPMAVLAPAGTADVV ASAAQVVSSWGFSITPDTLNQI ASEVGEQSIISRAGGAPTLAVG MAYILHGALGGMMDVAFWYH FAILFEALFILTAVD
24838	55206	A	24976	3	206	EPDFLPL**RRNHEQNYRDGKC TGSYRSLRTGR*SGQYDHHLRS DPGKSENGRSTGRRRCTGTSVA G
24839	55207	A	24977	3	982	GDAEPFVFLPR\RKDHEYSLDH YQHRFYLRSNRHGKNFGLYRT RMRDEQQWEELIPPRENIMLEG FTLFTDWLVVEERQRGLTSLRQ INRKTREVIGIAFDDPAYVTWIA YNPEPETARLRYGYSSMTTPDT LFELDMDTGERRVLKQTEVPGF YAANYRSEHLWIVARDGVEVP VSLVYHRKHFRKGHNPLLVYG YGSYGASIDADFSFSRLSLLDR GFVYAIVHVRGGGCKINLVVD NGKIVRAEAAQGKTNQGTLCL KGYYGWDFINDTQILTPRLKTP MIRRQRGGKLEPVSWDEALNY VAERLSAIKEKYGPDAIQTTGSS

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24840	55208	A	24978	1339	3640	SPLSTAGISICGPLLIITDVDLGT TVAGIKGMIATGEGTTEWNSV MVAMLLTLIPPVVIVLVMQRAF VRGLVDMRNKMAGLKLQAVT KSWDGKTQVIKPLTLDVADGE FIVMVGPSGCGKSTLLRMVAG LERVTEGDIWINEQRVSELRLIG YMSRKMGGGKNRREPHIDVKR GIFGLSITPEFSEPLAEDFLSRRQ YGIRFRNLETGNWYPELLDNVE PSFVWANDSWIFYYVRKHPVT LLPYQVWRHAIGTPASQDKLIY EEKDDTYYVSLHKTTSKHYVVI HLASATTSEVRLLDAEMADAE PFVFLPRRKDHEYSLDHYQHRF YLRSNRHGKNFGLYRTRMRDE QQWEELIPPRENIMLEGFTLFTD WLVVEERQRGLTSLRQINRKTR EVIGIAFDDPAYVTWIAYNPEPE TARLRYGYSSMTTPDTLFDLDI DTGERRVFKPPE/V/PGFYAA/SY RREPRW/IVSADGVKYSFV\APR QHFRRDAPVLSFLLFSDRAPFR NNGPRVVLLLGYYHPELLGVT YSQLSVHEARPKPLPIPHSRHRH VPTRNEMAQEKERPAGSQSLFR GLMLIEILSNYPNGCPLAHLSEL AGLNKSTVHRLLQGLQSCGYV TTAPAAGSYRLTTKFIAVGQKA LSSLNIIHIAAPHLEALNIATGET INFSSREDDHAILIYKLEPTTGM LRTRAYIGQHMPLYCSAMGKI
24841	55209	A	24979	1	248	
24842	55210	A	24980	839	1625	PDAFILTTKPAGAIPTSTSITRPIP FCPSFAPCENATPAAET/HQRNT RPEWRFTFAFFLFAIFRNAVNT VTMSIRKGIGVHHNAANLVPW MTKFFQRFGIAFQSRGAVFHQH HHAGYAGQRGKTALAEQRLVF GFGINKQMRAVPLIGEVYQFSG *CQRQSFTADGFTDSNAFNNIS GNSTARDKLFIAGYGNRYFHC GVNAQIIFMQELGDFRHFVIF/A QKGNEYHGDTRISPGRFRRGHH PLGALRLAASVERSGNGHRA
24843	55211	A	24981	2538	2864	GSSLINSKVMP/SF*QQNRKFAY KRAGVATDEFHAESFVRGRAP MKRKL*LFMQLGGDVIQPFDGF IAGNTVYRCQQLAVGDAVGKI LHNRYAFRQQSTVIQQQCRHLP
24844	55212	A	24982	1	1281	

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24845	55213	A	24983	1	2180	METLNLYADLRSVTGEALLLL DEPGVGVDPISRRELWQMVHE LAGEGMLILWSTSYLDEAEQCR DVLLMNEGELLYQGEPKALTQ TMAGRSFLMTSPHEGNRKLLQ RALKLPQVSDGMIQGKSNIVGI KDTIDSVGHLRTMINTVKSVRP SFSVFCGYDDHLLNTMLLGGD GAITASANFAPELSVGIYRAWR EGDLATAATLNKKLLQLPAIYA LETPFVSLIKYSMQCVGLPVET YCLPPILEASEEAKDKNRPLVD LEHAALQVGKGIIPPPLREYGAS EVRSVTRAFNHMAAGVKQLAD DRTLLMAGVSHDLRTPLTRIRL ATEMMSEQDGYLAESINKDIEE CNAIIEQFIDYLRTGQEMPMEM ADLNAVLGEVIAAESGYEREIE TALYPGSIEVKMHPLSIKRAVA NMVVNAARYGNGWIKVSSGTE PNRAWFQVEDDGPGIAPEQRK HLFQPFVRGDSARTISGTGLGL AIVQRIGDNHNGMLELGTSERG \GLSIRAWLPVPGTRAQGTTKE GAREDAVEFFAKLGFVNQGEIT TPTTTPIRHFLMIKPVATLDDIL HRGDWCAQLQQAWYEHIPLSE KMGVRIQQYTGQKFITTMPETG NQNPHHTLFAGSLFSLATLTGW GLIWLMLRERHLGGTIILADAHI RYSKPISGKPHAVADLGALSGD LDRLARGRKARVQMQVEIFGD
24846	55214	A	24984	875	1150	
24847	55215	A	24985	1507	1974	
24848	55216	A	24986	1	1006	
24849	55217	A	24987	1491	1703	RECRYATNGKNNGCCRSAGSD FSSRLRYVR*PFIYTQ*SCGIGH CPGTDIRAKIRRTARFIKNYGTY CPS
24850	55218	A	24988	1	1758	
24851	55219	A	24989	1773	2165	PSRGVEVNSGWNWQATNRRVI RNFDDLDQLIIPGTARNAQTCIF NFVTVTMTLNNCRRIVQLANQ/ DYRQPTGTAVAETHGTAEIALL ATNFNVAVFIAPLGNQRHNRVL TVWHKFRRVGVLHVGNMASVI N
24852	55220	A	24990	1	141	SPGKIRPVIAAAMKQIKEFMSP DSDFFRYMKTPTSATR*YNDCG TGQ

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24853	55221	A	24991	1430	1933	PIIVCMGSLTMPDSACMAPFPPS AVRRWNSSFPPTFSAHTSSPCA CYPRCYRTVKGVL**HHR*W/V LISTPGRGAYAASKYALEAWSD ALRMELRHSGIKVSLIEPGPIRT RFTDNVNQTQSDKPVENPGIAA RFTLGPEAVVDKVRHAFISEKP KMRYPVTHGDLWR
24854	55222	A	24992	1318	4265	LAIVALFLDLQNHIFSKGFWPS DKFYAAKVEEQNQRHQRYHGT SYNLEPDIKSSPGGLRDIHTLQ WVARRHFGATSLDEMVGFGFL TSAERAELNECLHILWRIRFAL HLVVSRYDNRLLCVHPTLLTTL DIHGEAQIWRREVSSRYGQYPK AQAAQPDQLMSDYFFRVSLAM QNKTLLFSLDDTLVNNALQTLN KTRPAMVDVIPTDGIVPLYINPQ GIAKLLRNETLTSLPKNLEPVFY NAAQTLLMPKLDAL
24855	55223	A	24993	1	454	MGFDDTRDRALFEDSAMSQQP TVPDRLRWLLQTFKYQKNIRI* STPRKKPMRHSIWNIWGSRRC WSNPKRTFMSISVRGNMAAIM SFHTSAVMRSHCSILTTIKSRW ATLNTLILR
24856	55224	A	24994	65	330	
24857	55225	B	24995	1	1998	
24858	55226	A	24996	1175	1877	QQVPQKGPGRAKRHLHAAGW HWHQRDRCPEEKNVRQ*RRYR AVRFIII
24859	55227	B	24997	1	3117	
24860	55228	A	24998	1888	2412	ARFKHVGDGTVTHRLFRRAAQ IVRVV*RAVSHRQHFTGVDIHQ HGATRFSLVKGHRIVQFAINQR LQAFINTQRQVVRSLAVSRRNI FNYATIAVFTHNALTRLPGKPFI ETLLNALNPLTEHAARDLEDSP VRITAYIEDVDALAQAGADIIAI DGTDRPRPVPVETLLARIHH
24861	55229	A	24999	1	2457	

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24862	55230	A	25000	1	3019	MAALRQSFWSQLFDRVHIGLD FFDASINRIAAWVIGTRNMKKA LLRALLEPTAELRNWKRRAITL RVWHCWKSRNRCRGRRSGKCI ANVTIRQQDHQIETVFINQRLH ERMFPPFVLFAERLSGDEDLGL KAPILEALNDLGYEKPSPIQAEC IPHLLNGRDVLGMAQTGSGKT AAFSLPLLQNLDPELKAPQILVL APTRELAVQVAEAMTDFSKHM RGVNVVALYGGQRYDVQLRA LRQGPQIVVGTPGRLLD
24863	55231	A	25001	60	545	PSPFTAGASMAVERSTG\HEGE LVLETLVIDGDENT/CAGTRRSL RANA*CLFHPFRAGAEKLAEEV WFCRYPHCGCEQNTTTEEQRR TEWMVTESLADFLDPHDPGKT VEGYPAPKRARNRNRAEDHRQ RLRHRTRKKQTHGQRRRHRPE PAQRQPQTGTTD
24864	55232	A	25002	1410	1575	
24865	55233	A	25003	200	691	
24866	55234	A	25004	1336	2028	
24867	55235	A	25005	1	345	
24868	55236	A	25006	671	1204	RTSDKLPFCRRSRMENLARFLS TTLKQLRQQRGWSLSRLAEAT GVSKAMLGQIERNESSPTVATL WKIATGLNVPFSTFISPPQSAT/P SLFPYDPQLCFEHLAIQMASGAI SESTPHEKGVIEHVVVIDGQLD LCVDGEWHTLNCGEGVRFAAD VTHIYRNGGEQTVHFHSLIHYP RS
24869	55237	A	25007	2251	2466	
24870	55238	A	25008	181	626	WQNFDTCGGDMLDKLDAALR FQQEALNLRAQRQEVLAANIA NADTPGYQARDIDFASELKKV MQRGRDATSVVALTMTSTQHI PAQALTPSTAELQYRI\PANPSL DGNTVDMDRERTQFADNSLQY QMSLSALSGQIKGMMNVLQSG N
24871	55239	A	25009	57	278	
24872	55240	A	25010	171	532	KPVQFAIADGNNQPLALLNIHL PVMMLAIAHGPLLPAFPPELLV LFDDS/PLSSRVLLINAFSGGSDT AMRRAGKGAPAFLLPELPIITV VSPFLPQSSPRRKPIMSKRIPSAV NQRNPRQ
24873	55241	A	25011	1	648	

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24874	55242	A	25012	158	514	VLQLIKAVWTQRTQKPSWLHP VDSAPGLQMELPASPVPCTCTP QPLGGRWDWALWSRGWRLLR RLGPHRSPRRS*GSGLWPWPAQ KGAPIVQRWAKGLLKCHQSGS PGRGGAESERGL
24875	55243	A	25013	1	693	
24876	55244	A	25014	119	304	DRRRCAHKITVIPKRMTIAGIRL PPQTVNI*LGNFLRALIASTAGI MTAQMVAHSPAPPIP
24877	55245	A	25015	361	540	
24878	55246	A	25016	191	446	AKRRLGVYDADCCSIDKTQSLS ACTTRNCGAYSKCLCGKYAKP VGGIPQPLQESHVR*CCNVMEL SPCSDFT**HPPGAVSQPQT
24879	55247	A	25017	1	2259	
24880	55248	A	25018	1	1170	
24881	55249	A	25019	3	1240	
24882	55250	A	25020	1	1259	MAGPRYPVSVQGAALVQIKRL QTFAFSVRWSDGSDTFVRRSW DEFRQLKKTLKETFPVEAGLLR RSDRVLPKLLGQASLDAPLLGR VGRTSRGLARLQLLETYSRRLL ATAERVARSPTITGFFAPQPLDL EPALPPGSRVILPTPEEQPLSRA AGRLSIHSLEAQSLRCLQPFCTQ DTRDRPFQAQAQESLDVLLRHP SGWWLVENEDRQTAWFPAPYL EEAAPGQGREGGPSLGSSGPQF CASRAYESSRADELSVPAGARV RVLETSDRGWWLCRYAGAGPE ELDTSARNAGALTRRREIRDAA TLLRLGLAYGPGGMSLREVTA WAQLHDVATLSDVALLKRLRN AADWFGILAAQTLAVRAAVTG CTSGK/QIASCRWNSNQCARGR QR*MATTYGI*SSYLSVH*F*AN RQQRR

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24883	55251	A	25021	803	2061	AKPAARGGILAAPVRDTLFLYF RLKKNQRQEGFINTYPWPKKP GIFYMCVPIKGANAQDVAAFC VTARGRQNCLWESIARGPALIN NRGAARGRCNDRVVEVDHGFA VLTFNFQGVSPGEFTQTVDHFD FAAFRHTSQTTGQLIDHFLFPGT NLVDIGFRFAEDDTVFSQRFGF FDNFCYVQQCFRRDTADVQAN TAKGVVTFYDYGFQTYWVKV LDPGSEVVAEAGDGASAIDLAH RLDIDVILLDLNMKGMSGLDTL NALRRDGVTAQIIILTVSDASSD VFALIDAGAAGYLLKDSDPEVL LEAIRAGAKGSKVFSERVNQYL REREMFGAEEDPFSVLTEREL\D VLHELAQGLSNKQIASVLNISE QTVKVHIRNLLRKLNVRSRVA ATILFQSAAFRSRFRRATSDNV
24884	55252	A	25022	1	1569	
24885	55253	A	25023	2151	2709	YLREASETARRQFTLP\VILYNF RDLTGQDLTPETVTRLALQNEN IVGIKDTIDSVGHLRTMINTVKS VRPSFSVFCGYDDHLLNTMLLG GDGAITASANFAPELSVGIYRA WREGDLATAATLNKKLLQLPA IYALETPFVSLIKYSMQCVGLPV ETYCLPPILEASEEAKDKVHVL LTAQGILPV
24886	55254	B	25024	1	1201	

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24887	55255	A	25025	1	2209	MIGEIRDGETAEIAIKAAQTGHL VLSTLHTNSTCETLVRLQQMG VARWMLSSALTLVIAQRLVRK LCPHCRRQQGEPIHIPDNVWPSP LPHWQAPGCVHCYHGFYGRTA LFEVLPITPVIRQLISANTDVESL ETHARQAGMRTLFENGCLAVE QGLTTFEELIRVLGMPHGDGAA MDREENELGVSCIAVPVFDIHG RVPYAVSISLSTSRLKQLYAGLP VWCDGSRFFAQKARAIKCKQW GYVGAKSRQRWLFYAYDRLRK TVVAHVFGERTMATLGRLMSL LSPFDVVIWMTDGWPLYESRL KGKLHVISKRYTQRIERYNLNL RQHLARLGRKSLSFSKSVELHD KAAGGVPVLVRELLKAGLLHE DVNTVAGFGLSRYTLEPWLNN GELDWREGAEKSLDSNVIASFE QPFSHHGGTKVLSGNLGRAVM KTSAVPVENQVIEAPAVVFESQ HDVMPAFEAGLLDRDCVVVVR HQGPKANGMPELHKLMPPLGV LLDRCFKIALVTDGRLSGASGK VPSAIHVTPEAYDGGLLAKVRD GDIIRVNGQTGELTLLVDEAEL AAREPHISELSAFTFGTGRGYSA AFGVKCPFRKRALSDPCYAMR EVADFLINKGVDGLFYLGTGGE FSQMNTAQRMALAEEAVTIVD GRVPVLIGVGSPSTDEAVKLAQ HAQAYGADGIVAINPYYWKVA
24888	55256	A	25026	1	3395	MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKYIPCSWLGRINIVKMAILAK VIYRFNAIPIKLPMTFFKELEKT TLKFIWNQKGAASRSNPEPKNK LEDHITNSTIYRLSTKSCSVSGL KQTLLAESEALTSYSHRVFSAW DFGLCGDVHVRLRQRIILYELK GQVPALLLDDGTLLTEGVAIM QYLADSVPDRQLLAPVNSISRY KTIEWLNYIATELHKELKFSFH WSTTSHKGLGM

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24889	55257	A	25027	145	681	FNGATQRIFDARGKPSTYIGSIQ HVNADVDQRATTLQFFIGKDTP AGNAAATQGAGGGNVNLSQN AVGHLFTQLLRIERKTMVKVV GQHLAQFARGIDISRACYHMA ARFQCHQGMFVMKTVR*ADA NHIRFHCQQHGLRIVPHGCIPVF FCQRLPLGKAAVTDSYQFQIRC GCSSTKH
24890	55258	A	25028	696	953	LSGLCSVRRAYPGGRSCPGVP* FVGLVARRPGGG*GSCFVLLHP QRSGTGGCL*QPPFPGAGAGRK IRECIRVGRSAGHAAGGET
24891	55259	A	25029	3	506	RGKPSTYIGSIQHVNADVDQRA TTLQFFIGKDTPAGNAAATQGA GGGNVNLSQNAVGHLFTQLLRI ERKTMVKVVGQHLAQFARGID ISRACYHMAARFQCHQGMFVM KTVR*ADANHIRFHCQQHGLRI VPHGCIPVFFCQRLPLGKAAVT DSYQFQIRCGCSSTKH
24892	55260	A	25030	291	560	
24893	55261	A	25031	63	404	
24894	55262	A	25032	660	1073	LSHECSFWLTNQLVSPRAQTVS GELQPAYAHGVLCRQYPSAFE KASETPQSSNPCPSSYTIHPTVE NFQTCRNQHLSKGCLINAGRA GPSPGTGGWGELEVAAAARLQ GAWKRHLQSSRPPGQALFASPP *WTGSVQ
24895	55263	A	25033	272	511	GSDTALPSAIAAPLLAAMAWLP PRERGTLAH/QVLEHYQLAQLP VSAL/QMPLHCPPQAIAHHQQL/ EQQALASLQNWGVFHV
24896	55264	A	25034	1	3300	
24897	55265	A	25035	1117	1376	PPPIGLTYSSSASPLSLFCTVRKP FSRSCW*QTNSNPISSCPELVTP SE*L*PRRSIRLDSLSAVRGFAS RIWLSSAITFPSGSLA
24898	55266	A	25036	207	427	DEHLQQRKKPLFLNYGRTEQA SVK*RISWVQNPERSSLC*GILA A*NPMSVSGL*LT*HCLSARRY ELVCQPK

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24899	55267	A	25037	2012	2547	LKFARPKLWGIFRNRQYHHML ER\RSQAIDAPALDRGAALGAL MRLEHPNASAEAALTMLAQLS PAQSGEALHGLLALARHQLAC QPAFIAGFSSHLNQLSEADFINA LPDLRAAMAWLPPRERGTLAH QVLEHYQLAQLPVSALQMPLH CPPQAIAHHQQLEQQALASLQN WGVFHV
24900	55268	A	25038	1	150	DKASRGRSRQQS/CAVLQPLLVI PRQT/WVWSGPPANSSRPGEEG PDC*KEN
24901	55269	A	25039	1	150	DEASRGRNRQQS/CAVLQPLLV IPRQT/WVWSGPPANSSRPAEEE PDC*KEN
24902	55270	A	25040	96	389	PCLSP*LYPSGVHKSTFIYGFYN T*PCTSQSLFWQHSC*GSITSSS YFYLLPEEGTGSNLCCSAASAG DTQANRVWSGPPANSSRPAAE GHDCWKEN
24903	55271	A	25041	1181	1364	VSLGNIKFRQTGAPLGQSFQRK EQSAIFAVLQPPLVIPRQI/WVW SGTPADSSRPAAEGPDC*KEN* RVNRQPTEWEKIFPIYPYDKGLI SRIYKELKQIYKKKIKPPHQKV GKGYVFSKEDIYAANRHMKKC SSSLAIREMQIKTTMRYHLTPA NRGIEIINCPFLDDAASCIDPTYS SNIFPPVNLSWGLPMKPKEVKI KRQKKEHLLKDRDFSFQEPIMA LRTVILEILMEKEMDNSQRECIK DILTKHLVELSILARTFKNTQLP ERAIFQIKQYNSVSCGVSEWQL EEAQVFWAKKEQSLALSILKQ MIKKLDASCAANNPSLKLTYTE CLRVCGNWLAETCLENPAVIM QTYLEKAVEVAGNYDGESSDE LRNGKMKAFLSLARFSDTQYQ RIENYMKSSEFENKQALLKRAK EEVGLLREHKIQTNRCPSGTKL PEEGTVSNLCCSAASTGDTQAN RVWSGTPADSSRPAAEGPDC

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24904	55272	A	25042	42	963	VQEGCVRPFCCRSAGVCWRST PDSVCLGITSGGCRTAKTAACS FLWKLCPRGTPARCQVECSYTR CLS\SLLGGVSQAGGTRVRDPL EEEVCPLAELERCAGRSVAVFR ASRQEHLRLLKLTSQPPLPPGA LSQGDGSFIYKPLTGVAAFLSD ALPKRRNLERQSGYSTFEELCF QKRTWGRDAVRISDLLLGDHS HFGKCPISRLERAENMPVVSEL SAAGCSTEVNHVFVGIIWQKGK CSKYTAPSKSSVPVSSTRGHVHI TVQNPTLVPFVGKLNIDSPIGDR NIPVLTAGNCKTLGDLRSFPHN
24905	55273	A	25043	98	352	
24906	55274	A	25044	3	414	PEEALCALAELERCAGRAAALF RAERQKRLRLLKLHPQPPLPPG ALSQRDGS\LSISP*LGL\RLSFR DALPREQFYRLFTDRSDRVPEN SVTDVCHIESKMEPLRLGP/SNV SIMRPSLVCSFTTLVFISSNAQSS LVA
24907	55275	A	25045	2	1544	STTRGSPPQEARQYRHNQAYA YSIQGDGAEDDDERIVRFHTRL PVFMLPPTPRKTSWIVAPVLEV LARAIRHETEIQGIHTGTEDVPV SLFADDMIIYLDNLKDSSRKLL EVIRDFSKVSGYKINVHESVAL LYTNNDYAENHIKNSTPFTIGY VLAFVVMVIAVSCVRLLYAHN CTQHTSLKHKCQAWVVTTVDA AAFMTQATREERRIAYSAPGGY FFHILEVLARTIRQEKEIQGIQTG KEEVKVSLFADDMIIYLENLKD SSRKLLEVIKEFSKVSGYKINVD SRGSPTDLVIYKEEIVFLIVPKA KKSKIKVLASDPLCYAATTWR MTIIAGLPVEYNDRFIRGIAVFA PWRKTPGIYHQSHDPLCYAATT WRMTIIAGLPVEYNDRFIRGIA VFAPWRKTPGIYHQSHGACLG RRSRTITVVDAQPQVMDMDPT CSLFTTGQCLGEPDLLASARRL QFFSHQYSIAVLMANARGNSA\ LW\DNYGGLIVRADRGSLLLVG

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24908	55276	A	25046	1	1228	MLQSNRTAASHSPSIQPAIQPAI QPASQLSIHNLWTQFRHSTKIPV EWVNGEWLNGRMPEDHHEWQ CNYQNVQQFIDEGNYTSGDNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTRETVDFNGKHIHVR GAKLLFPAIQQPYPPLYFGGSSD VAQELAAEQVDLYLTWGEPPE LVKDFIEQVRAKAAAHGRKIRF GIRLHVIVRETNDEAWQAAERL ISHLDDETIAKAQAAFARTDSV GQQRMAALHNGKRDNLEISPN LWAGVGLVRGGAGTALVGDG PTVAARINEYAALGIDSFVLSG YPHLEEAYRVGELLVPLLDVAI P\EIPQPQPLNPQGEALRKK
24909	55277	A	25047	1	1075	MTIKGEQAKKQLIAAALAQFGE YGMNATTREIAAQAGQNIAAIT YYFGSKEDLYLACAQWIADFIG EQFRPHAEEAERLFAQPQPDRA AIRELILRACRNMIKLLTQDDT VNLSKFISREQLSPTAAYHLVH EQEAEHRFAMGELPDEVLEICQ RLAKLTEMLRGLAELFLNDLSE KTGSHDIVRLHRLILQMNRALG MFEAQSKLWRLASLAQSSGAP VTKWATREEREGQLHLWFHCV GIRVSDQLERLLWRSIPHIIVTS ATLRSLNSFSRLQEMSGLKEKA GDRFVA/SGFP/HLTTANRAKLL FPGCALSLPSTTKSSILPKWRPF SVSRWRAKNISVCWYCLPADG RCSAFSTM
24910	55278	A	25048	530	642	LKTLW/PAVQEPVPHRYHGATV FRIMQTIFIKQICRLLL*GTAGHF VCGITACHAAEAAHRLTVQPVP RILDQRRPAQLHSRQVTAAIRQ PLHRRQAVRRDAVCQPLLVVC VFRLMLPQQFPRLRVLHRLAFA GQAAFIVIAIVDGNTVAFAQVA DVCQPAVAIILPLLLCEFSGQVI MITLRPPVKAALLYQPVQRIVT EDAVAAVQEPVPHRYHGATVF RIMQTIFIKQICRLLL
24911	55279	A	25049	1075	1479	

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24912	55280	A	25050	2	588	RWSSLTSSRYGFCRCPESADKE CLHVKSAAGKKATNVGHYAG WLRTYSPHLAAHRVNFFFGINA HMDQRGPGRLMISCNEACGSA CYSNHSYMRNDKHAVRRADSG RAEGGGPRVKSVIKAPVITPKK KPVVSTLKHWVLMLAWVTCSP LTVL\SPDGEMFDVMEKYAFSA WKWKRLRLAISQATFHALLPE KIG
24913	55281	A	25051	912	1169	
24914	55282	B	25052	1	1665	
24915	55283	A	25053	43	302	
24916	55284	B	25054	116	1534	
24917	55285	A	25055	1	1017	NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTRETVDFNGKHIHVRGAKLLF PAIQQPYPPLYFGGSSDVAQEL AAEQVDLYLTWGDPADL\VNEI VEQVRAKAAAHGRKIRFGIRLH VIVRETNDEAWQAAERLISHLD DETIAKAQAAF\ARTDSVGQQR MAALHNGKRDNLEISPNLWAG VGLVRGGAGTALVGDGPTVAA RINEYAALGIDSFVLSGYPHLEE AYRVGELLVPLLDVAIP\EIPQP QPLNPQGEALRKK

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24918	55286	A	25056	1	2677	MVLNRLLTGLFFGSTPPRCHYD LIGADPDRTIRSVRLYWRHSLN ELISMLPKFNKELTRKLFKLQE MLPFLNLHMSPERMLQRMDSE KVVTFTTALMTGLSGAMASVL LLVMTVVFMLFEVRHVPYKMR FALNNPQIHIAGLHRALKGVSH YLALKTLLSLWTGVIVWLGLEL MGVQFALMWAVLAFLLNYVP NIGAVISAVPPMIQVLLFNGVY ECILVGALFLVVHMVIGNILEPR MMGHRLGMSTMVDGVRVLKD GTDLNQTGSFYLAARPYAEKN GAFIQGVLATFSEADALTRSQR EQSIALLAKTMGLPAPVIASLLE ISQPVSNHPIRTRLTAEVAALQQ QTADLFYENRLVPKKVDIRQRI WQPTRLEGKQFMSLNMFWFLP THGDGHYLGTEEGSRPVDHGY LQQIAQAADRLGYTGVLIPTGR SCEDAWLVAASMIPVTQR\LKF LVALRPSVTSPTVAARQAATLD RLSNGRALFNLVTGSDPQELAG DGVFLDHSERYEASAEFTQVW RRLLQRETVDFNGKHIHVRGA KLLFPAIQQPYPALYFGGSSDV AQELAAEQVDLYLTWGEPPEL VKEKIEQVRAKAAAHGRKIRFG IRLHVIVRETNDEAWQAAERFV LSGYPHLEEA/YRVGELLFPLLD VAIPE/IPQPQPLNPQGEAVAND LSPRRTVAASGDQLLAGAVGFS
24919	55287	A	25057	114	372	
24920	55288	A	25058	2270	2760	TSPIPSQIRQYSIA/VGSTGNLGL SIGIMSARIGFKVTVHMSADAR AWKKAKLRSHGVTVVEYEQD YGVAVEEGRKAAQSDPNCFFID DENSRTLFLGYSV/AGQRLKAQ FAQQGRIVDADNPLFVYLPCGV GGGPGGVAFGLKLAFGDHVHC FFAEPTHSPCMLL
24921	55289	B	25059	1	2460	
24922	55290	A	25060	1	993	

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24923	55291	A	25061	332	1349	ILYDSDIYRFSCRSGGHIPAVIY HLSAKRRTMENAKMNSLIAQY PLVKDLVALKETT/WGFIPATL HGVKGLPYVGLTEQDVQDAH\ ARLSRFAPYLAKAFPGKWLPTG GIIES\ELGAL\PAMQKRL\EKEY QQPISGQLLLKKDSHLPISGSIK ARGGIYEVLAHAEKLALEAGLL TLDDDYSKLLSPEFKQFFSQYSI AVGSTGNLGLSIGIMSARIGFKV TVHMSADARAWKKAKLRSHG VTVVEYEQDYGVAVEEGRKAA QSDPNCFFIDDENSRTLFLGYSV AGQRLK\AQFAQQGRIVDADNP LFVYLPCGVGGGPGGVAFGLK LAFGDRVHGLQA
24924	55292	A	25062	284	1494	RLSLPDMFPPVQQFPVSLHRAF YRYDKSAYYALRIAGIASRLNP RRFSPSILTPERRCVVTLRNDIR RDVLRHNQPRSTASTRQARRR MKSSCWHMPTTSKPQALSHTS NSPTTSISRPNWSYSNVCNRSRT MANLSGYNFAYLDEQTKRMIR RAILKAVAIPGYQVPFGGREMP MPYG\WGTGGIQLTAS\VIGESD VLKVIDQGADDTTNAVSIRNFF KRVTGVNTTERTDDATVIQTRH RIPETPLTEDQIIIFQVPIPEPLRFI EPRETETRTMHALEEYGVMQV KLYEDIARFGHIATTYAYPVKV NGRYVMDPSPIPKFDNPKMDM MPALQLFGAGREKRIYAVPPFT RVESLDFDDHPFTVQQWDEPC AICGSTHSYLDEVVLDDAGNR MFVCSDTDY
24925	55293	A	25063	1	333	

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24926	55294	A	25064	1368	2451	PAHAAPGGGC/VRSLACRFLWN MRVTGKSYSTLRRVLSAIWNW RMMRCALTRALVAFRVR/SSVP LAAVLAIYARENGAGTMFEPE AAYDEDTSIMNDEEASADNET VMSVIDGDKPDHDDDTHPDDE PPQPPRGGRPGLRGLTLRWFSV AAQRSDILDAVTLSLKVAALAT LIALVLGTLAAAALWRRDFFG KNAISLLLLLPIALPGIVTGLALL TAFKTINLEPGFFTIVVGHATFC VVVVFNNVIARFRRTSWSLVEA SMDLGANGWQTFRYVVLPNLS SALLAGGMLAFALSFDEIIVTTF TAGHERTLPLWLLNQLGRPRD VPVTNVVALLVMLVTTLPILGA WWLTAKATYLEKLKV
24927	55295	A	25065	1	2072	MSEQLTDQVLVERVQKGDQKA FNLLVVRYQHKVASLVSRYVP SGDVPDVVQEAFIKAYRELTPR RPYLLRAFYEWLLDNQLTPHL VVDVTLPGVQVPMEYARDGQI VLNIAPRAVGNLELANDEVRFN ARFGGIPRQVSVPLAAVLAIYA RENGAGTMFEPEAAYDEDTSI MNDEEASADNETVMSVIDGDK PDHDDDTHPDDEPPQPPRGGRP ALRVVNVIVAIIFTTKPTAMGIA VRFTTAKGETPAIPDVTTTTAVI GETARASVVAKCIGIIITTAVPIV VKPFANISPATTSVPRFFGLPAS SSHTLIGAIIGIGLTNALLTGSSV MDALNLREVTKIFSSLIVSPIVG LVIAGGLIFLLRRYWSGTKKRD RIHRIPEDRKKKKGKRKPPFWT RIALIVSAAGVAFSHGANDGQK GIGLVMLVLVGIAPAGFVVNM NASGYEITRTRDAVTNFAARES EASVIRHSNRFIETINGGRRCSR GITLTLHKLR\SAQPLL\AVLNR LEQKKPVGLRYDPQAQSLVCLP TQTRTGWNLNGFEVGFRPCVR LMIYGRSLEAQATASLAAATG YDSHIFDLFPASASAQIDTDTAV ILLCHDLNRELPVLQAAREAKP FYLGALGSYRTHTLRLQKLHEL GWS\RQETTQIRAPVGIFPKARD AHTLALSVLAEVASVRLHQEE

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24928	55296	A	25066	2	332	AGYSTRTALAIVNKPPSSAIPPT SGLASRKRNPASNDFNGCSRGC GGGGNAGRLNNGSKRSASTPP TIRPTNIAPP\AASPKAPPARWN VSSSGSAPAPRRRANPETQLR
24929	55297	A	25067	1	3192	MNKKFKYKKSLLAAILSATLLA GCDGGGSGSSSDTPPVDSGTGS LPEVKPDPTPNPEPTPEPTPDPE PTPEPIPDPEP/TPE/PEPTPEPTPD PEPTPEPIPDPEPNQNGAELSYN TEKTLTIRDSVFTYTENADGTIS LQDSNGRKATINLWQIDEANNT VALEGVSADGATKWQYNHNG ELVITGDNATVNNNGKTTVDG KDSTGTEINGNNGKVIQDGDLD VSGGGHGIDITGDSATVDNKGT MTVTDPESM
24930	55298	A	25068	1078	1317	
24931	55299	A	25069	135	361	SCSMLAGLCG*GSSSSVSITTCF ALSASTIA*PREPQQALPV*PLA LPNSSQDGTPMKATSIFSSPLCT RCTRPP
24932	55300	A	25070	469	841	RWWKQYAAAGFQCMCATAVS NLTRPVAA*TAAIPESKSPVLPN SPASTVRRS*PVSTMPPIRPGDG DHDPRFKAPSGTPHQPPRAGHS L\RRHG*TENCTAA*GQLRTPG DNGTVMSADTITFP
24933	55301	B	25071	1	2922	
24934	55302	A	25072	1	3849	
24935	55303	A	25073	1	2280	
24936	55304	A	25074	672	1045	GAVLSINCRTLSPAAASGENVA TPP/VTSNNNTPIINKPKPLALAE ATGVIIAPKPPSSAAPMASPVTF CAVHKPLIRPNIASGVCVCSIVY CSNELTALNQPNSARQTTPKIHI GIRPNRPMARN
24937	55305	A	25075	650	1465	RKPICAADICQLSASAGYSTRT ALAIVSGLASRKRNPASNDFNG CSRGCGGGGNAGRLNNGSKVI NVPAAASP*FQATPPVASNKPPI MGEITDPRRTVNMVIAPACIKF SRPTSAGVAANSAVTPSDAKKP SHKPSK*IASNDGSGSSALRHSP MKPMPQVPRASKITFLRS*RSA STPPTIRPTNIAPPVSVTESPTCQ VECVIIWICTGTATPSKPRDTIE MKRARNTARNAGCVSAGSSGS SAEVGSSNSKTSGSIASARAIET RCC

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24938	55306	A	25076	156	3092	LNRRWIANIAKLEAEQARKLK KTEKDSLKDEVLHSLLPRAFSR FSQTMMWIDTVNGLIMVDCAS AKKAEDTLAVLRKSLGSLPVVP LSMENPIELTLTEWVRSGSAAQ GFQLLDEAELKSLLEDGGVIRA KKQDLTSEEITNHIEAGKVVTK LALDWQQRIQFVMCDDGSLKR LKFCDELRDQNEDIDREDFAQR FDADFILMTGELAALIQNLIEGL GGEAQHSGTGSLPEVKPDPTPN PEPTPEPTPDPEPTP
24939	55307	B	25077	61	2118	
24940	55308	A	25078	132	280	RRRAALPERSGPGLDHRRVRH/ GCHVLPTPVTLVKRRKVSRVD AQWKSSV
24941	55309	A	25079	1	1449	
24942	55310	B	25080	110	550	
24943	55311	A	25081	657	805	RRRAALPERSGPGLDHRRVRH/ GCHVLPTPVTLVKRRKVSRVD AQWKSSV
24944	55312	A	25082	756	938	
24945	55313	A	25083	781	1257	
24946	55314	B	25084	1	2727	
24947	55315	A	25085	1	2286	
24948	55316	A	25086	1161	2024	VRSAVWPCLQRDPDCHHNRCG TGGTSRPGPARNPRIEPETCVG\ RIRNLGVLLYDADAMERAAST ENEKDLYQRQLDVFLDPNDPK VIEQAIKDGIPLSVIEAAQQSPV YKMAMEWKLALPLHPEYRTLP MVWYVPPLSPIQSAADAGELGS NGILPDVESLRIPVQYLANLLTA GDTKPVLRALKRMLAMRHYK RAETVDGKVDTRALEEVGLTE AQAQEMYRYLAIANYEDRFVV PSSHRELAREAFPEKNGCGLPF GDGCHGSDTKFNLFNSRRIDAI D\KTEPHP
24949	55317	A	25087	664	1065	VAPEPHHGRKQLCREGLGVFH PTHHITHHLGVSLSLLITIFDAQS VHGPDDGCQGLDSVAVDNRLV LFHVFSGEAIFMDDLHLLHNGA FS*FSSPEQE*F/PRLWRR*CHPL *GFSQSPCSARGRLSPLRSEYIP

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24950	55318	A	25088	434	1663	PAGAFPDIANDFGEKSLLMPGG AVINGDF\NNVLPVDLVDPQQV QEFVDHAWYRYPNDQVGRHPF DGITDPWYNPGDVKGSDTNIQ QLNEQERYSWIKAPRWRGNAM EVGPLARTLIAYHKGDAATVES VDRMMSALNLPLSGIQSTLGRI LCRAHEAQWAADAIENNYSRN PSQGYSTVPRSPHPKVDPILTKP SGPAGPEMTRKQTQREDRPRSR PSMTTSPTSNLKPSVPAFKGVG YLDSLDRIGAADYQPTEQDILR TRVKTTGIVETHFTFKNLHFRT EQASVHACYCRLFDVEGQRSE RKKWIHCFEDVTAIIFCVALSG YDQVLHEDETTVLSTRIVDGHR YSDHSTIACPAFGTYTLLELKEL ALSCSTLLHIPHQRSPAGSFLAD NLNCTQAAVIPEFGGF
24951	55319	A	25089	1	1247	MTFGGDQIFESLVYRSAFRHVY SRGSPWYLHTNSDLSFVESKKE LIAEHILETFPWNLKGLTEIPWG DASGESGAVGLGVLAAVHYHP QRQSLMEKLALNKDAVVLVIS TEGDTDQVIERLESDAVLRYGI EDVVTNLDVLERMQPSESLLRA VLHTKHLMNPEVLAAARRIVC QVVEEIMARLAKEVRQAFSGV RDRRRRSFIPLARNFDFKSTLRA NLQHWHPQHGKLYIESPRFNSR IKRQSEQWQLVLLVDQSGSMV DSVIHSAVMAACLWQL\PGIRT HLVAFDTSVVDLTADVADPVE LLMKVQLGGGTNIASAGEYGR QLIEQPAKSVIILVSDFYEGGSSS LLTHQVKKCVQSGIKVLGLGA LDSTATPCYDRDTAQALGNVG AQI\AALMPGELGSLAWENLLA

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24952	55320	A	25090	1	1691	MGAYLIRRLLLVIPTLWAIITINF FIVQIAPGGPVDQAIAAIEFGNA GVLPGAGGEGVRASHAQTGVG NISDSNYRGGRGLDPEVIAEITH RYGFDKPIHERYFKMLWDYIRF DFGDSLFRSASVLTLIKDSLPVS ITLGLCWYFVCRACVVTHALSL WQSASIEVPRTSATAKARKTEP GRQTKRKVRSSQTVAARQRIAT LPHSMTVCNPGLFHSQMADAL AHRYYGFNIAEPWDNGSEAML QRDIGLKSESRGLMAGKRCSCL KGECGWSLDMQARVSTCFYVR LLCGTELEDHRICIIDTCDNKCG PQRRYVIKFRELCLVNSTVTLV DQEYELTVTDPELYDGSSQALA GISDLSSIYATCDPGYSCTDRVT LVDVRKRQSKTGPYKEIGRYGI DRNRSPLNPGFRGKPDLMPSQC IACGACACACPANALTIQTDDQ QNSRTWQLYMGRCIY/CDGRCE EVCPTRAIQ\LTNNFVLTVTNKA DLYTRATFHLQRCSRCERPFAP QKTIALAAELLAQQQNAPQNR EMLWAQASVCPECKQRATLIN DDTDVLLVAKEQL
24953	55321	A	25091	1	866	

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24954	55322	A	25092	338	2388	CVQEPLITVSWRLFAIPAGMKF SLFLRCLFCFHLAARYLVLLCQ LH/SQGIKVLDFTGVQSGPSCTQ MLAWFGADVIKIERPGVGDVT RHQLRDIPDIDALYFTMLNSNK RSIELNTKTAEGKEVMEKLIRE ADILVENFHPGAIDHMGFTWEH IQEINPRLIFGSIKGFDECSPYVN VKAYENVAQAAGGAASTTGF WDGPPLVSAAALGDSNTGMHL LIGLLAALLHRELNMTVAEIVE REEWAGFRARETAALEAVTAP STVIATGGGIILTEFNRHFMQNN GIVVYLCAPVSVLEDFRQRTME VLRLAFLSSGILEFFTSLSIALVA VYFGFSYLGELDFGHYDTGVTL AAGFLALILAPEFFQPLRDLGTF YHAKAQAVGAADSLKTFMETP LAHPQRGEAELASTDPVTIEAE ELFITSPEGKTLAGPLNFTLPAG QRAVLVGRSGSGSRYCPYINHR NVRLGPIVTDVPWENSGDKSLP EATAQVISSGSGATKVEDGLGD LNKPVSNQNLVTGIDTPVYNAP SAGSAPFGVLADNMRYPILHKL KDRLNQTWYQIRIGDRLAYISA LDAQPDNGLSVLTYHHILRDEE NTRFRHTSTTTSVRAFNNQMA WLRDRGYATLSMVQLEGYVK NKINLPARAVVITFDDGLKSVS RYAYPVLKQYGMKATAFIVTT
24955	55323	A	25093	1810	2399	STFRNSDDEPYIVRPVAVAWRD YVPQPARNGLSNFTGNLEEPAV MVNYFLQGDPYQGMVHFTRFF HQHPSGLS*WVAGNIFQILCAN QPVRKRTRDNVQLLHSRGQRG VFRCSRRVLTGLVDRFGRTQTF HREAAGEFSGEITGVTDGAWR HFRLVLTTQAQRAEEARQQAIS GGTEPSAFPDTLPVDTEYVMNF
24956	55324	A	25094	1	577	MPVSTAVATVIKTKQVEFQLQ VGVPLYFRLRANPIKTILDNQK RLDSKGNIKRCRVPLIKEAEQIA WLQRKLGNAARVEDVHPISER PQYFSGDGKSGKIQTVCFEVIG CREEPDAEECHGDREQRRVFIR EDGFFVTKDLYPNRRA\GIISTT AVISPSQPPIIAPRVAQSSEPRSA AHALARAIRQSTTV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24957	55325	A	25095	51	407	TCPIRAQRVETLYDRAYREVFG WNPRGPTGRPNARHTG*SKEG GRTEADETDAADSGQRGMEQR SEMDRKPTGTTGQRSEKPRRTL ECLALHETRIFLPQRKETHSSDA HDMPGPPML
24958	55326	A	25096	3047	4131	AHSGQMYMPLSSCIRSCILGSV VMTCGFPQKSAGQKRQKTADC RKRPQLYTKSLSLS/AVKAILAK GYDPVKWRKKDKVLDAVLKE LESGKYSDGDKHAFDQMLHSI GKQGGDPYLVMADFAAYVEA QKQVDVLYRDQEAWTRAAILN TARCGSSMESKRLDNAALAAGI SPNYINAHGKPQSISAETKRRLL DAMHQRTATKVAVTPVPNVM VYTSGKKMPMVVEGSGEYSW LLTTEEGTQYKGHVTGGKAFN LPTKLPEGYHTLTLTQDDQRAH CRVIVAPKRCYEPQALLNKPKL WGACVQLYTLRSEKNWGIGDF GDLKAMLVDVAKRGGSFIGLN PIHALYPAIRRAPAHTARLLAV
24959	55327	A	25097	524	697	AANWWWKSRRNWR*KMTAM LDRIISHIIRTVRMSGSVAVTRAI AVPGLLLLLIIATA
24960	55328	A	25098	1	1938	
24961	55329	A	25099	33	226	

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24962	55330	A	25100	1	2314	MDRAGDGPIRPLSGPTDVYGDT VYLRDPGPNHGKTTNGPLRFVP LLPFGQQVFPRVTPNFWNPVSS AALPARYMQTIENAAVWAQIG DKMVTVGNIRAGQIIAVEPTAA SYYAFNCGFGKAFIDKGHLEPV QGRQKVEDGLGDLYKPLSNQN LVTWKDTPVYNAPSAGSAPFG VLADNLRYPILHKLKDRLNQT WYQIRIGDRLAYISALDAQPDN GLSVLTYHHILRDEENTRFRHT STTTSVRAFNNQMAWARVDRG YATLSMVQLEGYVKNKINNRA TEREELRVSKITVLILGVIAIILG VLFENQNIAFMVGLAFAIAASC NFPIILLSMYWSKLTTRGAMMG GWLGLITAVVLMILGPTIWVQI LGHEKAIFPYEYPALFSITVAFL GIWFFSATDNSAEGAHLRPIRR KKVYRFNYLRSDGPYQGWVSE RLLILRAISPGCSKLVHFPTLFDS LYRTLVKAGEKSGLLAPVLEKL ADYNENRQKIRSKLIQSLIYPC MLTTVAIGVVIILLTAVVPKITE QFVHMKQQLPLSTRILLGLSDT LQRTGPTLLATVFIVAVGFWL WLKRGNNRHRFHAMLLRVALI GPLICAINSARYLRTLSILQSSG VPLLDGMNLSTESLNNLEIRQR LANAAENVRQGNSIHLSLE/QT/ AIFPPMMLYMVASGEKSGQLG TLMGAQSHWECATVNAASRIR
24963	55331	A	25101	20	825	GFPRSRSCYASCTACRTHTYSA EK/QLTRALAKLARATSNEKLS QAFHAHLEETHGQIERIDQVVE SESNLKIKRMKCVAMEGLIEEA NEVIESTEKNEVRDAALIAAAQ KVEHYEIASYGTLATLAEQLGY RKAAKLLKETLEEEKATDIKLT DLAINNSFYKEDIFMNRIEHYH DWLRDAHAMEKQAESMLESM ASRIDNYPELRARIEQHLSETKN QIVQLETILDRNDISRSVIKDSM SKMAALGQSTADTTKNSTHRQ SNTRQGN
24964	55332	A	25102	2	269	GIIGLHLQQQEAVAVAIVRGAT RMLFATLVAVAAGERHYQRW ADC*CAAAG*NVVTVESRTAA ASSHYVGVSRQSHITAVISAPV DVPW

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24965	55333	A	25103	607	727	RQAVYRG**TAGQRANLLLLR RHSACALAAGESQSSCPAG
24966	55334	A	25104	465	574	
24967	55335	A	25105	3	636	AHTSGFGDKESEKVSPQRKLHA MSRTFFWEN\LRCHGNLGSPTY AFQISAIDRVNFALVVGLHLRH DYRNEKLGRSGRHYQAPVGNR SSADGMHRDPCSQLDICCILLG AGSIYGLYRYIEPQLPDVATLK DVRLQIPMQIYSADGELIAQYG EKRRIPVTDGPVMWFPFMIITTC VKGNFALNNQFREDMLNYNTE GIYGKNVNFENNKQT
24968	55336	A	25106	434	1205	
24969	55337	A	25107	368	532	
24970	55338	A	25108	722	934	
24971	55339	A	25109	82	420	ARADPHRAHTAGVNGVNARLR IFNADTCLRRHAQPCTGGEKDF RVRFRVFKLGSIRAEGEKLAQL QRR*NRRRIQGDRSQPNRD/RA VPEDLPSKERMPGRTALTVNSR SEWT
24972	55340	A	25110	618	788	WYPCCRNWRYLAGGDSGFCR GERA*R*IASQSGVT*AVATVV FPSVLAGLRITGHS
24973	55341	A	25111	186	1198	QKTAVSTSITALTRWGS/SRA/G KRGAVLRSRVTRGKYHYPSSW RETSSSVQNAPLMRQIKEVFLAI RIEQLLTKDEILELYLNKIYLGY RAYGVGAAAQVYFGKTVDQL TLNEMAVIAGLPKAPSTFNPLY SMDRAVARRNVVLSRMLDEG YITQQQFDQTRTEAINANYHAP EIAFSAPYLSEMVRQEMYNRY GESAYEDGYRIYTTITRKVQQA AQQAVRNNVLDYDMRHAIAA RHYVLWKPTANIRARYKAQGI ELPAVVPAGPDNPMGHHAIRL AAYGGVYLLHGTNADFGIGMR VSSGCIRLRDDDIKTLFSQVTPG TKVNIINTPIKVSAEPN

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24974	55342	A	25112	1087	3289	RLRSCGAQKNTFCNAAAGCRW RTTLSKMGGLLIAADLQDPVQ DMEMWQFHPTGIAC/AGVLVT E/GCRGEGGYLLNKHGERFMER YAPNAKDLAGRDVVARSIMIEI REGRGCDGPWGPHAKLKLDHL GKEVLESRLPGILELSRTFAHVD PVKEPIPVIPTCHYMMGGIPTKV TGQALTVNEKGEDVVVPGLFA VGEIACVSVHGANRLGGNSLL DLVVFGSARQVLHLQESIAEQG ALRDASESDVEASLDRLNRWN NNRNGEDPVAIRKALQECMQH NFSVFREGDAMAKGLEQLKVI RERLKNARLDATSSEFNTQRVE CLELHNLMETAYATAVYATFR TERRGAHSR\FDFPDRDDENWL CHSLYLPESESMTRRSDYTLEA DEGRDMMLLDALIQLKEKDPS LSFRRSCREGVCGSDGLNMNG KNGLACITPISALNQPGKKIVIR PLPGLPVIRDLVVDMGQFYAQ YEKIKPYLLNNGQNPPAREHLQ MPEQREKLDGLYECILCACCST SCPSFWWNPDKFIGPGSLLAGY RSGLIAGIPKCSARYLSGEKRSV AWQQIAAEIGISIDAQFNESLKG ISRDESLRRILQHGGKEGDFNSQ ERAQLAYRKNLLYVHSLRELT VNAVLPGIRSLLADLRAQQISV GLASVSLNAPTILAALELREFFT FCADASQLKNSKPGPGIFLAGC
24975	55343	A	25113	47	630	VGWETSFAQIRSRFLRIRFCRAY SSTLFVSAANPTT*G/QMVF*CG NGAQHKNILLLYRSIHGGFHFQ RGHHINTFNKRWRR**NRT*YQ RDVRATTGSGGGDRKTHLAGA VIRDITHRIERFTRRAGGNHNV QMFQVVDGRKCATAISTVLDM FGDHFGRQKIASCQRWLAKTIR TVQQPICKNIVRKPGCHSLA
24976	55344	A	25114	731	829	

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24977	55345	A	25115	2	3744	RLPFKYPVKVKPLPAPFSKILLN SPAIPQLPITMNGSDFSLPEGPM NRWENIQLTPETRLAPRAYFFS YDSVAQARTFARETSSLFLPLS GQW\NFHFFDHPLQVPEAFTSE LMADWGHITVPAMWQMEGHG KLQYTDEGFPFPIDVPFVPSDNP TGAYQRIFTLSDGWQGKQTLIK FDGVETYFEVYVNGQYVGFSK GSRLTAEFDISAMVKTGDNLLC VRVMQWADSTYEKDQDMWW SAGIFRDVYLVGKHLT
24978	55346	A	25116	1	2643	
24979	55347	A	25117	2499	2935	RSGGVACNCAVSASCMLVTVL PWLSLPV/SVFGLWDGFFASLG VTALLAATPA\W*GVKT*CRPG RSP/SLTVRLGSVISPMIGGLLLA TGGVALLPLLSLPALPPPPQPRE HPLKSLLAGFRFLLASPLVGGIA LLGGLLTMASAVRV
24980	55348	A	25118	676	1035	
24981	55349	A	25119	1	1842	
24982	55350	A	25120	1	1341	
24983	55351	A	25121	563	1360	PSVLRCRNWVI*SPYCISLPSRV SSLPFLVWIPVAR/CTAIGASRE AMLGVLVEPMLLLGLWVAAQ VAGSTNISNITDTVYHWPLSQSI PLVLALCACAFATFIEMGKLPF DLAEAEQELQEGPLSEYSGSGF GVMKWGISLKQLVVLQMFVG VFIPWGQMETFTAGGLLLALVI AIVKLVVGVLVIALFENSMARL RLDITPRDMIRIELDSWEQNGE AIKRTGQPLLLSLLVRNLLDNA VRYSPQGSVVDVTLNADNFIVR
24984	55352	A	25122	382	1424	VLLENLSEPPNQHDIIEILTVQR KEEETALSCRLVLRKLTETEPVI IFEGIEAPATLPADEVPVGKDEN DNVEVSRWGTPREFDFEVRDH VTLGEMHSGLDFAAAVKLTGS RFVVMKGQIARMHRALSQFML DLHTEQHGYSENYVPYLVNQD TLYGTGQLPKFAGDLFHTRPRH ECFRHIGSLGLATPLVTECMQW LFGIPHTLQLDAIIITCWIILNAIC VACGLQKGVRIASDVRSYLSFL MLGWVF\IVSGASFIMNYFTDS VGMLLMYLPRMLFYTDPIAKG GFPQGWTVFYWAWWVIYAIQ MSIFLARISRGRTVRELCFGMV QEFGCKSSTKIDNADFNQA

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24985	55353	A	25123	416	610	
24986	55354	A	25124	662	811	AQQLPGMSDWQNSQEQHQMK N*VRLFMRTSRKLMDRLNVLIK LWSPNRT
24987	55355	B	25125	1	3264	
24988	55356	A	25126	489	3256	PRVFSSATRSLVAMRRWVYRV RRIQYRRTTQTAVFHSTHGNYR EGQPVGTLIDDRYKANENVEL VHYAQPLLNEADSLAKVMPSDI PLKQRRWLGLQMLEGDIYSRA YAGEASQHLDAALARLRNEMD DPALHIADARYQCIAAICDVVS NTLTAEPSRFTTAVDKIVLNRFL GLPIFLFVMYLMFLLAINIGGAL QPLFDVGSVALFVHGIQWIGYT LHFPDWLTIFLAQGLGGGINTV LPLVPQIGMMYLFLF
24989	55357	A	25127	779	910	
24990	55358	A	25128	2203	2665	ACWARISAAVIQRSGMPGVRV CGRIKSCSKAVRCQRHVFATCV WNGRQVTSGAGTWSTIAWYSG VMSSAISSWSRPAIPFSAEA*TIG KSSC/YVGRVEVNEQIEYLIHNP IRTRARAVNFVDNNNRLQAVS KRFFGYEARLRHRAVKCVNHQ QH
24991	55359	A	25129	241	918	
24992	55360	A	25130	2142	2646	KGVCGTTNPAKI\QAILQAFHEI FGEGSCHIASVAVESGVPEQPF GSEETRAGARNRVANARRLLP EADFWVAIEAGIDGDSTFSWVV IENASQRGEARSATLPLPAVILE KVREGEALGPVMSRYTGIDEIG RKEGAIGVFTAGKLTRASVYH QAVILALSPFHNAVY

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24993	55361	A	25131	473	1765	KAWLMTGIVRHWKGRAVPPA EQLLEHLGNGKSFDSVAQAWD AAMADAKAEDTVLWGVEAFRI NAAVAKDDTQIHTHMCYCEFT DIMDSIAALDADVITIETSRSDM ELLESFEEFDYPNEIGPGVYDIH SPNVPSVEWIEALLKKAAKRIP AERLWVNPDCGLKTRGWPETR AALANMVQAAQNLRRGARAG CAADFAASARLAVGEALTNIA ATQIGDIKRIKLSANWMAAAG HPGEDAGLYEAVKAVGEELCP ALGLTIPVGKDSMSMKTRWQE GNEEREMTSPLSLVISAFARVE DVRHTITPQLSTEDNALLLIDLG KGNNALGATALAQVYRQLGD KPADVRDVAQLKGFYDAIQAL VAQRKLLAYHDRSDGGLLVTL AEMAVLSSLGQGGYFGHMII/D SGQYPGKSKTGQSTPDVAAQA RQSWIP
24994	55362	A	25132	602	2563	VVTTLTLVLTAVGSVLLLLFLV MKARMHAFLALMVVSMGAGL FSGMPLDKIAATMEKGMGGTL GFLAVVVALGAMFGEILHETG AVDQIAVKMLKSFGHSRAHYA IGLAGLVCALPLFFEVAIVLLIS VAFSMARHTGTNLVKLVIPLFA GVAAAAAFLVPGPAPMLLASQ MNADFGWMILIGLCAAIPGMII AGPLWGNFISRYVELHIPDDISE PHLGEGKMPSFGFSLSLILLPLV LVGLKTIAARFVPEGSTAYEWF EFIGHPFTAILVACLVAIYGLAM RQGMPKDKVMEICGHAL\QPA GIILLVIGAGGVFKQVLVDSGV GPALGEALTGMGLPIAITCFVL AAAVRIIQGSATVACLTAVGLV MPVIEQLNYSKRRGFTGRVEEN FGVCKGPSKYHSQHDAINRQG REASDAHGTLENLPLPLVPQPN AATALAALRASGLEVSENAIRD GIASAILPGRFQIVSESPRVIFDV AHNPHAAEYLTGRMKALPKNG RVLAVIGMLHDKDIAGTLAWL KSVVDDWYCAPLEGPRGATAE QLLEHLGNGKSFDSVAQAWDA AMADAKAEDTVLVCGSFHTVA HVMEVIDARRSGGKLCQMHVN VQDKIDEEINQVHICLCLVLVIV SGCKYVGYSLKCSEHYYSLVR

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24995	55363	A	25133	518	1079	TQKETNKRCSPLVGWYPAFRM AHFLASERSCYQKLSN\RKSH\P AVAGMVSGMTVANLL/EHSAG NVFKSGI*LALHLFIDRCF*YCG DGIGLFLGARYSRRGERKSART ISLFAQPGPVVNFRRHDVWQRR CVCLVQLRKAIHDVYFRFFGNG DDLYYDVSWARDGAGKYAKW QDFRTLFTTAHCSSD
24996	55364	A	25134	322	798	AQRAHVVGTVGKFDEDDADIL HHRHNHLAKVFGLRLFLIAELE FIKFRHPLYQLGDAFTKKLFHIL ILVVGGSIFNHVMQQRRHQRFI VEFHLGQNAGN\ATGCVI*GSPL ERVCPS*ASRATRYACRRRLIW SIARPAAKVSACCSAIATSK*RS KGQRVLLGNCHVEVAIREFT
24997	55365	A	25135	440	906	CGFSSLSRLPHSSYSAHHAVAPS VLMSASGRPRWSQWYRWIFRA GVYTGSIWFFICSTVRPHDASQ RRLSSLT/QVSQDFTFQPVNHQL WAGGKPTAGITVGKQ*W*PFIK FTVPGDDSGDGRGQGFLQIAAG KCRAQTFFSFCRAGKHDPCRRT VS
24998	55366	A	25136	1059	1541	TAPLLRPGCRLS*SAAHPAAPA QSTNQCPGDRYAATLPAHHRH TNHG*IADVHQHISATPASAAS YAPGFLKDGAPASERHRETGC GRDRPH*PSLYKLSGILRPYQPA SFPG*QQRAVLSAR*LLPVQCSL HSQRCRRRPHRLHRSAPAPGIR ERRSRR

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24999	55367	A	25137	236	2211	QGALMSEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSPSQRSYS VLRSKFDAWLMEQAEEAGAQL ITGIRVDNLVQRDGKVVGVEA DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVAVGVKELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNENT LSLGLVCGLHHLHDAKKSVPQ MLEDFKQHPAV\APLIAGGKLV EYSAHVVPEAGINMLPELVGDL HERSLIFVASGPAGNSKETASD KLEEALPTKNWEVPGANWNTP GNGIPSVPEKLKGMLSAPNYRR MVLPAPLQILLLQNAKGGELLG AAGGQIAFNLGSAVGAYCGGM MLTLGLAYNYVALPAALLSFA AMSSLLLYGRYKRQQAADTPV LAKPLGQLDNAPFRCENVNLIR EEIGFNALDKFKRTTGALLQLQ QALHPALGADLCGSTGFAVLFI SPVRGNTHLRHLVHIFGTDLDL NRHSVRADHRGVQRLIAVRFW NGDIVFHAARTRLVQAVHLAQ HAITGVRIIDDHAESVDVHDRV KTLLFEHHFAVNRIKMLLPTTD AARYSRFLQTPFDFRKNLLDHL
25000	55368	A	25138	1	1932	

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25001	55369	A	25139	1	1200	MAIPAFGLGTFRLKDDVVISSVI TALELGYRAIDTAQIYDNEAAV GQAIAESGVPRHELYITTKIWIE NLSKDKLIPSLKESLQKLRTDY VDLTLIHWPSPNDEVSVEEFMQ ALLEAKKQGLTREIGISNFTIPL MEKAIAAVGAENIATNQIELSP YLQNRKVVAWAKQHGIHITSY MTLAYGKALKDEGIARIAAKH NATPAQVILAWAMGGGPVE\W RR*QIWRGFSSAS*RHELYITTK IWIENLSKDKLIPSLKESLQKLR TDYVDLTLIHWPSPNDEVSVEE FMQALLEAKKQGLTREIGISNF TIPLMEKAIAAVGAENIATNQIE LSPYLQNRKVVAWAKQHGIHI TSYMTLAYGKALKDEGIARIAA KHNATPAQVILAWAMGGGPVE MAKVADMAGIFVSKLKTFNAG VKGSTLGASGPQYVMVPKKHA DQLRESLASGEIAAVQSTLVAD NTPLNSRVYTVRSGDTLSSIASR LGVSTKDLQQWNKLRGSKLKP GQSLTIGAGSSAQRLANNSDSIT YRVRKGDSLSSIAKRHGVNIKD VMRWNSDTANLQPGDKLTLFV KNNNMPDS
25002	55370	A	25140	2237	2404	
25003	55371	A	25141	307	642	
25004	55372	A	25142	1449	2084	NAPRCAYY\VDVIAVTMPTTCC TLKISPLCRELILTLANRTTTQR AEPMTRRLIQVLFDELPQQPQQ QLHLPVSSHPKIRTMVEMMAK GPVEWGALGQWAGFFAMSER NLARLIVKETGLSFRQWRQQLQ LIMALQGLVKGDTVQKVAHTL GYDSTTA\FITMLRKPGKTAGTS LYHRRYGVSLLSSAWGQVGPP RYCRQANSVLSDRFCVLI
25005	55373	A	25143	981	1103	
25006	55374	A	25144	222	379	
25007	55375	A	25145	1	1452	
25008	55376	A	25146	500	854	
25009	55377	A	25147	1	1374	
25010	55378	A	25148	2	167	
25011	55379	A	25149	781	1047	
25012	55380	A	25150	1	783	

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25013	55381	A	25151	442	857	LVKNPVKRMEIQQKNLTLFEYL DWWDVLFLLLESELLFANTWL AATSESVDDCSGVKPPSGKNGT *AMPSWAKASIIASSARCAMLY SFCTQTISAILRASATCVGVTLL RPICFTRPCCCISASTVRLASIDP SAGP
25014	55382	A	25152	3	4105	
25015	55383	A	25153	2	269	YKNPYIAAKIQPKTHDTLTPINP GRIKLWLMTKRPMWVVPERSN *IAARSLG*VGRM**P*QAGAE ATMYAGSTPIASATGTIAASAA A
25016	55384	A	25154	1	1370	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAVYGIAWMA ETMFAPACYGYYILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPFQSVKAD IATNPFKRPGGAFIRITQTFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC V\GVTEGAIPFAAADPLRVIPSI MVGSVGGAVTAALVGAQCYA GWGGLIVLPVVEGKLGYIAAV AVGAVVTAVCVNVLKSLARKN GSSTDEKEDDLDLDFEIN
25017	55385	A	25155	1	789	MKIIAGITPADSGTLEIEGNNYV RLTPVHAHQLGIYLVPQEPLLFP SLSIKENILFGLAKKQLSMQKM KNLLAALGCQFDLHSLAGSLD VADRQMVEILRGLMRDSRILIL DEPTASLTPAETERLFSRLQELL ATGVGIVFISHKLPEIRQIADRIS VMRDGTIALSGKTSELSTDDIIQ AITPAVREKSLSASQKLWLELP GNRPQHAAGTPVLTLENLTGE GFRNVSLTLNAGEILGLAG/TEL AETLYGLRTLRGGRIML
25018	55386	A	25156	1	1332	

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25019	55387	A	25157	1594	2220	MWVNPERGRAENTIIGGNATGI GTLNVQDQDSVITVRRLS*SAL KPGILVFKLTPAETERLFSRLQE LLATGVGIVFISHKLPEIRQIAD RISVMRDGTIAGTGFGDDFGFT HPLRQQRLPQHLVSFMRAAVQ QIFTLEIQRGVRPGCNVLAFGQ RGWTPGIVFQQVVELSLKFRIFL RTDKSFFQLAQSRHQDLWHVH AAKLTKIGVK
25020	55388	A	25158	14	237	KTTSFPAKLFNACRISLLASAE/ CQSEYFSIFSNMDLADTVMFL* GAIRFSDLVNEQIQHTFLIPGETI CRLSEVV
25021	55389	A	25159	1	1506	
25022	55390	A	25160	158	639	SGC*PGRPSLN/GRLDVLSAWS VSILRLGGMALEGSIAYIVINFC DVKPQRFRGLSVPAASITVVLIQ QFVLHRRELRRKLALPAHHLVT FTWGNVSAVDETRQWMVIKPS GVEYDVMTADD\RWWLR*PAV RWWKAAKNPLPIHQRIWRSTV AMPKLAVLC
25023	55391	A	25161	2	2886	SVPTIIFFFLPVLRFWRPGIQQA KKCHLFATGTQSRRNTLRQRT AKGIPQQRMTAKREEISIGILHV TPQQRRECRGDNRFTARFRRTP WRLLGHCVSAAVTGVLPAVAG SPLAYSDTDEFYPVAGGTMSQ HLPLVAAQPGIWMAEKLSELPS AWSVAHYVELTGEVDSPLLAR AVVAGLAQADTLRMRFTEDNG EVWQWVDDALTFELPEIIDLRT NIDPHGTAQALMQADLPQDLR VDSGEPLVFHQTTLGFI
25024	55392	A	25162	1	1659	
25025	55393	B	25163	200	646	
25026	55394	A	25164	1	3197	MPHRQHGPQMTPSHQRTTINR DQREQQPIGTAAPQTRPQSAPY CEPHTRRRTLQPHNRGFRTAKY TSTQARKYHMARPERSNDSDH PVHTRSRWNATQTERHTQHHV SPPSSLRTLRTNCTSHAHHRYH RHAQWHRVGLLDVKPTGVPSN TVFSPPKNALWADRVDTSRGR TTVEQDNHPNGGNVVGTPSDN NFWLETTGGDPNKEYYHHHHY NEDYCRYYPLLIAEPLLFPSLSI KENILFGLAKKQLSMQKMK
25027	55395	B	25165	1	2505	

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25028	55396	A	25166	159	1744	NSRISGLQQRYLMHIMVTQGGL MSLSIVHTRAALGVNAPPITVE VHISKGLPGLTMVGLPETTVKE ARDRV/RSAIINSGYEYPAKKITI NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEYELVGEL ALTGALRGVPGAISSATEAIKSG RKIIVAKDNEDEVGLINGEGCLI ADHLQAVCAFLEGKHALERPK PTDAVSRALQHDLSDVIGQ\EQ GKRVLEITAAAGHNLLLIGPPG TGKTMLASRINGLLPDLSNEEA LESAAILSLVNAESVQKLWRQR PFRSPHHSASLTAMVGGGAIPG PGEISLAHNGVLFLDELPEFERR TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHYQ GNHNRCTPEQTLRYLNRLSGPF LDRFDLSLEIPLPPPGILSKTVVP GESSATVKQRVMAARERQFKR QNKLNAWLDSPEIRQFCKLESE DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR
25029	55397	A	25167	127	503	NRCLLLTLLRCKGRNREEENDA EAESEKLKNKFNRPSGRLSYGD RMFDIGVNLTSSQFAKTVMML *RARLGLR*TTGLELRELLPLIP AEKL*/YETDAPYLLPRDLSAKP STSRYHCVIEARAWFK
25030	55398	A	25168	3	406	

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25031	55399	A	25169	1	1252	MFDIGVNLTSSQFAKDRDDVV ACAFDAGVNGLLITGTNLRESQ QAQKLARQYSSCWSTAGVHSH DSSQWQAATEEAIIELAAQPEV VAIGECGLDFNRNFSTPEEQER AFVAQLRIGADLNMPVFMHCR DAHERFMTLLEPQMVENYETLI FEAHSTDYQTPQSLRQLVIDHF AILKVGPALTFALREALFSLAAI EEELVPAKACSGLRQVLEDVM LDRPEYWQSHYHGDGNARRLA RGYSYSDRVRYYWPDSQIDDA FAHLVRNLADSPIPLPLISQYLP LQYVKVRSGELQPTPRELIINHI QDILAHTTQPVKANKQNKEEH AMPNIVLSRIDERLIHGQVGVQ WVGFAGANLVLVANDEVAED PVQQNLMEMVLAEGIAVRFWT LQKVIDNIHRAADRQKILLVCK T*WKWYWQKGSPYVSGRCKK LSTTFIAPPIDRKSCWFVKHPPIS
25032	55400	A	25170	2	319	YSSVFSLSASASFSSSRFRPLPT* KREKKTPISNRQYIGIANSVCEK TSGGVSNIPTTNAPTSTYGRFLR KSSGEVIPIQHSSTIATGTSKETP NAINSAITKLK
25033	55401	A	25171	1	1011	MIPHPKLEGDRSTQALPPTPVIR VTERRNLNWVGTTIGFVHTGK PLSFVYDMADIIKFDTVVPKAF EIARRNPGEPDREVRLACRDIFR SSKTLAKLIPLIEDVLAAGEIQPP APPEDAQPVAIPLPVSLGDAGH RRRRSGRVSEVSWRSGVMSFR RASGDKPQPKPKVMPEHAECPP AARRGQMMSICPCFALKIDIAD NKFFNGETSPLFSQSQAKLARQ FHQKIAGYRPTPLCALDDLANL FGVKKILVKDESKRFGLNAFK MLGAPEKCHRRKNDF*RRSDRI VLIRL*REFSSHQKGLRDRPAH KAVLGDNQLFSGGTGAPVWPG FAKRAVMF/TPLKNLLSAISIFN AKHGHILIIWPRLAAGGHSACS GITFGFGCGLSPLARRKLMTPE RQLTSDTRPDRLLRWPASPSET GSGMATGCASSGGAGGCISPA ASTSSISGINLANVLLLRKISLH AKRTSRSGSPGLRRAISKAFGTT VSNLMMSAIS
25034	55402	A	25172	1	510	
25035	55403	B	25173	1	1482	

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25036	55404	A	25174	704	1069	RLWQADCKENAG\GDYYWTFF PQPTFVSTQKYYCHVDNSCYM NFDFSAPEYHAHWRYGLLMVG ESQHGLGANAIQASQCFKAAN QPLGADATFLQQIKGEIICFGLFI TGVFSIDSAFCDIT
25037	55405	A	25175	1	639	MARVWLCDFIPYGYLPTLNAM PESTRKQIMPWTRLSGSLHTWN RTPNRRIGRYPSGLPPDSANRPR REPDACRSLHSPAKYRGNPNRD RLDHQQNGLPARGKDTPRSNK PSISQWTNTKPQPRHQPRGKKG HKSPAPEMPKPPQATSSTREQT KYGAAELWRSPWKTRYIELKA RGPMACVTISLNVCCAHLVRL VMVTLKQTDPIRNLGEMPSKSQ TKKAREVHLHSLHLQELAQEQ EPPARKRKTQWAVSERK
25038	55406	A	25176	82	356	AQCEEYRVPQTLKRNPKQCFDI SIRGGSQPCGIFSTPVRNTLQNM GQMGWLVAPG*WLWREIRKH NRWCACPRKPGRAGISMALRW GSGHA

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25039	55407	A	25177	1	2635	MNKSGKYLVWTVLSIMGAFAL GYIALNRGEQINALWIVVASVC IYLIAYRFYGLYIAKNVLAVDP TRMTPAVRHNDGLDYVPTDKK VLFGHHFAAIAGAGPLVGPVLA AQMGYLPGMIWLLAGVVLAG AVQDFMVLFVSTRRDGRSLGE LVKEEMGPTAGVIALVACFMI MVIILAVLAMIVVKALTHSPWG TYTVAFTIPLALFMGIYLRYLRP GRIGEVSVIGLVFLIFAIISGGWV AESPTWAPYFDFTGVQLTWML RLINRSIMMDFSLTEEQELLLAS IRELITTNFPEEYFRTCDQNGTY PREFMRALADNGISMLGVPEEF GGIPADYVTQMLALMEVSKCG APAFLITNGQCIHSMRRFGSAE QLRKTAESTLETGDPAYALALT EPGAGSDNNSATTTYTRKNGK VYINGQKTFITGAKEYPYMLVL ARDPQPKDPKKAFTLWWVDSS KPGIKINPLHKIGWHMLSTCEV YLDNV*TSVWRTCACPALRRA TQRYRRQSRAGNLRTSGEAIRR DMEWTSLRSE\DWEKGDTIKQC ISAATSCVYGVTGEGILEGGDA QILREPLPGTKLGLLNWPVFDA LESRSTRERDGKPGGEICGETA NILIRGPENRPLRRDPPGKP

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25040	55408	A	25178	216	1829	TVCRCHFVTTKHIGRERNQRAR QCLVGKTTDTQQHNCDIRVGE QADHTRANHQHCTQRYDHLTG NDQVHTKPTLEQRRQVTTEDT TEVSKQHRHPGEHRDLFQRTLN ISADDQRRLLLELQNDNLNHNR IWLRLAAQPEDHIYGCGEQFSY FDLRGKPFPLWTSEQGVGRNK QTYVTWQADCKENAGGDYYW TFFPQPTFVSTQKYYCHVDNSC YMNFDFSAPEYHELALWEDKA TLRFECADTYISLLEKLTALLGR QPELPDWIYDGVTLGIQGGTEV CQKKLDTMRNAGVKVNGIWA QDWSGIRMTSFGKRVMWNWK WNSENYPQLDSRIKQWNQEGV QFLAYINPYVASDKDLCEEAAQ HGYLAKDASGGDYLVEFGEFY GGVVDLTNPEAYAWFKEVIKK NMIELGCGGWMADFGEYLPTD TYLHNGVSAEIMHNAWPALW AKCNYEALEETGKLGEILFFMR AGST/GDIGG\YTTLFEMKRSKE LVLRWCDFSAFTPMMRTHEGN RPGEHWAF/DGDAKHRHLAVY
25041	55409	A	25179	277	488	
25042	55410	B	25180	260	1500	
25043	55411	A	25181	1	764	MQEWGRYTILSGCCNSALKGD VCLLYGFRVAGRRQASE*TPGA YNRVPSSKK*GFQLVLLPFSAN GKSPAY*RFSKSFAEDGEKDAG FPHPYAEAGYDNGGRRSGAGT LLSR*I*TGAGRGAWRV*RLTG E*MAGKRT*VTASGYSQR*IMV FLWSLYRSYRL/GRVRQHNGPR YLPVLARNWKMSAWVAAAW QGLTDMKRKTMKIRSGS\IVILA SGYAATAA*PLSGDRIFLP*PGK TG*RHGGTPSCAGFTGDY
25044	55412	B	25182	1	3117	
25045	55413	B	25183	270	388	
25046	55414	A	25184	2154	2279	
25047	55415	A	25185	614	623	RPNSGAR*GRGDKRSTQSVPET VRLLFCAGTFDQQPGNARWDD QYRCIRSGIVGVRAVLLGGDIL DTQPLPVELAETLGKSAE

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25048	55416	A	25186	1208	2813	CYGVAWPFDPTLKFEFWRYFT HALMHFSLMHILFNLLWWWY LGGAVEKRLGSGKLIVITLISAL LSGYVQQKFSGPWFGGLSGVV YALMGYVWLRGERDPQSGIYL RRGVIIFAPIWIVRRWFEMTPTQ WSNYFFENLFKYEWVQTRSPA GAIQFEAVDAPEIIPDPFDPSKK RKPTMLVTDLTLRFDPEFEKISR RFLNDPQAFNEAFARAWFKLT HRDMGPKSRYIGPEVPKEDLIW QDPLPQPIYNPTEQDIIDLKFAI ADSGLSVSELVSVAWASASTFR GGDKRGGANGARLAL\MPQTR TGDVTRRQPIRAL\PVLE\KIQKE SGKASLADIIVLP\GLFVVEKSA SAAGLSIHVPFAPGRVDARQDQ \TAIGMFELLEPIADGFRNYRAR LDVSTTESLLIDKAQQLTLTAPE MTALVGGMRVLGANFDGSKN GVFTDRVGVLSNDFFVNLLDM RYEWKATDESKELFEGRDRET GEVKFTASRADLVFGSNSVLRA VAEVYASSDAHEKFVKDFVAA WVKVMNLDRFDLL
25049	55417	A	25187	1520	1960	PVPLNFGWQRSTEVLICHVNSP STAAMTISPWRR**RRRTKQLS APLLLGVSAIGW/LTIILVAFMA WLLAKT/AFGRSFYATGDNLQG AR/QLGVRTEAIRIVAFSLNAER DFDDLRDSGPLIAMILFIMPTLS SISSRRLNPGVPSEI
25050	55418	A	25188	1155	1778	SASGGVMLKFIQNNREITALLA VVLLFVLPGFLDRQYLSVQTLT MVYSSAQILILLAMGATLVMLT RNIDVSVGSITGMCAVLLGMLL NAGYSLPVACVATLLLGLLAGF FNGVLVAWLK/IPAIVATLGT\L YRGLMSLWTGGHWFEGYPRIE KPSPPVAGVHHWCVTQIGGLRP AVAKRVGPDLPGDNKGAKGVL NTLDNYGVDGKCV

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25051	55419	A	25189	1	2227	MVTIAGHLGGLALVGLITYFGK WTYLWKEWLTSVDHKRLGIM YIIVAIVMLLRGFADAIMMRSQ QALASAGEAGFLPPHHYDQIFT AHGVIMIFFVAMPFVIGLMNLV VPLQIGARDVAFPFLNNLSFWF TVVGVILVNVSLGVGEFAQTG WLAYPPLSGIEYSPGVGVDYWI WSLQLSGIAVAHIAAQNVAVLL ISSDLEEIELMADRVYVMHQGE ITHSALTERDINVETIMRVAFGD SQRGVMLKFIQNNREITALLAV VLLFVLPGFLDRQYLSVQTLTM VYSSAQILILLAMGATLVMLTR NIDVSVGSITGMCAVLLGMLLN AGYSLPVACVATLLLGLLAGFF NGVLVAWLKIPAIV\ATLGTLG\ LYRSIMLLWTGGQWIEGLPAEL KQLSAPLLLGVSAIGWLTIILVA FMAWLLAKTAFGRSFYATGDN LQGARQLGVRTEAIRIVAFSLN GCMAALAGIVFASQIGFIPNQT GTGLEMKAIAACVLGGISLLGG SGAIIGAVLGAWFLTQIDSVLV LLRIPAWWNDFIAGLVLLAVLV FDGRLRCALERNLRRQKYARF MTPPPSVKPASSATSDFICIGIVA LPLTMVIVSGGIDISFGSTIGLCA IALGVLFQSGVPMPLAILLTLLL GALCGLINAGLIIYTKVNPLVIT LGTLYLFAGSALMLSEEQKNTK KTRQREDKKKEKKKQRKREEK
25052	55420	A	25190	1055	1206	SFALFSSSSPRSRP*FASTKS*TL TTGQVLPSTNVRFLTGNWGPPV VATG
25053	55421	B	25191	1	1386	
25054	55422	A	25192	1	449	MQDPLLALLEDYNKGDLEKQV PPAQSGPQPGKAGRDRPIVIML DPGHGGEDSGAVGKYKTREKD VVLQIARRLRSLIEKEGNMKVY MTRNEDIFIPLQVRV/AKAQKQ RADLFVSIHADAFTSRQPSGSSV FALSTKGGMCSYRGSGCLQ
25055	55423	A	25193	1536	1941	STSNQNSTALCRRRGLVHCIDG ANDDDSVMVWPSGSGRPWSAE PGAPQR\YAQLVVEDVELDLLH FIVFGDDVMLNVVLQGQAFML ALGLVTNVGVLAHAHHHALVS GVPNDGGGTWVGGRCVQQSQ LCTCWSHCQ

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25056	55424	A	25194	240	855	SRAGYAPAAAQKVASPYVRRE R*NQSD\PAVLTGIGERGK*LLS RDFFIAPLAGMIVEKRGAVHLA RWSVPVERKGQWQPAGLWAQ FFLADIVCPAATALPDTTAEDQ HIDHPAVVHVHVIPVVNTCAED NHRAPMRFMGGIGKFTGDGFNI LARHPGNLLTPGWGVRFDFSVI FRTVFIFQPAIEAVIRQYQIINAD HRTGVAID
25057	55425	A	25195	840	1157	QYAPTAQPARPADPFALPTVQA RLTPFCYLVAKGDWCVYRRSY SLWHSVASPRVRQSPRLGY*GY TANSPGILLAPLSLRGEMFLPQD APKSVPPYKRGKSVAIN
25058	55426	A	25196	1076	1339	LVCVASMPVEISTDASASSGVI VISSAMSGSWSAETKRRLAMV* PEPLHLWAISIPTTSGRFTSSLIS PFPAR*YSPARYIPRVWRV
25059	55427	A	25197	2	118	
25060	55428	A	25198	1809	3145	ARHKQHAYGYRYRQSPRCYGV SGKKRGLRYYGSWLAISGSSRI TR/LLCMYLRRFFIGVIGADIAN MGISAGAMWLLSVSQVSLAAV SQVVAVRVWPASSYTRVTVES NRQLKYKQFALSNPERVVVDIE DVNLNSVLKGMAAQIRADDPFI KSARVGQFDPQTVRMVFELKP NVKPQLFALAPVAGFKERLVM DLYPANAQDMQDPLLALLEDY NKGDLEKQVPPAQSGPQPGKA GRDRPIVIMLDPGHGGEDSGAV GKYKTREKDVVLQIARRLRSLI EKEGNMKVYMTRNEDIFIPLQV RVAKAQKQRADLFVSIHADAF TSRQPSGSSVFALSIQRGARPVG DRYVDHTMFDMVQSLTIADSL KFGKAVLNKLGKINKLHKNQV EQAGFAVLKAPDIPSILVETAFI SNVEEERPNGQPGHPLDPATTM GTLIDCAHADSVQ
25061	55429	A	25199	1	277	
25062	55430	A	25200	902	1006	
25063	55431	A	25201	2	1265	
25064	55432	A	25202	409	525	
25065	55433	A	25203	91	431	NHKPGNIDVARRIQRGFAGDQI GHLRPVERQCSPDKRRFIAADG REIRGKQRAGHIFQLLSRCLLQI LNHCQRRAAHFRFQLSNQRHQ QLLPV/HYHAAEREYPAGACLV RWLL

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25066	55434	A	25204	3	71	
25067	55435	A	25205	1	1212	
25068	55436	A	25206	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVWDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGPGRLPFNRIGLIRRITRRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSGLKRVYHSPG APDIREFTRDAIP
25069	55437	A	25207	5	402	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI
25070	55438	A	25208	48	219	PETCGHLWAYVWPSCAAV\GL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25071	55439	A	25209	1	912	

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25072	55440	A	25210	1	1857	MRVCARACVRTRTRMCVYAH TCVCVRTYAYVRVRVRVHVRA RVRVCAYARTRVRNSLSILPFIQ LTLATPIHHIHQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLIRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPLALLLAFLCSTSPGF GDPDGLGVIAYQDTVRPNAAT AISELNALAVKGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTLDDRVVAGSAGRYGGDGA GDSECVKIVAQEIRQTDRNIER DRSPRPSGERVRVRGKGGIEAN QPLSTAFTNQITIRQSIRLFSNQF VFHKGISRVVAGSSAIISNVSPG CILRTPNCRRGFPISCTGEGKAA YGWQRDGGHAEYLLAEEKDLI LLPDALSYEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDVY/V*IGVARVSWMNGRID SELRTRVRAYAHTRTRARTCTR TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
25073	55441	A	25211	3	1180	SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFVDL LPAQQRMKGENWYRGTADAV TQNLDIIRRYKAEYVVILAGDHI YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIEFVEKPANPPSMPNDPSKS LASMGIYVFDADYLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHPFPLSCVQSDPDAEPYLAR CGYAGNFMESEPRSGLIRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRPVPDPVELVLV AAEFITPGDPTPRLHGSGFIDIR QIHHQTRSHLEGVKTGIRFLNH FSGNPQGGIAHVNGVARFQVK QCHQAWGQQYAARLRFQARGI SLQIAIHRVDIIHRFDVRQL
25074	55442	A	25212	16	543	
25075	55443	A	25213	1	3387	

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25076	55444	A	25214	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTPFGVC TSASMNVPVLTLRIRTRVTGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/WVAGTFD*SVWF GHDTDVVTLYRFHEALCYSVT LRTPHRRVLRFKSQHPGELACFI SPVA
25077	55445	A	25215	905	4761	PPHNWMPSNATPGIAFVWCAY GAI/LPGDAPVPVVDDYRKVVR KDTKGLIARWKYFWMSVIALG VAFALYLAGKDTPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTDGLDGLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAVLLRQEFLLVIM GGVFVVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25078	55446	A	25216	269	1219	QTRTRRVQLQDLIEYVAIHQW/ FSDKHPVPFYSCIFDDSITNCYS WSISKDGYFIFGGAYPMKDGQT RFLTMKDKMSAFQFQFGKTVK SEKCTVLFPSRGQDFVCGKDNA FLIGEAAGFISASSLEGIIYALYS TDIPRSVLLKQPDKLNPAYWRA TRLVCITLFGQIVNTICMAAPDL RKWIMLSPVAHKGHHLEWVLH DMQILPVPRPSGCICSGSSTFFC NWGCPYDRPQWQLYPSMCLC VHIGPAPVRSEKVESKRAISKV DQDSAFRGCCRSGNRNGGRKI VAVSLKKVSGAAKPCGHFRST RYRVAYSTIIN
25079	55447	A	25217	1	1158	
25080	55448	A	25218	1156	1899	LKLGIRYPQCQRLVTHSLDGISL PLHTAH*SQSNSAENTHRAISLK AVPPFFTAERRGVNAEEHRNGR LINGECRQRFNVLRVANGVRN VQFAKARDRNDIASFRQIGFDT FQTEVAQHFTDFRVAGFAFAID DSDLLVRLHFTALDAANADNA NIAVVIELRNLHLERTVKVNVR RRNVVNNRLVQRGHVFRHIFV VQTRDTVQRRSVNDREVQLLV GRVEVNEQIEYYADAFVIMLER LCKVLCCR
25081	55449	A	25219	1	2583	

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25082	55450	A	25220	278	787	TLLSATRQVYALLSTKPAFFSS HSSFSTSSRLISSRAASSMDVAF PIAFSASKTVSIKFFSR*KLLRNS HRPPFMVMRSIIRSPSNVFMAS* FRFVSIPTLRIDAVRRSTIWCSTT ARFSSRADAKFIKNVFQQAIPDS AAKWFFPVPGFPLNAKFVHPVI SSSAMDFA
25083	55451	A	25221	866	1144	
25084	55452	A	25222	19	1203	NWNLTPYASLTGFTADNPEYH LSNGMKSKSVDTRSIYRELGAT LSYNMRLGNGMEVEPWLKAA VRKEFVDDNRVKVNSDGNFVN YLSGRRGIYQAGKDLDRFKNL VLVHAARYAADLSYLPLMQEL EKRYEGKLRIQTVVSRETAAGS LTGRIPALIESGELESTIGLPMN KETSHVMLCGNPQMTRRLIPAS VEVYHDSLC\RKIWHGWEQHIT ARYLVGADGANSMVRRHLYP DHQIRKYVAIQQWFAEKHPVPF YSCIFDNSITNCYSWSISKDGYF IFCGAYPMKDGQTRFTTLKEK MSAFQFQFGKTVKSEKCTVLFP SRWQDFVCGKDNAFLIGEAAG FISASSLEGISYALDSTDILRSAL RKPIRTEQGANGAIRELEKFRPA
25085	55453	B	25223	58	359	
25086	55454	A	25224	4	329	
25087	55455	A	25225	1	1008	
25088	55456	A	25226	1	1335	

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25089	55457	A	25227	3	1886	HRLNITAENDCRRLHCSLRDLS SLLQAVGRLAEYFIGDVFAARF NDALTVVERLVKVTLYGSQIKL YNIETAVPSVLKPDLIDVHAQS LAGGCRLSAHWLAQYCSEIHR QNTQQFVTLISTTMDAITPLIST KVQDKLLLSACHLLVSLATTVR PVFLISIPAVQKVFNRITDASAL RLVDKAQVLVCRALSNILLLPW PNLPENEQQWPVRSINHASLISA LSRDYRNLK\PSAGAPQRKMPL DDTKLIIHQTLQRLRKILWENIS G\ESTKSSTDFAYQFGCRESV\Q VSLGLFPAF\IHQSDVTDEMLSF FLTLFRGLRVQMGVPFTEQIIQT FLNMFTREQLAESILHEGSTGC RVVEKFLKILQVVVQEPGQVFK PFLPSIIALCMEQVYPIIAERPSP DVKAELFELLFRTLHHNWRYFF KSTVLASVQRGIA\EEQMENEP QFSAIMQAFGQSFLQPDIHLFK QNLF\YL\ETLNTKQKL\YHKK\I FR\TAM\LFQFVNVLLQ\VL\VH KSHDLL\QE\EIGHRHSYNMASV DF\DGFFAAFLPEFL\TSC\DGV\ DANQKSVLGRNF\KMDRLCPCL PGPAPHSPRMCTGWSTTCGLLT DSGNDSLAPWGLWKLLGPCLL PGGTRDFLLVAT

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25090	55458	A	25228	689	3053	VDCRMS/FSYIEKFTDFLRLFVS VHLRRIESYSQFPVVEFLTLLFK YTFHQPTHEGYFSCLDIWTLFL DYLTSKIKSRLGDKEAVLNRYE DALVLLLTEVLNRIQFRYNQAQ \LEEL\DDETLDDDQQTEWQRY LRHSLEVVAKVMELLPTHAFST LFPVLQDNL\EVYLGLQQFIVTS GSGHRLNITAENDCRRLHCSLR DLSSLLQAVGRLAEYFIGDVFA AR\FNDALTVVERLVKVTLYGS QIKLYNIETAVPSVLKPDLIDVH AQSLAALQAYSHWLAQYCSEV HRQNTQQFVTLISTTMDAITPLI STKVQDKLLLSACHLLVSLATT VRPVFLISIPAVQKVFNRITDAS ALRLVDKAQVLVCRALSNILLL PWPNLPENEQQWPVRSINHASL ISALSRDYRNLKPSAVAPQRKM PLDDTKLIIHQTLSVLEDIVENIS GESTKSRQICYQSLQESVQVSL ALFPAFIHQSDVTDEMLSFFLTL FRGLRVQMGVPFTEQIIQTFLN MFTREQLAESILHEGSTGCRVV EKFLKILQVVVQEPGQVFKPFL PSIIALCMEQVYPIIAERPSPDVK AELFELLFRTLHHNWRYFFKST VLASVQRGIAEEQMENEPQFSA IMQAFGQSFLQPDIHLFKQNLF YLETLNTKQKLYHKKIFRTAML FQFVNVLLQVLVHKSHDLLQE EIGIAIYNMASVDFDGFFAAFLP
25091	55459	A	25229	1	853	MISVANEIAEAGFDPQGRTSED LLDLAESRVFKIAESRANKDEG PKNIADVLDATVARIEQLFQQP HDGVTGVNTGYDDLNKKTAG LQPSDLIIVAARPSMGKTTFAM TLVENAGR\MLQDKP\VLIFSLE MPSEQIMMRSLASLSRVDQTKI RTGQLDDEDWARISGTMGILLE KRNIYIDDSSGLTPTEVRSRARR I\AREHGGIGLIMIDYLPLMRVP ALFDNRTLEIAEISRSLKALAKE LNVPVVALSHLNRSLEQRAEER PGNSDLGESGSIEQDADLIL

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25092	55460	A	25230	206	1073	VKITSWLMSNSALPGTLKLLAL ILKCSTCVRVLPRSELRNLER/Q GQLDSVGGFA/YLAEL/SKNTPS AANISA/YADIVRERAVVREMIS V/ANEIAEAGFDPQGRTS/EDLL DLAESRVFKIAES/RANKDEGR NPMFDDRGKRGEPSDLIIVAAR PS/MGKTTFAMNLVENAAML/Q DKPVLIFSQTKI/RTGQLDDEDW ARISGT/MGILLEKRNIYIDDSSG L/TPTEVRSRARRIAREH/GGIGL IMIDYLQLMRVP/ALSDNRTLEI AEISRSLKHFEKLALICGCRNNG TTRYCKSLLA
25093	55461	B	25231	1	483	
25094	55462	B	25232	287	635	
25095	55463	A	25233	1	2469	MPSDISLASCRLRATSRLFTDHR RQSDCMTAINRIPIVDDEDNVR RFETHCANNVRTALHLFADIHP DVVLMDIRMPEMDGIKALKEM RSHETRTPVILMTAYAEVETAV EALRCGAFDYVIKPFDLDELNLI VQRALQLQSMKKEIRHLHQAL STSWQWGHILTNSPAMMDICK DTAKIALSQASVLISGESGTGKE LIARAIHYNSRRAKGAFIKVNC AALRESLLESELFGHEKGLFER ANEGTLLLDEIGRM/PLVLQAIL RILQEREFERIG/GHQTIK/VDIAS LLAPTRLQAMVKEGTFREDLFY RLNVIHLILPPLRDRREDISLLA NHFLQKFSSENQRDIIDIDPMA MSLLTAWSWPGNIRELSNVIER AVVMNSGPIIFSEDLPPQIRQPV CNAGEVKTAPVGERNLKEEIKR VEKRIIMEVLEQQEGNRTRTAL MLGISRRALMYKLQEYDATGF FRDGMTIMVGGFMGIGTPSRLV EALLESGVRDLTLIANDTAFVD TGIGPLIVNGRVRKVIASHIGTN PETGRRMISGEMDVVLVPQGTL IEQIRCGGAGLGGFLNPTGVGT VVEERQTSIDTSTRKRPFELGRP SRNNDKGIRPRSGAGSEEYPRT LHDSLKRLQTDYLDLYQVHWP LRPFYCFGKLGYSWTDSAPAVS QLDTLDALAEYQRAGKIRYIGV SNETAFGVMRYLHLADKHDLP
25096	55464	A	25234	1	891	
25097	55465	A	25235	1	1614	
25098	55466	A	25236	1	946	

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25099	55467	A	25237	1055	1474	NGVKSKPPPNHQTGSAPGFSAI KNRTFAWPTLPNTSCWANTML IGSRELGIRSSQSGPLLGVRVWC /CRCRGTQG/HSQGKDG/IPENGI RAYKFTSS*ASFRNSACFRQPSR IKPLRKATWLLCGLSTRHLITK RLSSPDWA
25100	55468	A	25238	2036	2743	DLLIRQMPLLSRRVIPVIRVPVT GVLWKSFTPRITIFGH/ALIDQH SMIVAAQGLTPDHQLLLQIYDR ARVSASRIVHQAQIYGDAVVR YAFIEHRAEVFDFASIEGNEENN VWLCDCAKVYGHAQVKAGIEE DAIPTIHYSSQVAEYAIVEGNCV LKHHVLVGGNAVVRGGPILLD EHVVIQGESRITGAVIIENHVEL TDHAVVEAFDGDTVHVRGPKV INGEERITRTPLAGLL
25101	55469	A	25239	2234	2571	IMSSVDSSLVLPLKAMVPSRITL IRSAIWRISG/RLMRDKNNTHAS SKQLLQATKQAFGFRRGKRGG RFIEDQNPRVAHQPAEDFHHLA IGDIQRSCQTMQIKLAAQRRQQ VLH
25102	55470	A	25240	659	1206	WKSTSNTAKAKPGSVMAVDLR IPIRFGVMLSAA/FGDDVVDLIA QVDLVTTAVGPVVLERIAPAIA KGQVKRKEQGHESPLNIIACEN MVRGTTQLKGHVMNALPEDA KAWVEEHVGFVDSAVDRIVPP SASATNDPLEVTVETFSEWIVD KTQFKGALPNIPGMELTDNLM AFVERKLFTLKH
25103	55471	A	25241	332	683	ALPGR*RHVHLPGSAYEWNDA EPAQESDELSLKMLTAICWLTA TA/STSLKI*R*KVALRCLVGRIR RLRRIRQQCQLLMRRSRVLSGR LSSV
25104	55472	A	25242	1	841	MVKVAGECRVRASAHLPGLNR STKNTEDRGANNQEGTNTQKT RGETNERLKKNEHRDLRLARY PAKENNKQGDKNKPRTYEKLT GTVTHQEPPHHADQSPGLCLFR TSRAQVERGPTVLLLISQENQIE RYDSDNHSQLNLCLRVPTVTTQ RRDYDIAERYRQKGIKLPARKE RLMTIAERLRQEGHQIGWQEG KLEGLHEQAIKIALRMLEQGFD RDQGIA/RRASCQRQQRQSSLPT P/EHCCAISGATARKPAALPAAR IRRILVSIIRCTSGCPALSG

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25105	55473	A	25243	240	651	RCPPQSCLLAEGRWCG*K/CRK VSV*SNRYR*SRLSLGELLRAYS RNRDLPGF/SSGSARVLVATDV AARGLDIKSLELVVNFELAWEP EVNVHRIGRTARAGNSGLAISF CAPEEAQRANITSRPPHPAHIAS DHQSTP
25106	55474	A	25244	1455	1643	RDPHQICVAESVYLAAFVLLCA GLCVRRRSTTGARNAAAAC*N GLW*AEAQCPAYYVCPVVG
25107	55475	A	25245	549	641	
25108	55476	A	25246	1378	2084	PNFGYSPPASSCGQVSQNSS*LQ CSVSGRDKMLRTGPCARTVSSS YLMGVSFSRDA**DAR*VCACH NTIAALSASAERFTSCERASHSE ARSGCCNSVRVMSNNPCCPRSL IGVYDILFFQESTAKRCKRSLSG SGSACGKSRVRFTPYRPARRTP LRSTTSPISAASFPSGWECNAAS TCSAALRSTAITSLPSLAKFRAS SPSNSQTPRTAGLTGSAASESSI PQPQAAANS
25109	55477	A	25247	1134	1428	GPCGCCSSNVARCASQTSSRFA AV/WHGAIGAR*LNADNRPLWI EITREHAELPGKTGRRMETKQR RAITFTQRQNGFESHTPGAVFFS INNRCQFGDR
25110	55478	A	25248	96	535	RPQTTVQPALYVAEQSICSQPC* *FSTKCDRKPAAVLAPAGYAAL PVLFSSAKLDGSWLRWNSASG RRQNGSFSCAALASKRPASASS KLNSA**SLPSAVFAAPVRVAA SMIISGFCALASIRPSASTRRPSA SVFITSTFLPLR

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25111	55479	A	25249	1471	3026	SPLRSSVACRGWHRKNNRRGW CPRRGDPARPVRDSLQ\HATAIII VATPGRLLDHLQKGTVSLDAL NTLVMDEADRMLDMGFSDAID DVIRFAPASRQTLLFSATWPEAI AAISGRVQRDPLAIEIDSTDALP PIEQQFYETSSKGKIPLLQRTLV RFANGSARVLVATDVAARGLD IKSLELVVNFELAWDPEVHVHR IGRTARAGNSGLAISFCAPEEAQ RANIISDMLQIKLNWQTPPANS SIATLEAEMATLCIDGGKKAKM RPGDVLGALTGDIGLDGADIGK IAVHPAHVYVAVRQAVAHKA WKQLQGGKIKGKTCRRCYPLA APYVRHCSLVGRAASHQALWH VAGFGLYALFRRTGGCRLRCR YSGGLRLIRPTVAAGICRPDKT RKRRIRHRAPFPDAARAPYPAY RSQYNQFFFTNSDFSFIGPKPSM LQSMLCAPCNQADVFHFGANV SASKSYLFTFRSLMMVTLSPCS QQIAVSIFNDQLVAFLCRFCVV PLRRHIHGQMYMPLSS
25112	55480	A	25250	196	330	
25113	55481	A	25251	62	617	NRRLPSGGDEMSAQVSLELHH RI\SQF\LVQESSCWTDW\KFRD GVAQLRPKEVRF\TMRTTVNGQ TRVPRKGVQPPTTWIFNDTKDQ LERRIARLETGMAWAEEPPSRT RHLISNCQISETDIPNVFAVRVN YLLYRAQK\ERDETFYVGTRFD KVPPSE\DTTWRCLKRDIVLDQ AVITSHNLSVLF
25114	55482	A	25252	1	318	
25115	55483	A	25253	1	510	
25116	55484	A	25254	9	79	
25117	55485	A	25255	1	361	
25118	55486	A	25256	863	1245	FSQIYLARSALSSAHSSRSPWQH SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI
25119	55487	A	25257	909	1069	GILSPFLVFVRFVKDQIVVDVW YYF*GLCSVPLVDISVLVPVPCC FGYCSLVV
25120	55488	B	25258	1	1878	
25121	55489	A	25259	778	990	
25122	55490	A	25260	312	635	
25123	55491	A	25261	4047	4276	

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25124	55492	A	25262	1599	1776	WFPASSMSQPKKAQDQTDSQP NSTRGTERSWYHSF*NGSKQ*K KSNSSPTHFMRPASS
25125	55493	A	25263	1	162	
25126	55494	A	25264	1	3370	MNRAPIPKQSKDKTSRETKNTS RSKTRERTDELEGLSTDNHAET QHAETNTDMTHERYTQIRNHT YKTTHQMEDKRTKPKREKEIH NRPDDMAKAGIPRSILNTGHPG KLMQTEVHHVRTLKIMLKVYS RALQEELQFSSKAIGRLFPCAD DLLETHSHFLAQTHERSGYVPL CVCATHTKFYEFMEDVNTAYT KRHTMFRSLSMVSECLFSLING DDMFVTFAAMQAQQGRSSLV WLFSQLYLYSFISLFIYMV
25127	55495	B	25265	44	238	
25128	55496	A	25266	1	444	MPAEFITG\ERS\SEGFF\RIHAGI EQAISRGLAYAPYADLKNLDD KTIASFQQQLSDMGYKFQFITL AGIHSMWFNMFDLANAYAQG EGMKHYVEKVQQPEFAAKKD GYTFVSHQQEVGTGYFDKVTTI IQGGTSSVTALTGSTEESQF
25129	55497	A	25267	710	1395	DLPGISSKWVIAVIFGHLIVGIFI PPAIIVRAGIT*RQVR/WIAAHE GKAPQQIIIMAHLDTYAPLSDA DADANLGGLTLQGMDDNAAG LGVTLQLAERLKNTPTEYGIRF VATSGEEEGKLGAENLLKRMS DTEKKNTLLVINLDNLIVGDKL YFNSGVQTLEARHQRSFNTVKP WPDSVISNRPFAGNTGSVDDND EIQRNLNDTNYNRMWEYNNRG VGSKVVAEAKK
25130	55498	A	25268	2	2105	
25131	55499	A	25269	754	1133	RAANQHQTVDLTRLQTRIAQR LFNRHSQAIEQRQPQIFQFVLVK FAFPRFFLILPANVQWRLIATFC RFHTGVQGCQFTLVKRGPGDIR DYQQTNLDWYNSRNTTKLDES VNRV/HAAIQS*RQNGL
25132	55500	B	25270	1	1275	
25133	55501	C	25271	1	1167	

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25134	55502	A	25272	275	2424	SPAMHFQSFT/WQNNLDDNTIA SFQQHLSDMGYKFQFITLAGIH SMWFNMFDLANAYAQGEGMK HYVEKVQQPEFAAAKDGYTFV SHQQEVGTGVYAASGNSLLLM RALNAAWPGIIDCSNHFARLRC SVWSIPRSDLRCAAAFRTGRLA CCPAGDEKPYPSLRSSRWSGRG ATALHYYTAKRCRPDKTRQRRI RQPARALDVGCGVTALSDLPG CRTSQRCRPDKTRQRRIRQPAR ALDVGCGVTALSDLRGAALHG SLANYRVVNFLFRLPDAMILSV LLRSCPFVFPLLRRLRAGAPVGP YCTGTPITPLPSTRLFAPLPNRC SMAGMYGGLQPVPHPAIGARC LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMRCWRIL SGLRGARPNKIVCRIRRLRRIRPI LRLRFPRHSRVVFIFGGGNPRR AKQRQTGEEVEKCHQPQHGTK CCARGGFAACLVFEYVVVFWT SLPDSFCRKSFPTRIRGSMVPSL WDFPPGVDGRKGKTSWNGVPG PCVTCGLGLTCPESPCCPGLSLG DGYPEKVSVGPPIPLKFQAILQA FHEIFGEGSCHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS
25135	55503	A	25273	1	441	
25136	55504	A	25274	3	2919	AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQ/EAVRT VRARLQAD/VTGVPTVLVARTD ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRF AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT
25137	55505	A	25275	432	549	

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25138	55506	A	25276	652	2689	KFSVGYAVQNFNATVSTKQFQ VFSEQNTSSYFAEPQLDVNYYQ NDVVHFVTTRDDMPEATRVHL EPTINLPLSNNWGSINTEAKLLA THYQQTNLDWYNSRNTTKLDE SVNRVMPQFKVDGRMVFERD MEMLAPGYTQTLEPRAQYLYV PYRDQSDIYNYDSSLLQSDYSG LFRDRTYGGLDRIASANQVTTG VTSRIYDDAAVERFNISVGQIY YFTESRTGDDNITWENDDKTGS LVWAGDTYWRISERWGLRGGI QYDTRLDNVATSNSSIEYRRDE DRLVQLNYRYASPEYIQATLPN VNHHITMEHLHMKTRTQQIEEL QKEWTQPRWEGITVRPYSAEDV VKLRGSVNPECTLAQLGAAKM WRLLHGESKKGYINSLGALTG GQALQQAKAGIEAVYLSGWQV AADANLAASMYPDQSLYPANS VPAVVERINNTFRRADQIQWSA GIEPGDPRYVDYFLPIVADAEA GFGGVLNAFELMKAMIEAGAA AVHFEDQLASVKKMRHMGRT ASDQPWLAYAPYADLVWCEPP PPDLELARRFAQAIHAKYPGKL LAYNCSPSFNWQKNLDDKTIAS FQQQLSDMGYKFQFITLAGIHS MWFNMFDLANAYAQGEGMK HYVEKVQQPEFAAAKDGYTFV SHQQEVGTGYFDKVTTIIQGGT SSVTALTGSTEESQF

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25139	55507	A	25277	134	1695	FPDPARLPPVSVNHHITMEHLH MKTRTQQIEELQKEWTQPRWE GITRPYSAEDGGKLRGSVNPEC TLAQLGAAKMWRLLHGESKK GYINSLGALTGGQALQQAKAGI EAVYLSGWQVAADANLAASM YPDQSLYPANSVPAVVERINNT FRRADQI/QWSAGIEPGDPRYV DYFLPIVADAEAGFGGVLNAFE LMKAMIEAGAAAVHFEDQLAS VKKCGHMGGKVLVPTQEAIQK LVAARLAADVTGVPTLLVART DADAADLITSDCDPYDSEFITGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRF AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIHSMWFNMFDLA KAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQENRSSK QQQPLLTVGRIRRSRRIRQSVPR TGIGCASRRFNTAKPWADAVIS NRPFAGNTGSVDDNDEIQRNLN DTNYNRMWEYNNRGVGSKVV AEAKK
25140	55508	A	25278	230	380	
25141	55509	A	25279	432	1247	PSQEPSVHGRWMA*KGHSRIV* WRAYD*TH\FNPVLKKSVSLGS NIRHMLAEEATTEELDGT\GPV LV*PNRH*PAYWMRAYLNLKK MSCRSFRRKA*RW*CETQTVV HRDRVDQGNNHFDVVARHYH LYAFLRKERQLIFFKFKYARIQY AG
25142	55510	A	25280	243	430	RRPSYSVLQRLPSAVLLPYY*R DWYHRTAGRRRDGNAGRQHQ NGCYPDPPDRDGRRSAFRNP
25143	55511	A	25281	10	638	SSVPTAGSRYNHLRAPRYSPLF ANYSMSDRCCKPFG/LDSSTG* WFQ*RSVPLPILLPDTSRHQL*C SDPTRNGPA\QACQRFFHIVERV ARVHHARFAATVTVDHVVIDQ RFFQICRT/PWCRLHRHHWRSSS GTR*TF*SPARHFCLLHNDSSYR STARPTCSGTDVPDRRCSDAHL CDHWSGSRAHADTDAECWCL NPQPAPSLLQCRR
25144	55512	A	25282	803	1622	
25145	55513	A	25283	498	686	RRPSYSVLQRLPSAVLLPYY*R DWYHRTAGRRRDGNAGRQHQ NGCYPDPPDRDGRRSAFRNP

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25146	55514	A	25284	1	2063	MKNFMENVLRYLSDDKWKPD AKASMTVGTNLDTVYFKRHGQ VTGNSAAFDFHPDFAGISVEHL SSYGDLDPQEMPLLILNGFEYV TQVGNDPYAIPLRADTSKPKLT QQDVTDLIAYLNKGGSVLIMEN VMSNLKEESASGFVRLLDAAG LSMALNKSVVNNDPQGYPNRV RQQRATGIWVYERYPAVDGAL PYTIDSKTGEVKWKYHVENKP DDKPKLEVASWLEDVDGNRKR NFSNDARANGTAAFTDCETQT VVHRDRVDQGHNHFDLVARH YHLYAFRQFDGTSHVSSTEVEL RTVAFEERSMTAAFISWTECTL QIRTCPQNPTGKVWTCDELEIM ADLCERHGVRVISDEIHMDMV WGEQPHIPWSNVARGDWALLT SGSKSFNIPALTGAYGIIENSSSR DAYLSALKGRDGLSSPSVLALT AHIAAYQQGAPWLDALRIYLK DNLTYIADKMNAAFPELNWQIP QSTYLAWLDLRPLNIDDNALQ KAL\IDQEKVAIMPGYTYGEEG RGFVRLNAGCPRSKLEKGVAG LINAIRAKKSATMIDTTLPLTDI HRHLDGNIRPQTILELGRQYNIS LPAQSLETLIPHVQVIANEPDLV SFLTKLDWGVKVLASLDACRR VAFENIEDAARHGLHYVELRFS PGYMAMAHQLPVAGVVEAVID GVREGCRTFGVQAKLIGIM
25147	55515	A	25285	3	371	
25148	55516	A	25286	63	180	
25149	55517	A	25287	2	205	
25150	55518	A	25288	495	707	REFSSHQKGLRDRPAHKAVLG DNQLFSGGTGAPVWPG/HSENV VPVDPT\MKRLPDDVNHPALDY YWRLSFA

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25151	55519	A	25289	1	1713	MTWAYSPSYGKPLSVPQGIIGL MTRFGMDVTLAHPEGYDLIPD VVEVAKNNAKASGGSFRQVTS MEEAFKDADIVYPKSWAPYKV MEERTELLRANDHEGVK\APEK HCL\AQNAQHK\DWH\SIEEMM EP\TREGEAQNKHGRP\AEINGA SCKEGRSDQKAYDEKSRPDEM PIDDNVVLNKGDVLQVSGDAR RVKTIADRIGFISIHSQVTDLLAF CAFFVIGLMIGMITFQFSTFSFG MGNAAGLLFAGIMLGFMRANH PTFGYIPQGALSMVKEFGLMVF MAGEIQVDGNTIYPHIWKSCDG GVLFAKQYLLRLGIILYGFRLTF SQIADVGISGIIIDVLTLSSTFLL ACFLGQKVFGLDKHTSWLIGA GSSICGAAAVLATEPVVKAEAS KVTVAVATVVIFGTVAIFLYPAI YPLMSQWFSPETFGIYIGSVIEV GVDVPNASLMIIENPERLGLAQ LHQLRGRVGRGAGLLTACCST KRRFLKAAPEVTRTGLADDRSS GLPLQTGYELASMQGLVDVVR LSPQGTDTFAMLDAFRANENG AAPLPLTANSDCNGYWRRLAG
25152	55520	A	25290	629	1054	ASGRFREVTG/MEEAFKDADI/V YPQSWAPYKVMEERTVLLRAN DHEGLKA\LEKQCLAQNAQHK DWHCTEEMMELTRDGEALYM HCWPADISGVSCKEGEVTEGVF EKYRIATYKEASWKPYIIAAMI\ CPVNTPNQVHCSSNC
25153	55521	A	25291	235	780	
25154	55522	A	25292	1	2783	MTYRNNHQTGVAFLFQTKFCIE DGGVKTFDGYRVQTQSRHAEQ EVTDVEINLFCHPLCIIMQIFTV HISEELATFIVRGFRFRRGKAAI GIFLVNNQLQPDIVHRGFCTEH HDVRGIKHFTLVEHVITGSGFG NTRFTFFRAGNNKMPRLGVGA GWAVLQGVPVRFGVWPLPEYP AYACGKFNGAIRAGDAAQLAA YAQAFIQLHGPIDAGDGVNRA DHRAGDFFEIVFQNLFAIADVD LAINHAVNAQLRLRNP

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25155	55523	A	25293	365	722	TSCLSALAIK/QQHLDEKKELG HLSAGARRLILGIIVTF/CADSG VNLRYSAV*PAGAVYLPDAAV GGSADRTADAGALLGANVDCA VADRFLPLYLVALHLYAELGRS GQPGVRAYSALR
25156	55524	A	25294	798	1094	
25157	55525	A	25295	1	2780	MGIVASASVQAAEIYNKDGNK LDVYGKVKAMHYMSDNASKD GDQSYIRFGFKGETQINDQLTG YGRWEAEFAAWTDMFPEFGG DSSAQTDNFMTKRASGLATYR KTTSSAYRWPELNLQYHRCTS AARAMLLSGRPVMQINERTAV RRQMTVYLRVERIHEIDPLVSL SHSMSVIPIDVERPIAAAPCTPG LWRTKTPLRVPSTYPLRLPGRA RVVCHRTFRLHLCKDWVFMFS GLLIILVPLIVGYLIPLRQQA
25158	55526	A	25296	66	300	QSTYCDNPPVPVSRGL*P*RRSS STSSAGYQK*RYCQHRHDPASR IRTVQRTDSQRTVKRKFMLLVP EASVPASEIC
25159	55527	A	25297	240	424	RCSRDEHDFQLIANLRIVVITFA TFA*CTA*LPLGNHSVVAAH*A G*GGAPVTAQVFVQHG
25160	55528	A	25298	1	1425	
25161	55529	A	25299	1	471	
25162	55530	A	25300	1269	1390	
25163	55531	A	25301	601	1119	VAAGAV*RGH*NVQLGKLFFV ASDLRINAIAGGVVVFS*FIQGL TNAIGSGFNNARCRKPTGQVA ADGGRDAGFFTIANNQCTYAA GIFFQCSGEFVGIQFQFAIAGIGR DTNLRQRFIAGRTDGITQHRFQ LRLNRPQRGVAEQCTIARTLAIS SRMAVYLVRLLKVSISEL
25164	55532	A	25302	1666	1769	RLKRHPPLRPSWPPY*TGAHVW HFSPLANWKPGI
25165	55533	A	25303	1	1970	MKDDIFFRTSGGGVTLSGGEVL MQAEFATRFLQRLRLWGVSCA IETAGDAPASKLLPLAKLCDEV LFDLKIMDATQARDVVKMNLP RVLENLRLLVSEGVNVIPRLPLI PGFTLSRENMQQALDVLIPLNIR QIHLLPFHQYGEPKYRLLGKTW SMKEVPAPSSADVATMREMAE RAGLQVTVGEKWGVSIETQGA LGTENRLADEDIRRADVALLIT DIELAGAERFEHCRYVQCSIYA FLREPQRVMSAVREV

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25166	55534	A	25304	2804	3494	LSLAEWKCLNPSQRALYREVM LENYRNLEAVGQLQPQSTQRIP *GRICNGDRLTSQKGLDL\VLEA LPGLL\EQGGQLALLGAGDPVL QEGFLAAAAEYPGQVGVQIGY HEAFSHRIMGGADVILVPNRFE PCGLTQLYGLKYGTLPLVRRTG GLADTVSDCSLENLADGVASG FVFEDSNAWSLLRAIRRAFVLW SRPSLWRFVQRQAMAMDFSW Q\VAAKSYRELYYRLK
25167	55535	A	25305	1	1306	
25168	55536	A	25306	818	1658	
25169	55537	A	25307	2611	2826	
25170	55538	A	25308	609	2359	PPPKIAPVWGCRKKSLPARSKSI FCFALFFPFFLNGEIILPESPCPF WTLFRNDGGKKRDPLAPVYLL GKLTISPGPICPDMIGVLFDSTV RREVAHIGNVQHRFCGPLFLKL VEFIDFILTIDIAAIIRQYLVVICE VDQRINQIAIATRIFRTGYTAAD LRQHLMQLLIFLVVFTRFVALT TQFFHFFRCVTKNKDIVSTDMI QHLDIRTVQRTDSQRTVKRKLH VTGAGSFRPCQRNLFRQICRRN DQLRQANAVVRDEHDFQLIAN LRIVVDHFRYVIDQMNNVLRH VIGRSRLTAKNIHARYPLRIRVG LDAVIAEMASGLDPFWRPDVV HAHDWHAGLAPAYLAARGRP AKSEFTVHNLAYQGMFYAHH MNDIQLPWSFFNIHGLEFNGQIS FLKAGLYYADHITAVSPTYARE ITEPQFAYGMEGLLQQRHRERR LFGVLNGVDEKIWSPETDLLLA SRYTRDTLEDKAENKRQLQNA\ MGLKVDDKVPLFAVVSRLTSQ KGLDLVLEALPGLLEQGGQLA LLGAGDPVLQEGFLAAAAEYP GQVGVQIGYHEAFSHRIMGGA DVILVPSRFEPCGLTQLYGLKY GTLPLVRRTGGLADTVSDCSLE NLADGVASGFVFEDSNAWSLL RAIRRAFVL/WSRAGSWRYSAR AIRCCRKVSLRRQRNTPVRWAF RLAITKHFRIALWAARTSFWCP

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25171	55539	A	25309	1028	1632	TSASAGTARNFSSNFAVRTTGH STSEATSSSRLSLKSALPPILRAA SSASALMFFVIGDDFPTSRRISG Y*SALSMVNSGSPIKRWPRITRS D*MPRMVAGMTLSP/MQQGHG VHRTHEVHVVAPQRISFGIGSF AREVATIFGSSASVFRR*YRNH APNLLTLCSVCLQRRTPGQSPG RVFRFHDPVAFRQVSYFQRQTP IA
25172	55540	A	25310	1	336	
25173	55541	A	25311	1889	2257	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTVCTGRTKCTSL APQRISFGIGSFAREVATRRPYR DIKEGFSQREAALLPQSLRVPQ TGTWSAAGAQA
25174	55542	B	25312	1	735	
25175	55543	A	25313	1439	1744	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPMQQGHVPWQLMVVL WNTRQRWKPSSPDRYVNRAMS LPSRKGEMLKPAPCRK
25176	55544	A	25314	1209	1972	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTVCTGRTKCTSL APQRISFGIGSFAREVATIFGSSA SV/HFALHMGAIQQPFAFIGSQT LSLVNGNTATT\PQPSAALLGLP SASNAWAIAGPRFSISRSGCASA RLATFSARRRGASKPLNGCLLR ATLSSPDKFQQGSTGGMLWGV LRHSPKFSITADGREFTLHWPN TGAMTGCATPGEYVWYSTFDN TQRKYPHPWEL

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25177	55545	A	25315	1	1521	METQHRLMRTFQPRQQDWTY ALWGGVKLRWLFFFLWGLFLF AGEEELGIRQTRTNDFLVTGDN LLRIFRFDVGNEDKVRQQFAVV RIHREVFLVTFHGVNQRFSRHR EEFLFEFCVTPKLNEGTTQRTN NRGIAVLNTGHRHPDLVAAVE QQLQQFTHTAYQIVPYESYVTL AEKINALAPVSGQAKTA\FFHP GSETG\ENGVKMVRAHTGTPG V\IAFRGG\FHGRTYMTMALTG KVAPYKIGFGPFP\GSVYHVPYP SDLHGISTQDSL\DAIERLFKSDI EAKQVAAIIFEPVQGEGGFNVA PKELVAAIRRLCDEHGIVMIAD EVQSGFARTGKLFAMDHYADK PDLMTMAKSLAGGMPLSGVVG NANIMDAPAPGGLGGTYAGNP LAVAAAHAVLNIIDKESLCERA NQLGQRLKNTLIDAKESVPAIA AVRGLGSMIAVEFNDPQTGEPS AAIAQKIQQRALAQGLLLLTCG AYGNVIRFLYPLTIPDAQFDAA
25178	55546	A	25316	114	187	RSTISSVRYGDDAFKP*RQAWN VL
25179	55547	A	25317	105	317	YLFFLSRFNHWISMEKKLGLSA LTALVLSS\SWARVFSVCRKIW RQLPARQHCSSAGVLLALAFYC WPLPC
25180	55548	A	25318	1	593	
25181	55549	A	25319	1	729	
25182	55550	A	25320	1	1005	
25183	55551	A	25321	1	1361	
25184	55552	B	25322	1	2793	
25185	55553	A	25323	27	255	

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25186	55554	A	25324	225	1408	RIIYMHMESQKIWFALSTPMEIR NECCLPSHSSPKMYLGACLF\PL SSSWGIDDRDDLLRTIHRMIDN GHAARLAGFYHRWFRYSPCEW RDYLAELNEQGQAYAQFVAST AECCGEGGIKAWDYVRMGFLS RMGVLNNWLSEEESLWIQSRIH LRALRYYSNWRQYFAGYTFGR QYWQSPEDDHLPLLREFLAQET TDVDIIRRAYLALLPSFHTETDP QGFKQLRHAYDDALPIAQSPAK SVLQPEEYEWEALLVEMLGLL HRIAMVQLSPAALGNDMAAIE LRMRELARTIPPTDIQLYYQTLL IGRKELPYRTCQLHACTSADTP LRKIPRFSGKLHFYAFCPNIYSS YHSAAKYGGSCQPGSTAHRLG YYWRWHFIAGLCHADPHAHSS
25187	55555	A	25325	230	380	
25188	55556	A	25326	432	1247	PSQEPSVHGRWMA*KGHSRIV* WRAYD*TH\FNPVLKKSVSLGS NIRHMLAEEATTEELDGT\GPV LV*PNRH*PAYWMRAYLNLKK MSCRSFRRKA*RW*CETQTVV HRDRVDQGNNHFDVVARHYH LYAFLRKERQLIFFKFKYARIQY AG
25189	55557	A	25327	10	638	SSVPTAGSRYNHLRAPRYSPLF ANYSMSDRCCKPFG/LDSSTG* WFQ*RSVPLPILLPDTSRHQL*C SDPTRNGPA\QACQRFFHIVERV ARVHHARFAATVTVDHVVIDQ RFFQICRT/PWCRLHRHHWRSSS GTR*TF*SPARHFCLLHNDSSYR STARPTCSGTDVPDRRCSDAHL CDHWSGSRAHADTDAECWCL NPQPAPSLLQCRR
25190	55558	A	25328	803	1622	
25191	55559	A	25329	498	686	RRPSYSVLQRLPSAVLLPYY*R DWYHRTAGRRRDGNAGRQHQ NGCYPDPPDRDGRRSAFRNP

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25192	55560	A	25330	1	2063	MKNFMENVLRYLSDDKWKPD AKASMTVGTNLDTVYFKRHGQ VTGNSAAFDFHPDFAGISVEHL SSYGDLDPQEMPLLILNGFEYV TQVGNDPYAIPLRADTSKPKLT QQDVTDLIAYLNKGGSVLIMEN VMSNLKEESASGFVRLLDAAG LSMALNKSVVNNDPQGYPNRV RQQRATGIWVYERYPAVDGAL PYTIDSKTGEVKWKYHVENKP DDKPKLEVASWLEDVDGNRKR NFSNDARANGTAAFTDCETQT VVHRDRVDQGHNHFDLVARH YHLYAFRQFDGTSHVSSTEVEL RTVAFEERSMTAAFISWTECTL QIRTCPQNPTGKVWTCDELEIM ADLCERHGVRVISDEIHMDMV WGEQPHIPWSNVARGDWALLT SGSKSFNIPALTGAYGIIENSSSR DAYLSALKGRDGLSSPSVLALT AHIAAYQQGAPWLDALRIYLK DNLTYIADKMNAAFPELNWQIP QSTYLAWLDLRPLNIDDNALQ KAL\IDQEKVAIMPGYTYGEEG RGFVRLNAGCPRSKLEKGVAG LINAIRAKKSATMIDTTLPLTDI HRHLDGNIRPQTILELGRQYNIS LPAQSLETLIPHVQVIANEPDLV SFLTKLDWGVKVLASLDACRR VAFENIEDAARHGLHYVELRFS PGYMAMAHQLPVAGVVEAVID GVREGCRTFGVQAKLIGIM
25193	55561	A	25331	2	696	FLLLLWEIRKSSQQTTPTEMNA AEMAQLVAGVDEVGRGPLVG AVVTAAVILDPARPIAGLNDSK KLSEK\RRLALYEEIKEKALSWS LGRAEPPEIDELNILHATMLAM QRAVVGLHIAPEYVLIDGNRCP KLPMPAMAVVKGDSRVPEISA ASILAKVTRDAEMAALDIVFPQ YGFAQHKGYPTAFHLEKLAEH GATEHHRRSFGPVKRA/LGTCV LILVSRLSKPESEDVL
25194	55562	A	25332	2	63	
25195	55563	B	25333	138	182	
25196	55564	A	25334	356	706	ISDICAPNMVSAIHAIPYTATMA IIPERKTSFFEIDAGLVLVRIIISA PVSSINI*ITSTIDSGLPPKDGRRS ESAPRRATTAIAPRKIHIASQLL VVIIIRSLVGCRMRRWRVLSD
25197	55565	A	25335	1746	1873	

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25198	55566	A	25336	1998	3626	PKAARMANVPNNTTGTAMVGI SVA/RHILQEQIHHQEHQHNGFE QRFYHFVNRKLDEWRGVIRVE NLHS/AAGRMAVIPPVLP*WLS RYREHSRRLPA*SPKGEAASNP EVIARTLRKLKNQPELSEDTIKK AVESLSLELVLTAHPTEITRRTL IHKMVEVNACLKQLDNKDIAD YEHNQLMRRLRQLIAQSWHTD EIRKLRPSPVDEAKWGLCRNGK TACGKAYQITWAELNKQLEEK PRLQTCPSKFGSGPFYF
25199	55567	A	25337	243	604	PRFPFPLPPATSSVQTAMTDG*N ECERICVGYLRYSSHSAPDARR QRARTHVPVGKHALPALTKAT HPSWWWQCAAMAEDSTDARQ LKA*WGVNGFLDLRSATMDGR LYPVAMCLLPATK
25200	55568	A	25338	1	3287	MPITLRRSVEKEQLIEIANTIMPF GKYKGRRLIDLPEEYLLWFARK DEFPAEARYTHIDLHVPAPLLV MFTLDTRQSACDRNPHLPIHVC SSWTSPKCAPRLWTRALLPRTR TPPYATGTTIGSRASWFVTFPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLIHKM VEVNACLKQLDNKDIADYEHN QLMRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSAVVEETR EAVDTTSQPVAT
25201	55569	A	25339	1	1425	
25202	55570	A	25340	534	1391	RQKRRLYQTYWYKQQPRYLPP EHRQRHRHQSAGVSRPYSGYG EVRPLSQYQPEWQCWEPDVEW VRQPPQDAITDPDFFCFYQPGM TFEQFVREFAEWFSQKRPAAM MIGIRADESYNRFVAIASLNKQ RFADDKPWTGGHSWYIYPIYD WKVADIWTWYANHQSLCNPL YNLMYQAGVPLRHMRICEPFG PEQRQGL\WLYHVIEPDRWAA MCAR\VS\GYTTGGLYPGQARG AAV*TEALKPSGLPQVCALNQC LLSVHRYAGHVRQERCDGADG RPAVHERRQLL
25203	55571	A	25341	786	1009	HHSHEQQFQWPVGASGVDRW AVYLHQICPLTQFQY/WCRARQ EGIMSSPGQQVGFIA*VTSSFSP R*KGRRVSSA
25204	55572	A	25342	2446	2970	
25205	55573	A	25343	1	2184	

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25206	55574	A	25344	706	1293	IHRLLIRRIHQIIDLRIWQRTVEI HGAPVRFIQMAAWTHIAVLLT* QLRQLRAGFQRNSWAIFYFFHH RKQYIFHFDLRRFPVIMHALFC AVQRCADLMAHRRQKRRFCLA GFFCFRPCLSVFYHQFLQFSCTR FDLRRQLFAVAIQCMNIAFAAA LVDFDLPDIDGITLARQLAQQY PSLVLIGFSAHVIDETLQ
25207	55575	A	25345	1	3291	
25208	55576	A	25346	882	1019	
25209	55577	A	25347	1	2265	
25210	55578	A	25348	284	535	CVAASVTGTRVLIPPLLNNRSR RSPVRYVSKGNWWGSVCNCAS NNSNSVSR*SLPPMRSHAWRKV RRIMRQLPLERPRPGFTI
25211	55579	A	25349	131	208	LVRWLLSPGW*WKISPIISICLFP V
25212	55580	A	25350	1	3108	MDSQDKYFEATQTVYEWCGV ATQLLAAYILLFDEYNEKKASA QKDILIKVLDDGITKLNEAQKS LLVSSQSFNNASGKLLALDSQL TNDFSEKSSYFQSQVDKIRKEA YAGAAAGVVAGPFGLIISYSIA AGVVEGKLIPELKNKLKSVQNF FTTLSNTVKQANKDIDAAKLKL TTEIAAIGEIKTETETTRFYVDY DDLMLSLLKEAAKKMINTCNE YQKRHGKKTLFETYLTDHPVTF RERLQMSIYKIPLPL
25213	55581	A	25351	1	296	
25214	55582	A	25352	3	164	VGD/NVGTTARWGIFALIIVETL AWFTVVASLFAQHKQRAENLI QRLHLLWSFNP
25215	55583	B	25353	91	990	
25216	55584	A	25354	1146	1881	RCGVQ\WTMYIRAVFVNLTNP KSIVFLAALFPQFIMPQQPQLM QYIVLGVTTIVVDIIVMIGYATL AQRIALWIKGPKQMKALNKIFG SLFMLHNAFAWFYLGAFLLTVI AWFLLGNAQKMPQTTLQWGIL VFLGVVASGIGYFMWNYGATQ VDAGTLGIMNNMHVSAGLLVN LAIWHQQPHWPTFITGALVILA SLWVHPNKRFRNWLTLLAIAH GGVQSAPQAFAQGFGHHQTLA LKTLYYPMR
25217	55585	A	25355	1943	2287	
25218	55586	A	25356	44	274	

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25219	55587	A	25357	876	1400	YRHVRDSPGNDRLFETWRSAG CAARLLRQSGETRLLSRVVRDY GGRWPVSLLDGLPDATWCTEK RGGFCTCATGRAGEKWAQFPE\ SLLTNLANPKAIIYFGSVFSLFV GDNVGTTARWGIFALIIVETLA WFTVVASLFALPQMRRGYQRL AKWIDGFAGALFAGFGIHLIISR
25220	55588	A	25358	1	1428	
25221	55589	A	25359	421	797	IIFPFLLFHLCNQLSHLLQYAVV NAPVRRILPIQLLWQQLIQPGEK LKSIRRAIQHIGQTQIIGMFIQMP IMIAYETDRATGDGI/WAAH*T HEYPCHVRQSQFHENHDDVQE NPPHPWKIQTPGH
25222	55590	A	25360	1	1320	
25223	55591	A	25361	1	1251	MLLSIITVAFRNLEGIVKTHASL AHLAQVEDISFEWIVVDGGSND GTREYLENLNGIFNLRFVSEPD NGIYDAMNKGIAMAQGKFALF LNSGDIFHQNAANFVRKLKMQ KDNVMITGDALLDFGDGHKIK RSANRAGLFLIGYGAFRIIVEFF RQPDAQFTGAWVQYISMGQILS IPMIVAGTMKQYLELMQKVLD EGTQKNDRTGTGTLSIFGHQMR FNLQDGFPLVTTKRCHLRSIIHE LLWFLQGDTNIAYLHENNVTI WDEWADENGDLGPVY\ITTVL NQLKNDPDSRRIIVSAWNVGE/ LDKMALAPCHAFFQFYVPDGK LSCQLYQRSCDVFLGLPFNIAS YALLVHMMAQQCDLEVGDFV WTGGDTHLYSNHMDQTHLQLS REPRPLPKLIIKRKPESIFDYRFE
25224	55592	A	25362	3	1327	

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25225	55593	A	25363	1	2443	MGLIGFVLTALWIKLIHNPTDH PRMSAEELKFISENGAVVDMD HKKPGSAAASGPKLHYIKQLLS NRMMLGVFFGQYFINTITWFFL TWFPIYLVQEKGMSILKVGLVA SIPALCGFAGGVLGGVFSDYLI KRGLSLTLARKLPIVLGMLLAS TIILCNYTNNTTLVVMLMALAF FGKGFGALGWPVISDTAPKEIV GLCGGVFNVFGNVASIVTPLVI GYLVSELHSFNAALVFVGCSAL MTMSARSATGHECVFWCNGKP RRLAMRLIYWCAAAPTGDVVQ KLTGKWALIANSHRAGQPTRN VNEEVGQRLLEEMEWYDNYL NMGKTDRSANPSPGNKKGGLA NVVEKALGSIAKSGKSAIVEVL SPGQRPTKRGLIYAATPASDFV CGTQQVASGITVQVFTTGRGTP YGLMAVP/SH*NGNWKITASVT SIQPNTNELPNCCMNGVSTANT TSKSSLVICALR

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25226	55594	A	25364	1	2701	TFFLPAGEILPPRLEPQITLPVGS RRIISIAVTDLPEPESPHLRSGLG WASLCCFMVICKFFPAAEGLIL AAVCDSRGSRYWCNGNRRYG YASDLLVRCGATVMFSEVTEV RDAIHLLTPRAVNEEVGKRLLE EMEWYDNYLNMGKTDRSANP SPGNKKGGLGKRGSSKALWLP LLQIQARKQVGLRVYTVACVL RTGTWYDRNGPDWRVPGQLN MGNPAPETGRYRLAHPATPHD PRTTPDHPSHIKPHAPTNQQPDT LTPTHHHHTDTRDPSPPPPRTRT PRQSTHTTPPHPTTTTRHTDIHP PTHTNPPPPTRVLTRQLHHTNRI IPHRTHTTTCRRNHHNQMNTTT PPPPHTPQITHRHHNTTLREQTQ KHRQHIHGTQHHTTRKPPTPTT RQYNTSIVGTIGGG\MVERKVIE ESLQALQERKPRLFHGRMARN GADAVGSDCGGAMSVFISVHG MRPRLVLIGAGHVNRAIAQSAA LLGFDIAVADIYRESLNPELFPP STTLLHAESFGAAVEALDIRPD NFVLIATNNQDREALDKLIEQPI AWLGLLASRRKVQLFLRQLRE KGVAEEHIARLHAPVGYNIGAE TPQEIAIRVLAEILQVKNNAPGG LMMKPSHPSGHQMVVIRGAGD IASGVALRLYHAGFNVIMLEVE KPTVIRCTVAFAQAVFDGEMT VEGVTARLATSSAEAMKLTER

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25227	55595	A	25365	1	1262	MGNWHLSPCPAPAPGHSCLFL VGTSPRILAVPGHTGSKAINKA ALLLESYMSQALKNLLTLLNLE KIEEGLFRGQSEDLGLRQVFAG QVGG\QPLYAAKEPVPEERLVH SFHSYFLRPGDSKKPIIYDVETL RDVAPVLDVAGATPPTIRHQRV TALVAPKNGSRDVRSCAGKMP TDGSIRAVLLPFQVSTIGGVTYE RVGTKDQGPQCPHVQRSSAVR PGPEAAPGDNSYPPYEDRSTCG MQAPDASYSANPDLSFTWSPCL SEDALHTSPLYCTTPTSGGEAF KGLASDLVPHEDKMVLQNGKC FTSPRHTEWAVLRAGHALARG RNLLDLAAGGMAWVSMSQEC PGPGTICSRDLQGTECLRMIQIL PPKDPVTRGSTHCNAGTKRELE EFSSQVTLTALIQPLMQVSAQF RAADGAP
25228	55596	A	25366	2	176	
25229	55597	A	25367	1	1395	MRESLELPRDLLNCCDQNANS DMDMKSRLRGYQMEIMNLLG AGVKDFELESDDLVYLVEEISK QQSIHDVAWLLLVAFVYICEQR NDLKSELIFTREAEHKSLENLEP DHVPEELDTSARNAGALTRRRE IRDAATLLRLGLAYGPGGMSLR EVTAWAQLHDVATLSDVALLK RLRNAADWFGILAAQTLAVRA AVTGCTSGKRLRLVDGTAISAP GGGSAEWRLHMGYDPHTCQFT DFELTDSRDAERLDRFAQTADE IRIADRGFGSRPECIRSLAFGEA DYIVRVHWRGLRWLTAEGMRF DMMGFLRGLDCGKNGETTVMI GNSGNKKAGAPFPARLIAVSLP PEKALISKTRLLSENRRKGRVV QAETLEAAGHVLLLTSLPEDEY SAEQVADCYRLRWQIELAFKR LKSLLHLDALRAKEPELAKAWI FANLLAAFLIDDII\SHRWISPPE
25230	55598	A	25368	482	765	

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25231	55599	A	25369	1	1575	MGSVTKSRGPTDSSAFFQINRD YSFLDYILGGCQLMFTPWARLL QSTCCEQCSKKAHDQFLADLA SILPSNTTPLIVSDAGFKVPWYK SVEKLGWYWLSRVRGKVQYA DLGAENWKPISNLHDMSSSHSK TLGYKSLTISNPISGQILLYKSRS KGRKNQRSTRTHCHHPSPKIYS ASAKEPWILATNLPVEIRTPKQL VNIYSKRMQIEETFRDLKSPAY GLGLRHSRTSSSERFDIMLLIAL MLQLTCWLAGVHAQKQAFRF MRLVDGTAISAPGGGSAEWRL HMGYDPHTCQFTDFELTDSRD AERLDRFAQTADEIRIADRGFG SRPECIRSLAFGEADYIVRVHW RGLRWLTAEGMRFDMMGFLR GLDCGKNGETTVMIGNSGNKK AGAPFPARLIAVSLPPEKALISK TRLLSENRRKGRVVQAETLEA AGHVLLLTSLPEDEYSAEQVAD CYRLRWQIELAFKRLKSLLHLD ALRAKEPELAKAWIFANLLAAF LIDDII\SHRWISPPEVPDPKRRT
25232	55600	A	25370	1	1341	MAGGRKFPDGGDRTTLCGLSQ PGVLAPRSPEKRRAINQRYPSK TGQLPASITDMMRTARHHLSG NGISVPKGAELAHPSTVLELFAI SAKPIHPEELDTSARNAGALTR RREIRDAATLLRLGLAYGPGG MSLREVTAWAQLHDVATLSDV ALLKRLRNAADWFGILAAQTL AVRAAVTGCTSGKRLRLVDGT AISAPGGGSAEWRLHMGYDPH TCQFTDFELTDSRDAERLDRFA QTADEIRIADRGFGSRPECIRSL AFGEADYIVRVHWRGLRWLTA EGMRFDMMGFLRGLDCGKNG ETTVMIGNSGNKKAGAPFPARL IAVSLPPEKALISKTRLLSENRR KGRVVQAETLEAAGHVLLLTS LPEDEYSAEQVADCYRLRWQIE LAFKRLKSLLHLDALRAKEPEL AKAWIFANLLAAFLIDDII\SHR WISPPEVPDPKRRT
25233	55601	B	25371	1	1233	

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25234	55602	A	25372	1	2197	SHSRGSPGKAVDFTLVSHAAW FGLPHFSTPAFNGQAMMLIAPV AVILVAENLGHLKAVAGMTGR NMDPYMGRAFVGDGLATMLS GSVGGSGVTTYAENIGVMAVT KVYSTLVFVAAAVIAMLLGFSP KFGALIHTIPAAVIGGASIVVFG LIAVAGARIWVQNRVDLSQNG CNPAYAEHHQHPGYSDKLKTR VSFSCLRIISTNLRRECRAQFRF HVDASARHGFRLWQIQGVAQP VFIITIREVEAAMRATAFGTEVG RNSRCIRRFHQVIQFQALNALG VELAGIDSRDPRLKVLEEMKRT FHWGRQTISKHIKIWLGLMLGR AMTPLMLDATSGKLTVWDGA HAGAAMGILAVTADQNSAELA YYKSGSFRIEDVLWPSAVTDDN IKRNAFAADGSVNSYSVPFSSV PLLQRQGRIKYAVTLAKYRTNS NEQQESKFAQATLQWGGPWGT TWYGGGQYAEYYRAAMFGLG FNLGDFGAISFDATQAKSTLAD QSEHKGQSYRFLYAKTLNHLG TNFQLMGYRYSTSGFYTLSDT MYKHMDGYEFNDGDDEDTPM WSRYYNLLYTKRGKLQSLISKT RLLSENRRKGRVVQAETLEAA GHVLLLTSLPEDEYSAEQVADC YRLRWQIELAFKRLKSLLHLDA LRAKEPELAKAWIFANLLAAFL IDDI\SHRWISPPERIPSARKWT
25235	55603	A	25373	1	2754	
25236	55604	A	25374	1	652	
25237	55605	A	25375	1	1800	

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25238	55606	A	25376	1	2187	MAGPRYPVSVQGAALVQIKRL QTFAFSVRWSDGSDTFVRRSW DEFRQLKKTLKETFPVEAGLLR RSDRVLPKLLGQASLDAPLLGR VGRTSRGLARLQLLETYSRRLL ATAERVARSPTITGFFAPQPLDL EPALPPGSRVILPTPEEQPLSRA AGRLSIHSLEAQSLRCLQPFCTQ DTRDRPFQAQAQESLDVLLRHP SGWWLVENEDRQTAWFPAPYL EEAAPGQGREGGPSLGSSGPQF CASRAYESSRADELSVPAGARV RVLETSDRGWWLCRYAGAGPE ELDTSARNAGALTRRREIRDAA TLLRLGLAYGPGGMSLREVTA WAQLHDVATLSDVALLKRLRN AADWFGILAAQTLAVRAAVTG CTSGKRLRLVDGTAISAPGGGS AEWRLHMGYDPHTCQFTDFEL TD\SRDGER\LARFAQPPDEIRIA DGEFVWRPKCIRSLAFGEADYI VGVHWRGLRWLTAEGMRFDM MGFLRGLDCGKNGETTVMIGN SGNKKSP\GFPFRARFIAVSLPPE KALISKTRL\LSENRRKGRVVQ AETLEAAGHVLLLTSLPEDEYS AEQVADCYRLRWQIELAFKRL KSLLHLDALRAKEPELAKAWIF ANLLAAFLIDDII\SHRWISPPEV PDPKRRTNSLWRITKMVIWSLQ VAIRGTVSLTAPSLCNSACCCC VSTNSATTLNDFAFARSVIDLTI
25239	55607	A	25377	2	333	RLGVWQDILSRRASCYHGMEV WDKDSFGHISFDDQSMGYSHL GHIVENSVIHYA\ARLVIGADGV DSWLRNKADIPLTFWDYQHHA LVATIRTEEPHDAVARQVFHGE AFW
25240	55608	A	25378	3	235	VAVLEQRVHEPLAANAPPQLR VS/ARLGVWQDILSRRASCYHG MEVWDKDSFGHISFDDQSMGY SHLGHIVENSVIHYA
25241	55609	A	25379	1	774	
25242	55610	A	25380	1	1076	

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25243	55611	A	25381	1138	1737	SVSTEPSVAAFSSIKLRQDPP/H DNLHHQYN*GDIAFC\FTPYFH NCLCQS*WARAFQ*RANEF*R MNCTQLARTSGSHHLIPLTLRF* QICISSGQLIQYSVVCRFIHPPEH RLTIHPLAGQGVNLGFMDAAE LIAELKRLHRQGKDIGQYIYLR RYERSRKHSAALMLAGMQGFR DLFSGTNPAKKLLRDIGLKLAD
25244	55612	B	25382	1	735	
25245	55613	B	25383	1	1941	
25246	55614	B	25384	847	849	
25247	55615	A	25385	1	1227	
25248	55616	A	25386	324	1533	EGFMEHQRKLFQQRGYSEDLL PKTQSQRTWKTFNYFTLWMGS VHNVPNYVMVGGFFILGLSTFS IMLAIILSAFFIAAVMVLNGAAG SKYGVPFAMILRASYGVRGAL VPGLLRGGIAALMWFGLQRGS PFYDLIQTALSSPHKVTIEQFYR EVGVFLGIALIAVVISVLNNFFV SHYVFRWRTAMNEYYMANWQ QLRHIKGRTAFINAIMTLIAFLP VLVTLSAHVPELPIIGHIPYGLVI AAIVWSLMGTGLLAVVGIKLP GLEFKNQRVEAAYRKELVYGE DDATRATPPTVRELFSAVRKNY FRLYFHYMYFNIARILYLQVDN VFGLFLLFPSIVAGTITLGLMTQ ITNVFGQVRGAFQYLINSWTTL VEL\MSIYKRLRSFEHELDGDKI QEVTHTLS
25249	55617	A	25387	1526	1683	
25250	55618	A	25388	2709	2918	CWCFWHRRSCCGSVRYALSAV PGCQCPET*RRRFPHSAF*RFRS SETGQTGAYVSGPDLQPERLQR LWC
25251	55619	A	25389	1	1812	
25252	55620	A	25390	134	386	RLKPSAAIRRRVSSSRISTPLNPA STTAFVGTDCA\IPRLRATSGLA GSPLIQNRFCRARQPRWSAPVA RHAAVYARHRWNQII

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25253	55621	A	25391	181	1630	RIRQFCFYHHCVLTLAICAFIVIT LTIWVSFRVSVLVFAMADDIKV AVVGAMSGPIAQWGDMEFNG ARQAIKDINAKGGIKGDKLVGV EYDDACDPKQAVAVANKIVND GIKYVIGHLCSSSTQPASDIYED EGILMISPGATNPELTQRGYQHI MRTAGLDSSQGPTAAKYILETV KPQRIAIIHDKQQYGEGLARSV QDGLKAANANGVFFDGITAGE KDFSALIARLKKENID\FVYYGG YYPEMGQMLRQARSVGLKTQF MGPEGVGNASLSNIAGDAA\EG MLAPVLITVDQPFVQAGFQPLR RLLPAHETGRRTRAYGVGRLT RQIRRQIATTFRHNAQAAESKD FQWYRCDPCQLFHLMNRQHAR QHHASNVKMAMIKVNRLFIGR RSLHRYVALNMRITLGGVLHH GEVGEDQRVGTQLRRHIHGAL PTGVTVRMRKSVNRDVKFAA MLMDKTHRFLQFFLGKVKAGE
25254	55622	A	25392	2	505	
25255	55623	A	25393	1	2038	
25256	55624	A	25394	188	1771	GKQTSTSPAGWENSLRMRYT\ MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK TTGTARYAYEWHEEAPNAAYG YIVGSAIAKGRLTALDTDAAQK APGVLAVITASNAGALDKGDK NTARLLGGPTIEHYHQAIALVV AETFEQARAAASLVQAHYRRN KGAYSLADEKQTVNQPPEDTP

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25257	55625	A	25395	356	849	GSACRVREIPRPASQMP/HTLPA GSRPPGSEAEPGPEAAPPPARRE AHQIPRPRRGHLPSSPGPRTHVA AHNIRVVTEAHADSHALLSDLG AAPFVVMSRILRVDGDEDPPHV DESIQPTTENAVVFRPVQLTSAI ETGGKEEPYGLSAASLGRAESS AASLAGRR
25258	55626	A	25396	154	379	LVPRLKLGDLPSEINPLSSCSLV REKDPPTTSCTHT\TNPRNISPIS NPDSTGNRTVQLTW*PLPEPLE LWPKAL
25259	55627	A	25397	4761	5127	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQT\TSPRNISPISNPHTR TSKRLNRSGQAFLQNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL
25260	55628	A	25398	1	753	MGSWLQGLRAMVFALNYMVT RVRNKKDPPTTSGPQT\TSPRNI SPISNPR/PKETRFICGPKTPAPL MDWEGSLPLMFNHCRDTSLIIH PCFQGVRPCRDACLSPSPLAASP AFLGKGQVPLNPFFTLSGKSRF SGGGASTPTPSFHVSTPSLLFW GRGKYPSTPSSPLVASPAFLGK GQVPLNPFFTLSGKSRFSGEGA KAPETITDAELRVTLTVEAAVC STIALSLGWEILPRHWGKEEVT KTIYYPVIP

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25261	55629	A	25399	174	2238	LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQT\TSPRNISPISNPRQR RHILSMDPKLRRRSWTWVGSLP LVFNHCRDASLIIHPGFRGVRPR RDVCLGPSPLATITDAELYVTL TVEGKSIPFLIDTEATHSTLPSFK GPVALASIHVQNVQIKRDKEGH YIMVKGSIQQEELTILNMYAPN TGAPRFIKQVLNDLQRDLDSHT IIMGDFNTPLSTLDRSTRQKVN KDIQDLNSALHQADLIDIYRTL HTKSTECTFFSAPHRTYSKIDHI VGSKALLSKCKRTEIIINCLSDH SAIKLELRIKKLTQNHSTTWKL NNLLLNDYWVHKEMKAEIKM FFEINENKNTTYQNLWDTFKAV CRGKFIALNAYKRKQERSKIDT LTSQLEELEKQEQTRSKASRRE EITKIRAELKEIETQKTLQKINES RSWFFEKINKIDILLARLIKKKR EKNQIDAIKNDKGDIATDPTEIQ TTIREYYKHLCPNKLENLEEMD KFLDTYTLPRLNQEEDESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AKFYQRYKEELVPFLQKYKEEL VPFLLKLFQSIEKEGILPNSFSEA SIILIPKPGRDTTKKENFRPISLM NIDAKILNKILANQIQQHIKKLI HHDQVGFIPGMQGWFNIRKSIN VIQHINRTKDKNHMIISIDAEKA FDKIQQPSC
25262	55630	A	25400	3	267	EKDPLTTSGPQT\TSPRNISPISN LRLFAFTWTDPDTHQAQQITW AVLPQGFTDSPRYFSQAQISSLS VTYLSIILIKTHVLSLPIMSD
25263	55631	A	25401	167	408	LGSRTFPWEINPPSSCSLLREKD PPTTSGPQT\TRPRNISPISNLVS GLFLLSSPTSLTIPQPLSSFNLDD TLQSLPSLNF
25264	55632	A	25402	142	441	LRLGDLPWEINPLSSCSLLCEKD PPTTSGP\PRNISPISNPVSGLFLL SSPTCLTIPQPLSPFNLGATLQSL PSLNFNSFHFLVETKETRFIRGP KTPAP
25265	55633	A	25403	79	381	LGSGDLPWEINPLSSCSLLREKE PPTTSGPQT\TRPRNISPISNPELA TLAGNLATGPRNARSPGFLLSH VLSVWDPTENQTVQLTWQPLP QPLELWPKAL

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25266	55634	A	25404	1	511	MWKGPKGLDMYGKSSVSPKTS DILGRDTLLLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLPWEINPLSSCSLLHE KDPPTASGPQT\TSPRNISPILNR VSEVSDHAGTPALVLHP
25267	55635	A	25405	570	1182	LGSGDLPWEINPLSSCSLLHEK DPPTTSGPQT\TSPRNTSPISNLH ALKGLKPAITRLLQHGLLKPINS PYNSPILPVLKPDKPYKLVQDL CLINQIVFPIHPVVPNPYTLLSSI PPSTIHYSVLDLKLAFFTIPLHAS SQPLSAFTWADPDTHQVQQIT WAVLPQSFTDSPHYFSQAQISS LSVTYLSIILIKTHVLSLPIVSD
25268	55636	A	25406	489	615	LRNTWNSPRLMACALHSGSPSC TWGPYS*SGLSENLASQRVCPP YQNENVGRVRDTEIKEHCYEES SYRAATQIQVRKVGIITEPYPFM ASLRTHCIICETCYEMKISFSKS LNPLEKNKKSQPANCAVKEVS EQLRRRQAFSVAAGLKGKGSP AQSIRKNLQKPYQHFQTLQQLL PLQWAPCYGPSNFATHGTHQG LWLVLSTVAAQAVPGALIAEA TALLAWIQGAVS
25269	55637	A	25407	579	715	LGSGDLPWEISPL\SCSLLHEKD PPMTSGPQT\TSPRNISPISNLR
25270	55638	A	25408	1553	1896	
25271	55639	A	25409	964	1332	SCRFIRIYQGACCNLHPGEINSH VAHTKPVWWSLHTDTHENCHL NTAVFFYHWLALEFFLNPLRR/ CSC*HSLPGQFPVSLCLRVLSVD CAHPWGKPEAPGS*HPGPWQFS SLPSPLWPLYQHP
25272	55640	B	25410	1	717	
25273	55641	A	25411	590	1142	PNSSWMRGEPKKDPPTTSGPQT \TSPRNISPISNPR/PKETRFICGP KTPAPLMDWEGSLPLMFNHCR DTSLIIHPCFQGVRPCRDACLSP SPLAASPAFLGKGQVPLNPFFTL SGKSRFSGGGASTPTPSFHVSTP SLLFWGRGKYPSTPSSPLVASP AFLGKGQVPLNPFFTLSGKSRF SGEGA

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25274	55642	A	25412	1	790	MGLVHLQRQSYWTVQRSSINH FLGCNPHTGKDKTLYMRWTKS FRKVEDPPTTSGPQTDQPKKHL TKFKSETKETRFIHGPKTPAPV MDWEGSLPLVFNHCRDASLIIH SHFKGVRPRRDACLGPSPLAAS PAFLGKGQVPQPLISLCPDPLFP HPNLISLRPNPLCPHPDLVSLCP DPFPAFLEAHKNFQTPEPQQPGI PPEPPPPGACYKC/HEI*PPGQG MPAAQDSS*AMS/LSVRDPTGN QTVQLTWQPLPEPLELWPKAL
25275	55643	A	25413	1	736	MQAMEKWKREAKVETEKDQK NQYQQTWLSDSASGYRYTKLP FYFRHNNLIPALAHLLFLDSLYS DLLTAAFFMQFWLSAQMSSDQ RGLPGYLLWAEEISLLEISELTS GKQDSSWPEVKAGLKKEANYL SSDSARLHPGEINSLVAHTKPV WWSLHMDTHEIWCRDSNWGD LPWEINPLSSCSLLHEKDPPTTS GPQT\TSPRNILPISNPPSSKHQE KPPEAISTLPNAAATAAAAVGS LLWSL
25276	55644	A	25414	1644	2010	LGSGDLPWEINPSSSCSLLREKD PPTTSGPQT\TSPRNISPISNPHTR TSKRLNRSGQAFLQNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL
25277	55645	A	25415	1	1035	MGKEYSLDVKKSIKVFKDNRS QGNRLQKLGLEDTDREDAMGF GSHRAKLTVVAALGACHCPEN EGQTVLPSSTSGRSDKRERVSA GYTPPFFVKEGVPSPLFKLHVV RCCSIQSHHSRRSQNCAEDVIR KTKTDQAVSSMSSAPVTVQQL NIIPALLVALTCGWAFCLMVSQ EQYDEASKQAASFSNNAVIPVY MSHMSKTLYKSEVFPINTYAQK ICFIAHTKPVWWSLHMDAHEI WCRGRRSTDLPWE\INPLSSCSL LREKDPPMTSGPQT\TSPRNISPI LNQELATRAGNLATRPRNACSL GFLLSRISSVWDPT*KFGLVQLT LGKPLPEPLELWPKAL
25278	55646	A	25416	174	393	LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQT\TSPRNISPISNPGET KETRFIRGPKTPAPVMDLGRQP SLGV

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25279	55647	A	25417	2	4574	WDVLGAVIGTECGTIESGLSMV FLKDGERKLCTPSMDTTGYGN LRFYFVMAKWIYIPENVVKGR KEIILVLDFTWCMVHRGICDPG NSHENDIILYAKIEGRKEHITLD TLSYSS/L/SSLYWPVMSQILFW QRTVH*TWL\QL*DGIPDIPNVY F*KLWQFQALLLP*LLLYPWC* SQLWLWCLGQW*GPGFQQRW AASANYIFP*QLTIQNNLRRTTR *CKAVWNSVQMVATVSFFPER RCMGY**DYHDICA
25280	55648	A	25418	1	363	
25281	55649	A	25419	1	301	
25282	55650	A	25420	2	309	
25283	55651	A	25421	3	512	YIGPSCLKFCSGRGQCTRHGCN\ CEMASQTFPMFISESFGSSRLSS YHNFYSIRGAEVSFGCGVLASG KALVFNKDGRRQLITSFLDSSQ SRIISVELPGDAKQFGIQFRWW QPYHSSQREDVWAIDEIIMTSV LFNSISLDFTNLVEVTQSLGFYL GNVQPYCGHDWTL
25284	55652	A	25422	2	878	
25285	55653	A	25423	1	750	
25286	55654	A	25424	1	1404	

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25287	55655	A	25425	1	2506	GCSRLLVTVDLNLTNAEFIQFY FMYGCLITPNNRNQGVLLEYSV NGGITWNLLMEIFYDQYSKPGF VNILLPPDAKEIATRFRWWQPR HDGLDQNDWAIDNVLISGSAD QRTVMLDTFSSAPVPQHERSPA DAGPVGRIAFDMFMEDKTSVN EHWLFHDDCTVERFCDSPDGV MLCGSHDGREVYAVTHDLTPT EGWIMQFKISVGCKVSEKIAQN QIHVQYSTDFGVSWNYLVPQC LPADPKCSGSVSQPSVFFPTKG WKRITYPLPESLVGNPVRFRFY QKYSDMQWAIDNFYLGPGCLD NCRGHGDCLREQCICDPGYSGP NCYLTHTLKTFLKERFDSEEIKP DLWMSLEGGSTCTECGILAEDT ALYFGGSTVRQAVTQDLDLRG AKHDYILLPEDALTNTTRLRW WQPFVISNGIVVSGVERAQWA LDNILIGGAEINPSQLVDTFDDE GTSHEENWSFYPNAVRTAGFC GNPSFHLYWPNKKKDKTHNAL SSRELIIQPGYMMQFKPFGFCRS DSWQLVQTQCLPSSSNSIGCSPF QFHEATIYNSVNSSSWKRITIQL PDHVSSSATQFRWIQKGEETEK QSW\AIDHVYIGEACPKLCSGH GYCTTGAICICDESFQGDDCSV FSHDLPSYIKDNFESARVTEAN WETIQGGVIGSGCGQLARYAH GDSLYFNGCQIKRAATKPL\DL
25288	55656	A	25426	146	10561	GGGGGGGGGGMERSGWARQT FLLALLLGATLRARAAAGYYP RFSPFFFLCTHHGELEGDGEQG EVLISLHIAGNPTYYVPGQEYH VTISTSTFFDGLLVTGLYTSTSV QASQSIGGSSAFGFGIMSDHQF GNQFMCSVVASHVSHLPTTNLS FIWIAPPAGTGCVNFMATATHR GQVIFKDALAQQLCEQGAPTD VTVHPHLAEIHSDSIILRDDFDS YHQLQLNPNIWVECNNCETGE QCGAIMHGNAVTFCEP
25289	55657	A	25427	1	296	

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25290	55658	A	25428	1	557	MARSLGVLVALPFPLPVGFNAE EAHNIVKEFSPGKSHPRESLSQQ RETLVQAGAFHWFGWRGKEK LKPKFNTFGRLPNEMLEQWLSP TNQCVDGV/LKGGED\YNHNNI NQWTASIVEQSL\THLVKLGKA YKYIVTCAVVQKSAYGFHTASS CFWDTTSDGTCTVRL/WENRT MN\CIVNVFCHCLFVL
25291	55659	A	25429	178	2270	VRRLFCVQTGGSPVGRGSLHHL WLVFSHVLSLLCSPCLLAPGM WGFHDRDLVLRKALYTMMRT GAEREALKRRWRWQQTQQNK ESGLVYTEEEWEREWTELLKL ASSEPRTHFSKNGGTGGGHLPP EGKPLHGCSSLLRSGKGGHVK AEPSRLQQSQAKPPLTSQIRALH FPIPSQINEKPGAGHWSAKLHFP YWQLGEAGEEEGSSPPDIMRCL LTCLSVPSTAVIPLTDSEHKLLP LHFAVDPGKDWEWGKDDNDN ARLAHLILSLEAKLNLLHSYMN VTWIRIPSETRAPLAQPESPTAS AGEDVQSLADSLDSDRDSVCS NSNSNNGKNGKDKEKEKQRKE KDKTRADSVANKLGSFSKTLGI KLKKNMGGLGGLVHGKMGRA NSANGKNGDSAERGKEKKAKS RKGSKEESGASASTSPSEKTTPS PTDKAAGASPAEKGGGPRGDA WKYSTDVKLSLNILRAAMQGE RKFIFAGLLLTSHRHQFHEEMIG YYLTSAQERFSAEQEQRRRDA ATAAAAAA\PPPPPRP/ERPPRRP ETEGVPVPERASPGPPTQLVLK LKERPSPGPAAGRAARAAAGG TA/CPGGRRAACERQRTSAWPQ PPGASAPERHPRAGVGRAGRG VRAGRGGAAAVRHVPAAEPLA VVAELQPGARRRPAHRQHGRV AGARGARGPTGRGGDRGGGRA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25292	55660	A	25430	404	1116	SLGPLMLSGQKLQTSYTMEYY AAIKR/DKIVSLVGTWLELEAIIL KKLMQEQKTKYHMFLLDSLSH GMQQAERVLIADGTMLLSAQY QFENNLLVPILRVSFRKSLQRKE EPGRKAKKSQTSGEGIKKRRFW FEWKEPVALSSQGWYEAKGSE RPEKGHLGLLRAESFQDLRTAL ISKPYFSVPGKVGPAIKCPETLP ELKTYPQYGVTLGEPVRNEQQ QASSFPSLSNTHLSKKRNES
25293	55661	A	25432	1571	1782	WLLCRLPPRVPDQL*WCGCQPE KCAGAEFQDGSAMPLPSRTCPH SPRMCTGWSTTCATTDSATTA CPLAL
25294	55662	B	25433	69	1160	
25295	55663	A	25434	14	437	LQTSHPYPTTSKC/PPP/CEKPSP TSL/C*RRSAPHLQPPE
25296	55664	A	25435	782	997	MMLCQLQRPV/CGSHSCSRG/C PPAQ/CPSPVPVPSPQSAFPVPQS PSSTCPNPSHPIHPIPMVPSSWSG HWDSK
25297	55665	A	25436	1117	1815	GDAHTEQCLQNLYPRGSRPPLP LESHPSSSKHSPKACPTGRS/CG PWK/CPGPEVRP*PPPSCTR*DP HFRGLLEGLLEPRHVTCLALCG PQRVLYWPVYHERLGEGWDW CPSSWPGA

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25298	55666	A	25437	1261	2757	ALGKDEKSQGPPIQTGGLGPRL FRLPSSQGQERRFAAAKAPSSL VPHNGSPLSCWRGLREEGGLSL ATLWTPCGVGSGVPAAPPSAW CDLGKLLVCWRGQNRGPRSTQ TDVRRHEARSRQRRRKCVAAP VAPRSRRWRCPAALAAPAVAV PVVFALIFLLGTVGNGLVLAVL LQPGPSAWQEPGSTTDLFILNL AVADLCFILCCVPFQATIYTLD AWLFGALVCKAVHLLIYLTMY ASSFTLAAVSVDRCAVPG\HPL GRAVGAGVGGGVLNVGLVWL LAALFSAPYLSYYGTVRYGALE LCVPAWEDARRRALDVATFAA GYLLPVAVVSLAYGRTLRFLW AAVGPAGAAAAEARRRATGRA GRAMLAVAALYALCWGPHHA LILCFWYGRFAFSPATYACRLA SHCLAYANSCLNPLVYALASR HFRARFRRLWPCGRRRRHRAR RALRRVRPASSGPPGCPGDARP SGRLLAGGGQGPEPREGPVHG GEAARGPE
25299	55667	A	25438	1	1624	MKDKSKTLGLEASIFRNNWKC KSIFEGLKGHQEGYFSQMIISYE KIPSYRKSKSLTPHQRIHNTEKS YVCKECGKACSHGSKLVQHER THTAEKHFECKECGKNYLSAY QLNVHQRFHTGEKPYECKECG KTFSWGSSLVKHERIHTGEKPY ECKECGKAFSRGYHLTQHQKIH TGVKSYKCKECGKAFFWGSSL AKHEIIHTGEKPYKCKECGKAF SRGYQLTQHQKIHTGKKPYEC KICGKAFCWGYQLTRHQIFHTG EKPYECKECGKAFNCGSSLIQH ERIHTGEKPYECKECGKAFSRG YHLSQHQKIHTGEKPFECKECG KAFSWGSSLVKHERVHTGEKS HECKECGKTFCSGYQLTRHQV FHTGEKPYECKECGKAFNCGSS LVQHERIHTGEKPYE\CKECGK GFS\GGYHLTQHQKIHTGEKPF KCKE\CGKAFSWGSSLVKHERV HTNEKSYECKDCGKAFGSGYQ LSVHQRFHTGEKLYQRKEFGK TFTHGSKLVHERTHSNDKPYK YNECGEAFLWTTYSNEKIDTDE

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25300	55668	A	25439	32	447	VLGGSMMFREGQRGNRQKGP KKRRNLALSSALLASTA\PAGG QPRHWRPG*CCLRQQL*PLQGN WAPVSPLQGHRSQLRAGYSISS FLQMFAP*VQGAARAQPAPGA AVPRGSGRQGGPRAVDLHGFR VGWNRLRAASM
25301	55669	A	25440	1	858	
25302	55670	A	25441	147	1088	SRTTYKGKSSFQTYSDYLRWES FLQQQLQALPEGSVLRRGFQTC EHWKQIFMEIVGVQSALCGLVL SLLICVAAVAVFTTHILLLLPVL LSILGIVCLVVTIMYWSGWEMG AVEAISLSILVGSSVDYCVHLVE GYLLAGENLPPHQAEDARTQR QWRTLEAVRHVGVAIVSSALT TVIATVPLFFCIIAPFAKFGKIVA LNTGVSILYTLTVSTALLGIMAP SSFTRTRTS/CPQGPGCRAAGRG PGAGCLPRAPAERL*DSPARRG LPIARDGLWTLAPLVPWVGDR SCFPARLQLAVSPGLGPGRPAG
25303	55671	A	25442	1	1596	MGVSVRVDCGCARASEFLGRP RGAVRGADPGSGLTETCAQSR TWARARSKGGFRLTLNFYGPR YPSEGTSRGQRSEALPFLDIQHP TPLGRPRMLQSRGEMVRSWGP VVEGKLGFCPPLTVFPGGLRGP HPGLAGERENFARGAKQEACL LQGPGDAGLTHPCPATGYFPEA SCTSRSIRMFINSQERQLADMSL FIADSWLCYSGIICWKSLEHQR GASLSCVYMEGKGGNIWMKAS NVLPLCQMLPTSGHSKSDLFGG LAVEKQMRQDHHILLHDRSGF QLAVTSPLLTRLGKGHIIQVPV YVLDAPSRWLGGLRLFRDSSCG LVLSLLICVAAVAVFTTHILLLL PVLLSILGIVCLVVTIMYWSGW EMGAVEAISLSILVGSSVDYCV HLVEGYLLAGENLPPHQAEDA RTQRQWRTLEAVRHVGVAIVS SALTTVIATVPLFFCIIAPFAKFG KIVALNTGVSILYTLTVSTALLG IMAPSSFTRTRTS/CPQGPGCRA AGRGPGAGCLPRAPAERL*DSP

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25304	55672	A	25443	1	2355	MDHPGFREFCWKPHEVLKDLP LGSYSYCSPPSSLMTYFFPTERG GKIYYDGMGQDLADIRGSLEL AMTHPEFYWYVDEGLSADNLK SSLLRSEILFGAPLPNYYSVDDR WEEQRAKFQSFVVTYVAMLAK QSTSKVQVLYGGTDLFDYEVR RTFNNDMLLAFISSSCIAALVYI LTSCSVFLSFFGIASIGLSCLVAL FLYHVVFGIQYLGILNGVAAFV IVGIGVDDVFVFINTYRQATHL EDPQLRMIHTVQTAGKATFFTS LTTAAAYAANVFSQIPAVHDFG LFMSLIVSCCWLAVLVTMPAA LGLWSLYLAPLESSCQTSCHQN CSRKTSLHFPGDVFAAPEQVGG SPAQGPIPYLDDDIPLLEVEEEP VSLELGDVSLVSVSPEGLQPAS NTGSRGHLIVQLQELLHHWVL WSAVKSRWVIVGLFVSILILSLV FASRLR\SASRAPLLFRPDTNIQ VLLDLKYNLSAEGISCITCSGLF QEKPHSLQNNIRTSLEKKRRGS GVPWASRPEATLQDFPGTVYIS KVKSQGHPAVYRLSLNASLPAP WQAVSPGDGEVPSFQVYRAPF GNFTKKLTACMSTVGLLQAAS PSRKWMLTTLACDAKRGWKF DFSFYVATKEQQHTRKLYFAQS HKPPFHGRVCMAPPGCLLSSSP DGPTKGFFFVPSEKVPKARLSA TFGFNPCVNTGCGKPAVRPLVD

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25305	55673	A	25444	1	1737	MLYAAECLRNVMKLQVIPSAL NEALQAQSTWSDLGLASHALS STWCLHGESAAWSQPAVVECG QPRDQLQTHSEAWLCALVATF SQELEQFAVTGAQISDRQGHAV CTAPPRGRPSTLMTNLVCASSA DECGGGKTETQTAGGRLQGAE TRSRGQLTRLITRTQAAEPRWF LQLLKRSANRSRALTRPFSGLSS DGARRLRLSFVSAVSSADTKPT VPVSSDSSGRDGCGETRAEAGP GGPHVAQPQRVAPPAAAARDF RKPRGLNRQNVSP/PGPGEQGP G/PRPQKPAGRAP\PEPQGEPGL GLFPR\GRPPRSFPGSPADPAAS VSHTQGPSPDTGLPGTCQNRLP NPAAVDEQTCTRGSLNCRLSRS PRVSERRGPEGTPGRRPAAPPQ CAGTRGLSPRADLGAAIRTPRA PYRPHGQGRPSRHNCDSVSSQG WPPHSCWWKTTSNGMPWKAS FCSRTAQPANQNTGNHERGLRS VAMFGDRASREATPALSLCESQ GCFEDEKEVFSPEPHVETSDEPL PICSGPGDGWGDPIARPGRGNN LSPGTSAWEVPRWIRVTGEDW LSTGPAECVFINDLTT

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25306	55674	A	25445	2	1642	LLSSISAWFGPPASTPAFTMSIR VTQKSYKVS\TSCPRAFSTRSYT SRPGSRISSSSFSRVGSSNFRGDL GGGYGGASG\MGGITAVTVNQ SLLSPLVPEVDPNIQAVRTQEKE QIKTLNNKFASFI\DEVGFLEQQ NKMLGTKWSLLDQQKTA\RSN MDNMFESYINNLRRQLETLGQ EKLKLEAELGNMQPLVEDFKN KYEDEINKRTEMENEFVLIKKD ADEASMNKVELGSRLEGLTDEI NFLMQLYEEEIRELQSQISDTSV VLSMDKSRSLDMDSIIAEFKAQ YEDIANRSRAEAESMFQIMYEE LQSLAGKHGDDLRRTKTEISEM NRNISR\LQAEIEGLKGQR\ASL GGRPLQDAE\QRGKSWPIK\DA NAK\LSEAGSPPLQAGPKQDMG R\QLREY\QKLMNVKAGPWTIE\ IATYQESCLEGEEEPGWSLGCQ NMSI\HT\KTTQRGYAGRPEPPP MGGFTSP\GFSYKPGAPGFGSG AGS\SSFNRHQLSPGAVVVKKIE TRDGKLVSES\SNVLPKVKQLR QPLPSLPLLRCPRGLGKEAPYP
25307	55675	A	25446	1	1280	MAYLCNAICMTHMVTLDPVDQ ALPGATTATSVPGPQCDASCM MLFAVVPFNGIALAATQGAQS MLPPRVQGSLSSKPSTRRGRDA PGLQVSQAPPPRRGFAVGRRYS PPALAPGRCAAPHGGGRKELPT RRPGHGMAPKFPDSVEELRAA\ GSESFRNGQYAEASALYGRAL RVLQAQGSSDPEEESVLYSNRA ACHLKDGNCRDCITDCTSALAL GPFSIKPLLRRASAYEALEKYP MAYVDYKTVLQIDDNVTSAVE GINRGPGLKEDTTQKRWNSLPS ENHKEMAKSKSKETTATKNRV PSAGDVEKARVLKEEGNELVK KGNHKKAIEKYSESLLCSNLES ATYSNRALCYLVLKQYTEAVK DCTEALKLDGKNVKAFYRRAQ AHKALKDYKSSFADISNLLQIEP RNGPAQKLRQEVKQNLH

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25308	55676	A	25447	1	1297	MHLLSAYFVPGSMLVGSGYM MVNITDVSPPSWSFLCSMLITTT QGAQSMLPPRVQGSLSSKPSTR RGRDAPGLQVSQAPPPRRGFAV GRRYSPPALAPGRCAAPHGGG RKELPTRRPGHGMAPKFPDSVE ELRAAGNESFRNGQYAEASAL YGCALRVLQAQGSSDPEEESVL YSNRAACHLKDGNCRDCIKDC TSALALVPFSIKPLLRRASAYEA LEKYPMAYVDYKTVLQIDDNV TSAVEGINRMTRALMDSL\GPE W/RALKLPSFPLVPVSAQKRWN FLPSENHKEMAKSKSKETTATK NRVPSAGDVEKARVLKEEGNE LVKKGNHKIAIEKYSESLLCSN LESATYSNRALCYLVLKQYTEA VKDCTEALKLDGKNVKAFYRR AQAHKALKDYKSSFADI\SNLL QIEPR\NGPAQEVAGREVKQNL
25309	55677	A	25448	3	491	GITFTHSPAATGGGAQRVRRRD PPPGVQLRNMAQETNHSQVPM LCSTGCGFYGNPRTNGMCSVC YKEHLQRQNSSNGRISPPATSV SSLSESLPVQCTDGSVPEAQSAL DSTSSSMQPSPVSNQSLLSESV\ ASSQLGQYICGTKAVPETEDVQ ASVSDTAHV
25310	55678	A	25449	1	860	HLLLLAIDYNLPIAGVLMESQY LGASPKRLVIPNLYAHRKSLAT LEPYAPRRPMPIARRYAIPYMS HHNGYIGDVYYRLTVEEKKSSF IARRSILTTEFTIRRTKKVPVPSI NMSSASPLEDESRPSAGVQLRK GRYRLLRDRYRPGCNSVGESPR KSSFSDDIMATESRESIFAEEPR TGEHSVRGPVSNQSLLSESVAS SQLDSTSVDKAVPETEDVQDSL NASPTKQQCG/DVQTVDLYSNN KELFAQKCYRHRYISRLKKCCL CHELVPRDTIKSPESLSVGS
25311	55679	A	25450	880	1196	SPTTRRGTPGTCLKPTACAGAA *PGCSARRTCASAAPLSTCPPSS CAAPPPAPAAVPSTPRPTSPSPW AAPASPSRRRTQTASTPASTNR APSSCWAPTTRPLAP
25312	55680	A	25451	254	579	IEKISLEPKNRPSPQIPNLVGP/R LFLVPGDFQSQVPNFLPFKPSSG PHPAAGKGQPFSFLPAWRSTGP ERATPGPGRPAACSALEAPSLR GPSGYSAQEPPRRPISARI

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25313	55681	A	25452	6	1442	RSELIRHSWPRHAQLRGARART AVSIRECISVHVGQAGVQIGNA CWELFCLEHGIQADGTFDAQAS KINDDDSFTTFFSETGNGKHVP RAAMIDLEPTVVDEVRAGTYR QLFHPEQLITGKEDAANNYAPG PPTPGGKESIDLV\LDRIRKLTD ACSGLQGFLIFHSFGGGTGSGFT SLLMERLSLDYGKKSKLEFAIY PAPQVSTAVVEPYNSILTTHTTL EHSDCAFMVDNEAIYDICRRNL DIERPTYTNLNRLISQIVSSITAS LRFDGALNVDLTEFQTNLVPYP RIHFPLVTYAPIISAEKAYHEQL SVAEITSSCFEPNSQMVKCDPR HGKYMA\CCMLYRGDVVPKD VNVAIAAIKTKRTIQFVDWCPT GF\KVGINYQPPTVVPGGDLAP VQRAVCMLSNTTAIAEAWARL\ DHKFDLMYAKRAF\VHWYVGR GDWKKGEFSEAREDLAALEKD YEEVGVDSVEAEAEEGEEY
25314	55682	A	25453	3	618	SSAGREPDPSDLPRRLCFTHRLP AARRWVQLCVHASPEPGGQGV CPGRSERMVIRVFIASSSGFVAI KKKQQDVVRFLEANKIEFEEVD ITMSEEQRQWMYKNVPPDKKP TQGNPLPPQIF\NGDRYCGLLVS FSVICIKNPNWHNLFLLIPWSGI NPYCEQDSSFSENVGDEILKNS GVPRDFTSILIQKERKSEKVKG VDQGHR
25315	55683	A	25454	3	424	SWTMAATIQAMERKIESQAAH LLSLEGQTGMA*S*GTPPCCPG AAAGSRSSCCAAGSPRSPAASA AARTPAAGSPARPTCPPAGSRT PRLSSRNQPASSRPSRFDLLGKA GEQPAIQSSSPWPESWLPSSTK
25316	55684	A	25456	268	445	
25317	55685	A	25457	3	205	
25318	55686	A	25458	27	272	AKCSGQGPGRVRAQGERADHE CPGAGAGGGGCNSAASAREES SRLISG\SLQMQNVSLASRRKEE EVRAAAAGGAAAGRPRV
25319	55687	A	25459	1	253	
25320	55688	A	25460	2145	2399	

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25321	55689	A	25461	174	1309	HLLCCRAQRRPQTPPAARGLEA CSEGALKMPEAPP\LLLAAVLL GLVLLVVLLLLLRHWGWGLCL IGWNEFILQPIHNLLMGDTKEQ RI\LNHVLAACGSPGNAQSVLG GHLTPNCEQKEW/APLNVGDK KGQDSWDALISREQPALPCLLG NLGAYFGLLQLLRMAR\LLVNQ GARLIHHSRFNPDLCPPSPKRM\ VDFAGVKDKALFQVTL\VCGAS PETFHPPSLKKKYDVGHNWTW VFLDHWKDRYL\PDTLLLE\EC G\LLPEGGQLLLAEQRLSSPGAP \DFL\AHVSREPACFG\CT\HYQI VPWKYRE\VVDGLGRRPI\YKG P\GSEAGALTAPPRPPSRALSPK PGTEGARPWLLLTLVRLRACVL NAKSHARAESLRA
25322	55690	A	25462	2470	3460	SGPCPRCCAECRPYKTRPRSRV PGTHGPGPADHGQPPCCMAGA HPPRPQAWMLLQTHSQDCEGK VGCGGIFCPCYHHCKHTHHHH HHPHHHHYHYHHHNHHQHHH HHHHHHYHHYHSHYHHYHHH HLHHH\HHHHHHPYPHHYHHH RGQDHHPHPHHHH/HHHYHHH HYHHHYHPHHHPHHHHQPQH HHHQHYHHHYHHHHPHHPHH PHHHHHYHYHHHHHHHY\HPY PHHYHHHHHHHHHPHPHHHH/ HHHYHHHPHHNHYHHHHHPH HHHRPHHHHRHQHPHHYHHH HPHPCHHHRLHHHHRHHHYHH TSSVQGPGSQPAGASLPGQACR
25323	55691	A	25463	1	407	DAERQEALGIVRRIGTDTEAAT EPAGATVPAAAAAARIGTVGP QPPAMPRRKRNAGSSSDGTEDS DFSTDLEHTDSSESDGTSRRSA RVTRSSARLSQSSSRISRSCSKS GSLLALRSLLTLPEE*PVVSSSL

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25324	55692	A	25464	3	2539	RILYIPDGHRAPGASQSGNWEH PLLLLEPGNLASSPSMSLAYPHP CGLTIHQEHRRAHEELAYTPND RASSTGHPAFIEDGNPSPVLAFA ASPRPNDSYILKREPPESCEKER VFEEATTRGKYGEGAKQETFTF ALTLVFIQCVINAVFAKILIQFF DTARVDRTRSWLYAACSISYLG AMVSSNSALQFVNYPTQVLGK SCKPIPVMLLGVTLLKKKYPLA KYLCVLLIVAGVALFMYKPKK VVGIEEHTVGYGELLLLLSLTL DGLTGVSQDHMRAHYQTGSN HMMLNINLWSTLLLGMAVSCP DQGPELVPRCPFVQALEKPSWK NLHQQDLFATCYWHNEGESCV SCHGKTLSSKTQGGILFTGELW EFLSFAERYPAIIYNILLFGLTSA LGQSFIFMTVVYFGPLTCSIITTT RKFFTILASVILFANPISPMQWV GTVLVFLGSTQIILDNLKILNTS AKTLLYKTPLSWQELEGERASS CAHKRSASWGSTDHRKEISKLK QQLQRTKLSRSGKEKERGSPLL GDH/VSAGSTEGVPS/RASPQGP LSCDSAPACT/VSLEGLNQELEE VFVKEQGEEELLRILDIPDGHR APAPPQSGSCDHPLLLLEPGNL ASSPSMSLASPQPCGLASHEEH RGAAEELASTPNDKASSPGHPA FLEDGSPSPVLAFAASPRPNHSY IFKREPPEGCEKVRVFEEATHQ
25325	55693	A	25465	845	1316	LSLGDSAQCLLPHASWCQVAG HPAFLEDGSPSPVLAFAASPRPN HSYIFKREPPEGCEKVRVFEEAT S/RRVLTGPFLTSCPDK\NKVHF QP\TGSAFCPVNLMKPLFPGMG FIFRNCPSNPGISSSPGQPQATTS EGSGSLQGLPTAIRAMAAHPYH Q

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25326	55694	A	25466	1077	1506	CDACGRRCRTCRTFCLGLQPAG LDGHHHRHPDCWFPWSPRHR* GMIIDVFSRYSGSEGSTQTLTKG ELKVLMEKELPGFLQILTNEDE PLVTIPFLSHSCSLAYLLTTSGN RVNALLKWLLKLGERWQMTE EGIKGQRSGHGPEQAENPLGDS VPQDTTKDVPLTQHRLHQGLE AGVPKTSVPARPGLPVPALQHA QIPGPCERALLHCHNGPQRLQH SLQGEEQRETHLRGQDWPCTL QMRTLKREVHALPGGRAGGAA REGLGASICETGEHQMTNFQVP RWPPCFPGQAGPVLGTGTRHG LDLLSGRPGTVRKGSSVARIMK EEVTVTKQSAADLRHTGQGPT CCVLSGGRCGSQACSRRPFSLL LGDESEPHGRGPFAAALHHRR NPLNDVMLVGDDAGPAGHFAS VYNPLAWTVTTIVTLTVGFPGV RVTDEAGHPVPSQVSGIQRCLQ GMKAPPVTVTVSGEKGSCLCA SCVLCLEHPYFPLVPWLPPVFR DSVIPSSTSPQEAVLADVGFRN NVPQRAQLKPQKQILTPF
25327	55695	B	25467	31	783	
25328	55696	A	25468	846	1392	PDPAAHRFGHPTLHPGSLRTSS GAGTWYQNPQHHNDHDYYHH HHHHDDHHYHYHHHHHHHHH HHYHHHHHHHHHHHHHHHHH HHHQHHHHHHHHYHHHHHHH HHHHHHHHHHHHHDQHHHHH HHHHHHHHHHHH/HF/HHHDH HHHHHHHDHHHHHHHHHHH HHHHHHHHHHHHHDHHHHH YP
25329	55697	A	25469	181	412	LRSDQQTRKFVSRSSGACSPPTT TELSWPPSLLPSL*FHSPSSQP* MNHSASTTSPLPSFITERESILAT EWDTARN

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25330	55698	A	25470	1	848	MPSLNTIVSPLGSPHTSLIPPML LSANLPFDTTIMIKLQTACSAPI HNLQRPCGENLRTSTFVRRLDR NLVKSPQPGGGGQPSRQWEAR GAEPQGRRDPSEVQ/RPAGRGF GRISRAPRKPSRAPTPTQGLGPP LGAGGQGSLASCRPARKNARPP TRAAAHSAHPHSHWHSHARPQ PQSPSAAGQSGDPWPPARVPPP PLLRLPQRRTAGRTPVDAPARG IFTLSLSSSHSKSSGKHRGARKT PEMWPLFRGSLSKLSRRRKVSP SAALHWRLRRTQKRLCC
25331	55699	A	25471	92	1083	TMRTHGHRKGNITPWGLSGVG GL/ETGRALGEIPNVDEGLMGVI AAVAIVLVSLLFVMLRYMYRH KGTYHTNEAKGTEFAESADAA LQQRERALDSSRDSHLETLGAC PGRNGGGLALQEATPRDPGRR WPPQRPPFAPRRWEKIWAHGPL GSAGQHQLTGRKVLVEGLGCI CMAHTDLQNTSVAKMAINRPN EYAQVSLENDVSCKVKAVQAP QRLHWPSVDADTGGRGAVHIA FPKHVEPETPFAHTIPARNSWT KWSSEHILETLSPQKPALPWAP RQQGRPLGLTAPISKRLGPGDG PEGEAGERLAQAHFINTRPPST GPPGTPAAD
25332	55700	A	25472	73	424	RPGMWSTRSPNSTAWPLSLEPD PGMASACTTMHTTTIAEPDPG MSGWPDGRMETSSPTIMDIVVI *CAIAAEAIVLVSLLFVMLRYM YRHMGTYHTNEAKGTGVADS ADACPAGDPA
25333	55701	A	25473	139	546	RPGMWSTRSPNSTAWPLSLEPD PGMASASTTMHNYHHCRSLIPG M\SGWPDGRMETSTPTIMDIVVI AGVIAAV\AIV\LVSLLFVMVAL TCNRA/HRGTYHTNEAKG\TEF AESADAALQG\DPAL\QDAGDS SRK\EYFI
25334	55702	C	25474	142	408	

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25335	55703	A	25475	44	727	ARAGSRSRGLPFCGTAGPPPKA TLWGGLLRLGSLLSLSCLALSV LLLAQLSDAANNFEDVRCKCIC PPYKENSGHIYNKNISQKDCDC LHVV\DPMPVPGA\NVEAYCLR CECKYEE\RSS\STIKVTIIIYLSIL GLLL\LYMVYLTLVEPILKRRLF GHAQLIQSDDDIGDHQPFGKCT RCASPLPQFEPTCWNKVEYAQ QALESFQVQEQRKSV\FDRACC PQLNLGN
25336	55704	A	25476	11	1323	VVLLVSVNTEAEESEKAATEQR /PLEGTDQTLDVEEEQEESKAA ACGSKKRVVPGIVYLGHIPPHF QPLHVRNLLSAYG/RSPSHYDL WNLKYLHHFTWSHHSEHLAFE RQVC\HRQHLRVEVTQAKCETI FYLQSVEWGQCFLAVDGDLAH PDGSWTFAQRPTEQELRARKA AQPVGKVLNYYPTQLSLECEVP SQPMGTGHSHRGLCQDVKVIN VPVSFVWCALVAGLLVVVPPPP PQAPEAEVSDISLKRGLQREIEQ CRRDIQNFPFPCASEELASQLFP LMEVPQGRGTTGFMNAPLTTS EVRGLKKELKPLLDDPERVAEQ IDQFLGSKLYTWTELMSILGILF SKEERNMICRAAMGAWERDYP AGQNIPAADVTFPARDPQWNN NNAAHQKNMRDLQELIIKGIKE SAPRPQNLTKAFDEQQEKDEGP
25337	55705	A	25477	1	490	GTSGTRPLVSVNMEAEESEKA\ ATEQEPLEGTEQTLYAEEEQEE SEEAACGSKKRVVPGIVYLGHI PPRFRPLHVRNLLSAYGEVGRV FFQAEDRFVRRKKKAAAAAGG KKRSYTKDYTEGWVEV\RDTR\ IAKRVA\AALLK*PMGARRRSP FRYDLWNLKYLHR
25338	55706	A	25478	2	574	

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25339	55707	A	25479	160	1548	KTSSQTLSLALTMFQRLNKMFV GEVSSSSNQEPEFNEKEDDEWI LVDFIDTCTGFSAEEEEEEEDIS EESPTEHPSVFSCLPASLECLAD TSDSCFLQFESCPMEESWFITPP PCFTAGGLTTIKVETSPMENLLI EHPSMSVYAVHNSCPGLSEATR GTDELHSPSSPSILPNKMLSVHV GTAIHNQAALCQSVESYWQCGI QLLTQFQSQSKLGQLLAATCKE LPGPKESRRTAKDLWEVVVQIC SVSSQHKRGNDGRVSLIKQRES TLGIMYRYVLEPLVLTIILSLFV KLHNVREDIVNDITAEHISIWPS SIPKKQMSSRTFMSQEETVCRA AHTPSLPEEKWVEQLIYALVVA AARIMAMWGPNAAWLVFLAA AGPPPLTPPHSPP/PPPPPPALGR WMGPPLRDSASGLPRPPPGRISE DSGAWACGPALCPRPAIPSPAP ALRVPEALRLWGTCSV
25340	55708	A	25480	1	380	FTSPKTARNWGWLMQVRNQR LVLGKAGGKKGSPLEQRGGNG HHGGTRLICALV\LVS\MRPLAT FAEPQTETCTVAPRERQNCGFP/ GVSRPPQCANKGCCFDDT\VRG VPWCFYPNTIDVPPEEECEF
25341	55709	A	25481	3	2367	
25342	55710	A	25482	2	1230	WRRSRRRRPPAPQAGGGDFRA GISPPTGKKSLGLMEPQGNHYR CRCLQVAGSQAWARCVSMPEL VVQKVVGHP/LVLLSVVDHFNR IGKVGIQKCVIGLFWGSWQKK VLDVLNSFAVPFDEDDKDNSM WFLDHDYLENMYGMFKKVNA RERIVGWYHTGLKIHKNGITIN ELMKRYYPNSVLIIIDVNPKDL GLPTEAYISVEEIQDDGTPTLKT FEHVTSEIGAESYLEKVATGKL RINHQIIYELQDVFNLLPDVSLQ EPIKAFYLRTNDQMVVVYLASL IHSVGLTDPFC\VALHNLINNKI ANQDGDKKEGQEKKES/KKDR KADKGKDKDKEKSDVKKEQK NHCLKEKYRFRQDSLPDDPRVL GLELTPPVARQYSPQDLSEIPRH ADFRCDPAHFQLWWSQGETPS

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25343	55711	A	25483	3	1042	DRYCCRCLRVAGSQAWRAGC VAMPELAVQKVVVHPLVLLSV VDHFNRIGKVGNQKRVVGVLL GSWQKKVLDVSNSFAVPFDED DKDDSVWFLDHDYLENMYGM FKKVNARERIVGWYHTGPKLH KNDIAINELMKRYCPNSVLVIID VKPKDLGLPTEAYISVEEVHDD GTPTSKTFEHVTSEIGAEEAEEV GVEHLLPDIKDTTVGTLSQRITN HVHGLKGLNSKLLDIRSYLEKV VTG\KLPINHQIIYQLQDVFNLL PDVSLQEFVKGFYLKTNDQMV VVYLASLIRSVVALHNLINNKI ANRDAEKKEGQEKEESKKDRK EDKEKDKDKEKSDVKKEEKKE
25344	55712	A	25484	257	1566	GLEHLCNPRWPLLFLRAMDST VPSALELPQRLALNPRESPRSPE EEEPHLLS/SLAAVQTLANVIRP CYGPHGRQKFLVTMKGETVCT GCATAILRALELEHPAAWLLRE AAQTQAENSGDGTAFVVLLTE ALLEQAEQLLKFGLPRPQLR/EA YATATA/EEKQVGQL/AAAGIN VAVVLGEVDEETLTLADKYGI VVIQARSRMEIIYLSEVLDTPLL PRLLPPQRPGKCQRVYRQELGD GLAVVFEWECTGTPALTVVLR GATTQGLRSAEQAVYHSIDAYF QPCQDPRLIPGAGATEMALAK MLSDKGSRLEGPNGPAFLAFAR ALKYLPKTLAENAGLAVSDVV AEMSGVHQGGNLLMGVGAEGI INVAQEGVWDTLIVKAQGFRA VAEVVLQLVTVDEIVVAKKSPT HQQIWNPDSKKTKKRPPPVEK

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25345	55713	A	25485	145	1918	PLEYFQRSVSGVPQLLFLEHLC NPRWPLLSLRAMDSTVPSALEL PQRLALNPRESPRSPEEEEPHLL SSLAAVQTLASVIRPCYGPHGR QKFLVTMKGETVCTGCATAILR ALELEHPAAWLLREAGQTQAE NSGDGTAFVVLLTEALLEQAEQ LLKAGLPRPQLREAYATATAEV LATLPSLAIQSLGPLEDPSWALH SVMNTHTLSPMDHLTKLVAHA CWAIKELDGSFKPERVGVCALP GGTLEDSCLLPGLAISGKLCGQ MATVLSGARVALFACPFGPAH PNAPATARLSSPADLAQFSKGS DQLLEKQVGQLAAAGINVAVV LGEVDEETLTLADKYGIVVIQA RSWMEIIYLSEVLDTPLLPRLLP PQRPGKCQRVYRQELGDGLAV VFEWECTGTPALTVVLRGATT QGLRSAEQAVYHGIDAYFQLC QDPRLIPGAGATEMALAKMLS DKGSRLEGPSGPAFLAFAWAL KYLPKTLAENAGLAVSDVMAE MSGVHQGGNLLMGVGTEGIIN VAQEGVWDTLIVKAQGFRAVA EVVLQLVTVDEIVVAKKSPTHQ EIWNPDSKKAK\KHPPPVETKKI
25346	55714	B	25486	1	642	
25347	55715	A	25487	3	395	FLPVNLTHDWQGSSALATLERP LSQVRLKRFVGTLIAFMVSAIVI LATASMAVASITESVQTAAFID NMARNVSNKLLLQQGIDQKIL ALLQSLEAALEYVGEQQDALA FQQQ*NCNWGHKHICIISLPWN
25348	55716	A	25488	3	358	HEPMCGETHQALQGAMEKLW SRFMELMQE/KKVDLKERVEEL EHCCI*LSGERQTPSGSGKPGHG KESCTLVRGAPASESCPPAGEYI ALYQSQRAVRKEEECISRLAQD KGEVKVKLLE
25349	55717	A	25489	1	250	VQCGGIPPGQNNKEEMEVLPEP PPPINRKKDKSYATAMGPFLRQ EALSGELLACLVIQD*QGNWV YKPISFNIYKKLRKSIRG
25350	55718	A	25490	1	702	
25351	55719	A	25491	1	252	
25352	55720	A	25492	1	122	LAPLVTYFSSLSLGFFNLKGKL APSSWRC*GLNEIIRGKH
25353	55721	A	25493	3	505	

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25354	55722	A	25494	1	3345	MRVGFRDIVGSLSEYSFGCPVN YEVFHSVWITILCCLMANDRKP QFLYFFQFFSFHGGRNLMSSFH PGNGHNDSRRSVFYANEKWEF LDPTPKDLEESIVQEEKKEPTPE GNKVSQRLKNLPHTSLKAKQL LQTSSTNRGTVITATRLAFDLRT QSTKCSHPASGSSGHSTDFQLE GEWGLWDLGTKGFKLPYSLSI DIDNVKSPHFPHELKTLTVSLGS NRRMGLEKKECHQKQGALREQ LQVHIQNVEILVSE
25355	55723	A	25495	296	1350	TLWLQGEQPSTQEIHEKV/LNE AMGAMMYHTIILTREDLEKFK APRVIVQIGSGYDNVDIKAASE LGIAVCNIPSAAVEETPDSTICHI LNLYQRNTWLYQALRGQAVA VRAKAFGFSVIFYDPYLQDGIE RSLGVQRDLLYQSDCVSLHCN LNEHNHHLINDFTIKQMRQGAF LVNAPHGGLVDKKALAQALKE GRIRGAALYVRESEPFSFAQGP LKDAPNLICTPHTAWYSKQASL EMREAAATEIRRAITGHIPESLR NCVNKEFSVTSAPWSVIDQQAI HPELNGATYRYPPGIVGVAPGG LPAAVEGIIPGGIPVTHNLPTVA HPSQAPSPNQPTKHGDNREHSN
25356	55724	A	25496	694	1185	PKPFKEGTIRGAALDMHESEPF SFAQGPLKNAPNLICTPHTAWY SEQASLEMREAAATEIRRAITG CIPESLRNCVNKEFFVTSAPWS VIDQQAIHPELNGATYRYPPGV VGVAPGGLSAAMEGIIPGGIPV THNLPTVAHPSQAPSPNQPTK* MK*KQMGEVA*GAARIRGETL GLNGFGCTGQA/VAVRAKAFG FSVIFYDPYLQDVVERSLGVQR VYTLQDLLYQSDCVPLHCNVN EHNNHLINDFTIKQMRQGAFLP PKPFKEGTIRGAALDMHESEPF SFAQGPLKNAPNLICTPHTAWY SEQASLEMREAAATEIRRAITG CIPESLRNCVNKEFFVTSAPWS VIDQQAIHPELNGATYRYPPGV VGVAPGGLSAAMEGIIPGGIPV THNLPTVAHPSQAPSPNQPTKH

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25357	55725	A	25497	290	1251	PFMLYVSISTLYIAFCHILNLYR RNTWLYQALWEGTRVQSVEQ MGEVA*GAARIRGETLGLNGF GCTGQA/VAVRAKAFGFSVIFY DPYLQDVVERSLGVQRVYTLQ DLLYQSDCVPLHCNVNEHNNH LINDFTIKQMRQGAFLVNAARG GLVDEKALAQALKEGTIRGAA LDMHESEPFSFAQGPLKNAPNL ICTPHTAWYSEQASLEMREAA ATEIRRAITGCIPESLRNCVNKE FFVTSAPWSVIDQQAIHPELNG ATYRYPPGVVGVAPGGLSAAM EGIIPGGIPVTHNLPTVAHPSQA PSPNQPTKHVDNREHPNEQ
25358	55726	A	25498	1	1538	MLLQKTQFEYAFKKKRKLEES KKRGAGPASSDPRWRGSSQTA PHASEVSGAPLGRSCETTRDTG VGPSPRQWLGAGAGTWQHRA RAASTPSSRGLRALQTWGGGE VMNGPLH\PPPPRVALLD/SRNC TVEMPIPKDLATMAFCDTHSTQ EIHEKILHEALGAMRYHTITLA RADLEKFKALGVIVRIGSGYDN VNIKAACELEIAVCNIPSAAVEE TANSTICHILSLYRRNTWLCQA WARKHVCYSMGQIREVALGG AHIGGETQG\LIGFGSTGQAVPV RAEAFGFSVIFYDPYLQDGIERS LGVQRMSQGAFLVNAARGALV DEKALAQALNNGKIR/GAALDV PQSELFSFAQG\SLEMREAAATE IRRTITGCIPESLRNCVNKEFFVT SAPWSVIDQQAIHPELNGATYR YLPGFVCVAPGGLPAATEGIIPG GIPVTHNLPTVAHPSQAPSPNQP TKHGDNPEHPNEQSRECRKVII QIHLRPRDSEKLMNSEKTNLTV FLADSGHMHY
25359	55727	A	25500	1	2595	
25360	55728	A	25501	561	1023	SGHDAYREQIQEYRVISLLLNP N\DHVNKCQSTNDAYPTGFRIA VYSSLIKLVDAINQLREGFERK AVEFQDILKMGRTQLQDAVPM TLGQEFRAFSILLKEEVKNIQRT AELLLEVNLGATAIGTGLNTPK EYSPLAVKKLALKSLAFVGNLF
25361	55729	A	25502	2	227	
25362	55730	A	25503	262	428	

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25363	55731	A	25504	389	2310	ATSGPPGRSLGSACTIWVLVWT GSIPIYSFHGKVEKYMCFHNMS DDTWSAKVFFPLEVFGFLLPMG IMGFCCSRSIHILLGRRDHTQD WVQQKACIYSIAASLAVFVVSF LPVHLGFFLQFLVRNSFIVECRA KQSISFFLQLSMCFSNVNCCLD VFCYYFVIKEFRMNIRAHRPSR ATEEVSKNLVAMKEILYGTNE KEPQTEAVAQLAQELYNSGLLS TLVADLQLIDFEASLGLHGLEQ AVDLALPIAQAQGEVLNNGKC MDQFPVDVYQGGAGT\YVNMS TNEVLANIGLGLMGHQKGEYQ YLNPNDHVNKCQSTNDAYPTG FRIAVYSSLIKLVDAINQLREGF ERKAVEFQDILKMGRTQLQDA VPMTLG\QEFRAFSILLKEEVKN IQRTAELLLEVNLGATAIGTGL NTPKEYSPLAVKKLAEVTGFPC VPAEDLIEATSDCGAYVMVQG ALK\RLAVKMSQI\CNDLRLLSS GPPG\SSIMPAKVNPVVPEVVN QVCFKVIGNDTTVTMAAEAGQ LQLNVMEPVIGQAMFESVHILT NACYNLLEKCINGITANKEVCE GYVYNSIGIVTYLNPFIGHHNG DIVGKICAETGKSVREVVLERG LLTEAELDDIFSVQNLMHPAYK
25364	55732	A	25505	133	375	
25365	55733	A	25506	3	505	ARGREGVSRRERPLLSARRLGA EWDSAGAETASGLQVPRLGGS WPQTSVFSAAVKARGCRIATLP MDLIGFGYAALVTFGSIFGYKR RGGVPSLIAGLFVGCLAGYGAY RV\SNDKRECKKCHWFTAFLPG LPSMGVRFKRSKKIM\PAGLVA GL\SLM\MILRLVLLLL
25366	55734	A	25507	244	696	

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25367	55735	A	25508	1	1442	MGQLHQAQASADIATSRLQQT SLTDVTRHQQFFSTYNTDDFIQ FTATYREQTRTRRQRQYAVNH VTFFFGKCTFRDRHRHRVIGIVL NIGLTFPAHQTQDGIGSTRSQR QSRLVANKVATRNLVKHFDDD REANRGIQEAQTEHHHRGVLV NESRQRFGCQQHNRHRNHYRR HHHRQMVNHPYCSNYRIQRED GVKDDNLCDDHPETGIQLYASL LLQVFFFAANIYGWYAWSRQT SQNEAELKIRWLPLPKALSWLA VCVVSIGLMTVFINPVFAFLTR VAVMIMQALG\LQGVMPELQA DAFPVWDSCMMVLSIVAMILM TRKYVENWLLWVIINVISVVIF ALQGVYAMSLEYIILTFIALNGS RMWINSALIHQVVLDLIQQGIVI VWRDHLHMQRLHRLLAYHPC MYLVHIADFRDFPAHTRLQVQ RFPAIPVHLQVIHSRYLSTVATR YAESEATPVSGALGLLCPTLPIV
25368	55736	A	25509	133	375	
25369	55737	A	25510	2	471	AFAQRETAGRRVGQRWCGDCF RTPGTALGGSWPQTSVFSAAV KARGCRIATLPMDLIGFGYAAL VTFGSIFGYKRRGGVPSLIAGLF VGCLAGYGAYRV\SNDKRECK KCHWFTAFLPGLPSMGVRFKRS KKIM\PAGLVAGL\SLM\MILRL VLLLL
25370	55738	A	25511	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
25371	55739	A	25512	59	882	SRLKNASIFVASPSGKKAKGKK VAP/APAVVKKQEVKKVVNPLF EKRPKNFDIGQDIQPKRDLTSFV KWPPLYQRQRAILCKWLKVPP EINQFTQALDHQTAALLLQLAH KYRSETKQEKKQRLLALAKKK AAGKGGIPTKRPPVLRAGVNTI TTLLENKKAQPVVIAHDVDPIE LVVFLPALCHKMRVPYCIIKGE ARLGRLVHRKTCTTVAFIQVNS EDKGALAKLVGAIRTDYNDRY NEIRRHWGGNVLGPKSVACIG KLEKAKAQELATKLG

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25372	55740	A	25513	1	833	GTRPKMPKGKKAKGKKVAPAP AVVKKQEAKKVVNPLFEKRPK NFGIGQDIQPKRDLTRFVKWPR YIRLQRQRAILYKRLKVPPAINQ FTQALDRQTATQLLKLAHKYR PETKHEKKQRLLARAEKKAAG KG\DVP\TKRPPV\LRAGVNTFT PL\VENKKAQLVVIAH\DVDPM RGWLSFLPAL\CRKMGVPYCIIK GK\ARLGRLV\HRKTCTTV\AFT QVNSESQRRLWAKLVEAIRTN YND\RYDEIRRHWGGNDLRPK\ SVARI\AKLEKAKAK\ELATKLG
25373	55741	A	25514	1	1176	MEKELVDHTGLFLSAHASEAL ALKLMIYSEVAHKLRAVRSQH PDMGVSLPLTPANSCPKTIERM RRSRELEREKDQSIETDHLPWA FGSTFLKTPLSCKTLMKYICYA FIINLSFVKGVSAVTLMMSEES NMQMQFSVSITSGFGPFKSHIIA AIPNAERKESQGEKMAPAPAVI KKQEAKEVVNPLFEKRLKNFGI GQDIQPQRDLTRFVKWPHYIRL QRQRAILS\AHKYRPETKQEKK QRLLAQAKKKATSK/EDIPTKR PPVLRAGVNMVTTLVENKKAQ LVMTAHDVDPIELAVFCLPAPC CKKGVPYCIIKGKARLGHLVHR KTCTTVVFTKVNSEDKGALAK LVEAIRTNYDRYDEIHCHWGG NVLGLKSVAHIIKLEKAKVKEL
25374	55742	A	25515	2	524	
25375	55743	A	25516	144	412	AGSCPFAAGPGPLGSGRCFVLIR FILIQNRAGKTRLAKW\YMQFD DDEKQKLI\EEVHAVVTVRDAK HTNFVGVSGTFKIILPPLWLASN
25376	55744	A	25517	38	476	
25377	55745	A	25518	235	892	RSRVGTNRLFGETYPRASPGPQ STALLTAYKKMTDLVAVWDV ALSDGVHKIEFEHGTTSGK/REV VYVDGKEEIRKEWMFKLVGKE TFYVGAAKTKS/ATINIDAISGF AYEYT\LEINGKSLKK\YMEDRF KNPPILWVLHM\DG\ENFRIVLE KDAMDVWCNGKKLETARDFC KMSDTISDDTKVDEQERALSRT PEDKWNFRPAVPMRGERGSPS HCGQAH

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25378	55746	A	25519	1	1233	MQLKFPGRQKIHISKKWGFTKF NADEFEDMVAEKRLIPDGCGV KYIPNRGPLDKCHHGKCVATG TSYMCKCAEGYGGDLCDNKN DSANACSAFKCHHGQCHISDQ GEPYCLCQPGFSGEHCQQGLLG GVREMLRCKVRSNIVTMKAKL SFRICMTLTILANMWPRPILGG VDQIPIKPKSKVLYLGAASGTT VSHVSDIIGPDGLVYAVEFSHR AGRDLVNVAKKRTNIIPVLEDA RHP/HQPDQ\ARSVALNAHTFLR NGGHFLISIKANCIDSTASAEAV FASEVRKLQQENLKPQEQLTLE PYERDHAVVDYSSSSATEQRRT ENDSDKLTEVGFRKLVINFSKL KEDVRTHHKEVKNLEKRLDEW LTRINSVEKTLNDLMEAENHGT KKYVTQAQASVAYLIKWKKG
25379	55747	A	25520	78	978	AAGHSAKKSCLSLLPAWSFPLG STRAQWHVRRLQARISGGGRH RCGRRGQ\GKTRRRMGPMVVS VEPHRHEGVFIYRGAEDALVTL NMVPGQSVYGERRVTVTEGGV KQEYRTWNPFRSKLAAAILGG VDQIHIKPKSKVLYLGAASGTT VSHVSDIIGPDGLVYAVEFSHR AGRDLVNVAKKRTNIIPVLEDA RHPLKYRMLIGMVDVIFADVA QPDQSRIVALNAHTFLRNGGHF LISIKANCIDSTASA\EAVFASEG EKLQQENLKPQEQLTLEPYERD HACV\VGVYRPLPKSSSK
25380	55748	A	25521	230	314	QMPGNNPAFSA*CDAGASYQA YVNSAIY
25381	55749	A	25522	1360	1848	RFRALV/TEGFSLRELFPVATVL VASST\VTKRFIFLLAAD\VRLA LRRSI\THPFVRKQELTVYTLNN ELENLLTNVVNQAQQGGKVML DSVPVDPNMLNQFQSTMPQVK EQMKAAGKDPVLLVPPQLRPL LARYARLFAPGLHVLSYNEVPD ELELKIMGALM

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25382	55750	A	25523	91	1184	AAACSPPPPARLTYGSETLRGG DCSKMAAGCCGVKKQKLSSSP PSGSGGGGGASSSSHCSGESQC RAGELGLGGAGTRLNGLGGLT GGGSGSGCTLSPPQGCGGGGG GIALSPPPSCGVGTL\LSTPAAA TSSSPSSSS/APASSSSPGSRK\M VVSTE\MC\CFCFDVLYCHLYGI \QQP\RPPRFTNEPYPLFVTWKIG RDKRLRGCIGTFSAMNLHSGLR EYTLTSALKDSRFPPMTRDELP RLFCSVSLLTNFEDVCDYLDWE VGVH\GIRIEIHQCKKASKR\TA TYLPEV\AKEQGWDHIQTIDSLL RKGGYKAPITNEFRKTIKLTRY RSEKMTLSYAEYLAHRQHHHF QNGIGDPLPAYNHYS
25383	55751	A	25524	3	154	
25384	55752	A	25525	575	1707	TALLLTQSLFGGLFTQTHMKFG AVTRJ*NRKTGNSKKQSTSPPPK ERSSSPATEKSWMENDFDELRE EGFRRSNYSELREDIQTKGKEV ENFERNLEECITRITNTEKCLKE LMELKTKARELCEECRSLRSRC DQLEDCLLKKLHSHQANPEFDL ITEHLTLCIRISIQIKAYLSLSKA QSSLSHRPPTYLAYLFNGFRLF KNLKAYLHPGEINSFIAHTKPV WWSLHTDAHEIWCRDSDLKLV PTLPLIPLEAALRNITHSLSIPPP KNFRRPNTSTLFCVIFLINIRRQE YQASEPKPSHRIPCDLQRIKYLG IQLTRDVKDLFKENYKPLRNEI KEDTNKWKNIPCSWVGRINIVK MAILPKPLLVIPRQTGSGMDPQ QTSGDLQKCLTVLRKTNKQKAI ASTSRKRMTMQKLHLKEKLINS KDQRTNDKNHMIISIDAEKAFN KTEHRFMLKTLNKLEINSRWIK DLNVKPKTIKTLEENLGNTIQDI VMDKDFMTKTPKAMATKAKI DKWDLIKLKSFCTAKETIIRVY RQPTERESIFVIYPSDKGLISRIY KELAIPGKGNSSNVSKDSKMSK HQKMQGENKHD

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25385	55753	A	25526	110	569	TALLLTQSLFGGLFTRTRMKFG AMTRIG\DLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGCLPWSFTLSGKSR FSGEGANHHGHRASGNSHSGS
25386	55754	A	25527	2	464	LFGGLFTRRRMKFGAVTRIR\DF PWEINPLSSCSLL/CEKDPRTTS GPQTDQPSKHLTNLKSASTPPP YNPFITSPPHTRSGLQFRSTSSPP APAQQFTLKKVAEAKGIVKVN APFSLSDLSQISVRLGSFIKYEKS SPVHGSFGSNPETLYSPRP
25387	55755	A	25528	162	206	
25388	55756	A	25529	74	446	TAMLLTQSLFGGLFTWTRMKF GAVTRIG\DLPWEINPLYSCSLL SRFKKIKACYHSPATSWPFKTY KLSLQLPHFTCPKTRQALQVSS GAVPYQPNCFAYPPCGAQPVPS FVLNTFLHNSLCRA
25389	55757	A	25530	66	311	FGAVTRIG\DLPWEINPLSSCSLL REKEPPTTSGPQTNQAKKHLTN FKSGACYTCRKSGHWAKECPQ PGIPPKPRPICVGPH
25390	55758	A	25531	728	825	MKFGAVTRIG\DLPWEINPRSSC SLLHEKDPPM
25391	55759	A	25532	291	311	TALLLTQSLFGGLFTQTHMKFG AVTRI*NKKNNTK
25392	55760	A	25533	1	1056	
25393	55761	A	25534	245	487	TALLLTQSLFGGLFTQTRMKFG AVTRIG\DHPWEINPLSSCSLFQ EKDPPTT/SGPQTDQPKKHLTNF KSTSFVFSSCIPPP

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25394	55762	A	25535	818	2391	TALLLTQSLFGGLFTQTRMKFG AVTRIG\DIPWEINPPSSCSLFLP/ RLPLLHFPGAGPSTPQPLL/HSPS AASPAFLGQGQDLINLVFKVYN NRKKLQFLASTVTQTPATSPAH KNFQTPEPQQPGVPPEPPSPGAC YKCQKSGHQAKECPQLRIPHLS YAWTFNDNPLYVQEDNRRFVS QETGNLYIAKVEPSDVGNYTCF ITNKEAQRSVQGPPTPLVQRTD GVMGEYEPKIEVRFPETIQAAK DSSVKLECFALGKIDDSIREKG AIRIKPSSILMRCNCLVQSPILVG EGWTGARCQGKSSTANPKLSL KSRTSNKKMKAFMSALQATFE EETLQRVNSFFMHNVLDNCLLP NSGTCLFETAPPEWEQKIQNTH LSIYDNLLWECKASGKPNPWY TWLKNGERLNPEERIQIENGTLI ITMLNVSDSGVYQCAAENKYQI IYANAELRVLGSQLVHFRENGT CLSDEVIRDSDFMSGMTVVHAF TSGSQGTTTENQDELQIKFISAR HSQATEGINSTSAKFD
25395	55763	A	25536	425	749	IASLLTQSLFGGLFTWTHMKFG AVTRT/RGDLPWEINPLSSCSLL HEKDPPTTSGPQTDQPKKHLTN FKSAQLKASGK/DLQKPYQHFQ TLQQLLPLQWAPCYGPSSVSI

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25396	55764	A	25537	2	2204	IDMIFTPGPPSTPKHKKSQKGSA FTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFVKVERQVQDMG KKLDFLVDMHMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSDLKTIICNYSETGPPEPPYSF HQVTIDKVSPYGFFAHDPVNLP RGGPSSGKVQATPPSSATTYVE RPTVLPILTLLDSRVSCHSQADL QGPYSDRISPRQRRSITRDSDTP LSLMSVNHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGETDTDTDPFTPSGSMPLSST GDGISDSTVPLFLSSEILQKQVG QSITSMLGFLSRGPSMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFSLLSVTSYS SFAFHKFSVAVYNISNLKTVDP AKFPTRYCYCLNNRTNDLSDFT ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFICVMTGKSGR NLSDFWEIEEKYPIINYTFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIG\DLPWEINP/LSSCS LLHEKDPPTTSGPQTDQPKKHL TNFKSAARPTFLGQGQVPLNPF SFTLSGKSCFPRRQEPPNRLFPH PNLLSLCPNPLFLCPNPFSTFLE GKNHHPHPFSVSQVFSLGLPPS LWEHSPMAHRLRVQPRQQPPDI HKQVISLQSGHSLLVKSQSWSQ DPIKFQLPHHHKNTASVCINPSV
25397	55765	A	25538	110	542	TALLLTQSLFGGLFTRTRMKFG AMTRIG\DLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGCLPWSFTLSGKSR FSGEGASCSLPG
25398	55766	A	25539	1	781	MPLQPLATPFTSPGSPSVAQVT TNTGEPGFAQQEYAETPQTTAR PPHPHPALRALQASVHQTPRLG DCLGSSESATALHGSGEPNKLA PPGRPTERGGLFKCSVPLRTVR GCRAGLRGTETVPSSLQRQPAG DVGWINNKSTTALDRTPTDTQ RTRRPRPPKQKQRGRALKERPR DSDSAREGPLKAVAGLFGGLFT RTCMKFGAVTRIG\DLPWEINPL SSCSLLHEKDPPTTSGPQTDQPK KHLTNFKSDLLSLATED

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25399	55767	A	25540	1571	1781	TALLLTQSLFGGLFTRTRMKFG AVTRIG\DLPWEINPSSSCSLLRE KDPPTTSGPQTDQPKKHLTNFK SA
25400	55768	A	25541	2150	3195	TVLLLTQSLFGGLFIWTRMKFG AVTRIG\DLPWEINPLSSCSLLH EKDPPTTSGPQTDQPKEHLTNF KSDED
25401	55769	A	25542	4688	5149	TAMLLTQSLFGGLFTRTRMKFG AVTR/IRGTDLPWE\INPLSSCSL LREKDPPMTSGPQTDQPKKH\L TNFKSGACYTCWKSGHWAKER PQPGIPPKPRPICVGPHLKIRTCS THLGQATPRAPGTLAQGSLTDS FPDLLGLAAEDSHCLIASEAP
25402	55770	A	25543	1	433	MAAFPAALNRPTRARARRRRIS AHSAASAAAAVVVAGTARGM VPGSEGP\CRA\GDEVADWEIVI EGTANLGPYFEGLRKHYLLPAI EYFNGGPPAETDFGGDYGGTQ YSLVVFNTVDCAPESYVQCHA PTSSAYEFVTWLDGIK
25403	55771	A	25544	1	235	
25404	55772	A	25545	1	301	
25405	55773	A	25546	2	438	
25406	55774	A	25547	1058	1494	KSVRLVVN/YLRTQKAVVRVSP EVPLQNILPVICAKCEVSPEHVV LLRDNIAGEELELSKSLNELGIK ELYAWDNRRVPSAVPMQGPWP AEHFLQVNEQPPAGSPSPCPSSS SSSSGLRGGMQTANGPACALTP TCAQTDCPCPTSH
25407	55775	A	25548	1	3965	RRFQPLPSAALRRCPPPARVGG RWVSAEKVNEGGSGGGGSQRL TRRARSTARVPAPGTMDAPRAS AAKPPTGRKMKARAPPPPGKA ATLHVHSDQKPPHDGALGSQQ NLVRMKEALRASTMDVTVVLP SGLEKRSVLNGSHAMMDLLVE LCLQNHLNPSHHALEIRSSETQ QPLSFKPNTLIGTLNVHTVFLKE KVPEEKVKPGPPKVPEKSVRLV VNYLRTQKAVVRVSPEVPLQNI LPVICAKCEVSPEHVVL
25408	55776	A	25549	1	388	

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25409	55777	A	25550	1	1748	MVLARVARRPAGSAEAQASLA GKAALPERARKMSSPGIDGDPK PPCLPRNGLVKLPGQPNGLGAA SITKGTPATKNRPCQPPPPPTLP PPSLAAPLSRAALAGGPCTPAG GPASALAPGHPAERPPLATDEK ILNGLFWYFSACEK\CVLAQVC KAWRRVLYQPKFWAGLTPVLH AKELYNVLPGGEKEFVNLQGF TARGFEGFCL\VGVSDLDICEFI DNYALSKKGVKAMSLKRSTIT DAGLEVMLE\QMQGVVRLELS GCNDF\TEAGLWSSLSARITSLS VSDCINVADDAIAAISQLLPNLA ELSLQAYHVTDTALAYFTARQ GHSTHTLRLLSCWEITNHGVVN VVHSLPNLTALSLSGCSKVTDD GVELVAENLRKLRSLDLSWCP RITDMALEYVACDLHRLEELVL DRCVRITDTGLSYLSTMSSLRSL YLRWCCQVQDFGLKHLLALGS LRLLSLAGETPVSALTLAVTTH PHLVHPPNLPGPCANSHPARTH SPGSEAEEEGGAARPSPPEPWA ARTEPPSDPAAGCPLLTTTGLS GLVQLQELEELELTNCPGATPE LFKYFSQHLPRCLVIE
25410	55778	A	25551	1	377	MRRLTRRLVLPVFGVLWI/DGA AVLLGNQEEVGGAD/WDLKCR PL/EVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTSGDNHTL/SRPSLR*RQRP*IP CIRSQHGNRKRIPRRRIFI
25411	55779	A	25552	222	287	
25412	55780	A	25553	2	918	GHCEVNRDWLQPLLHRVKEDY TRVVCPVIDIINLDTFTYIESASE LRGGFDWSLHFQWEQLSPEQK ARRLDPTEPIRTPIIAGGLFVIDK AWFDYLGKYDMDMDIWGGEN FEISFRVWMCGGSLEIVPCSRV GHVFRKKHPYVFPDGNANT\YI KNTKRTAEVWMDEYKQYYYA ARPFALERPFGNVESRLDLRKN LRCQSFKWYLENIYPELSIPKES SIQKGNIRQRQKCLGISKGRTTK KPQT*S*A\LCQGQRRRCQSPRV WGLSHYTQADSFQGELVALFSS FTFVSLGAPVVSCSFARMGD

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25413	55781	A	25554	84	2804	PRGSWRCRRDLKCRPLSHSDA DWDDLWDQFDERRYLNAKKW RVGDDPYKPVCFSTSGRVSGSP AIRAIPDTRHLRKKATSNSLSRQ QLASPLPRSSYCGVTPGPIAIGP LWTSGSLRTPNHIDTVFAPGLP QPWFHLNYLRAMPSLSSAPKCT LLVYCTDLPPTSIIITFHNEARST LLRTIRRPPAVSTSQMAMTAAA LTPAPLRTYSVHLSCRAHQLVP MPQRKKYDETWVREHTKHSKI SLFPSCRLHFSCLSRRRMAVGS GKFQVMGDLGEPFLRVRWLRI WTLGPDFHGSALNSVLNR\TPT HLIREIILVDDFSNDPDDCKQLI KLPKVKCLRNNERQGLVRSRIR GADIAQGTTLTFLDSHCEVNRD WLQPLLHRVKEDYTRVVCPVI DIINLDTFTYIESASELRGGFDW SLHFQWEQLSPEQKARRLDPTE PIRTPIIAGGLFVIDKAWFDYLG KYDMDMDIWGGENFEMMTVQ VLQPRRSEALICTWKVHHLTRE STALLIALVQAPFTGPQAKKLQ QSPCPAMLAPEYAPEASVLVCT VSLLTYTTLQSEISFRVWMCGG SLEIVPCSRVGHVFRKKHPYVF PDGNANTYIKNTKRTAEVWMD EYKQYYYAARPFALERPFGNV ESRLDLRKNLRCQSFKWYLENI YPELRYPSYLLELWLAESRGPQ LAWSGEETDNDQLDEGFYVYQ

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25414	55782	A	25555	1	2439	MPLKKKGDEPQMEKYIQERSM LAPPSCSDHRDTHSRCIPHIQRL FQCPLGPWFQGEQRNQARGEG GALHPLPVTAGTVALPGAAQPT PARGNVTESLQGATVKLVCKK TSFIFIYCQHPAQCLALACDHEC IDLCTHVASTSLCLRGYQGMKR TIERALTATLAQGTAVPPFPSDV PSQKDAAVRGKGDGSEWERTL TMKRSNLNSEKILPAILLLTEFP RHQSPCSFDKPHHPNTLGCWLP TVLETRGGTNGQSSGKREATLC PCPLLGLPISEEDCVPPALLLPPR G\LPPGLQLSWAPVPQFPPLGPS SLGIPA/LPLVLNLGCLPSLVCPP TSAHTSEVAPSLKSPAEPSPPAR LPRSHQPALSREMRHSDYSVSV HAICWDHDFYTLVTHYMNNTS PISSKRSSDKLNPHVLVVQDSM TILSLHNHLALAGQDMMVWEP RKTLQRRQQPDSSSHSPPPALV ECHPLEPEPLVAGIMYSFSGLQ GVGLRDRAVDETNKRNEKRTL EMSRVEALSSFENSEFGCPPSIN TREITGNSLEGNVKKGVSVPNC TAPGKRTEKKYSKIHEMVKHS GNCKRTDGIWEEYGWSWRLH MKKVFPGFMLVKGGEDAAPGT KEIKSVSGIFQRGKKKPRGRKE KNRKKRGFAFSKETNFVYLLIL VCLIGKVVVWLTSACAEKPKP HGEATCRHSGPSAPLNFQPTRV
25415	55783	A	25556	2	1178	AKCVEVCGKREPPSMSPLNQSA EGLPQEASNRSLNATETSEAWD PRTLQALKISLAVVLSVITLATV LSNAFVLTTILLTRKLHTPANYL IGSLATTDLLVSILVMPISIAYTI THTWNFGQILCDIWLSSDITCCT ASILHLCVIALDRYWAITDALE YSKRRTAGHAATMIAIVWAISI CISIPPLFWRQAKAQEEMSDCL VNTSQISYTIYSTCGAFYIPSVLL IILYGRIYRAARNRILNPPSLYG KRFTTAHLITGSAGSSLCSLNSS LHEGHSHSAGSPLFFNH\VKIKL VTVALKRKEDSAARERKATKIL GIILGAFIICWLPFFVVSLVLPIC RDSWWIHPALFDFFTWVGYLN SLINPIIYTVFNEEFRQAFQKIVP FRKAS
25416	55784	A	25557	3	146	

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25417	55785	A	25558	45	592	PSPPPPARAPSARTRRAPIPAAG QGRARPPRTVSRCGSAAMATKI DKEACRAAYNLVRDDGSAVIW VTIKYDGSTIVPGEQGAEYQHFI QQCTDDVRLFAFVRFTTGDAM SKRSKFALITWIGENVSELQRA KTGTDETLVKEVVQNFANEYVI SDRKELEEEFIKS\ELKKAVGAN YDAQTE
25418	55786	A	25559	249	1808	INGGTLTVTLSVTNQGAETLPF GTGWHPYFPLSPQTRIQAQASG YWLEREQWLAGEFCEQLPQEL DFNQPAPLPRQWVNNGFAGWN GQARIEQPQEGYAIIMETTPPAP CYFIFVSDPAFDKGYAFDFFCLE PMSHAPDDHHRPEGGDLIALAP GESTTSEMSLRAYNDTNRRSDK AFTPHPTCFPSNQNNSASPPTIT PDTATIAPVSHKAFAGNALRSII SDGKLTAGSVINNASAGAVPIP ASIIVCTIGISAAVGMTNKHPAT AIDTTHIMLLSTAPSAWGNNQT RAAPNTSLLAAYRFLIDSRDTE TDSRLDGLSDAFSVFRCHSIMN CVSVCPKGLNPTRAIGHIKSML LQLPPNVEKFAGAYLIQFALFQ PLTHNRLMFFGAFADFLHADQ TFPGQITAAVKGQFVRRRLRFF AIISPSRTLS/YHTP*PRR*PR*SN FVTGRDAGRGLYNRQ*KTS/PS SICSA*GANPVVHHAMTVKFA* WQPIMKISSTSFPSMRPLSHMK TINGLTTFVAW
25419	55787	B	25560	1	567	
25420	55788	A	25561	1	741	MLILISPAKTLDYQSPLTTTRYT LPELLDNSQQLIHEARKLTPPQI STLMRISDKLAGINAARFHDWQ PDFTPANARQAILAFKGDVYTG LQAETFSEDDFDFAQQHLRMLS /GLPYRLEMGIRLENA\RGKDLY QFWGDIITNKLNEALAAQGDN VVINLASDEYFKSVKPKKLNAE IIKPVFLDEKNGKFKIISFYAKK ARGLMSRFIIENRLTKPEQLTGF NSEGYFFDEDSSSNGELVFKRY EQR
25421	55789	A	25562	3	320	IGLVLPISVRKRHAASARCLVN RRPMPRLHGLPGIPMRPPSLPRV RHAGTVFRRHRKRGSPMAY*Y GHSDVVKHREALVADLCHKAA FQLCRGQRHCRPALWRHR

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25422	55790	A	25563	1600	1908	
25423	55791	A	25564	142	326	TRRAPSAISSRCCCNSHQTSKSS LVRTSSSLRSSSHLRTIA*CSSV HLPISCMQIRPSQAR
25424	55792	A	25565	1	1599	
25425	55793	A	25566	393	611	HSRAVCRFYPAKTSPFPVRRCR YRQFVPR*HQNE*AGRE*QPCSI ATVLPYRALPSLAHPRLSADQL PAAHL
25426	55794	A	25567	971	1628	
25427	55795	A	25568	3	1895	
25428	55796	C	25569	1	2505	
25429	55797	A	25570	1	3345	
25430	55798	A	25571	457	790	PSFRRRYRQVVVISVRKRHAAS ARCLVNRRPMPRLHGLPGIPMR PPSLPRVRHAGTVFRRHRKRGS PMAY*YGHSDVVKHREALVAD LCHKAAFQLCRGQRHCRPALW RHR
25431	55799	A	25572	1662	1767	
25432	55800	A	25573	3	603	RLRSLFFLPDKMKLKDCVMIKK IFALPVIEQISPVLSRRKLDELDL IVVDHPQPPSGDYTLHPLPPIIR ANRPNRFRINAGCTRTFTLSTPI NVFRHKILRTQEFPSLTHHAYSP LLVVINKAKFDGLSPEFQQALV SSAQEAGNYQRKLVAED/LAK NHRRHERSGRGS/LSPISTAKPL ATHWGIRFATCLLKMCRRELIC
25433	55801	A	25574	2271	2519	HRQLVIVFQQPLVSGFHEAELS LDDAKWVLHP\ARMLAFMYSM LMAVLFLRGCCFKVLTLPGRSA ISQSTSTSASSSRCGAPW
25434	55802	A	25575	931	1213	
25435	55803	A	25576	1	2767	MIAILSGLRCSIVANYIYAENNL FWLRLNNPKAIWCLRICTFATV IGGTLLSLPLMWQLADIIMACM AITNLTAILLLSPVVHTIASDYL RQRKLGVRPVFDPLRYPDIGRQ LSPDAPLTTTRYTLPELLDNSQ QLIHEARKLTPPQISTLMRISDK LAGINAARFHDWQPDFTPANA RQAILAFKGDVYTGLQAETFSE DDFDFAQQHLRMLSGLYGVLR PLDLMQPYRLEMGIRLENARG KDLY\QF\WGDII
25436	55804	A	25577	395	467	
25437	55805	A	25578	1	675	
25438	55806	A	25579	1	4014	

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25439	55807	A	25580	1802	2385	RKISAPALIKSRTG*EMASLPTS/ HDKQIEQALADVDVPIVGVGGS YHLAESYPPVHYIATDNYALVE SAFLHLKEKGVNRFAFYGLPES SGKRWATEREYAFRQLVAEEK YRGVVYQGLETAPENWQHAQ NRLADWLQTLPPQTGIIAVTDA RARHILQVCEHLHIPVPEKLCVI GVMNRRTVRSPFRESLKISP
25440	55808	A	25581	1	1568	MVKQLKLVSFLLRPGDSKQGY DKHSSLQVGLMIPVCSCIRFRKP SEQSFKFEEGTDAAFHGFWLW PCTMLNVTPIKGMMTVIYEFPV DSETTLQNYDIYFTNEELTDEQ KSLIEWYRDVFRPEDLRLVESV QKGLKSRGYRGQGRIMADSSG SGISEHAWCMSRGAQGRQFCK GAKMSQVLITGATGLVGGHLL RMLINEPKVNAIAAPTRRPLGD MPGVFNPHDPQLSDALAQVTD PIDIVFCCLGTTRREAGSKEAFI HADYTLVVDTALTGRRLGAQH MLVVSAMGANAHSPFFYNRVK GEMEEALIAQNWPKLTIARPSM LLGDRSKQRMNETLFAP\LFRL LPGIILLEELNWKTWAERWNS MLGPRAVKVFFSLAFLPGTLEP AQILFPTQRQGKKAALLLGLW KLEIYSDNRRSPEVSTAWNSPP TGKLDNKQYMIMIPRKRETNTT TRGASNARLDPPSRKGYKGHY ETIGHALEHDKQSQGSYNVEHT IKRQTPRVRRCTSIIAGIYQELG
25441	55809	B	25582	1	1560	
25442	55810	A	25583	1	2115	
25443	55811	A	25584	3036	3957	RIYDAVSEPAEPVDCPRNPVCR FY*QYRDHRGKTVYDVASGDA LFISELG/PLPENVTWLSPEGEFQ KWN/GTAWVKDTEAEKLFRIRE AEETKNNLMQVASEHIAPLQD AADLEIATEEEISLLEAWKKYR VLNSRAMALILTPDLIRSNTACF CSSFVLAGQTAKAAADDGLFPP IFARVNKAGSPVAGLIIVGILMT IFQLSSISPNATKEFGLVSSVSVI FTLVPYLYTCAALLLLGHGHFG KARPAYLAVTTIAFLYCIWAVV GSGAKEVMWSFVTLMVITAMY ALNYNRLHKNPYPLDAPISKD
25444	55812	A	25585	1	2490	

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25445	55813	A	25586	368	761	LYCEACIMAFRMSEQPRTIKIY NLLAGTNEFIGEGDAYIPPHTGL PANSTDIAPPDIPAGFVAVFNSD ESSWHLVEDHRGKTVYDVASG DALFISELGPLPENVTWLSPEGE FQKCSGTTRVKNAKA*TLF
25446	55814	A	25587	1	809	MPVSSYERGHAEKRVVQECCG INLTSSANTILSDCERVNGYCVL CHTTRALVTGNHHRNAVYAET PSNSRINYIVSSHNAFRMSEQPR TIKVYNLLAGTNEFIGEGDAYIP PHTGLPANSTDIAPPDIPAGFVA VFNSDESSWHLVEDHRGKTVY DVASGNALFISELGSLPENVTW LSPEGEFQKWNGTAWVKDTEA EKLFRIREAEETKNNLMQVASE HIAPL\QDAADLEIATEEEISLLE AWKKYRVLLNRVDTSTAQDIE WPALP
25447	55815	A	25588	1	2301	
25448	55816	A	25589	718	1131	
25449	55817	A	25590	279	513	CRRIDTWQPIYQTCGRLMAVEL LTVVTHPLNPSQRLPPDRYFTEI TV/SHRMEVVKEQIDLLAQKAF SLAYLSPCESGL
25450	55818	A	25591	1	407	PQDNAKKLRPHQLSSDEGHTG MGGTAKDVGFVSMRTYSWISS ALPKRLGGGVMPIGATIATEEV FSVLLGNPFLHTTTFGGNPLAC AAALATINVLL\GRTYRLRLSK KAICCWTVSVNWRGNIPIWYR KRVVKGC
25451	55819	A	25592	1	2079	
25452	55820	B	25593	1	700	
25453	55821	A	25594	1427	1845	ACISGFSTETSASGRVSVITDAS LFRVLPRVCGMAVAATKRSGRI TTSEALCCANQLRRRPCVSPTR STPSWLSCAV*ICTSGTT*MKR VPNARHCWICSSLIPHSGLHPQP ITAKFAPIALSSSVTSPFSSVTFG *IN
25454	55822	A	25595	2	295	
25455	55823	A	25596	1	900	
25456	55824	A	25597	1	1422	

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25457	55825	A	25598	2	535	YGNREQRAVSSHTNTWVNRAL ARGWSSLGYRWWVSAWTPSR RFISQLMSRPVDASAAKVKRSA SVPCGSIPFGNCFSVRLRILSASC GCIILPVRFSSSSGSEIPSTISSGSI TLPLDLDIFWPSSSRIRPVM*TV WNGTCGLPFSSLMKCMVIMIM RAIQKKMMSKPDTITLVGWN
25458	55826	A	25599	442	1368	RRTMAAFACGVVRDASEVIRPS STLVPLVGEKHAKGLFGTIVDN FYLVALIFAMGTSLGLATPLVT ECMQWLFGIPHTLLGFI/LYNAI CVACGLQKGVRIASDVRSYLSF LMLGWVF\IVSGASFIMNYFTD SVGMLLMYLPRMLFYTDPIAK GGFPQGWTVFYWAWWVIYAI QMSIFLARISRGRTVRELCWIL WTVLGSNTLLLIDKNIINIPNLIE QYGVARAIIETWAALALNNGN MWGFFILWFIGPGTLVNAWQNI RAQFVHHILRRNGIADGFRHLA ALTIHGKAVGQYLTIRRFTLHR
25459	55827	A	25600	2468	3907	
25460	55828	A	25601	3	3738	YKTNYTDNSEYYANVGFNVKP VKRDGKMSVMSDPDTAIYPFPP KPTPLSIDEKAYYREKIKRLLTE RNAVMVAHYYTDPEIQQLAEE TGGCISDSLAMARFGAKDPASN LLVAGGGTCRSVVINAVFSYVT NVWGWAFEWYMVVMLFGWF WLVFGPYAKKRLGNEPPEFSTA SWIFMMFASCTSAAVLFWGSIE IYYYISTPPFGLEPNSTGAKELG LAYSLFHWGPLPWATYSFLSV AFAYFFFVRKMEVIRPS
25461	55829	A	25602	1331	1456	
25462	55830	A	25603	549	588	
25463	55831	A	25604	19	1629	

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25464	55832	A	25605	1	1995	MVGVRFALGLMWLTLIVAETIS ANSGIGYLAMNAREFLQTDVV VVAIILYALLGKLADVSAQLLE RLWLRWNPAYHLKEATLSAEQ AARIREMTVITSSLMMSLTVDE SDLSVHLVGRKINKREWAGNA SAWHDTPAVARDLSHGLSFAE QVVSEAHSAIVILDSRGNIQRFN RLCEDYTGLKEHDVIGQSVFKL FMSRREAAASRRNNRVFFRSGN AYEVENVPDPGVEQADDIILRIT ATAICGSDLHLYRGKIPQVKHG DIFGHEFMGEVVETGKDVKNL QKGDRVVIPFVIACGDCFFCRL QQYAACENTNAGKGAALNKK QIPAPAALFGYSHLYGGVPGGQ AEYVRVLKGMWGRLNDAQPG FRSSRPLRYGAGIMTLLNISGLS HHYAHGGFNGKHQHQAVLNN VSLTLKSGETVALLGRSGCGKS TLARLLVGLESPAQGNISWRGE PLAKLNRAQRKAFRRDIQMVF QDSIST\VNPQPNRLHIV/RFPLT RLNQYQPSFSTDLYHGTLKPAS LTMSGVVLLGRM/PRKTSQQV QWA\CIARTDKASMPTVYSESL FVEPLERVLYVAVILTQIIRGLR DTEIETINPDIAVHFALCFHGLG SIPTKGAEKSPFLTIHKVRVKPD IPSPVSIMAPCRAHPTCEALFNN STALHSPWFCDSL
25465	55833	A	25606	179	371	CVLQYTHWPACSTVA\HSRRW* NRRRLRLAVTKTGSLFSHRCAG ARLAFSKKLRCRDALPASRS
25466	55834	A	25607	544	983	SVQNPRVNWIHAALQRTGRGR RRHEQHGEDHFVNGAAGVHQ AANGLVNPPRHQVFGAHQAKG DGENHRQRGAPDGDLQRDGHF GEVILPLAEIGREEVGGERRHV AAVFDQ/S*AGPFPRPATRRPTR RVQRPSSEARTSCAWVGRW
25467	55835	B	25608	1	1746	
25468	55836	A	25609	1	858	
25469	55837	A	25610	98	288	LCRNNGEPLARSGAAMGALLD REHSRHP\PDLEG\GSQQQVCDS GGSVTAANTSGGQQVKAQLEL

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25470	55838	A	25611	1934	2812	RPQTYSDAQPGFRSSRPLRYGA GIMTLLNISGLSHHYAHGGFNG KHQHQAGLNNVSLTLKSGETV ALLGRSGCGKSTLSRVLVGLES PAQGNISWRGEPLAKLNRAQR KAFRRDIQMVFQDSISAVNPRK TVREILREPMRHLLSLKKSEQL ARASEMLKAVDLDDSVLDKRP PQLSGGQLQRVCLARALAVEP KLLILDEAVSNLDLVLQAGVIR LLKKLQQQFGT\ASLFITHDLRL VERFCQRVMVMDNGQIVETQV VGEKLTFSSDAGRVLQNAVLP AFPVRRRTTEKV
25471	55839	A	25612	1	515	MLAVECRSLPFPPLVQPVRYTD VTVKDDYNPETEQYTLTISQRT PATPDQAEKQPLHIPFAIELYDN EGKVIPLQKGGHPVNSVLNVTQ AEQTFVFDNVYFQPVPALLCEF SAPVKLEYKWSDQQLTFLMRH ARNDFSRWDAAQSLLA/ILHQA ERRASSARSAAVSAGACG
25472	55840	A	25613	1	1053	
25473	55841	A	25614	1	1521	
25474	55842	A	25615	430	1120	QTASTFLKRGKCASRQSKLCGN RRRKRRQRISSYCLLRGTACSP AHQPDAFHQKRGNAGRHYAEC VLQYSSCSTRYS\PGR\TQLINLF EVADGKRLVDLPGYGYAEVPE EMKRKWQRALGEYLEKRQSLQ GLVVLMDIRHPLKDLDQQMIE WAVDSNIAVLVLLTKADKLAS GARKAQLNMVREAVLAFNGD VQVETFSSLKKQGVDKLRQKL DTWFSEMQPVEETQDGE
25475	55843	A	25616	407	1176	AYSTSLRVKICRKTSTLLLRSRV TQIRSNTKSTKRAAHCSLTASC PPRCSIHATTVTSTTPCLWRRIA TMLRALARLLLRICFSGRTLKIA CLLLLVAGATILIADR/AALYHA GKVKWLLVSGDNGRKNYDEA SGMQQALIAKGVPAKVIFCDY AGFSTLDSVVRAKKVFGENHIT IISQEFHNQRAIWLAKQYGIDAI GFNAPDLNMKHGFYTQLREKL VIAKGHGSLLTDLPVAKAGTM WAIEIDDVARHSRSHL
25476	55844	A	25617	3	168	NPFYSAMR\KSAGIRHILARHVE GASHMAEGYTRATAGNIGVCL GTSGRCCFRLCW
25477	55845	B	25618	169	1227	

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25478	55846	A	25619	489	740	AIARSCADYHPANFRHHRAAA RAGDDYLSRRAERQPGAKAGG SRLRAGKRPCSAFRYW*CAAG E*SVGEKIMAGDVISPKRRL
25479	55847	A	25620	146	475	
25480	55848	B	25621	38	191	
25481	55849	A	25622	662	4568	
25482	55850	A	25623	20	2661	AGHIHRPRYQHGVGTESTSIMS VASRSAERVFLTKFESWKNFPI NRGRNKMAKMRAVDAAMYV LKKEGI\TPAFG\VPGAA\INPFY SPMRKHG\GIRHILARHVEGAS HMAEGYTRATAGNIGVCLGTS GPAGTDMITALYSASADSIPILC ITGQAPRARLHKEDFQAVDIEAI AKPVSKMAVTVREAALVPRVL QQAFHLMRSGRPGPVLVDLPF DVQVAEIEFDPDMYEPLPVYKP AASRMQIEKAVEMLIQAERPVI VAGGGVINADAAALLQQFAEL TSVPVIPTLMGWGCIPDDHELM AGMVGLQTGHRYEKYTEGRKI VHIDIEPTQIGRVLCPDLGIVSD AKAALTLLVEVAQEMQKAGRL PCRKEWVADCQQRKRTLLRKT HFDNVPVKPQRVYEEMNKAFG RDVCYVTTIGLSQIAAAQMLHV FKDRHWINCGQAGPLGWTIPA ALGVCAADPKRNVVAISGDFD FQFLIEELAVGAQFNIPYIHVLV NRPAANGAQGSCHPDAPAVFR SSIFIRKSEEKLVVTMNELSASR ALPEETMPGRFELKPTLEKVLH APDNFLFMDPLPPMHRRGIIIAA IVLAVGFLLPSDDTPNAPVVTR EAQLDIQSQSQPPTEEQLRAQL VTPQNDPDQNLYRKASQKSSR KLPKRDLPHILTPFRAPMASVC AKRKGQVLHQQYSLKKYRYK
25483	55851	A	25624	1	570	
25484	55852	A	25625	312	873	APRSRVQAKIAASNTGELNALQ QLGFS\LVEGEVDLAL\PVNNA\ SDSGAVVA\QETDIPA*RQLASA AFAQSRFRAPWYAPDASSRFYA QWIENAVRGTFDHQCLILRAAS GDIRGYVSLRELNATDARIGLL AGRGAGAELMQTALNWAYAR GKTTLRVATQMGNTAALKRYI QSGANVESTAYWLYR

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25485	55853	A	25626	2	922	FSPPGLHDAGEAVFWRVNKSA NYGVLDKLARGYADLSKAESQ WDEMMRTAGSLKLGTIHASINS LFENITAAPADPILGLADLFRAD ERPGKINLGIGENPSCCRTSSSP VFDAAIWPAPVNNASDSGAVV AQETDIPALRQLASAAFAQSRF RAPWYAPDASSRFYAQWIENA VRGTFDHQCLILRAASGDIRGY VSLRELNATDARIGLLAGRGAG AELMQTALNWAYARGDHMI/R I*RTAGGGNRTRLYAVGNG*RQ TVWRWRFYPSLPAVAGATFWQ RQSVTDAVLHRFAGDGGAAAR YPAWR
25486	55854	A	25627	911	1441	AIPSISCFLLAIKALILSAIWLNA TPSRSKLEPSSKWIRSLRCPSPN RCAAASSFNISCQWFLSEYGPP NQVASGKTSPFVIVFKQPRYRA VTKPNCRLMMRNGCSTLARML PVMYAMLMPVLFLRGCCFKVL TLPGRSAISQSTSTSASSSRCGA PW*PASAETNCSSPCSRLPS
25487	55855	A	25628	1	1247	MERVLDNLLNNALRYCHSTVE TSLLLSGNRATLIVEDDGPGIAP ENREHIFEPFVRLDPSRDRSTGG CGLGLAIVHSIALAMGVNAQA DFMKLTGADEQIAAYCFKMPF VFHLIEEVSRNFGYALCLINIDH KAALNITQRTAANILLDGQMQ HAVDQAFTQRTARQGSTFVQY ARLARKLATANICWSYFVPVR ASIEPLTWENAFFGVNSAIVRIT SEAPLLTPDALAPWSRVQAKIA ASNTGELDALQQLGFSLVEGEV DLALPVNNASDSG\AVVAQETD IPALRQLASAAFAQSRFRAPWY APDASSRFYAQWIENAVRGTFD HQCLILRAASGDIRGYVSLREL NATDARIGLLAGRGAGAELMQ TALNWAYARGKTTLRVATQM GYTAALKRYIQSGANVESTAY WLYR
25488	55856	A	25629	1	1925	
25489	55857	A	25630	402	664	TARRLLFFRD/RTARVAVPNAA VVLPFPLPVKTMIIPRSLGRRRS GGICRPLGYLVAMDAIDGLQN ADNSNGESRIATSSFRSRSARR

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25490	55858	A	25631	920	1237	IARPGCHLSHCHSEPSGRLSK*P FSCNSLKTGDF*PI*GLIQTQIFS PFAFRRRIIPSGSGKVSGSHSKS HHWKAFIQKQSKWKTCSGRLR SAIPSIKLFTVASS
25491	55859	A	25632	1	1341	MVHRFGIRVRFVALGFYQDVIL PVRAHRHEWGHYVHLCASIQR QIDVSFARDATSHSSCPVTGVR FWGYPFAANKVVIAGFELEGET MTRPGLICAEGGLLVMIVSLRS ELYDSYHEFTRQRVTEIVEKAA NHLPAVVEMMTLHRCAINRHN FVRRVGPAGISTFFASSPDGVN AGFSTFRVVFTCQRSRPLQRHS HADVQTATLLLNTVNLEQKQA NAILSGLSDMIPNSSPESAPEIQL LQSRMILGKTIAELNLRDIVEQK YFPIVGRGWARLTKEKPGELAI SWMHIP*TLSKNRPTPFS/DGLS DMIPNSSPESAPEIQLLQSRMIL GKTIAELNLRDIVEQKYFPIVGR GWARLTKEKPGELAISWMHIP QLNGQDQQLTLTVGENGHYTL EGEEFTVNGMVGQRLEKDGVA LTIADIKAKPGTQFVLSQRTELE AINALQETFTVSERSKESGMLE LTMTGDDPQLITRILNSIANNYL QQNIARQAAQDSQSLEFLQRQL PEVRSELDQRKKNSTFIASSAIR
25492	55860	A	25633	170	935	LTQEDTRINLIPMAVESLHLPTQ MLINGGETYAWRNWKRGGQY KSATLNTGQPHVRARELVDSD TLASDAARLTCRHGLALPALFT LIAVVTSLLSPQFIRQILWSRLT KTR*AGDQLDAYSTTEWSGSA TDTHGWGKRPLYTGR*RVHRQ WYGRPASGKRWRCADYRGH* GQTRNTVCPEPAYRTGSD
25493	55861	B	25634	42	755	

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25494	55862	A	25635	793	2127	RYCKGTVMDQIRLTHLRQLEA ESIHIIREVAAEYSNPVMLYSIG KDSSVMLHLARKAYYPGTLPFP LLHVDTGWKFREMYEFRDRTA KAYGCELLVHKNPEGVAMGIN PFVHGSAKHTDIMKTEGLKQA LNK/YTTSRAKERIYSFRDRFHR WDPKNQRPELWHNYNGQIN\K GESIRVFPLSNWTEQDIWQYIW LENIDIVPLYLAAERPVLERDG MLMMIDDNRIDLQPGEVIKKR MVRFRTLGCWPLTGAVESNAQ TLPEIIEEMLVSTTSERQGRVID RDQAGSMELKKRQLIELIINVH NLLKNGFGFQVKVNRIALLAIN VEFFFRLVQLAAHFSSGTLAQD KLCSWFGLNVRDSQRNAIFFQT LADHTIDGELFTFQCIVAVFPNL PIYSYATIYVSSSSIPISSEESPSIR FACSQTSRQPPVSDSRFCVSQV
25495	55863	A	25636	360	566	GAETMGDLLWVVGILLMCSLS TLVLVWLDPRLKS*RT*A*CGA LTSHQAINNGRNEKRKPIRESDP LKA
25496	55864	A	25637	1	312	LLRKSVSVIIKGTIKTIIGFMLLQ AGSGILTSTFKPVVAKMSEVYG INGAISDTYVMQDG*APELGLS PGRFLRHDTDFVLQLGIVMVRL AGDGSLNINAQANN
25497	55865	A	25638	517	796	PTARFGWVKGVDLPAD/CNRQ DRFAIDVRVQGS*\WGCVLPLF RVLLFVSCALLLVSVSCVLRLL FCCSS\LSLFLSGLGGGRSPKAG DVFRDRR
25498	55866	A	25639	47	411	AIKVRELSIKLKMC/YSLIKTLH G*KYRNFMVIGSMVFGKKAITH VAGVKRRTAVVVGFKVFDIQR SQFRIVVTGDLAQLLYRVIKVIT CGHFVRQHGIVLCAGVLHVGD RYQAHVKTLGGLI
25499	55867	A	25640	1	1488	
25500	55868	A	25641	2	298	CCICL/YSYAPIDVW/WG/WNTA GQVQAA*TLKAASSSIVTIPLRN TFIFNYSLSGLRRRRLIIRSRRHS THASNITLIAASTASRIGWFASA YHTRSNHGR
25501	55869	C	25642	1	2064	
25502	55870	B	25643	1	1116	

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25503	55871	A	25644	312	620	SACRCCLVVVPLFVCL/GSSLSL APTFPLLASFSSSRASRVVAFGL GSLRAGSALCLPCAAVVLALRS AGTCLEWWWWHSVVLPPETK RLPSTSLIPYPASVSI
25504	55872	A	25645	2	2237	
25505	55873	A	25646	692	6383	RMSRSSDYDQYRSRNALIRRHI EKMDASLHVGTKEFDISKVSEV DSVDDLLIDNAARYLLKDWKG VGELVNGVEVALEYTAERGIAL LKQNPELYWQILAEAASIAQVG GEVWIAPKFERNGLRLLANSEI GAASQLQTYHRVDPGRPCKLD LSGGMSQRVMIAMAIACRPKL LIADEPTTALDVTIQAQIIELLLE LQQKENMALVLITHDLALVAE AAHKIIVMYAGQVVETGDAHA IFHAPRHPYTQALLRA
25506	55874	A	25647	856	1467	
25507	55875	A	25648	1823	2014	SQEIALMQFRPRLTGASGSP*RP PHRTLLRSDQNAATIPQKRASA LIPLMRILPVRYGHLLLC
25508	55876	A	25649	1	218	
25509	55877	A	25650	2740	3293	IFAVNLILQCHVGGTHHQRFLL FAGNGDAGNQIRERFPNAGG/E LQSPDVALLLRPAFWRRPQSSA AAAHGE*SRGSVPEAPYTRRQF ALPAPPIKCAPLPERQRPSVPSR HLRLPACPGYKNRASSAKPSYS FLAQRQHLQRLSPLPQNQNLPQ RRRDQRQRAGAMSARVPDLISS SRSMRRTS
25510	55878	B	25651	1	1875	
25511	55879	B	25652	1	2981	

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25512	55880	A	25653	1	1649	MTFRNCVAVDLGASSGRVMLA RYERECRSLTLREIHRFNNGLH SQNGYVTWDVDSLESAIRLGL NKVCEEGIRIDSIGIDTWGVDFV LLDQQGQRVGLPVAYRDSRTN GLMAQAQQQLGKRDIYQRSGI QFLPFNTLYQLRALTEQQPELIP HIAHALLMPDYFSYRLTGKMN WEYTNATTTQLVNINSDDWDE SLLAWSGGQQSLVWVAEASGE WGVLACTLFAWNRNYFVLLFV GVFLSSFGSTANPQMFALAREH ADKTGREAVMFSSFLRAQVSL AWVIGPPLAYALAMGFSFTVM YLSAAVAFIVCGVMVWLFLPS MRKELPLATGTIEAPRRNRRDT LLLFVICTLMWGSNSLYIINMPL FIINELHLPEKLAGVMMGTAAG LEIPTMLIAGYFRQTSGPTAYGR SVGRIRRSRRIRQSCYYQRIFSL LACELANALERPENFCGMHFFN PVHRMPLVEIIRGEKSSDETIAK VVAWASKMGKTPIVVNDCPGF FVNRVLFPYFAGFSQLLR/ERRG FPQDRQSDGKTVWLADGPGIS AGRCGH
25513	55881	A	25654	1590	2855	RNLLGEAADPVSGPHSAIYRPD WPKSGDCACQGPIKGSANRPA VVPHVHGP\SEDLEVFLNVFGE LPQPLIDTQILAAFCGRPMSWG FASMVEEYSGVTLDKSESRTD WLARP\LPERQWEYASPNVWY LLPITAKLMVETEASGWLPAAL DECRLMQMRRQEVVAPEDAW RDITNAWQLRTRQLACLQLLA DWRLRKARERDLAVNFVVREE HLWSVARYMPGSLGELDSLGL SGSEIRFHGKTLLALVEKAQTL PEDALPQPMLNLMDMPGYRKA FKAIKSLITDVSETHKISAELLAS RRQINQLLNWHWKLKPQNNLP ELISGWRGISAVKSSEAGLGAL SATSGFGKLQIQHQAFTLRTRT TDQHTLLAGTLFIAKILIPMVSF TFQYCCFAVPQATYCHRIAPIL GNGAMKPGRKIS

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25514	55882	A	25655	1	3315	MDELRLVLMTIIHIKLPPIRRAD GSFGNDLTTGAGFNDRKTVPR YARVHVYRCRKVICIFTKRIPFC LDVPAHRALVVMKGTLYGMP VVAAAFEFAFMGGSMGSVVGA RFVRAVEQALEDNCPLICFSAS GGARMQEALMSLMQMAKTSA ALAKMQERGLPYISVLTDPTM GGVSASFAMLGDLNIAEPKALI GFAGPRVIEQTVREKLPPGFQR SEFLIEKGAIDMIVRRPEMRLKL ASILAKLMNLPAPNPEA
25515	55883	A	25656	246	422	RHADTDLRR*ISDRFSPAPPADP ANGGR*TPRHAAKRRDPGTPV QPARKPSKPTRLLR
25516	55884	A	25657	884	1276	LVTRQLSPGNRCNVFAFSSAVE TSLTCQGWLSPVCAVCQAISSS HNASIQVRSPAASCGSPFCSKRP SALWWTSVSPFLSPRRRTSGAN AESVSAT*SKRRSSARRSASARS TLSGAALRSRTASNEWRS
25517	55885	A	25658	649	1427	LPLLGWSMSPRMTAQLACDAL QMALWRRKRPRNVIVHTDRGG QSVQQFRALKRHITASRETERF YLDVQKQFPKVTAQKVIVSEA GASVYSASELAAQEFPDLDVSL RGAVSIARRLQDPLAELVKIDP KSIGVGQYQHDVSQTQLARKL DAVVEDCVNAVGVDLNTASVP LLTRVAGLTRMMAQNIVAWR DENGQFQNRQQLLKVSRLGPK AFEQCAGFLRINHGDNPLDAST VHPEAYPVVERILAATQQALKD LMGNSSELRNLKASFLDNEEN WPLLLDALIPVANTCEMILMPA CFGLADDKLWRWLNEKLPCSL MLLPTLPPSVLGIRLQNQLQRQ FVRQGGVWIECGDGGDTTTITI TQR**PAGRVYRSPGSLSGGGT HSGSNTAGTERSDG
25518	55886	A	25659	1	1878	
25519	55887	A	25660	1	4329	

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25520	55888	A	25661	2514	4173	PTSCLPDDYVGHCRGVSAAHF AGSVSCVRLLSACARPLWRHL GLALLRVWCRTFLLLSALASVF CPCSVVWGRLLFSASLSVVVW GGVFLSPLGSLSPRGTARLGAA CRSRED/RRR*WRGIFNRDTFAS AVPASVNPDKPCAPAACIRFTS TSAY*VGCSDRNA/DAEASGEG WRRFGDATLSTGQFGGEAREE VILGLIGSQA\KTGGNTPKASAV RKITLVAWPALETGLTMLSM** IG*ETRVFSVFEPSSKSIVPSSRT VTFSSNASRRIAL*ISGSASFDSL IVFA*QPPSKLNTPSSSQPCSSSP IRRRFGSVERVVLPVPERPKNT ATSPFSPTLAEQCIEAIPSAVFA APVRVAASMIISGFCALASIRPS ASTRRPSASVFITSTFLPLR*VMI SPSLNALPLIRLSAQQRNSFTRL FSPRVMANASAPVTVAAPPMS DFIESINAVCLMQARVHWRFFI ASWVVIQPPAIPENVLNRVRLC AAPGTLCLTTFVSSSGDR*NAL CNRCNRPAPCFRSSAIRFATVLA ARRHDWVWPISPLIPRPSS

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25521	55889	A	25662	2221	4400	RGCVVSGKSSCSKTNLPSDDKR TGASCPLRDLFLRYLRAHALVT AEQLAHEFSLGIAIVEEQLQQLR EQGLVMNLQQDIWVSDEVFRR LRLRSLQAAREATRPVAATTYA RLLLERQGVLPATDGSPALFAS TSPGVYEGVDGVMRVIEQLAA SAINASLWESQEFVYGKPVYAV GENYSQGQYYLASFANKIWLSP QGVVDLHGFATNGLYYKSLLD KLKVSTHVFRVGTYKSAVEPFI RDDMSPAAREADSRWIGELWQ NYLNTVAANRQIPAEQVFPGA QGLLEGLTKTGGDTAKYALEN KLVDALASSAEIEKALTKEFGW SKTDKNYRAISYYDYALKTPA DTGDSIGVVFANGAIMDGEETQ GNVGGDTTAAQIRDARLDPKV KAIVLRVNSPGGSVTASEVIRA ELAAARAAGKPVVVSMGGMA ASGGYWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTD GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADARH STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEIN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA
25522	55890	A	25663	1	1665	
25523	55891	A	25664	475	1182	
25524	55892	A	25665	242	3059	
25525	55893	A	25666	1761	1970	
25526	55894	A	25667	455	1137	GTKPRDIDHILGTFITPGMPKGG KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHD VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG
25527	55895	A	25668	1108	1932	
25528	55896	A	25669	1496	1631	
25529	55897	A	25670	462	1152	
25530	55898	A	25671	545	598	

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25531	55899	A	25672	1	1761	MRGHNWIDMDQARQQSTPHT DRKICHKNDRPRTTPLRKIDAH PHTLIILPAESTLSTTKYKLRAL LVENTNKDKSAVSVVFRGSVL HQQAANFPNLMLCFQLKNGVN ACNDFIMLFVDDNAAGSIERAA SPCINEKQHAFSESVPAIAAVRG LGSMIAVEFNDPQTGEPSAAIA QKIQQRALAQGLLLLTCGAYG NACKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKLT PVIQPRASGEYNEEFSLLPVVN YLKDKLSNPVRLVKDYLDGVD VAEGELVVLENVRFNKGEKKD DETLSKKYAALCDVFVMDAFG TAHLRAGFLLTGI\GKLRCSLRC AGPLLAAELDALGKALKEPARP MVAIVGGSKVSTKLTVLDSLSK IADQLIVGGGIANTFIAAQGHD VGKSLYEADLVDEAKRLLTTC NIPVPSDVRVATEFSETAPANL KSVNDVKADEQILDIVRDLDAA NVVINAVFSYVTNVWGWAFE WYMVVMLFGWFWLVFGPYAK KRLGNEPPEFSTASWIFMMFAL LYVCCRTVRLGREIHRRAQIVH IDIEPTQIGRVLCRISVLSLMLKR
25532	55900	A	25673	1	984	
25533	55901	A	25674	1	1181	MMAVSAPYVGDNIDDGGIYTQ SETHTISSDCVLDTAAMWTPLS AVIGCTTNPAQYPANAAEVYN KDGNKLDLYGKVDGLHYFSDN KDVDGDQTYMRLGFKGETQVT DQLTGYGQWEYQIQGNSAENE NNSWTRVAFAGLKFQDVGSFD YGRNYGVVYDVTSWTDVLPEF GGDTYGSDNFMQQRGNGFATY RNTDFFGLVDGLNFAVQYQGK NGNPSGESFTSGVTNNGRDALR QNGDGVGGSITYDYEGFGIG\Y TQTYNATRVGSLGWANKAQNF EAVAQYQFDFGLRPSLAYLQSK GKNLGRGYDDEDILQICCMSDP TQNRQASAKLALPCQVALLSSA SPHHAFTPSTSIIQPAHIIIHSSPP PWASSHSISTHQQHTQCSSSSNT LAVH
25534	55902	A	25675	1	147	

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25535	55903	A	25676	683	947	QVRDSLQQGRERRIALSIGWLV WREGCQDQCELEAGGASALTR RGSCRELDPAPFATMLLFCPGC GNGLIVEDG\QRCHASTDAVPP
25536	55904	A	25677	12	393	RGSCRELEPAEFETMLLFCPGC GNGLIVEEGQRCH/RAVACNT\ CPYVHNITPQGNTIWKYPKLKE CGSDVLGGAAAW\ENVDSTAE SC\PKCEHPRAYFMQLQTRSAD EPMTTFYKCC\NAQCGHRWRD
25537	55905	A	25678	234	567	YVDETDDCFENNRCGQPVNGA YSPAGLSRVAADASLTTPHAK* TLRSLTLHQHDKTRTELLNDVA GALALDDKLGRSTNQLSGGEW TPSLARPFLLLGPRKMRLLPLH LPP
25538	55906	A	25679	1	794	HCDGKHFTGVGKIMSIGMQLQ DVAESTRLGPLSGEVRAGEILH LVGPNGAGKESLTGREWPEMP TVKGTIQFPGHPLEAWSAKK\L ALLRAYL\SQQQTPPFPPPVWH YLTLHQPDKTRPELLNDVAGA LALDDKLGRSTNQLSGGEWQR VRLAAVVLQITPQANPAGQLLL LDEPMNSLDVAQQSALDKILSA LCQQGLAIVMSSHDLNHTLRH AHRAWLLKGGKMLASGRREE VLTPPNLAQAYGMNFRRLDIEG HRMLISTI
25539	55907	A	25680	12	414	RAAPSRNLPPRMPIPIAAPIAAR PIITAAAMYSRSIFRFSMTVSSLF QLKRSSVGKLMFFRRHRQIDDR QNHEDEGLQRNDQDVENGPRH IQDPL*PPRQETSNQNEDQLSGV HVTEQSQTEGSWFGQHAYPF
25540	55908	A	25681	568	724	RFSLGTVLDGIYPHQYDGYSR WSAKRYL*WRNL*SGTHRSC* VNNFTRSNKK

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25541	55909	A	25682	1	974	MNGKLQSSDVKNETPYNIPLLI NENVISSGISLISLWHTYADEHY RVIWPRDKKKPLIANSWVAVY TVTGCGNSDRLNNIRTLRA\MA REFSIDVLDEMLQQFRVVTPDR PEHKQLPQHELAERQEKISTWL ELMKADGINPEELLGN\SSAAA PR\AGKKRQPGSAKYLFT\DVN GETKTWTGQGRTPKPIAQALAE DCHGKPEYGSAVHGCRCDDGS AGNLCFDLNRHCGLGVRLRPR KINGDYRSRFCHAGETGVCAG AETTQMAESGVSGAGLAVRGE RDGKRSPLQIAIMMNGSSGQAI SSNVIILQLFLVEVIKSLRMLYM
25542	55910	A	25683	1	1359	
25543	55911	A	25684	1	918	
25544	55912	A	25685	72	690	PAPVAGAHCPLGLHRSSEHQEP QLRHVARWPSS*SWLCHGTFR KLLPGKKRRGGNKKF*GRRAR GVGCVVSRVWCGPACACSLRR WLAHTVHWVFTEAQSIKSHSS DMWPDGLALSPGCAMGPSGSC SRGKNVGGATKNFRGVHNIYC HKPIPTTQHESKYARQTTTEEC TQTSSHDFRTTFSAVMQQRLQI ARNLVTHPKLVFMDEPTGGLD VSVQARLLDLLRGLVVELNLA VVIVTHDLGVARLLADRLLVM KQGQVVESGLTDRVLDDPHHP YTQLLVSSVLQN
25545	55913	A	25686	1334	1545	RSQSRLERSCSVTGSM*RVSPA RSFRRITKRVLAAARLAT*LPAS GRRTGVGVSVDSEFPSELLSSSF TD
25546	55914	A	25687	1784	2125	WLQHIHPQLLRCPVLRAQNVW IRTLYDRH/RFVTRGTLGWIETG DF/DKVPPDLRFFAGGDRSI/RG YKYKSIAPKYANGLDIGKSPAA GAISPCLTFVMSARRGGHRGQS ASGCRA
25547	55915	A	25688	931	1213	NLHPAPAKRRAPARPQSRLAHR QRGRMRGAPRPFRQRQIKLCY ARCTPTICPTKVKSRSNTVTSG* TWSPRQRAKWWKSAKPPSAGL TSSARHP
25548	55916	A	25689	999	1243	VDPVPWLPMALDITSTAPARQF RKRIIASLMPT/WGTSLRRYSVP PRRSGWKRWRFPPTGSTTCRPP FPAVCSSVCRLPATW

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25549	55917	A	25690	1225	2341	ARTFRLSNFGGSTRARGVYWD PNSDLCPTLDFSYKMPLLKNPL EQYYLVQGGFKRTDLNDTESD STTLVASRYWDLSSGWQRAIN LRWSLDHFTQGEITNTTMLFYP GVMISRTRSRGGLMPTWGDSQ RYSIDYSNTAWGSDVDFSVFQA QNVWIRTLYDRHRFVTRGTLG WIETGDFDKVPPDLRFFAGGDR SIRGYQY\KSIGPKLPNGD\LKG ASKLITGSLEYQYNVTGKCTK WQFGEWLAPGEVRLAPGATLA TPELVASCSTEGLNGLAANFHA ELRARLPWHGGAMKPRPVHLN TWEGFYFDLQPDKVKALATAA AALGVERFVLDDGWFNARHH DRAGLGDWWPDATKFPQGLG ELVAHVNPFYA
25550	55918	A	25691	45	233	SSYPRWWAAWWASTTARPSTR WRSSPR*SATTWASSPSPTSP*I HDRPGIGATHSSRFIPLK
25551	55919	B	25692	1	558	
25552	55920	A	25693	324	657	
25553	55921	A	25694	831	1244	WQPGGR*WSRQRSADGTGPDD LAAAYFPGDRFYRN*PSERC*H RRG
25554	55922	A	25695	1	1215	
25555	55923	A	25696	1	840	
25556	55924	A	25697	1	1365	MPQNRGGFLDKKNPGAPLEGA VYVNCFTRFPGIGYEGRTAVFC GAAKVPPGLNYRGIGAFPGGNF ASKRSRGRNLAGARCLRFCPK\ WQ\NYSETASVQQQN*SVLARA IERGINAPLA\SSCGRFFDAVPA ALGCAPATLSYKGEAACALEA LAASCHGVTHPVTMPRVDNQL DLATFWQQWLNWQAPVNQRA WAFHDALAQGFAALMREQAT MRGITTLHPEGLERMSAGHES WLERRNGELGEGKGSKAYPTG DHKGADLYDDSNFLIQNIFVED TRGLLRQGREDLIERYKDPLNE NPKRCVEQLANWHKELEEYKK ASRIDIKPSREYASTIMNAIWTG EPSVIYGNVRNDGLIDNLPQGC CVEVACLVDANGIQPTKVGTLP SHLAAMMQTNINVQTLLTEAIL TENRDRVYHAAMMDPHTAAV LGIDEIYALVDDLIAAHGDWLP

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25557	55925	A	25698	1	950	MPDEENRFNALKAVFSQLMTD ATLTPLFNYHYRISAPPGVNGL SMKRAVVVFSGGQDSTTCLVQ ALQQYDEVHCVTFDYGQRHRA EIDVARELALKLGARAHKVLD VTLLNELAVSSLTRDSIPVPDYE PEADGIPNTFVPGRNILFLTLAA IYAYQVKAEAVITGVCETDFSG YPDCRDEFVKALNHAHKEKLD EDCKRRMYTNPLRVLDSKNPE VQALLNDAPALGDYLDEESRE HFAGLCKLLESAGIAYTVNQRL AVNPEFKADPVVDIYLVASGA DTQSAAMALAERLRDELPGVK LMTNHGGGNFKKQFARADKW GARVAVVLGESEVANGTAVVK DLRSGEQTAVAQDSVAAHLRT KEKDSVEIYENENDQVEAVKRF FAENGKALAVGVILGVGALIG WRYWNSHQVDSARSASLAYQ NAVTAVSEGKPDSIPAAEKFAA ENKNTYGALASLELAQQFVDK NELEKAAAQLQQGLADTSDEN LKAVINLRLARVQVQLKQADA ALKTL*IPD*RPDAGLRCKRSPR SPAVCTDRQNAHEIPRPDSHLM PERR*EAPALPDFLNPARAAG
25558	55926	A	25699	1	3314	MKISRLGEAPDYRFSLANERTF LAWIRTALGFLAAGVGLDQLA PDFATPVIRELLALLLCLFSGGL AMYGYLRWLRNEKAMRLKED LPYTNSLLIISLILMVVAVIVMG LRAMLMAMEPIWESDFHTLSY GFRPERSVHHAIRTVKLQLTDC GETRGRWVIEGDLSSYFDTVHH RLLMKAVRRRISDARFMTLLW KTIKAGHIDVEDKRAASEGVPQ NKIISPLLSNIMLNEFDQYLHER YLSGKARKDRWYWNN
25559	55927	A	25700	997	1716	PYLTASSSAFQQLHLSGENHRD DGCAGYSRRTLAAQLQCHCEC DHNLPPDTPRLPRSGVVLPARF PRPLHTLISALHRRVLTRHARH ESSTLNPQRLPPAHRFFACQSRY VPGPAEYSYAVRSTDESG*A*W LRVPPNLIALTVQRSLPDLALPA QNCPPCRSMLEPAPYILLGMLA TWPACPG\HEVG*SHSAHPDEP ETLQTVSR*YRRFGRPVH*SVH VVGRYPHQACQCYLSSTAE
25560	55928	A	25701	1	769	

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25561	55929	A	25702	1	3707	MVRSAVVAGIAQAALPQSVVA WEYLVEDYDRIRNDIEAVLPEF ADYNQRIRHPGGFHLINAAAER RWMTPSGKANFITSKGLLEDPS SAFNSKLVMATVRSHDQYNTTI YGMDDRYRGVFGQRDGYRDN CEEIAQLAEDCGNLFAVTVFRC PAGANLQGNRNVHCIDDLGKD RFNDIRNVQAAELLAEMAISSA QRRMRAAKKVVRKKLTSGPAL PGKLADCTAQDLNRTELFLWK GEQNALLRGFPAVRLHSLL
25562	55930	A	25703	1	369	LPSHGAGLGTCSLPCLSLPPTP WAPVQPEPPRRAPPPAPWRPVP LTTQGLRN/DEHRVQDWQAAP PAAPLKVCKYTNQHPVFSTRFV NAPIDTLYLAALVRTWRTFMSS SRIVNTPIGTLYLAQ
25563	55931	A	25704	1	444	MRLHSSALGRSMGLGAVEQGA ALVGEAPAAQEPTEAGEGSGM AGCSPKACPAGRQLRPGPA\AA PSAGPPSPRPPGTPAGPQAPRAA PVPARASPSTPPCKLRERAAAF A/EPRKGLPQCSGGLKGSSSAA KVGAQAEEAPRASESCEDC
25564	55932	A	25705	1767	2130	YTGQRLRRVYWVPQQCQPTCA ALDFSPSLSCLPA/AAGLRTYSQ PCLSLPPTPWAPVQPEPPQ*APP PAPRRP\AHRPPKG*GVQAHGA G\RQAAPPAAPVRDPLG\KPAGL LSLVGTWRTFMS
25565	55933	A	25706	654	832	RRCARFLAGP*LPSHGAGLGTC SPPCLSLPPTPWAPVRPEPPRRA PPPAPRRPVLCVFS
25566	55934	B	25707	1	537	
25567	55935	A	25708	1	455	HCGSVIGGFLVSLTLRTKLRTL AVSVTALTVVCLEFIPSDVRMR SVSSFWWVRSLAGSRVKLQTF AVTVTALKAASLELFVPPGGLV VSLASGVKLQTAAAGK/RCLPV LRHAPALLSPWVVDGTGHRGA GGGAHRGGSGRPGAHGGGGRL
25568	55936	A	25709	1	314	SACREVWRERHEREPGLRGAL AGQLEFRVGVGLVRPALGGAG QPGAALDFSPGLSCLPA/AAGL GTCSPPCLSLPPPPWAPVQPEPP RRAPPPVHGAQSHRPPKG

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25569	55937	A	25710	144	519	HPGQRLRRVYWVPQQCQPIGA ELDFSPSLSCLPA/AAGLGTCSP PCLSLPPPPWAPVQPEPPQRAPP PAPW/WLSPIDHPRAEECECTA QDWQAALPAAPVWDPLEMSG LFDRAEKRYIRSFARKDSM
25570	55938	A	25711	271	743	ARTWNVPKVCVRIKANSHSIFT GLSCLPAGQGSGPAARHA*ASD PLRGLLCGPSLLDE/PPPPAPWR PVPSTTQGLRSAGEQRGTGRQL HLSAAPVRDPRGEAIWAPESGR SAASILKPARPPAHREERTTPDA PP*EL*HSPRRSAASLREDPWLH S
25571	55939	A	25712	1043	1348	GPARNRAQRRRAGTAGGPITPS AAAGPGAKPLIARRRQGWPAA PSAGPAKPTPTRISSWPAS\QPA AAVPARASPSTTLFKLREWAPA LASPERGSHSATVG
25572	55940	A	25713	22	226	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKAVDTQ RH
25573	55941	A	25714	166	714	
25574	55942	A	25715	1	462	

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25575	55943	A	25716	1	924	MFAIISYSSLAAVLLTATLTAAG IISFPVALCLVIGANLGSGLLAM LNNSAANAAARRVALGSLLFK LVGSLIILPFVHLLAETMGKLSL PKAELVIYFHVFYNLVRCLVML PFVDPMARFCKTIIRDEPELDTQ LRPKHLDVSALDTPTLALANAA RETCALATPWTDDGRKYAYSA ASGGRRSATKVMVVVTDGESH DGSMLKAVIDQCNHDNILRFGI AVLGYLNRNALDTKNLIKEIKA IASIPTERYFFNVSDEAALLEKA GTLGEQIFSIEDMDLGDEVYTV GRPHPMIDPTLRNQLIADLGAK PQVRVLLLDVVIGFGATADPAA SLVSAWQKACAARLDNQPLYA IATVTGTERDPQCRSQQIATLED AGIAVVSSLPEATLLAAALIHPL SPAAQQHTPSLLENVAVINIGLR SFALELQSASKPVVHYQWSPV AGQGKWLANPELLEADADAEY AAVIDIDLADIKEPILCAPNDPD DARPLSAVQGEKIDEVFIGSCM TNIGHFRAAGKLLDAHKGQLPT RLWVAPPTRMDAAQLTEEGYY SVFGKSGARVSSIPCAVPCVWA RVADGATVVSTSTRNFPNRLGT GANVFLASAELAAVAALIGKLP TPEEYQTYVAQVDKTAVDTYR YLNFNQLSQYTEKADGLLKPRF RPWQRKILDTLATYHEQHRDEP GPGRERLRRMALPMEDEALVL
25576	55944	A	25717	1	417	MGVLNNWLSEEESLWIQSRIHL RALRYYSNWRQYFAGYTFGRQ YWQSPEDDHLPLLREFLARYER PMKNCWKILDIEETTDVDIIRRA YLALLPSFHPETDPQDFKQLRQ AYEEALRIAQSPAKSVWQPEEY EVAEHEILLAFRALLASDSERFL PSAWQRFIQQLNYCSMEEIDEL RWSLCTIAMNTAHLSFECVVLL AERLRWLQEENTGEIDEEELGS FLYAIAKGNVFNFQTILHLPVA RRPDICTQHNDQSRCEGYQILS DKRGHQHGGGITALYQCGNAD PRAKGERLFFDAPA*CASSARV CVLSLAGASKKSRSPFARGSAL PHWYRAVMPPPCW

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25577	55945	A	25718	1680	2058	YRAYAPAFLPLSPSCPPLWRHC GSGRGENRRRDSSAHGPYAPRR QPDMPAHRQS*SFV/PASCSAC MDEPHKRLTVTAGTECGTSASS AALRAILKPCSSVCSSFFLLLLL PPPPPSSSSSSFFFLF
25578	55946	A	25719	1115	3549	NPDRLLQLNLILETSK*QQMGD TRKKRS/NLTVAPIISPLKRYEQ HTELSRHINVVNLGDRNRRQQL ILDQGKSSQRNIYLSHVAQKIPG RATYALSHSVDMITIQLGTLLR CAPPHRRRYAGRFFCRSAGNFL NVQGFDAVLVAVKHDLLLCLT IAPSLIVCTRLRSPWCGALRRCS TDGRSDLASSGVMFSIDTESAL TRWCLSLPHGALGKIIAEGLLS VIASKASAIVTTVAVVPVTRRSS LVNWHSGGSGLWRCNRTDERD QQASQGTTRMGRTQRNYSPTR QAIHKTGSPTMATTSNTEQPPH EKPNTLTQHPRNPDRTIHPKAT HNELTQDTPQRDAKQNGEKTQ RKKNCLSELNDAEDQAERFQD RLMLKLQVTTKPCSMTRLRDC AGIWSAANRWSGIGIDRMIMLF TNSHTIATLFSSRRCAHRNKFH LMNEAVRRLLRSSFRKSVLRRD ASFHDNQRVHSLQLLKERKKSL IHGRICAAKASLFQTRRYRWQK APLFSAQFRGRNRAVTHNRWV TTTTAIERTRARGLRPNSGRGF HSSPAWQLRHRKCRRCARRYH TVYWIKRRRSVARASTVVSGRI TSRRGENRRRDSSAIAHMLHAA KQTCLRIAVMIIRAASCSACMD EPPSDLTVTAGTDAGLAPAGYA LNERRDLLHALTKSTALRTAHR GPNRTGWLNRRIVRFVMTALF
25579	55947	A	25720	606	1562	
25580	55948	A	25721	688	762	
25581	55949	A	25722	492	737	SLPSGATLPPPALLLASAPDTA* WRCRER*YHLPAYAALSPAVA HRASLYSTLPSSVPWRRQCAGF RARRSPEQAWAYPAR

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25582	55950	A	25723	335	903	WVHDLPARKGSSARNIMLKSA PLRGHTRTRRKKMNIIEANVAT PDARVAITIARFNNFINDSLLEG AIDALKRIGQVKDENITVVWVP GAYELPLAAGALAKTGKYDAG IALGTGIRGGTAHFEYVAGGAS NGLAHVGQDSE\IPVAFGVLTT ESI/EQAIERAGTKVGNKGAEA ALTALEMINVLKAIKA
25583	55951	A	25724	3644	4545	SEAWPWRTAGTCLLCLNTT/AH VDKAIESRTVVADVLAKFENAL TGKLLTVSFQAHEAVIHGHHPA PEENLQVLAALRLQYLQGDYT LHAAIPPLEEVYSLQRLKARISQ STKTFTPCERLEKRRTSFLEGTL RRSFRTGSVVRQKVEEEQMLD MWIKEEVSSARASIIDKWRKFQ GMNQEQAMAKYMALIKEWPG YGSTLFDVECKEGGFPQELWL GVSADAVSVYKRGEGRPLEVF QYEHILSFGAPLANTYKIVVDE RELLFETSEVVDVAKLMKAYIS MIVKKRYSTTRSASSQGSSR
25584	55952	A	25725	1	735	
25585	55953	A	25726	147	504	STCPASAPPRPSAGPRILSGSSAS GSPLGSSSASSPAVHKG*RFWL TG*CGP*VSAGNK\LFERWDGS VQSIIPLQILESQGSKNLEVFFRG WMVAMDNRFVGLKGDSQQLS GQRIFKLG
25586	55954	A	25727	1	639	
25587	55955	A	25728	1	1247	

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25588	55956	A	25729	1	2376	MAEVEEKKQRIFRKFTYRGVD LGQLLDMSFEQLRQLYGARQL RRLNHGLWRNAEAQAAFAAE APMLGQEGGADHREAGSGEDA PAGYDHPSQDGGQQGGRLQRQ DLQPGGDQAGDDRPRPGRVLH HLQAQRGKKPM/ISTVTFGQ*P DPPLRAGQRL*RC/RLLIYGRGK CWALSGNP/RSGKTTLLKSISAR LTPQQGEIHYENRSLYAMSEAD RRRLLRTEWGVVHQHPLDGLR RQVSAGGNIGERLMATGARHY GDIRATAQKWLEEVEIPANRID DLPTTFLRATHTVKMFSIPGYSS PGQLLDPETNINIGTSYLQYVY QQFGNNRIFSSAAYNAGPGRVA TAIVLTLYIIYMVGFFATSGELT YEVWIGFFASAFTKVFTLLALF SILIHAWIGMWQVLTDYVKPLA LRLMLQLVIVVALVVYVIYGFV VVWGMRAALQISQSGQTCALL SKVFPTRSHTVSAQGGITVALG NTHEDNWEWHMYDTVKGSDY IDAGRKRQEEGDWNSGVGDPS DAGDRKHQLKAAQLRPEAIKQ RRIANRLKRRTQFPRHLKGFVN TLKPIHGGCSVGTKCPQMASLP EGLHHPVKLVFLGKPGCLLTDR PLKGPNTAKPVAVDLNASATAI TSYSLYGGSMILLFLASTLYHAI PHQRAKMWLKKFDHCAIYLLI AGTYTPFLLVGLDSPLARGLMI
25589	55957	A	25730	219	652	SASWREAICLSRCRLPRSATAR GAGRGGCGLADRRASRQGKNL EAESAQEQNGHQHRIHESQHPC QGGAPVSHHQAAVRLRESQIQ GAAEKR*PTGDVIHPGQPVSGG /LK*YPSIPTCLLTTRTASLLKPP GVRTSVCWQQLPR
25590	55958	A	25731	1902	2100	RKFFSSSSGRS*PVRCSKL*SSID A*PLERIKRSRSYQVGSVGLCL RKSFHSTSAISAMPIGAPG
25591	55959	A	25732	3223	3669	

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25592	55960	A	25733	1	4325	MPEPPTHSMGSCAAGASLTSTA PCSTAPSPIDHLRAKECERTAQ DWQAAPPAALVRDPLAALVRT WRTFMSSSRIVNTPIGTLCLAQ GFQWFSVLSQVHASTDQEIQE MHDEQANPQNAVGTLDVGLID SVCASDSPDRPNSFVIITANRVL HCNADTPEEMHHWITLLQRSK GDTRVEGQEFIVRGWLHKEVK NSPKMSSLKLKKRWFVLTHIPG LLQEFREDALNWGPDEKIFKET ELVNDMDKINGRIERAE
25593	55961	A	25734	501	2871	TGCCCLRKTDCRRRESARGVH AVYRRICARSMLLYRESVRPKA VTARVAVEAGIADYWYKYVG LNGAIVGMTTFGESAPAELLFE EFGFTVDNPLASRAVRLRLPFN NDQVEAAVGWKLAVERHNGP TALILSRQNLAQVERTPDQVKE IARGGYVLKDSGGKPDIILIATG SEMEITLQAAEKLAGEGRNVR VVSLPSTDIFDAQDEEYRESVLP SNVAARVAVEAGIADYWYKY VGLKGAIVGMTGYGESAPADK LFPFFGFTAENIVAKAHKVLGV KAGSHIPRKKYDVPGKKSFSPV KYSTIGSPSPERPVSITTIPNSFVI ITANRVLHCNADTPEEMHHWIT LLQRSKGDTRVEGQEFIVVEKL IRGLAMEDSRNMFALFEYNGH VDKAIESRTVVADVLAKFEKEP VGKHLPTYDGQIAMGLESTAS VTRKHSSPSSLQNALSCETATSL IERRVRMALGTGDRRGLNTWL ARLPMEAKEKDEWRYWQADL LLERGREAEAKEILHQLMQQR GFYPMVAAQRIGEEYELKIDKA PQNVDSALTQGPEMARVRELM YWNLDNTARSEWAN\LLKNKS KPDRAHLPGYASTTQWWILSV QATI\AGNLGDHLKERFPLANN DLSKRYTSGKKIPQSYAMAIAR QKSAWNPKVKSPVGASGLMQI MPGTATHTVKMFSIPGYSSPGQ
25594	55962	A	25735	1	1195	

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25595	55963	A	25736	1931	2676	FCGNTHQTYLGWVGGVANSEA *GEKWGTPDLVG/AERTETIQR LLGVCPEQGEGKIYIDGKQVDI RNCQQAIAQGIAMVPEDRKRD GIVPVMAVGKNITLAALNKFTG GISQLDDAAEQKCILESIQQLKV KTSSPDLAIGRLSGGNQQKAIL ARCLLLNPRILILDEPTRGIDIGA KYEIYKLINQLVQQGIAVIVISS ELPEVLGLSDRVLVMHEGKLK ANLINHNLTQEQVMEAALRSE HHVEKQSV
25596	55964	A	25737	1491	1667	TNGQWRAFYC*MRSGRNIRRR GEDISGGAGVSPRESPE*REVPE MGPGGAANRGTKRV
25597	55965	A	25738	419	823	VTLVAITRPIHVNRLRQYLVAIS LNETFGPSCKPSRSPCSSLSTCC WNAGVMHKK*VQGGRLCSYR N*SICLVVISPVVMGKRCIS*RC TAVLAALTVTVPSGVVAAHSV MLPRLPMKRSSIVPLPSNWRTS
25598	55966	A	25739	591	968	VKQCKQADEH*EQSLIPLERRR TTPLSVPQL/GKALTTVSFCASG GTSVNSLSHTS*ECMASAVAVK FTFPNLAVNFCTAAMAGPKVA LTSTLARIQAGSLARTGGRAYR WSRSTMLAKSFWCLMAL
25599	55967	A	25740	764	1005	QARPRAPRRAPYPILIRSSIITLIY /DGQRLGHLDDGTDSWNHVPT LNGQCTLVLIHEYVDTRGPEIK TILVISWWNILVFH
25600	55968	A	25741	463	786	
25601	55969	A	25742	3	646	
25602	55970	A	25743	1	3008	MTMLQIVGALILLIAGFAILRLL FRALISTASALAGLILLCLFGPA LLAGYITERITRLFHIRWLAGVF LTIAGMIISFMWGLDGKHIALE AHTFDSVKFILTTALAGGLLAV PLQIKNIQQNGITPEDISKEINGY YCCFYTAFFLMACSDQRRLRG AMDKRYKFILVGFGEVFVFNLE SLDSGKKIHLLRRSHEEVMGSV MRTGTIDKGILPFIHHTRGNEIL FIPALFILFSLGGAVFGMGEEAV AFAIIIA

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25603	55971	A	25744	2	3494	TITNLRPAAPGICEMAQGLSAG GEYTGASIFVAEYSPDRRRGFM GSWLDLRSIAEIELGAGGVGLIS TIVGEANFLDWGWRIPFFIALPL GIIGLYLRHALEDTPAFQQHVD KLEQGDREGLQDGPKVSLKEIA TKYWRSLLTCIGLVIATNVTYY MLLTYMPSYLSHNLHYSEDHG ALIIIAIMIGMLFVQPVMGLLSD RFGRRPFVLLGSVALFVLAIPAF ILINSNVIGLNLLPAMFPTHIRYS ALLLEMKN
25604	55972	A	25745	1	277	
25605	55973	A	25746	902	1006	
25606	55974	A	25747	2	1265	
25607	55975	A	25748	409	525	
25608	55976	A	25749	91	431	NHKPGNIDVARRIQRGFAGDQI GHLRPVERQCSPDKRRFIAADG REIRGKQRAGHIFQLLSRCLLQI LNHCQRRAAHFRFQLSNQRHQ QLLPV/HYHAAEREYPAGACLV RWLL
25609	55977	A	25750	3	71	
25610	55978	A	25751	1	1212	
25611	55979	A	25752	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVWDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGPGRLPFNRIGLIRRITRRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSGLKRVYHSPG APDIREFTRDAIP
25612	55980	A	25753	5	402	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI
25613	55981	A	25754	48	219	PETCGHLWAYVWPSCAAV\GL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25614	55982	A	25755	1	912	

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25615	55983	A	25756	1	1857	MRVCARACVRTRTRMCVYAH TCVCVRTYAYVRVRVRVHVRA RVRVCAYARTRVRNSLSILPFIQ LTLATPIHHIHQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLIRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPLALLLAFLCSTSPGF GDPDGLGVIAYQDTVRPNAAT AISELNALAVKGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTLDDRVVAGSAGRYGGDGA GDSECVKIVAQEIRQTDRNIER DRSPRPSGERVRVRGKGGIEAN QPLSTAFTNQITIRQSIRLFSNQF VFHKGISRVVAGSSAIISNVSPG CILRTPNCRRGFPISCTGEGKAA YGWQRDGGHAEYLLAEEKDLI LLPDALSYEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDVY/V*IGVARVSWMNGRID SELRTRVRAYAHTRTRARTCTR TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
25616	55984	A	25757	3	1180	SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFVDL LPAQQRMKGENWYRGTADAV TQNLDIIRRYKAEYVVILAGDHI YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIEFVEKPANPPSMPNDPSKS LASMGIYVFDADYLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHPFPLSCVQSDPDAEPYLAR CGYAGNFMESEPRSGLIRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRPVPDPVELVLV AAEFITPGDPTPRLHGSGFIDIR QIHHQTRSHLEGVKTGIRFLNH FSGNPQGGIAHVNGVARFQVK QCHQAWGQQYAARLRFQARGI SLQIAIHRVDIIHRFDVRQL
25617	55985	A	25758	16	543	
25618	55986	A	25759	1	3387	

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25619	55987	A	25760	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTPFGVC TSASMNVPVLTLRIRTRVTGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/WVAGTFD*SVWF GHDTDVVTLYRFHEALCYSVT LRTPHRRVLRFKSQHPGELACFI SPVA
25620	55988	A	25761	905	4762	PPHNWMPSNATPGIAFVWCAY GAI/LPGDAPVPVVDDYRKVVR KDTKGLIARWKYFWMSVIALG VAFALYLAGKDTPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTDGLDGLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAVLLRQEFLLVIM GGVFVVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25621	55989	A	25762	1	1448	MCHVLLAGRQRRTAGPEHALT PPECGSAAIGPAVYKWAHATG VMIPDRPRSPHAGAEERHWHH PQPELISQRLGSFSSGPTKYIHEF QYLTLSYNLTWSDLNVILTFILP LDEWERVFSLAQSHTDNCRLH KPDLQEGIREVPQEDPQWNYQ ENSPGIARRDYMISCLVEGLKK AAYKAINYDKLKETTQGTDKN PAQSMACLAATMRHFAALDPE ALAPHRDVNHGIKLTCKTIRSSI DISREIRAPRECRSTEMASWHPP ADLTECPVESGYSVLSGRTDCQ YSHTVRRACLTTIDSRPAVRQL LKIREVQLLSLLRGCVRSRRSGS INAQYCRCLERVVTLPFFDSGPS LMNHAPHLYFAWQQLVEKSQL MLRLATEEQWDELIASEMAYV NAVQEIAHLTEEVDPSTTMQEQ LRPMLRLILDNESKVKQVLQIR Q\DGLAKLVEQLRHLSKKHHLD TDSTSSSLPGVRTPYSPIRGGEE

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25622	55990	A	25763	1029	1665	RPESISSVASKTRLGRSFHGAAR RTREYHSSTCNASIAAAATV\A AQGHPDTTSTPPASVDTTATNT QTPAVTAPAPAVDPQQNAVVS PSQANVDTAATPAPTAATTPDG AAPLPTDQAGVTTPVADPNAL VMNFTADCWLEVTDATGKKLF SGMQRKDGNLNLTGQAPYKLK IGAPAAVQIQYQGKPVDLSRFIR TNQVARLTLNAEQSPAQ
25623	55991	A	25764	658	1307	SNRLYTDVESINEIEGIYMKLRF ISSALAAALFAATGSYAAVVDG GTIHFEGELVNAACSVNTDSAD QVVTLGQYRTDIFNAVGNTSAL IPFTIQLNDCDPVVAANAAVAF SGQADAINDNLLAIASSTNTTT ATGVGIEILDNTSAILKPDGNSF STN\QNLIPGTNVLHGLAFRAR CVSTANLRVPRPICFDPGSSYQA NTIGSGRCADCQPDA
25624	55992	A	25765	167	232	
25625	55993	A	25766	441	686	
25626	55994	A	25767	206	331	
25627	55995	A	25768	674	900	VVPICTMLEEALERQNLTASLC G*LKKACGRSWQTSPIKRSLNG AKFSRTSIIMGFITAEKWSGWEI WSARNVTS
25628	55996	A	25769	41	222	
25629	55997	A	25770	17	525	ESLECSGPSWNASGTQSGFYCH RIAPILPEKRLARMVEKTWGLG LRRRTGFRRQNLGGGTGTLVE CTSENS\KPSKSSFRKQRRGQRR EGH*SLRR*IRRERTERMQASR VTWNSFPQVPAAKKPSSLSESG *P*ATNYTREQDSMWNCVHHY WQPPTSVSRLVHLNSG
25630	55998	A	25771	698	1051	PYLRIRLTALISRSSTVMRILFAI SKRPIT*PKRPKPTTMTWGLSSL THGFSSSSSGPLNWRDSHLSTSF ISNGVVIMESVTVTSNNAIWSPS SSVAAVNTSRTPEAAIKRNTGR SK
25631	55999	A	25772	1	2204	

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25632	56000	A	25773	3	891	RYRNQDDHELQIHTGTRFYVEL CGFRVNPPWLATDVTHAAMAL LTLVTTGLHIVGEWGKHATPPV PYSICSNPPRRAAYITVWRNRPC TLGDHLFSIAYPRGLRYDMGG GGEGTAWANVRQALARTTGR AQHWTKDNAKSSREARHPRQN KTKTHLGKPVLRWV/DPSFDQS KYDSIVWNPI/TYYPVPKPSTQV GQKV/LDKILNYTNTEMKEAIA H/DTSKEGLQFYEVVPVALVVA GTQMATGLRTMDTRLYFEGELI DAAPNKPVIKVVRQGEEPDWP SKGDAGDGEKVPSSLSESG
25633	56001	A	25774	1	285	
25634	56002	A	25775	1	302	SFSSFTQRTASVIISSTSTQSRLA TSPILAIARARTSRRCPEKPQLG YPDSAAHVFQQDRATKYVINR NSKKP*ICSACRSTVSTRQHRR WRGSLQPLSQ
25635	56003	A	25776	307	473	
25636	56004	B	25777	67	809	
25637	56005	A	25778	44	301	
25638	56006	A	25779	1	1519	MINRLQHTVYTHKWNSYRTEP DRRHTALRNSFCLVRLNDSSHS RSLDSKQGHTEITFAATEHPPSP VSLRIHDVAFDDGRQTSRAPCF NLEQPGKLDCTKRLISDCWVM HPGESWHGFKDIPDNWSMLDPI KISILAPGMGEDGELEETGVPA ALVTAWLGRHGIVPTRTTDFQI MFLFSMGVTRGKWGTLVNTLC SFKRHYDANTPLAQVMPELVE QYPDTYANMGIHDLGDTMFA WLKENYSGARLNEAYS/GLPSII ERHVVDAQGYRGGGMLCSCES NFCVSLLRIQAS
25639	56007	A	25780	461	789	HHVLSELQQLYTAYRSVDHIID HSLAIARAPQRRRCPEKPQLGY PDSLQHVFQQDRATKYVINGTS KKP*ICSACRSTVTHGHTDAGE EVWNPFAVLVPSGKDARVWG
25640	56008	B	25781	1	990	
25641	56009	A	25782	1	3066	
25642	56010	A	25783	583	904	WGIRTTDFQIMFLFSMGVTRGK WGTLVNTLCSFKRHYDANTPL AQVMPELVEQYPGR*FTGVRK KSNN*FRQFGGVDTAGNNL\SEI FSASASAEIFPANSFCNRLA

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25643	56011	A	25784	331	660	TGIQLPGAP*SQPWSTRRRAVV RPLYRVN*AVP*NR*VIRSKRA MPKRTDIKSILILGAGPIVIGQRL GWRDSDGVRLCGVLGSQENVC ELDEKGEERWSISGTSSEFTR
25644	56012	A	25785	1	798	MSDAEDGARTTLGSGNAVERL ADALSQQNVTVIKSTSLDDGFA ILSSNEAIDCLMFSYQMEHPDE HQNVRQLIGKLHERQLNVPVFL LGDREKALAAMDRDLLELVD\ EFAWI\LEDTADFIAG\RAVAAM TRYRQQLLPPLFSALMKYSDI/Q SEYSWAAPGHQGGVGF\TKTPA GRFYHDYYRLLRVAWVLHKTE CRLINFPETPIFGNSFRYDIEVSN ESPDEEVKLRRHHLARCMKNF KTDIYFVSTFEPSTKSVDLLTVE TFAGT
25645	56013	A	25786	211	414	RVCECIQLRRIEIFRFMISSQPNL PEDLHPQIIAKPSQKRLIEQ*SSK LTVTKARRQGSRYKSSRFFS
25646	56014	A	25787	1694	4974	LSLLSAK/PVYMVPSRNRYGIIG PI/YPQEMQPETLQKKISE/SPLT KDKAGQKPSYCVV/TNCTYDG VCYNAKEAQD/LLEKTSDRLHF DEAWYG/YARFNPIYADHYAM RG/EPGDHNGPTASYIHVREGV GRLNFFRFNQAYMMH/ATTSPL YAICASNDVAV/SMMDGNSGLS LTQEDCWVMHPGESW/HGFKD IPDNWSMLDPIK/VSILAPGMGE DGELEE/TGVPAALYSNLCLSSG TTGLSTEALLE

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25647	56015	A	25788	1	1709	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK LSASLTSMRTLKSVFSEIYHENR GRYGYRRVTLSLHREGKQINH KAVQRLMGTLSLKAAIKVKRY RSYRGEVGQTAPNVLQRDFKA TRPNEKWVTDVTEFAVNGRKL YLSPVIDLFNNEVISYSLSERPV MNMVENMLDQAFKKLNPHEH PVLHSDQGWQYRMRRYQNILK EHGIKQSMSRKGNCLDNAVVE CFFGTLKSECFYLDEFSNISELK DAVTEYIEYYNSRRISLKLKGL TPIEYRNQTYMPRVNCPLFDTL RIPDIGGVVRARAIAKLLNDTD MAIIDKRRPRANVSQVMHIIGD VAGRDCVLVDDMIDTGGTLCK AAEALKERGAKRVFAYATHPIF SGNAANNLRNSVIDEVV/DLRY HSAER*NQITAERAYSDPVRKI
25648	56016	A	25789	2902	3271	SSAARHCAGCGDVRSVCRSGR ADAPRMHPGESWHGFKDIPDN WSMLDPIKISILAPGMGEDGE/P TRTTDFQIMFLFSMGVTRGKW GTLVNTLCSFKRHYDANTPLA QVMPELVEQYPAFVINQ
25649	56017	A	25790	185	663	SPVPSSRPSTRHRLPDGSSSSQFS SAIAARKVVNSCILCSKICQN*F NRRAASPLKRLP*SGASGMIT\P NQPAPAQ/PAK*LYTRLDEVKP* *KITHGNGVSFCPTG*A*RTGIS ASSRDLEVQSKKRSFPALNWPA VYCCSALGSAPKCKPIPFLRAT V

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25650	56018	A	25791	684	4208	NGLFWLFQPWLFADETRRRLE ERFRDRYQIIHHSSQVCHSDQA VYVLTQERVNERDDIVDIDLFV IDEFYKLAFRQLKSGDIDHQDE RVIELNIALSKLLKVSRQFYLTG PFVNSIRGLEKLGYPHTFVSTDF NTVALDVKTSASKRMTTKPSS KRWGKSRTCVDADHIKNGIGL HFGALPRALQQYTADQFNAGK LRFLLCTSTIIEGVNTIAKNVVIY DNRAGSTRTISADIINSVICGLN TLKSFDTRWALL
25651	56019	A	25792	1	896	
25652	56020	A	25793	231	721	IITAEKGRSREQQLAIL\PLNLAD MRQLQQQHSQTRLADTAADGL RHFTAQQRLMPLQLQAIFVTGQ RQLMLQRVGY/R/LHGSPWRKA QTHLPVPGSTPEYRRSDPHGPA LTGCSSHHNPVRARRGMTIAQL AANPDKEYRARSFAIARSRPLA SRSGYETVTPGC
25653	56021	A	25794	1	933	MLEAAVCLCVFVSCSLAEGRA CCRVAVSIPVSVRARIHLLESDH LGRFREPKSIPRKDAQMDTFRT MVREPATFLDQVDGLQQSDDIL RLLPPELATLGITELEYEFYRRL VEKQLLTYRLHGESWREKVIER PVVHKDYDEQPRGPFIVCVDTS GSMGGFNEQCAKAFCLALMLI AIANKWRCY\IMLSS\TEIVRYE LSGPQGIEQAIRFLSQQFRGGTD LASCFRAIMERLQSREWFDADA VVISDFIAQRLPDDVTSKVKEL QRVHQHRFHAVAMSAHGKPGI MRIFDHIWRFDTGMRSRLLRR
25654	56022	C	25795	83	1108	
25655	56023	A	25796	1	747	

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25656	56024	A	25797	25	1741	IMERLKRMSVFAKVVEFGSFTA AARQLQMSVSSISQTVSKLEDE LQVKLLNRSTRSIGLTEAGRIYY QGCRRMLHEVQDV\HEHLYAL NNTPIGTLRIGCSSTMAQNVLA GLTAKMLKEYPGLSVNLVTGIP APDLIADGLDVVIRVGALQDSS LFSRRLGAMPMVVCAAKSYLT QYGIPEKPADLSSHSWLEYSVR TDNEFEL\IAPEGISTRLIPQGRF VTNDPMTLVRWLTAGAGIAYV PLMWVINEINRGELEILLPRYQS DPRPVYALYTEKDKLPLKVQV VINSLTDYFVETPTPLSSLTSLPT IEICCMVSIPGTNQRLRPFTGFA THRLQSDLLLQVMTISRGRFSR SARFNGPTPSGRRLIRVIISTESG SRSSNPRTTGCFEEHCDHYRAII DSADGLPMVVYNIPALSGVKLT LDQINTLVTLPGVGALKQTSGD LYQMEQIRREHPDLVLYNGYD EIFASGLLAGADGGIGSTYNIM GWRYQGIVKALKEGDIQTAQK LQTECNKVIDLLIKTGVFRGLK TVLHYMDVVSVPLCRKPFGPV DEKYLPELKALAQQLMQERG
25657	56025	A	25798	1	1005	

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25658	56026	A	25799	1	2392	MEMVAASKMRKSQDRMAASR PYAETMRKVIGHLAHGNLEYK HPYLEDRDVKRVGYLVVSTDR GLCGGLNINLFKKLLAEMKTW TDKGVQCDLAMIGSKGVSFFNS VGGNVVAQVTGMGDNPSLSEL IGPVKVMLQAYDEGRLDKLYI VSNKFINTMSQVPTISQLLPLPA SDDDDLKHKSWDYLYEPDPKA LLEQCSCMLRSPAWGITSTDTT RARTDLACPIWLLLDPYPKLMG NAPKALASVDKRGVPVNTILVS ALVTALCVLINYLAPESAFGLL MALVVSALVINWAMISLAHMK FRRAKQEQGVVTRFPALLYPLG NWICLLFMAAVLVIMLMTPGM AISVYLIPPLQTNTFNSTTIAMA DYQMESLSAEINFAAAKLARA CADEWTARTPEKPRYVAGVLG PTNRTASISPDVNDPAFRNITFD GLVAAYRESTKALVEGGADLIL IETVFDTLNAKAAVFAVKTEFE ALGVELPIMISGTITDASGRTLS GQTTEAFYNSLRHAEALTFGLN CALGPDELRQYVQELSRIAECY VTAHPNAGLPNAFGEYDLDAD TMAKQIREWAQAGFLNIVRGC CGTTPQHIAEMSPGRKRLTRAE SSSVPSTLPGKAWLEHALPLIAE QL/QGRRSAVFIPF\AGVTQTWD DYTAKTAAVLAPLGVSVTGIHS VVDPVAAIENAEIVIVGGGNTF
25659	56027	A	25800	412	1115	LAGEVMDLLLLSNSTLPGKAW LEHALPLIAEQLQGRRSAVFIPF AGVTQTWDDYTAKTVAVLAPL GISVTGIHSVVDPVAAIENAEIVI VGGGNTFQLLKQCRERGLLAPI TDVVKRGALYIGWSAGANLAC PTIRTTNDMPIVDPQGFDALNLF PLQINPHFTNALPEGHKGDPRL FR\IRELLVVAPELTIIGLPEGNW ITVSKGHATLGGPNTTYVFKAG EEAVPLEAGHRF
25660	56028	A	25801	1	360	MDHAIAGIAVQFRGGNLLRFK AFQQRVKYRMCQAERAINRLF NIAVKRLTGNRLDDKSKQHIIDI AVDIPKWSDHLHIIRRKHHDPT QDSGTHLPAVADDGFRTSVRN RSA*HIRYLTRC*KALNRNKLPP RN*TAIPAMA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25661	56029	A	25802	1032	1233	LVQFLRICFHILQRF/LPSH*RQK DESLRALPVSFLCWRTDSDFPA DISYQNYR*YNREPYLPRPDSG
25662	56030	A	25803	1	1394	MTRDGLANKALAVARTLADSP EIRQGLQKKPQESGIQAIAEAVR KRNDLLFIVVTDMQSLRYSHPE AQRIGQPFKGDDILKALNGEEN VAINRGFLAQALRVFTPIYDEN HKQIGVINDSRWSIIWSVLFGM LVGLIGTCILVKVLKKILFGLEP YEISTLFEQRQAMLQSIKEGVV AVDDRGEVTLINDAAQELLNY RKSQDDEKLSTLSHSWSQVVD VSEVLRDGTPRRDEEITIKDRLL LINTVPVRSNGVIIGAISTFRDKT EVRKLMQRLDGLVNYADALRE RSRLEHILHNQRVPFIMKLHHR MLRHFIAASVIVLTSSFLIFELV ASDRAMSAYLRYIVQKADSSFL YDKYQNQSIAAHVMRALAAEQ SEVSPEQRRAICEAFESANNTH GLNLTAHK\SRAYAAHYKPHPL TATQLWK\RSTITRF*SGSGRQP PPG*LRFRSWDGRREISLLSRSL
25663	56031	A	25804	3	219	
25664	56032	A	25805	14	265	
25665	56033	A	25806	744	1566	FASWLRVFSITNCAAPVTSESC ALDLGSAEAKAWIGVENPHRA DVLTELRRSTVARVCTGRAGPR PRTQALLRFLADHSRSKDTVLK EVPEEWVKAQGLLEVRSEISDK NLYLTRPDMGRRLCAEAVEAL KAQCVANPDVQVVISDGLSTD AITVNYEEILPPLMAGLKQAGL KVGTPFFVRYGRVKIEDQIGEIL GAKVVILLVGERPGLGQSESLS CYAVYSPRMATTVEADRTCIY NIHQGGTPPVEAAAVIVDLAKR MLEQKAF\GINMTR
25666	56034	A	25807	596	745	
25667	56035	A	25808	151	660	STTERLGDDFVRAANIILHCEG KVVVSGIGKSGHIGKKIAATLA STGTPAFFVHPAEALHGDLGMI ESRDVMLFISYSGGAKELDLIIP RLEDKSIALAPNSRTVIT*CWFS AGDGGLPGPDYGQDFAAHPAG AGALYKCRDLINDNILRTVSCQ SHDDGDIRGMAFARQ
25668	56036	A	25809	314	583	
25669	56037	A	25810	1	2982	

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25670	56038	A	25811	120	790	EGLKTKGEKASPPSCLSFCKNE FVISSTDYALSQSQSGGVMHRQ SFFLVPLICLSSALWAAPATVN VEVLQDKLDHPWALAFLPDNH GMLITLRGGELRHWQAGKGLS APLSGVPDVWAHGQGGLLDVV *APDFAQSRRIWLSYSEVGDDG KAGTAVGYGRLSDDLSKVTDF RAVFRQMPKLSTGNHFGGRLV FDGKGYLFIALGENNQRPTAQD HRVPSWYK
25671	56039	A	25812	707	1141	ASHTATSPRPVRLSSSIASITLAV NATCGMASSRRIR*CTLFSKRA PSAPAGWERAKSSSLNPRACMT AIASASPIIRVLTVLEVGAKCIG QGSRSDSTELSPFIKMVPPNSLT TALAVIPPFSLSDTLPEVLISLSLI YNTLF
25672	56040	A	25813	215	2160	EINSITSRLSIIPRSPCSASAGWT KKAGVPVLASVAAIFLPMWPD LPIPETTTLPSQCKMILAARTKS SPR/RSNIMTHIRIEKGTGGWGG PLELKATPGKKIVYITAGTRPAI VDKLAQLTGWQAIDGFKEGEP AEAEIGVAVIDCGGTLRCGIYP KRRIPTINIHSTGKSGPLAQYIVE DIYVSGGKEENITVVGDATPQP SFVGPDYDTSEKLMIVRKKPIG VQMLYQVGTVSMLLYTRTIIQT KMTPRTIVTISHSVRNAGDSFFS IASNQPMPPTAKKIEPLAISLLS AEAPTRLSELKARIGEPRWSIEA IKPMPISTHKPNMQAITPPARRA ILSPCACESRSRQEPCPPGCHCS CPNHSCRSRLKGVLSMEQYLL QQKHVGTPPGPFRPPDTNQPCW KTKPSQREEYTRRVGFTGHSNQ GAKIIRTHIICRRRTSFALERPGD GFQAVVGGTVLMGLPRTKNVG LPVTILGRVHRRSSERFPRTSES AINRKDAGPKDPVRQRLAYKK HPMERRHGPHVVARTFGRAIPT LGPHRTVLSTRFQVAKNPLGPI GPSPLAVLTWTVPRPKNGRRG GKQRARIICQSRREASCNNVCL ARSSGVFKGFSPVSSSGEHTGN KYSAYSFSLCPLFVFLPLSGRLL

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25673	56041	A	25814	11	613	RLSSVFVSKSLASWRSCNCSFS GPLVRLTIRP\LSPPDVRLLLSPS VVHAYNCPHQETQRHHTHHLT P/RLPNHGQIAISAMVYSSPATN/ SMLRQLLIQHVEQIGSVPLVMD AISLVEAHD/RSAAG*SRPLY*R AN*SSRY*VSYARKRVRQAKSR /HGKPSKKVLAKRAVPNRVCRC CNRVKRRCICQPKRRKCMTLPV RATR
25674	56042	B	25815	1	1920	
25675	56043	A	25816	247	1182	EAVMRQTKTGILLANLGTPDAP TPEAVKRYLKQFLSDRRVVDTS RLLWWPLLRGVILPLRSPRVAK LYASVWMEG\GSPLMVYSRQQ QQALAQRLPEMPVALGMSYGS PSLESAVDELLAEHVDHIVVLP LYPQFSCSTVGAVWDELARILA RKRSIPGISFIRDYADNHDYINA LANSVRASFAKHGEPDLLLLSY HGIPQRYADEGDSLRELYAVA NPNPGPGMGVLLAYMFFGRGS AKQSAGGSGLDGLLRRTPPITP GGYFSVFVWKSLGSWRSCNCS FSGPLVGLTIRPRFTAGRSPTSF AQRCTCL
25676	56044	B	25817	1	651	
25677	56045	A	25818	1	1647	
25678	56046	A	25819	1	1506	

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25679	56047	A	25820	645	2161	LDRCALNVTAQPSIECQVANAC LSPKGEFEYLQIDAPTPQALLSE IEKCWHRHRNVWPDHTINLAL AIHGQVDPVTGVSQTMPQAPW TTPVEVKYLLEEKLGIRVMVDN DCQLHYCKTAILNWSRKMALS RQKFTFERLRRFTLPEGKKQTF LWDADVTTLACRATSGAKAFV FQSVYAGKTLRMTIGNINDWKI DDARAEARRLQTLIDTGIDPRIA KAVKIAEAESLQAESRKTKVTF SVAWEDYLQELRTGISAKTKRP YSTRYIADHINLSSRGGESPGLG LLLAFTLFGKGMSKRSAPGAMI IHFLGGIHELYFPYVLMKPLTII AMIAGGMSGTWMFNLLDGGL VAGPSPGSIFAYLALTPKGSFLA TIAGVTVGTLVSFAITSLILKME KTVETESEDEFAQSANAVKAM KQEGAFSLSRVKRIAFVCDAG MGSSAMGATT\FRKRLEKAGL AIEVKHYAIENVPADADIVVTH ASLEGRVKRVTDKPLYGPAVV
25680	56048	A	25821	2	341	
25681	56049	A	25822	218	469	LICAQGRRSPSRESTRQPKVLTL ACHNGSVSVVVLSPNSLYIEVV VPS*CNAATGPVVTCLYKGKFQ PILILLVTSTRVSSCI
25682	56050	A	25823	1	3966	
25683	56051	A	25824	2	728	
25684	56052	A	25825	528	1123	DAEEGPDHRYLSSAHGGGSAS QPPSCAVTACRWPWRGRGCRA GVWNQPTAAQGRSWPVGKTSC *GQGSTCKSQTWGFRGQRLPQ DAPAPPASLCASFHLVEAGASA DSGDTRRMTIR/FASKTVARAK RIIRVLRFSPLWVATRSLASTAI KIACCASEPGSFLQLWKPRSMA PVHRCTWHEACPEGQRQMSCV SSTGL
25685	56053	A	25826	1	492	

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25686	56054	A	25827	1740	3858	ADAAGTEKTATVSRYHFYLRY PRSGRSVIDVRSWWRFSIMDAL SRSIPRAISICARGKPVVTAKFK QGTMPEPSNKAIILPIRFFPGVV LMIIKKSGGRWQLSLLASVVIS AFFLNTAYAWQQEYIVDTQPG LSTERYTWDSDHQPDYNDILSQ RIQSSQRALGLEVNLAEETPVD VTSSMSMGWNFPLYEQVTTGP VAALHYDGTTTSMYNEFGDST TTLTDPLWHASVSTLGWRVDS RLGDLRPWAQISYNQQFGENI WKAQSGLSRMTATNQNGNWL DVTVGADMLLNQNIAAYAALT QAENTTNNSDYLYTMGRTRWL TLIGTIITQFALGSVYTWSLFNG ALSAKLDAPVSQVAFSFGLLSL GLAISSSVAGKLQERFGVKRVT MASGILLGLGFFLTAHSDNLM MLWLSAGVLVGLADGAGYLL TLSNCVKWFPERKGLISAFAIGS YGLGSLGFKF\IDTQLLETVGLE KTFVIWGAIALLMIVFGATLMK DAPKQEVKTSNGVVEKDYTLA ESMRKPQYWMLAVMFLTACM SGLYVIGVAKDIAQSLAHLDVV SAANAVTVISIANLSGRLVLGIL SDKIARIRVITIGQVISLVGMAA LLFAPLNAVTFFAAIACVAFNF GGTITVFPSL\ICGSIIASLFGGFY VTFYVIFALLILSLALSTTIRQPE QKMLHFTYLTTSALFPAGPKRN
25687	56055	A	25828	2	356	
25688	56056	A	25829	1	1307	MYETLEEVLRSSGDPADQKYV ELKARAEKALDDVKKRKLYC WRRRQICALRRISRSPYPGHQL ECIASFDRNFEAMQKEMYGQF ENTFMMYLPRLCEHCLNPSCV ATCPSGAIYKREEDGIVLIDQDK CRGWRLCISGCPYKKIYFNWKS GKSEKCIFCYPRIESGQPTVCSE TCVGRIRYLGVLLYELTAQQFF PVWPPDHFVHPF*TLYVLPAPP SR*CDRVQLMASLQSVARASRE YRWYGFSR*TPRKALALAQLRP AESSPTAPDCN

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25689	56057	A	25830	583	1369	RHQLNSIASPAGGRWKDIGWF NFPQSNLCLKREKQDESCSLTQ ALPSELKVSADNVSLTGAVSLA SMLTEIFLLQQAQGMPEPGWG RITDSHQWNTLLSLHNAQFYLL QRTPEVARSRATPLLDLIKTALT PHPPQKQAYGGT\LPLPVRFMA GPDTNLANLGGALKFNWTLPG QPDNTPPGGELVFERWRRLSDN SQWIQVSLVFQTLQQMRDKTP LSLNTPPGEVKLTLAGCEERNA QGMCSLAGFTQIVNEARIPACS
25690	56058	A	25831	199	543	
25691	56059	A	25832	1	642	EASIFRRLSVYDNLMAVLQIRD DLSAEQREDRANELMEEFHIEH LRDSMGQ*SARPGRCRAGAQ* CV*CR*PRSGQPRQTVRRAE*IS DSQPVRGQFLHG/VRSPPESDCP MLSRRCSM*NSSISSFARSSRCS ADKSSRICSTAIRLS
25692	56060	A	25833	3	329	
25693	56061	A	25834	1974	2195	
25694	56062	A	25835	1	615	
25695	56063	A	25836	2	166	
25696	56064	A	25837	2	189	STPGNWRFTTTYPLNCATRWK M*FLIVATMAPSVYWSLPRNIA AAKPTTPPTPSRRSGARGK
25697	56065	A	25838	64	354	
25698	56066	A	25839	1123	1845	
25699	56067	A	25840	1120	2097	
25700	56068	A	25841	124	548	CRQMVGTRRGGEQGKEVIDGY GKPATFYQMQDNGKPVEGHAS QMHYELAKDFVVLTGNAYLQ QVDSNIKGDKITYLVKEQKMQ AFSDKGKRVTTVLVPSQLAKA YKG\VAW*KTSA*PSTPGKLSV CWGQTVPVRPPLSTWL
25701	56069	A	25842	77	514	
25702	56070	A	25843	2487	5738	RRAAGLPGRNDAGLARSHQWA GSADTGSEKQHELQLRIQGEPV SGQLNLAGSFDRKEERWKG\TL SNTRFQTPVGPWSLTRDIALDY RNKEQKISIGPHCWLNPNAELC VPQTIDAGAEGRAVVNLNRFD LAMLKPFMPETTQASGIFTGKA DVAWDTTKEGLPQGSITLSGRN VQVTQTVN\DAALPVAFQTLNL TAELRNNRAELGWTIRLTNNG QFDGQVQVTDPQGRRNLGGNV NIRNFNLAMINPIFTRG
25703	56071	A	25844	538	777	

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25704	56072	A	25845	489	2797	TRRRRRTMIALIQRVTRASVTV EGEVTGEIGAGLLVLLGVEKDD DEQKANRLCERVLGYRIFSDAE GKMNLNVHQAAGSVLVVSQFT LAADTERGMRPSFSKGMSQLP GLSRETRESIAMYHLRVPQTEE ELERYYQFRWEMLRKPLHQPK GSERDAWDAMAHHQMVVDEQ GNLVAVGRLYINADNEASIRFM AVHPDVQDKGLGTLMAMTLES VAPYFSGSETGMMTLNRYRLR HMAKQGNRSAKRVEKLLRKPD RLISLVLIGNNLVNILASALGTI VGMRLYGDAGVAIATGVLTFV VLVFAEVLPKTIAALYPEKVAY PSSFLLAPLQILMMPLVWLLNA ITRMLMRMMGIKTDIVDMLLS VLDLEKM/TVDDIMLPRSEIIGI DINDDWKSIL/R/QLSHSPHGAIV LYRDSLDDAISMLRVREAWRL MSEKKEFTKETMLRAADEIYFV PEGTPLSTQLVKFQRNKKKVGL VVNEYGDIQGLVTVEDILEEIV GDFTTSMSPTLAEEVTPQNDGS VIIDGTANVREINKAFNWHLPE DDARTVNGVILEALEEIPVAGT RVRIGEYDIDILDKLSFCFRYSN HRRTNRTTIQRITFLHNAQYVT WRNVIRFHHCDGLMHIRVQWD VSFGDHFNAKLTHNIQHRLQRQ LNAFNHRRHIRVSFISHFQRTIQ AINHRQQFVDEFLQREFVGFFNI
25705	56073	A	25846	87	199	QPASVQTAGAGCRL*LHQRQW RECLVLDSKRRGDGVL

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25706	56074	A	25847	1167	3306	GKSMDKELPWLADNAQ\LELK YKKGKTPLSHRRWPGEPVSVIT GSLIQTLGDELLQKAEKKKNIV WRYENFSLEWQSAITQAINLIG EHKPSIPARTMAALACIAQNDS QQLLDEIVQQEGLEYATEVVIA RQFIARCYESDPLVVTLQYQDE DYGYGYRSETYNEFDLRLRKH LSLAEESCWQRCADKLIAALPG INKVRRPFIALILPEKPEIANELA VPALREFLAATKMPATCTLKGL GAVEADYPYYLGMLGMHGTK AANFAVQECDLLIAVGARFDD RVTGKLNTFAPHASVIHMDIDP AEMNKLRQAHLRDEHSWRYD HPGDAIYAPLLLKQLSDRKPAD CVVTTDVGQHQMWAAQHIAH TRPENFITSSGLGTMGFGLPAA VGAQVARPNDTVVCISGDGSF MMNVQELGTVKRKQLPLKIVL LDNQRLGMVRQWQQLFFQER YSETTLTDNPDFLMLASAFGIH GQHITRKDQVEAALDTMLNSD GPYLLHVSIDELENVWPLVPPG ASNYKKHHKLKQTFGVKIIPDV HDPSQAQPVADVVNVIQLPAFL ARQTDLVETHGENRPGQMGNI VDKFKEGGNEKVILCDRGANF GYDNLVVDMLGFSIMKKVSGN SPVIFDVTHALQCRDPFGAASG GRRAQVAELARAGMAVGLAG LFIEAHPDPEHAKCDGPSALPL
25707	56075	A	25848	1	695	MATRASVTPMSLFSAGTCLLST SCVLSPVGDTAEESCWQRCAD KLIAALPGINKVRRPFIALILPEK PEIANELVGLECPRTHFHSKEW LKVVANDPTAVRKLEHYWSQD IFSDREASYMSHENHFGYAACA ALLREQGLAAIPRLAMYAHKE DCGSLLVQINHPQVIRTLLLVA DKNKPSLQRVAKYHKNFPHAT LAALAELLALTEPPA/RPWLSN HRRQKAACTAKSTR
25708	56076	A	25849	823	1091	CVRFARINCSDRRSRCFAGFNH VLNKALGVHINHFG/YSACAP* CRYPPHAAGEFYPDPCRHKGTT GYRHRQGYPPPGEPPPRASWLD LR
25709	56077	A	25850	714	875	EFSSARISRTSRLKYTNGCCRL WSAFCRLRTATTVPPARP*QLR PDRSRAQCQ

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25710	56078	A	25851	2730	2893	WPVGERLAPGDYPVI*TGQLCT AAGD/EWRR*KVRRHQPLWRG FPNRRYMAWRSA
25711	56079	A	25852	750	929	SFHPAGRRYLYRHSSRSGNITN GCCRLWSAFCRLRTATTVPPAR P*QLRPDRSRAQCPV
25712	56080	A	25853	2	2427	CRQHHRWHSGSTAVYRRVLITS KCWNVFIRTKTWTVSILTTSVV CASARRVCVPAPRAVSSRCLSV TTLIPSASTPW*LAHRISLAAR* AFWFNCRIPAGIDNVKVLERIH PDKDVDGFHPYNVGRLCQRAP RLRPCTPRGIVTLLERYNIDTFG LNAVVIGASNIVGRPMSMELLL AGCTTTVTHRFTKNLRHHVEN ADLLIVAVGKPGFIPGDWIKEG AIVIDVGINRLENGKVVGDVVF EDAAKRASYITPVPGGVGPMT VATLIETRYRQGKMFDGSSIGG WKGINESDMVLMPDASTAVID PFFADSTLIIRCDILEPGTLQGYD RDPRSIAKRAEDYLRSTGIADT VLFGPEPEFFLFDDIRFGSSISGS HVAIDDIEGAWNSSTQYEGGN KGHRPAVKGGYFPVPPVDSAQ DIRSEMCLVMEQMGLVVEAHH HEVATAGQNEVATRFNTMTKK ADEIQIYKYVVHNVAHRFGKT ATFMPKPMFGDNGSGSPPSQPQ SQPTPPEILLQALLSAGCFYAVY YVTYKTRLRKRVADVPRRPLFT MNRVETNLTWVILMGIALVSV GIFFMHNGFLLFRLNSYSQIFSS EVSGVALKRFFYFFIPAMLVVY FLRQDSKAWLFFLVSTVAFGLL TYMIVGGTRANIIIAFAIFLFIGII RGWISLWMLAAAGVLGIVGMF WLALKRYGMNVSGDEAFYTFL
25713	56081	A	25854	502	885	
25714	56082	A	25855	233	738	SNSCKRTKIISDVTSVFHAIFPAI KITAPNSPRLRVNDSATPLTSAG ESSGSTTLQKLCQRVAPSVSAA SSYSGPNLFQHRLHGTHPKRNA GKGHSHRNPQPCIGDFDIKLRQ PFTVKTLYVKEKGQR*GGDRV LPAQRVNPSAHQAACGLGSDS GLGSTPSADRKRR

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25715	56083	A	25856	1	2363	MRRQDTGRRGRKRRDAGRWQ WRYWGKGSFTPMNATWDVAG KGEWHDSTITLTDLSTGFDQLQ YGTMTVEKPRLILDKPIVWVRD AQHPSFSGALSLDAGQTLFTGG SVLPPSTLKFSVDGRDPTYFLFK GDLHAGEIGPVRVNGRWDGIR LRGNAWWPKQSLTVFQPLVPP DWKMNLRDGELYAQVAFSAA PEQGFRAGGHGVLKGGSAWM PDNQVNGVDFVLPFRFADGAW HLGTRGPVTLRIAKQRKEMRN NNLRQFKLLGPDVGFDSINDRP MAEELSKLLSKQNEENLLPKTI LYCLNPRDNEVLGTMIENGASF AANPLYFDPKNIVELAIEAGCN CVASTYGVLASVSRRYAHRIPF LVKLNHNETLSYPNTYDQTLY ASVEQAFNMGAVAVGATIYFG SEESRRQIEEISAAFERAHELGM DGGWIGLMIKPLGRWSLIMEID EGFAVGMSPAELSAEQLLSKL WLWEGKAERYGWGRKSMDKE LPRLADNAQLELKYKKGKTPLS HRRWPGEPVSVITGSLIQTLGD ELLQKAEKKKNIVWRYENFSLE WQSAITQAINLIGEHKPSIPART MAALACIAQNDSQQLLDEIVQ QEGLEYATEVVIARQFIARCYE SDPLVVTLQYQDEDYGYGYRS ETYNEFDLRLRKHLSLAEESCW QRCADKLIAALPGINKVRRPFIA
25716	56084	A	25857	1	4440	MNRFDGAKQNVVGADAHHLA DTAVKRNQSLFQLRASGHPRLP AGGGKAVFHGRFAAKKIEAVA FYFRHLIALLVVQMHFKLVKG NVDVVFTAQLIDSTVQLIDSTTT VTQFTHIQTQLMRSVEWLTDN GSCYRANETRQFARMLGLEPK NTAVRSPESNGIAESFVKTIKRD YISIMPKPDGLTAAKNLAEAFE HYNEWHPHKAGTLTNEQWQQ VTAELHDRMMETVFFALDDAE QLFAHHQPTPVTSVDLLGQG

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25717	56085	A	25858	1	3705	MEEYGGVDVRLYRIPDPMAFL RQQKNLHRIVVQPQYLGDGLN NTLTWLWDNWYGKSRRVMQR TFSSQSRQNVTQALPELQLGNA IIKPSRYVQNNQFSPLKKYPLVK QFRYPLWQAKPFEPQQGSRGL YLVEAMVGGYRATTGGVVSDT VALSKVSSKELLVWTAGKKQV NEPGSEIFGLTALRITAENQDCA SLTPETFLPRIHVIKGVNISTATV CRQCEDAPCANVCPNGAISRDK GFVHCEARTLHLFAKT
25718	56086	A	25859	123	923	TDSPYERGHLMSNLLGPRDAN GIPVPMTVDESIASMKASLLKKI KRSAYVYRVDCGGCNGCEIEIF ATLSPLFDAERFGIKVVPSPRHA DILLFTGAVTRAMRSPALRAW QSAPDPKICIS\YGACGNSGGIF HDLYCVWGGTDKIVPVDVYIP GCPPTP\AATLYGFAMALGLLE QKIHARGPGELDEQPAEILHGD MVQPLRVKVDREARRLAGYRY GRQ\VADDSFTQLGQGEEQVAR WLEAENDPRLNEIVSHLNHVVE
25719	56087	A	25860	1337	1516	KLKSKSAKRHKFITPILAWRILI HYLQRVAV*WGSRLL*LFLITIP SRWRLLPHNTGKG
25720	56088	A	25861	1	545	MARLAALKACETVYSMGVRSH RRSPLEHLWQLKDQLVNEGEL VLETLVIDGDENTVLVPGDRYA QMRNVYFIPSALALKNWLKKC GFVDIRIADVSR/ITTTEEQRRTE WMVTESLADFLDPHDPGKTVE GYPAPKRARNRNRAEDHRQRL RHRTRKKQTHGQRRRHRPEPA QRQPQTGTTD
25721	56089	A	25862	620	1117	
25722	56090	A	25863	1	1188	
25723	56091	A	25864	231	407	
25724	56092	A	25865	1	501	
25725	56093	B	25866	1	2373	
25726	56094	A	25867	1	2211	

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25727	56095	A	25868	2093	3589	GGINGKNFWFFLSPFTPCVGRC HSRVQLANSHLVDVDETPPSSA AVHLYATDADSIGNCGTDREFC PCNPIRRHAFCCERLQNGYHRS GYAFHLGHYGDRKVITNFYSLI AKNHLSHWLETLPAQIANWQR EQQHGLFKQWSNAVEFLPEIKP YRLDLLHSVTAESEEPLSAGQI KRIETLMRNLMPWRKGPFSLY GVNIDTEWRSDWKWDRVLPHL SDLTGRTILDVGCGSGYHMWR MIGAGAHLAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPL/GIE QLPALKAFDTVFSMGVLYHRR SPLEHLWQLKDQLVNEGELVL ETLVIDGDENTVLVPGDRYAQ MRNVYFIPSALALKNWLKKCG FVDIRIADVSVTTTEEQRRTEW MVTESLADFLDPHDPAIFQIWP CTFMHAYHAFFDPVSHHRACQ NLTTFVPDTHQIAIRNTKACSIF VSFALRTTHSCAISHSSLEDPPAI LFKIADRMEQNLELLATAGNLG
25728	56096	A	25869	231	1785	DDEVHRYSELRTRTVPSYPPER SGEAKTAAQRAGTAFRRGRGA GVPFNLQQRSDRWCS*RSQQN A*RLIGLHGQNSRSVPQLPMES ASVA*RCGSIIEKTTLSSRPFYW CPGCQHYADRFGA

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25729	56097	A	25870	1818	3311	RMAIQFRTLSLRWCWKISLVSS FTVVKAMTIRIVAMRQLLRQQ KQRTFVC*SS/TVDGVLSDGLIY MGNNGEELKAFNVRDGYGIRC ALTSDIEVAIITGRKAKLVEDR\ LPHWGSLTCIRGSQTN*SPLAIC WKNWRLP/QENVAYVGDDLID WPVMEKVGLSVAVDDAHPLL GTEIDAYIENADYQYNKKRLRE IDRRVRYLTKCLENLKIVDYSP QQEGKVFFGAWVEIENDDGVT HRFRIVGYDEIFGRKDYISIDSP MARALLKKEVGDLAVVNTPAG EASWYVNAIEYVKPRLNQTVR LLLEHEMGQVWISGEISNFTQP ASGHWYFTLKDDTAQVRCAM FRNSNRRVTFRPQHGQQVLVR ANITLYEPRGDYQIIVESMQPA GEGLLQQKYEQLKAKLQAEGL FDQQYKKPLPSPAHCVGVITSK TGAALHDILHVLKRRDPSLPVII YPAAVQGDDAPGQIVRAIELAN QRNECDVLRPCVWCRRVRCRR
25730	56098	A	25871	1	3465	
25731	56099	A	25872	1	3126	
25732	56100	A	25873	1	1722	MSSLSQAASSVEKRTNARYWI VVMLFIVTSFNYGDRATLSIAG SEMAKHIGLDPVGMGYVFSAF SWAYVIGQIPGFVDIFSGFGIIV ALFTLRFLVGLAEAPSFPGQSRI VGDWFPAQDRGTGVSIFTPFIL RKGDLRPIWVVILMAGQLHAL MSTLEDTPFSNKAGMRLRRWI NAAVMRLNPLACLATRSNQVN WLLLTGNISVYPVGSSEPTRRR STPINSTPHFNKTILPINARYSPT LPSSDGTRWTTRIDDKPTVGHK FARYWDVELREIP\MRPG\QLFR DPKRMIEGCAENPL\GV\VPTFG VTYAGNYEFPQPLPDALNKFQ ADPGIDIDMHIDAASGGFLAPF VAPDIVWDFRLPRVKSISASGH KFGLAPLGCGWVIWRDEEALP QELVFNVDYLGGQIGTFAINFS RPAGQVIAQYYEFLRLGREGYT KSTQPARGSPPANNCQAQPETP DRAVIHPTDGYESAATIIVLSPP TASDSDPAHRDQRVVKTDAWS VVPGSTSEYPRRYKAEWFCQPF AVLPAILAWSAALWRYQPRAR RRKADYGCRALNSLKNELTTP

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25733	56101	A	25874	1	2385	
25734	56102	A	25875	1	1767	
25735	56103	A	25876	1	2079	
25736	56104	A	25877	368	1261	TSPRARPAAQGSRGAFL/HLTE KGVNRFAFYGLPESSGKRWAT EREYAFRQLVAEEKYRGVVYQ GLETAPENWQHAQNRLADWL QTLPPQTGIIAVTDARARHILQV CEHLHIPVPEKLCVIGIDNEELT RYLSRVALSSVAQGARQMGYQ AAKLLHRLLDKEEMPLQRILVP PVRVIERRSTDYRSLTDPAVIQA MHYIRNHACKGIKVDQVLDAV GISRSNLEKRFKEEVGETIHAMI HAEKLEKARSLLISTTLSINEISQ MCGYPSLQYFYSVFKKAYDTT PKEVFAIVNSEVML
25737	56105	A	25878	1	868	MTSLKNSMKWDEERFGLEYDL DIYMIVAVDFFNMGAMENKGL NIFNSKYVLARTDTATDKDYLD IERVIGHEYFHNWTGNRVTCRD WFQLSLKEGLTVFRDQEFSSDL GSRAVNRINNVRTMRGLQFAE DASPMAHPIRPDMVIEMNNFYT LTVYEKGAEVIGM\TPPLFGQE NFQNVILTCALEDPTRKVVLKP LCRPPLSLCNRRKRVMCRIFTSS ASTLRLSRRCAVCWNSRITVSM RSSRRVTSVWLSAPTPIILSPAIF IVRWWLLDSNPLIYYKAWSCW CSRK
25738	56106	A	25879	2097	2512	NTPVRPDVGT*TEEHGGAESGE *RNSRELRENDKA*LHQYHAQP DGKNLAEAFEHYNEWHPHSAL GYWRTVD/DMRGR*PQEPSLMI RAGRSSSPVQWQRIPLLIPGRKG DRMQKTVIPGSLFAGMPYAQPS IKTELAG

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25739	56107	A	25880	71	2613	QRKPTSSRKGLSARMMSGLTG TITTVSTGWCTTRGHNMKSRW SKVAIFTTR/SGRRVAKRVWRR ERDLTGWMSLSRKPQVTWYG WDGDRLTTIQNDRSRIQTIYQP GSFTPLIRVETATAVRRRRRWQ WGIPAGTVQMLDRLESEILADR VSEESRRWLASCGLTVEQMKK TSIHASIVRHKLLTAEQALKLLG EMFVYHMPFNRALGMELERYE KEFAQLAFKNQPMMVGNWAQ SILHGGVIASALDVAAGLVCVG STLTRHETISEDELRQRLSRMGT IDLRVDYLRPGRGERFTATSSLL RAGNKVAVARVELHNEEQLYI ASATATYMSKSMFLAVATILIS KSSLSRLRRPSTIVCGIPISSISAN ITPGRSLRSSSSTSKTLCTQFAV QFLSKLLYAEGFVHVHRQNRH LERRDSVRPYDASFVVVLLNRR SYHTRYPDTVATHRQDLVTAIF TLYGGFQCFGVLGTQLEDVTNF DTTFDQQPTLAIRAWIASHHVT DICNFRGSDIAIPVDAEVVFTID VSTSSEITHRRNVDLFPDQLTVT RSQTFTAYERLSTALTVAQVCG VQRLCNYYSARLTPLPGPDSTR ESNHRLAQITQYARQLASSPSII DNRSRQHLNDVGLTAWDCVIIS QIIGFIGFQARTIATFQAYLGHP VRWLPGLEIQNYADASLFADES LRWRSSYEVEKLPEEHTKSSTA
25740	56108	A	25881	71	3478	CCLSSHPSTTATALRSLSPVRK WPKISALIPWEWAMCSLLSHGL MLSGRSLVAWCWTVLVQNAS TSGRSLSGRCLPCCKASSISLVD SALSFLLFTLRFLVGLAEAPSFP GNSRIVAAWFPARKGTGIINE\IS P\LANTALEGLGGSGDALCTQC EAEGFRHITYYLDRPDVLARFT TKIIADKIKYPFLLSNGNRVAQG ELENGRHWVQWQDPFPKPCYL FALVAGDFDVLRDTFTTRSGRE VALELYVDRGN

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25741	56109	A	25882	90	629	PGDWGRRQLIGS*KTPGSVFKK GKSSTPN\DPFLKDKTQDRSGL ATFTMDGQI\RLFYQ\DISGNHS GK\QSLPPAQVIVSNSVDHLKIT GVEDHKPIFAGAGKPYQNLRQF IDEGNYTSGDNHTLRDPHYVED KAHKYLV/FEANTGTENGYQG EESLFNKAYYGGGTNFFRGSSR VDLQAC
25742	56110	A	25883	1	3066	
25743	56111	A	25884	104	547	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLFKFLKNGLNFLLHSVGTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDADDVLSTEVKRVITS SASNITPAFFCS
25744	56112	A	25885	3	4288	
25745	56113	A	25886	2	2222	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSLP QHTIPDVFIWMLSNNRRVAYA RIASKDLLYSPVAGQMGKHCG KIKTHFLKIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWNSWP LQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKDFRLL GQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLM\SWHDRFPDWKAG RILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPPLPARWPIH*C SWHDRFPDWKAGRKGSDAHRF GSWKFQLQRVSG\SATFTWGG KIR\LYSADYSGNHYGKQSLPS GQVNGSNSDDTLKINGVEDHK TILDGDGKTYQNVQQFIDEGNY TSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQSA KKRDAELANGALGIIELNNDYT LKKVMKPLITSNTIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSLKIDWIIER YQLPQSYQRMPDFRRRFLQVC VNEINSRTPMRLSYRMGVRGK
25746	56114	B	25887	1	2640	

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25747	56115	A	25888	1291	1629	
25748	56116	A	25889	1187	2925	NSLQRSHPNAANS/WHNKLWR SHSDSDLSDHHEPICKPGLELN KKDITTSADQIAEVKTMESHPPI PPVFVEHMVPQDANQKGLCTK ERMICLEFTSREFHAGQIEDELN LNDINGCSSGSTLEDPQFNDDSP EARKITRRWRIGEAADLVGVSS QAIRDAEKAGRLPHPDMEIRGR VEQRVGYTIEQINHMRDVFGTR LRRAEDVFPPVIGVAAHKGGV YKTSVSVHLAQDLALKGLRVL LVEGNDPQGTASMYHGWVPD LHIHAEDTLLPFYLGEKDDVTY AIKPTCWPGLDIIPSCLALHRIET ELMGKFDEGKLPTDPHLMLRL AIETVAHDYDVIVIDSAPNLEDP RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFTDKEE LLKQQASNLHEQKKAGVIFEAE EVITLLTSVL
25749	56117	B	25890	1	1954	
25750	56118	A	25891	1	454	MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEVYTK VFALDVAARHRAIR\VPRQQGD YRTRIWKFEDGLSNVLVIQLNK LIICVMCLVRDCDVLKTYFHL
25751	56119	A	25892	10	144	FLFIGKGFLKGIT*PGQIVQRG*E KKSNT*FRQFGGVDTAGNNLT

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25752	56120	A	25893	888	892	TVDLDACTKGVLTFTTALLAG GANQAFAKENTKKAYKETYGV SHITRHDMLQIFKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTSGDNHTLRDPHYV/EDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFTDSRGSK MTIDDLWKFELENDDLEYLVE ENSKQKTIQDVIWLFLTAYTHI RGATQAFAKENNQKAYKETYG VSHITRHDMLQIPKQQQNEKYQ VPQFDQSTIKNIESAKGLDVWD SWPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTPGDNHTLRDPHYVKTKAMR

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25753	56121	A	25894	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAFA KENNQKAYKETYGVSHITRHD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNSIDS WKNAGRVFKDSDKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHYGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGD GKTYQNVQQFIDEGNYTGDPL EAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRT PDFRRRFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIKIAWIIERY QPPQSYQRMPDFRRRFLQSRPA CMHDWLCAEALAWSIQTASYL VTMQVNLTSLSSDTDRDLSVVS NSGWVSSGSLVRFNTIKTSSGEI KRTVPRILPDPDDPRSAIAEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLLPKAVHLA
25754	56122	A	25895	3	2356	
25755	56123	A	25896	1	2610	
25756	56124	A	25897	1	2496	
25757	56125	B	25898	1	3198	
25758	56126	A	25899	1	5274	
25759	56127	A	25900	1	585	
25760	56128	A	25901	1	2469	
25761	56129	A	25902	1	1914	
25762	56130	A	25903	1	2259	
25763	56131	A	25904	1367	1959	KLVTLHMDLSWR\NSGYQSQE T*K*PANRPVKRPH*GGI*\FSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSF/DGEGSIYSR*A HGAA*PSHRKDRESADLGSDG QNDKGH\QYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESHKLQQSAKKLDAELSNGA LGFIE

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25764	56132	A	25905	1	2418	
25765	56133	A	25906	3	1918	
25766	56134	A	25907	1242	1463	
25767	56135	A	25908	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETYGVS HITRHDMLQIPKQQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVGD NSIDSWKNAGRVFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNEGI LPISEPPIKQDFRLLG
25768	56136	A	25909	610	2303	SLPNLDNAAICSSSSSPTRTR*SL SEGATQ\AFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNSIDSWKNAGRVFKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSLGTLQGFPAPAWLALAHP VHPLKHKSGGSNRLSAAIWGIK RKPARVCPGTGIHASSQIQGEW RTECAVGPKAKAKATAGWRR GNNQHISSTYDINRADTQVRRA VNNYDIIVMSNSFNGQSEHQTY ESIVIDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEPDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTGAWRNA LSIWEPVCNEIFDRLIKPRWEIR
25769	56137	A	25910	1	2103	

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25770	56138	A	25911	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFFKR GAIFRVHKHAVNPMSPKCRRPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKET/YPKQQQNEKYQVPQF DQSTIKNIESAKG\LDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYTSGDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGINSNDI YMLGYVSNSLTGPYKPLNTTG LVLQMGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ MNNASTMSKRTSAGCHCWQG
25771	56139	A	25912	1	3987	
25772	56140	A	25913	1	2235	

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25773	56141	A	25914	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL/VFEANTGTEEHPQPQ\ERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIAYLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHLPDLCSPSQDAQTTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTV
25774	56142	A	25915	1	2448	
25775	56143	A	25916	1312	1974	
25776	56144	A	25917	2	1778	
25777	56145	A	25918	1366	2673	
25778	56146	B	25919	1	1938	
25779	56147	B	25920	1	2262	
25780	56148	A	25921	1	2100	
25781	56149	B	25922	7145	7154	
25782	56150	A	25923	2085	11232	VNSEGSEPADRKKPVHTEEAM NMTIKKIVKQATVLTLTTALLA EGATQAFAKENNQKAYKETYG VSHITRHDMLQIPKQQQNEKYQ VPQFDQSTIKNIESAKGLDVWD SWPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLK\INGVEDH KPILDGGGKTYQNVQQFI
25783	56151	A	25924	153	293	

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25784	56152	A	25925	420	687	
25785	56153	A	25926	242	491	WLHVQPLHDEHHCWI*YPADT DGVRPAFQRSPALSPEHGCVPY TPARQGSVRSKGPCTSALLYVE CSIAAPDRKHSCHKSDQS
25786	56154	A	25927	2	113	
25787	56155	A	25928	779	862	NSTLPRCASTTFARY*AIPIKVFS ILP
25788	56156	A	25929	282	443	FSAGFLNLRYAQKFPSSYPPV** CYRPIYYPASDPCRNRLLYPAD VPYQALLD
25789	56157	A	25930	3	89	
25790	56158	A	25931	614	823	
25791	56159	A	25932	1229	1427	
25792	56160	A	25933	1965	2682	FAVPCRTSFGSIETVSHPGRDT* SA*AYRVQVDSHRPRLAHNVQ HRT*RGEVLLAGVPRHVAEREI ATLAGSFSLHEQNIHNLPRDQG PGNTVSLEVESENITERFFVVGE KRVSAEVVAAQLVKEVKRYLA STAAVGEYLADQLVLPMALAG AGEFTVAHPSCHLLTNIAVVER FLPVRFSLIETDGVTRQLLGVSY RILAMGHAEFLIQIADMRNDGG WRDFQFSGNLVMDEPNRSAQT YIKLVKSRLGTTKR
25793	56161	A	25934	261	563	RHSRGRSALRQISPEC*IHVCSPP PVQQLHPGYGNAIPLSYGHRNQ PDESDDAPVPPGWCQRYNLHQ KSTAHCGGYTIHADLVKTRCW LAPHRLPPGPGR
25794	56162	B	25935	1	1329	

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25795	56163	A	25936	761	3224	RGGAVTAKAPPDISAISALTAV KHGNCSSLTPLLNPPGSDVIVC AEMDEQWGYVGAKSRQRWLF YAYDSLRKTVVAHVFGERTMA TLGRLMSLLSPFDVVIWMTDG WPLYESRLKGKLHSNEGDAVL LEIEQEVSSVDSSFNSTLGPTFN TRTIQNAVLVKTGETVVLGGLL DDFSKEQVSKVPLLGDIPLVGQ LFRYTSTERAKRNLMVFIRPTII RDDDVYRSLSKEKYTRYRQEQ QQRIDGKSKALVGSEDLPVLDE NTFNSHAPAPSSRWALAQRIGV SRVDMQQHVRRPPVNLSPKRE NVIAGYLSNSVARKQRHIQTGT VFHQLMNLLRDGINIIFMNFKY QFIVYLHFLLSPKWVMYNRKC VNGMLLIASVPATWMLSRYRS SHRWIAKEIPMGKTQPLPILLLG /GGRRIGLALA\WHFIIQKQPVIV SYRTHYPAIDGLINAGAQCIQA DFSTTDGVMAFADELLKSTHG LRAILHHASAWMAEKPGAPLA DVLACMMQIHVNTPYLLNHAL ERLLRGHGHAASDIIHFTDYVV ERGSDKHIAYAASKAALDNMT RSFARKLAPEVKRQTATRAGH RGINQLSRYYRRALARQNQRR MVELRSLRFMYRHRPRSFVLW QATRLHRLNIAVRHRKPDARPL PAIQRNTDIAIKQPKRAVITGNH HRSTFVPTRLAQTGSEIRRHAM
25796	56164	A	25937	3	543	
25797	56165	A	25938	209	343	LSPPMSSFLATVFRSIAWLLTAK SIRYRTT*RWIRCAAVWLTMD
25798	56166	A	25939	547	640	
25799	56167	A	25940	174	583	
25800	56168	A	25941	2001	2610	DVLV\RKHNGHWTVELYSDSIP RLQINQHYASMCNNARNDGDS QFIRSNLQDAKWLIKSLESRND TLLRVSRCIVEQQQAFFEQGEE YMKPMVLADIAQAVEMHESTI SRVTTQKYLHSPRGIFELKYFFS SHVNTEGGGEASSTAIRALVKK LIAAENPAKPLSDSKLTSLLSEQ GIMVARRTVAKYRESLSIPPSN QRKQLV
25801	56169	A	25942	329	484	TRQLSLLVRMTL*AFVRKRRSS LA*KPLWSWLSSVKSQPGWKL MLARWKSF

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25802	56170	A	25943	1	1785	
25803	56171	A	25944	2493	2696	
25804	56172	A	25945	1	1861	
25805	56173	A	25946	456	700	
25806	56174	A	25947	1	2413	MPVIKVRENEPFDVALRRFKRS CEKAGVLAEVRRREFYEKPTTE RSRYDLVDRNNNIVLEYRKKEL VRLTLTDPVTGKSGEVKSLVSS LQTKYALKGYNVEATALEAAG GKVVTTGKDILVRKPTLDLPLE VRRKMWFKPFMQSYLVVFIGY LTMYLIRKNFNIAQNDMISTYG LSMTQLGMIGLGFSITYGVGKT LVSYYADGKNTKQFLPFMLILS AICMLGFSASMGSGSVSLFLMI AFYALSGFFQ\ST\GGSCSYST\IT \KWTPRRKRGTFLGFWNISHNL GGAGAAGVALFGANYLFDGH VIGMFIFPSIIALIVGFIGLRYGS DSPESYGLGKAEELFGEEISEED KETESTDMTKWQIFVEYVLKN KVIWLLCFANIFL\YVVRIGIDQ WSTVYAFQELKLSKAVAIQGFT LFEAGALVGNGCSYAQGMWG KTAETSDLQDLLIAALQGLSAW AVKAREYGIINHDVDSFAPRAF FSTLTNVNFDSPRIVGYAREAIA LREALKAQCLAVDANARVDNP MADLQLVSDDLGELQRQAAEF TPNKDKAAIGENILGLRLLCLY GLKVFNGREDQLDSCYHGNRQ LRGSLRLLFLAFIRQRLRDLIITA HRVIRVNRQHAALGVKHCRLP GITGNRIQRQATQYRDRRGTGQ NQCMRGDMQQLFADIANVAN TFAQIIAGRGRKFGANLLHIAD
25807	56175	B	25948	1	3738	
25808	56176	A	25949	1518	2124	DCFCGSRHDKLPSAHQCSAKPG SDRFWRSHADAAYAHDGGIQP VLCASRSNGCLQKPKCHTIVSG RCPLQQIGS\SVFPSGDAANVAS FSCACDNAGSAQHRTLLLGKQ FFNCRNAFHFNRNSRQTALKSG ISWVTFQLILKQQPRPVIMTKM AIGFRKV*SQRNIIRHLLVYIFKF ADGGCFVVIFLCLQRFIETGINN KMG
25809	56177	C	25950	1	747	
25810	56178	A	25951	168	332	CAWRAVCAAW/PTGASC/CNN DRFVFQILRSFEHDNSEDKPGP GMPPHGWRTQFWGG

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25811	56179	A	25952	1	2706	
25812	56180	A	25953	1	1062	
25813	56181	A	25954	1	855	
25814	56182	C	25955	1	2412	
25815	56183	A	25956	279	713	RCDAAAGAVLHSAGLLRHCGY WQRGKPDRWSRRPGNYADRIC RRWFCAGGVGDRQYELCQLLA YTVSATRRGTGYCLYRDSRGR TGLPVV*HLSGAGLYGRCRFAG VRWCVRHYRRTATSGIPAGDY GGRVRGRNAFCHPAVAP
25816	56184	A	25957	1	769	MDFAETELEFIKFWGDIITNKLN EALAAQGDNVVINLASDEYFKS VKPKKLNAEIIKPVFLDEKNGK FKIISFYAKKARGLMSRFIIENR LTKPEQLTGFNSEGYFFDEDSSS NGELVFKRYEQRAECRIVTRHL SFSGDVCLDHDRRDDHEELSY GGAAVAAVLVIEPNKLAFDGS GYLAWEGLICMQEIGKC/YRRT SGDCA*VAGRAQTG*VSGWAL SRGKNQPGVGCEAGARRHARE ARIGDERHRLAPRDML
25817	56185	B	25958	1	2472	
25818	56186	A	25959	4300	4492	DCGGVRSQRPDQR*DWNR*GA GGESDS*SLATGGQAAEGVAV WRYSARWR*PLFAGRCARAGG D
25819	56187	B	25960	49	3000	
25820	56188	A	25961	266	812	LLRWRPGALALGHKLVAGEIR QQRMDAWRAACLQNPQGILCC ARGGQRSHIVQSWLHAAGIDY PLVEGGYKALRQTAIQATIELA QKPIVLIGGCTGSGKTLLVQQQ ANG/VDLEGLARHRGSAFGRTE DELGKLAQTSTSSPAHWRETSK CGGFLCPIFLTNMRTPLPVCAT VLPYLAIATV
25821	56189	A	25962	761	874	
25822	56190	A	25963	2	304	MAAYGSGIFAQTYIEAFGISTIQ PASCSPVNQYITAAFVLFGNVA HALLIALQRRNRRHLQRRKGA VIVIAFNTSQGA/VPAFCCQP*S RYASPPCCSFSTA
25823	56191	A	25964	109	777	
25824	56192	A	25965	5	187	ITHKKPPPSWRSALLPAAGVFS RRYMPALCE*HWAS*RMRAEA TETFSDCTMPIIGMMMS
25825	56193	A	25966	1	711	
25826	56194	A	25967	757	1026	
25827	56195	A	25968	1	750	

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25828	56196	A	25969	1	1065	MKVLEKRNNASSEPEEKNEIRA AREHAGFTLQELVCLGASGRK VQGEAANAEEEVAAGELDNIA KITNEGSYTEQQIFNEGYMWLS TLMKIKENKISCSWATQSHFQG SIDAGELEHLTPERVWKETESA LTTRNPQVFFQVLRDCGALRVL FPEIDALFGVPAPAKWHPEIDT GIHTLMTLSMAAMLSPQVDVR FATLCHDLGKGLTPPELWPRHH GHGPAGVKLVEQLCQRLRVPN EIRDLARLVAEFHDLIHTFPML NPKTIVKLFDSIDAWRKPQRVE QLALTSEADVRGRTGFESADYP QGRWLREAWEVAQSVPTKAV VEAGFKGVEIREELTRRRIAAG LRG*VSRSHPHLPNAEPKNH/AS NYLIPSMPGVNRSVSSNWR*PA RLTCAAE/HGFESADYPQGRWL REAWEVAQSVPTKAVVEAGFK GVEIREELTRRRIAAGLRGMPT
25829	56197	A	25970	2373	2597	SADDKADSVA*YLRLASA*TNS CRPYRRPSAPVCRRAPAI*G*TP QNYGPPSSCPAGGFWRYPVDPP RFSGFVH
25830	56198	A	25971	2616	2777	TSVRKRFSTLSGKPVAKAGRKR PPPCR*TPTANGHPKPCRPPVW CHPAPVARP
25831	56199	B	25972	1	1449	
25832	56200	A	25973	1076	1477	CAVRRSITWCKLSSKTPVRPLR PSTYRDCLTVSIALTPPASEKVK RRPVPAVKSAMKVPPGAAQSR KRVWLVSPFPTCEFLASNSRGK KISVSLSALSPRWTS*PKARWA ARRLTTNLVVRH*TATSVLMK KK
25833	56201	A	25974	1	3552	
25834	56202	A	25975	196	493	KRCRFADRPGDPGRQGTPAATT FGGMSFVTILPAPIPELSPMVTP GLITT*LPIQTLLPIVIGKEYISPF FLNSWCTGCPVTERVTLGAIST LSPIVTV

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25835	56203	A	25976	1	3917	MTDKHQQHRYVAAPGPFVGD KCQVAGDPLMLRRALSNLLSN ALRYTPTGETIVVRCQTVDHLV QVIVENPGTPIAPEHLPRLFDRF YRVDPSRQRKGEGSGIGLAIVK SIVVAHKGTVAVTSDARGTSGL DDFFIDVVYWVRRIKRKLSVYR RIPRMSYRELYKPDEQPLAIMV PAWNERASSAIWRAGGTTLDT KFLFVGLPGPILGSCKVPFEFLE VACPPSGGPVGPPWRRPCRGA AAAICASPAAIILAPT
25836	56204	A	25977	3	292	GDMQRLNSLFC/SVAYSVLEQP DEDEGRDSINIVNPSGRPIIVSSG ATPAVREYAAHGFHLYGLRQR VGEVRVDLQREQIYASKPCGST IGISLVVR
25837	56205	A	25978	2	181	SARRLR/RSKHRFRILNRRYSHA HS\MLGDMQRLNSLFC/SVAYS VLEQPDEDEGRDSINIVN
25838	56206	A	25979	1	2781	
25839	56207	A	25980	1	2554	
25840	56208	A	25981	635	741	
25841	56209	A	25982	91	501	LWIRLAKRSGKAIKERRDFIFRL CTHRVRQGTALLRLFQHSGGN RLMKLDNQHLRLRISNHRAFHF RHRTTVKQSQQTFRYPWLYRV RHWGQKPKTDNFHGLLARIFG NSRSKTWGENR*EHSVLEQPDE DEGRDEY
25842	56210	A	25983	2153	3062	APVMPPERLPVIAVRQYPTANC CSDCLAAASRFFLASVAAPEQT DADTRRSRVAVGRRKTRSNSA NQPRPRRDWRELQLMDRLARV AQARASFAARETLRIGDAMEQ MMEGLNKVMHGEPRQEKELR KLADDINVLYTAIKLYLARMPK EELAEEESRRWAEIIEMSLNLEQ ASDIVERMG\GELVDKSWAAR RAFSLDGLKELDALYEQLLSNL KLAMSVFFSGDVTSARRLRRSK HRFRILNRRYSHAHVDRLHQQ NVQSIETSSLHLGLLGDMQRLN SLFCSVAYSVLEQPDEDEGRDE
25843	56211	A	25984	135	308	KLSLRLGIFPRPSLFPRPTPSPST PAPAS*PAPS*VSPSPRTATPSCP TSYSSFPCH

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25844	56212	A	25985	3	663	ARGKKPPRRGKEDFWDLSIATR VSVNPIKFPVEA*PFLKP\LQQV S\GPLGGRLPLPIPGNLLLQVAD GTLSLTGTDLEMEMVARVALV QPHEPGATTVPARKFFDICRGL PEGAEIAVQLEGERMLVRSGRS RFSLSTLPAADFPNLDDWQSEV EFTLPQATMKRLIEATQFSMAH QDVRYYLNGMLFETEGEELRT VATDGHRLAVCSMPIGQSLPSH
25845	56213	A	25986	1	1077	
25846	56214	A	25987	1	1323	MHSGTFNPQDFGWQGLTLTPA AAIHIRELEILDEYGIPNAWQGE TNFWGSTAVSIDRLAAYKDVD VLCFDHDNSKDMDALMATPL WQAMPFVRAGRFQRVPAVWF YGATLSAMHFVRVLDNAIGVIV ATALTWMNFSQALPRSQWAQ AAWSPDIDVIEQMIFHYSLLPRL AISLLVGAGLGLDVRYYLNGM LFETEGEELRTVATDGHRLAVC SMPIGQSLPSHSVIVPRKGVIEL MRMLDGGDNPLRVQIGSNNIR AHVGDFIF\TSKLVDGRFPDYRR VLPKNPDKHLEAGCDLLKQAF ARAAILSNEKFRGVRLYVSENQ LKITANNPEQEEAEEILDVTYSG AEMEIGFNVSY\VLDVLNALKC ENVRMMLTDSVSSVQIEDAAS QS\AAYVVMPMRLEGSPPLGNP EFQKISSPCALYIALCSKARHHT GRYLGLCGL
25847	56215	A	25988	211	475	GAIGVFTAGKLTRASVYHQAR RFMQRETVWLVEDEQGIADTL VYMLQQEGFAVEVFERGLPVL DKARKQVPDVMILDVGLPDISG FELCRQLLALHPALPVLFLTAR SEEVDRLLGLEIGADDYVAKPF SPREVCARVRTLLRRVKKFSTP SPVIRIGHFELNEPAAQISWFDT PLALTRYEFIVLKT\LLKSPGRV WSRQQLMDSVWEDAQDTTSH VVAFATILQGISRDLRRRILPYCI RCRRERCTGTALWQ

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25848	56216	A	25989	1661	2499	QMAHDEQWLTP\R\LQTAATLC NQNAPRDGSPLWLGVDLGTCD VVSMVVDRDGQPVAVCLDWA DVVRDGIVWDFFGAVTIVRRHF DTLEQQFGRRFSHAATSFPPGT DPRISINVLESAGLEVSHVLDEP TAVADLLQLDNAGVVDIGGGT TGIAIVKKGKVTYSADEATGGH HIFLTFAGNRRISLEEAEQYKRG HGEEIWPAVKPVYEKMADIVA RHIEGQGITDLWLAGGSCMQP GVAELFRKQFPALQVHLPQHSL FMTPLAIASSGREKAEGLYAK
25849	56217	A	25990	915	1518	PSGHAPDLNGAPATAHQPGGR YPAPRSVRRATDNGYPAGDPLE WRSTAQVFVSSRRRVSLPNDRK TVLTRCWSAAH*FALPAPLCRD RTGERKNRRFHTPTRCGRGFCP APAASRRCAGRRRGDASGRAY RRPAPSHCPVQ*RGHRKSTTTSS TSRRRPGQSARPYSGPEYRE*Y CSAQRFFHNDGSRPPVVRQAGR AQFP
25850	56218	A	25991	1	1254	
25851	56219	A	25992	675	835	VRWCWIFPSQ*TLFQKRAGHA APSADVLHESCQHFLNLLNRLG RHYDFGEGEP

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25852	56220	A	25993	1	2255	MRESPTRDDSKNTVNTTIRIRIH NSYTEQLQIVTNSYCTKQWHV HHTAKPYAHIQRPATPDAQLTK MQEEEEVEPEPEMEAEVEPEPN PEEAETESESMNQRDVRGTVRI VLKTFNNCRDTVFVAFEVNNT VSLLVATTDMTSGDTAIVVTTT GFAVFFQQRSKSAANEVQILAF FQGDVSFFPVATTTDTLSVTFN FPFNYQGVNDFDFDFKQFLHSS FDFCFGRVFSNFEYLHGARAHA CIPPSACIGEVLETSSFDIRVSVY RSSCVCVRLRESSTGDRYFGGL SLQMMRKATGLTDITSDTPGNT DDQRWHPEHGLTQRMQKEQE LVKEPEGAARDGDGEAEAWGE VKAKSSGCVGTRASSHLFRCNV CELHFKESSELLQHPCTPSGERP FRCGECQKAFKRPSG\LRQHER THSAERPFKCDLCPMGFKQQY ALMRHRRTHKTEEPFKCGLCE KGFGQPSHLLYHQHVHTLETLF KCPVCQKGFDQSAELLRHKCLP GAAERPFKCPVCNKAYKRASA LQKHQLAHCAAAEKPLRCTLC ERRFFSSSEFVQHRCDPAREKPL KCPDCEKRFKYASDLQRHRRV HTGEKPYKCPNCDKAFKQREH LNKHQGVHAREQQFKCVWCG ERFLDVALLQEHSAQHSAAAA AAEGAYQQTLHHPRRQQQQY WQLLCARNNVKLCMHILFSPH
25853	56221	A	25994	98	596	YSGIIMAQSKLYPVVMAGGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQPRFIVAHQMRQLNELSENIIL EPAGRTTAPTIAPAALAANRHS PESAPLMLVLATDHVIANEDAV RAPVK\NAIPYPKKGKLVTFGIG LDGRVPRYNM
25854	56222	A	25995	3	554	
25855	56223	A	25996	1	222	

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25856	56224	A	25997	1	1043	MKVKVLSLLVPALLVAGAANA AEVYNKDGNKLDLYGKVDGL HYFSDNKDVDGDQTYMRLGFK GETQVTDQLTGYGQWEYQIQG NSAENENNSWTRVAFASLKFQ DVGSFDYGRNYGVVYDVTSW TDVLPEFGGDTYGSDNFMQQR GNGFATYRDTDVFGLVPTRLHP ARVCCALRELKDAGADRIWYI ADAFRAGLSVDGVFNLTNIDR WFLHINRAKDKNHMIISIDAEK AFDKIQQPFMLKTLNKLGIDGT YFRIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISDFSKVSGYKINVQKSQT FLYTNNRQTESQIMSELPFTIAS RRIKYLGIQ*IRY*WDVFQNNK SYL*QTHSQYHTEWAKTGSIPF ENWHKTGMPSLTAPIQHSVGSS GQGNQAGEGNKGYSIRKRGSQI VPVCRRHDCLSRKPHRLSPKSP
25857	56225	A	25998	1	3339	
25858	56226	A	25999	1440	1880	AAQHASVYLYQNRIRGAVPPV RFFHADQRTRRDGADGKQRHA TETLCRIAEKISSSREQDWLHCD ERQSLYEWTW*PYSPHSGRSQK EKRQT*TAILDAYCADCFRCGR GVFARRERRTKRDRPGNAGTG GDCPCWLRRQYECVRL
25859	56227	A	26000	1	2277	
25860	56228	A	26001	1	1845	
25861	56229	A	26002	56	113	QQQPNPTRDQLQLAILHNIRGIR KIYG*IQSATREAG*GHSPQY
25862	56230	C	26003	1	2317	
25863	56231	A	26004	3	2168	
25864	56232	A	26005	670	2541	
25865	56233	A	26006	98	944	YSGIIMAQSKLYPVVMAGGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQHRFIVAEQLRQLNKLTENIIL EPAGRNTAPAIALAALAAKRHS PESDPLMLVLAADHVIADEDAF RAAVRNAMPYAEAGKLVTFGI VPDLPETGYGYIRRGEVSAGEQ DMVAFEVAQFVEKPNLETAQA YVASGEYYWNSGMFLFRAGRY LEELKKYRPDILDACEKAMSAV DPDLNFIRVDEEA/FLACPEESG DYAAMGRTGDAVVPLSLGAH

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25866	56234	A	26007	3	417	
25867	56235	A	26008	507	717	WPEAEYLDNADAVLAMYHD/Q GLPVLKYQGFGRGVNIT/LGLPF IRTSVDHGTALEWRTCKPMVP DSIVSCIL
25868	56236	A	26009	5	378	MAVCSSLSPRRSPAFL/HDFTDV WTHHLVFGVNP*RGLIHGTALT DHVG/ENGNYSSD*IHGTALTD HVGKTETILPTKYANIYSINTSK DRFLTKPAFAEVVLFLHPRELQ TCSFFLSQNMLVKVGHQRHWF TEVDVTLTEITQLA
25869	56237	A	26010	1	469	MQKEYAYWMDGLKTCKPDNR KNALSNFGWYPSQPLLGRSRY ATTESWVEDIATAKSNPNRLPL KFTATCALPLRLAGFQ\PRWMD NPQQLNTLAPPASYRSI*TA*CL K*KNPRPRQQSCRR*RDGNQYE TLANARQKGIEKTCGTINKAG MPITT

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25870	56238	A	26011	2	1854	CGGTLARACDGCLNGEFAA/LI TGPVHKGVINDAGI/PFTGHTEF FEERSQAKK/VVMMLATEELRV ALATT/HLPLRDIADAITPALL/H QPKYLDNADAVLAMY/HDQGL PVLKYQGFGRGV/NITLGLPFIR TSVGHG/TALELAGRGQ/ADVG SFIRPYSAIK*L*NAGASVRWLS ERRICRAITGPVHKGVINDAGIP LPVIPSFSKSVRRRKRCDDAGD RRTSRGAGNDALPLRDIADAIT PALLHNRNILITPTPCWRCTRSG SSRAKIPGLRARCDITLGLPFIRT SVGHGQPLNWRDVANRCWQF YTPLFCHQMIVKPMHNRIPRAT YRGAVKSAIGLGCCCLKASATR CAYRWRRSGRRDQSRFRYFEIA GIRSRGINFIACPTCSRRNLMLS VRLTRWSNAWRYHHSDGRFD YRLRGECPGEALVSTLGVTGG NKKAASMKMGAQRPSGQQDM IDQLEARIRAKASQRTKRVELT FSRLKNNNVEKQDTALFALYQ RRLRCVRKVRRYVMAAVSAGC GGGVCAVSAYMPLNRLPNAQE ANNEYTSFENCIKCTVCTTACR VTLRNNDPKLPYLVKAGLKMK RVTRSPRRYCAAASATHRFNDE RAGKVQGMPDINKLPADRETC STLTCARSRQNQTNPYPANRAA NAYQVVLATKALEKVSMKSP WQHKVSSPAAVRHLPSITQRRT

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25871	56239	A	26012	1	1504	MGIVASASVQAAEIYNKDGNK LDVYGKVKAMHYMSDNASKD GDQSYIRFGFKGETQINDQLTG YGRWEAEFAAWTDMFPEFGG DSSAQTDNFMTKRASGLATYR KTTSSAYRWPELNLQYHRCTS AARAMLLSGRPVMQINERTAV RRQMTVYLRVERIHEIDPLVSL SHSMSVIPIDVERPIAAAPCTPG LWRTKTPLRVPSTYPLRLPGRA RVVCHRTFRLHLCKDWVFMFS GLLIILVPLIVGYLIPLRQQAAL KVINQLLSWMVYLILFFMGISL AFLDNPRPYLADSVPDRQLLAP VNSISRYKTIEWLNYIATELHK GFTPLFRPDTPEEYKPTVRAHSE KKLQYVNEALKDEHWICGQRF TIADAYLFTVLRWAYAVKLNL EGLEHIAAFMQRMAERPEVQD ALSAEGLKGSRHLSAGARRLIL GIIVTFSLILALICVTQPFNPLAQ FIFLMLLWGVALIVRRMPGRFS ALMLIVLSLTVSCRYIWWRYTS TLNWDDPVSLVCGLILLFAETY AWIVLVLGYFQVVWPLNRQPV PLPKDMSLWPSVDIFVPTYNED LNVTPDELKQVLDVAAALKAL RAENISTKVFNSGLGISVFRDNS TRTRFSYASALNLLGLAQQDLD EGKSQIAHGETVRETANMISFC ADAIGIRDDMYLGAGNAYMRE VGAALDDGYKQASGFSEPAMR
25872	56240	A	26013	2903	3024	
25873	56241	A	26014	123	335	
25874	56242	A	26015	2634	2787	
25875	56243	A	26016	1477	2485	NPEQLMVKTQRVVITPGEPAGI GPDLVVQLAQREWPVELVVCA DATLLTNRAAMLGLPLTLRPYS PNSPAQPQTAGTLTLLPVALRA PVTAGQLAVENGHYVVETLAR ACDGCLNGEFAALITGPG\HKG VINDAGIPFTGHTEFFEERSQAK KVVMMLATEELRVGLATTHLP VRDIADAITPALLHEGIAILHHD LRTKFGIGEPRILV\GGLNPHAG EG\GPMGTEEIDTIIPVLNELRA QGMKLNGPLPADTLFQPKYLD NADAVRPMYHDQGLPVLKYQ GFGRGVNITLGLPFIRTSVDRGT ALELAGRGK\ADVGSFITALNL AIKMIVNTQ

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25876	56244	B	26017	1	3432	
25877	56245	A	26018	1385	2536	KSSQSHLITGMLEHVFVKSGDT PSR/LPELMNGAQALANQINT/F VLNDADGAQAIQLGAN/HVWK LNGKPDDRMIED/YAGVMADTI RQHGADGL/VLLPNTRRGKLLA AKL\PDASRTGETH/TVEWQAP AVAITRTATQARQSNSVDLDK ARLVVSVGRGITDSQTLRLYYI RLPPSLMGMRLTVFLLPICGFH RVGPPTLLSVLATNRNRNAKVF AHKNAPKFRSHTASEQWKSSIA HNKGVHPRVTSHTHARHSLME TDIPHNIHSGHASPADITRHRAQ VFNSVPKMASPIGDRVPTLHTQ HNSPANTGKAQSLLTCGPAAES CCRLIPRQMVSLVFRLKARLLLI TTELPKGLVPVATISGTGNFGN TQSANPYRPSENTDLSLS
25878	56246	A	26019	926	1293	LSPNPKEPSCRTRLKKSGFFTRI SAGAEPLMAIPARLSNSLACGA RDSAAKE/GFVVVPVCVAVEA DIAELDDEERDEFMADVGFT\V GVKEVRAWTIPVGATAPQAAG KIHTDFEKGFIRAQT
25879	56247	A	26020	1	1278	
25880	56248	A	26021	678	1526	ERNTNTCEVVPNRKRAYASHD MELSISPVGKGASKGEVNPADD IEVINTELALADLDTCERAIHRV QKKAKGGDKDAKAELAVLEK CL\PQLENAGMLRALDLSAEEK AAIRYLSFLTLKPTMYIANVNE DGFENNPYLDQVREIAAKEGSV VVPVCAAVEADIAELDDEERDE FMQELGLEEPGLNRVIRAGYKL LNLQTYFTAGVKEVRAWTIPV GATAPQAAGKIHTDFEKGFIRA QTISFEDFITYKGEQGAKEAGK MRAEGKDYIVKDGDVMNFLFN
25881	56249	A	26022	1177	1605	
25882	56250	A	26023	1	644	MDNHIALDFLLASECGSVYVY ATTHGRNMAGARALWRATGM TDADFGKPIIAVVNSFTQFVPG HVHLRDLGKLVAEQIEAAGGV AKEFNTIAVDDGIAMGHGGML YSLPSRELIADSVEYMVNAHCA DAMVCISNCDKITPGMLMASL RLNIPVIFVSGGPMEAGKTKLS DQIIKLDLVDAMIQGADPKIN/D YQSRGRRCPNRCFRCKNQAGS
25883	56251	B	26024	1	1944	

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25884	56252	A	26025	1	1488	
25885	56253	A	26026	1	1919	MNKAHFVSNLGATKCCPLSFLP YRWRRVIAFVVAFYFRHLIDLL VVQMHFKLVKGNVDVVFTAQ LIDSTVQLIDSTTTVTQFTHIQT QLMIQRAGTKCRKEDFRHCVGI LEPEWYPIIVVRVVVDVSQFEV RSQSLIFAVGEGITCIYTQFITHA VVRLTVNFHVVAQLSSPDWNR PETLPVRSHVTSITQFEVVTGFQ TEAPSVGVGATVNVSTVAHGC RQVVVEVRVAQATINKDVVRE VSRRVDVGSLAVLIHLTRTVIH VTFSEACSRTDDPLSVVTVNFGI NTDHDAVNILIIVDGAVVAVEV TTEVAYPCAAVISQAMTRVGQ TSTNGVWTISSVNAFQIRTGAA RSLAPPWSLTEKVFCGTTMER MRAALEAIMPFTESSSATQAPY LPCGRECGLAVRQFFGRGEGIE TVAYLFRIIRVVRTRVLSIGGFS RTRISSTPVKIATLRQNRSDCHA AMIADTYRQVTPTDPFSRHPFS RVLRGLFFIIFKDTKAHNGIGMI GGVNRRADYLNLLEKVFGDRV SSPQWQATLKAIVPSYGRKLNG DVAATERELQYTSEVVGLNYD KPQAADNNRQHKVRAARSRRQ NRPDRGSQIADSTAGARCRFQT PTAGDGA*SAASTAAPI/MLNLL EKVFGDRVSSPQWQATLKAIVP SYGRKLNGDVAATERELQYTS EVVGLNYDKPQAADNNRQHK
25886	56254	A	26027	1	2130	
25887	56255	A	26028	1144	1309	PGGSTPMAVEDPDFRSSERVLR FQPAVSVYGPEQPAV*DYAQTS YLRTRPRRSDP
25888	56256	A	26029	1	3546	

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25889	56257	A	26030	1097	3332	TRVLVLDHRLLRCLYATVCAG ASWGMNPVVCSQQIDPQFHTM LMICASEEAQRMQQASEDEFN RALNIAFDNRLGLCKVESARQV FPLTGRYARQFASHRLALVGD AAHTIHPLAGQGVNLGFMDAA ELIAELKRLHRQGKDIGQYIYL RRYERSRKHSAALMLADSFVR TTHALRRSHGGFPRLDDAAAL RFANRRTSCERNDDNTWSRSL YADLKNGTAQNIRAKFVFIGAG GAALKLLQESGIPEAKDYAGFP VGGQFLVSENPDVVNHHLAKV YGKASVGAPPMSVPHIDTRV\L DGKRVVLFGPFATFSTKFLKNG SLWDLMSSTTTSNVMPMMHV GLDNFDLVKYLVSQVMLSEED RFEALKEYYPQAKKEDWRLW QAGQRVQIIKRDAEKGGVLRL GTEVVSDQQGTIAALLGASPGA STAAPIMLNLLEKVFGDRVSSP QWQATLKAIVPSYGRKLNGDV AATERERKTLHVIFNDLRPEQC EAGKSPSRVQLQTWTNGGMLN APLSLRLTLVEKLASMLDPGHL ALTQIAQHLALLQKMDHRQHS AFPELPQQIAALYEWFSARCRW KEKALTQRGLLVQAGDQSEQIF TRWRAGAYNAWSLPGRCFIVL EELRWGAFGDACRLGSPQAVA LLLGDLLEKATQHLAESINAAP TTRHYYHQWFASSTVPTGGEH
25890	56258	A	26031	115	654	HATQTMTPWFLYLIRTADNKL YTGITTDVERRYQQHQSGKGA KALTGGSARSPLIKKALAEQLP GIPIAGGDDFGSVTAGLAR*RF HQRHGPCWSMKAESLQLCRAD CQRRFQPMSFGGHFRHYRLSVC WRYRFIRPEHKTAFTARFPVDN RLGQMVAKPFHLLNATTGNIC GCFNTKRP
25891	56259	A	26032	1	348	
25892	56260	A	26033	1	906	
25893	56261	B	26034	59	910	
25894	56262	A	26035	1	3684	
25895	56263	A	26036	1	2634	

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25896	56264	A	26037	1162	3478	LVRFGLLPLAYSARCFSARSED RPKDECETCCIKYPNGRNVLSQ EIHQVFVLNGIQSMSGYVYNLG NELASMQGLVDVVRLSPQGSS AREAFSHSLDLARLAEKRGYH RYWLAEHHNMTGIASAATSVLI GYLAANTTTLHLGSGGVMLPN HSPLVIAEQFGTLNTLYPGRIDL GLGRAPGSDQRTMMALRRHM SGDIDNFPRDVAELVDWFDAR DPILEPTHNGRRLCSTVRHPRM GYTPGVEPTTGPLGQGLANAV GLAIAERTLAAQFNQPDHEIVD HFTYVFMGDGCLMEEGWFTD DTAKRFEAYHWHVIHEIDGHD PQAVKEAILEAQSVKDKPSLIIC RTVIGFGSPNKAGKEEAHGAPL GEEEVALARQKLGWHHPPFEIP KEIYHAWDAREKGEKAQQSW NEKFAAYKKAHPQLAEEFT\RR MSGGLPKDWEKTTQKYINELQ ANPAKIATRKASQNTLNAYGP MLPELLGGSADLAPSNLTIWKG SVSLKEDPAGNYIHYGVREFG MTAIANGIAHHGGFVPYTATFL MFVEYARNAARMAALMKARQ IMVYTHDSIGLGEDGPTHQAVE QLASLRLTPNFSTWRPCDQVEA AVGWKLAVERHNGPTALILSR QNLAQVERTPDQVKEIARGGY VLKDSGGKPDIILIATGSEIEITL QAAEKLAGEGRNVRVVS\LASS
25897	56265	A	26038	1	1033	MNKSPKTRDIQEEELEVLLEEE AAGGDEDREKEILIERIQSIKEE KQKGLGLAAGWTADVSSRRPG ASQLPPPPTHPIPQYRGWGPPD QHLLSTLWTNVGSYKSGSFLQL GGWCMNLDMDLNSEESRWLF RRHWDTGGIKPHERKRAVAHL TLSEREEIRAGLSAKMSIRAIAT ALNRSPSTISREVQRNRGRRYY KAVDANNRANRMAKRPKPCLL DQNLPLRKLVLEKLEMKWSPE QISGWLRRTKPRQKTLRISPETI YKTLYFRSREALNHLNIQ\HLA RSHWLWPGERY\NRNGERGPV TLWTG/TPISDGSRTSVKRALGQ WGEHLSRRNAFFPLCATVV

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25898	56266	A	26039	797	1440	PAMRLTAMRCISMKSRLPASR MQFCATVRWKYRCHREPTLSA QHGAFRSINPTPRNSRGNCWKK REMKWANWPIWCR*KN*RERS LSAICCASRK/TGQFVLPPARYH LRRSHSLRHGRRHTRKGERGTI NIVNGTPIHERSRNIDNRRSLGH WEGDLVSGGVGTVIGVVTGVII FTVINYGLTYIGVNPYWQYIIK GAIIIFAVALDSLKYARKK
25899	56267	A	26040	687	1106	GSLSLTALLPDTAEREEIRAGLS AKMSI/RAIATALNRSPSTISRE/ VQRNRGRRYYKAVDAN/NRAN RMAKRPKPCLLDQ/NLPLRKLV LEKLNIQHLRRSHS/LRHGRRHT RKGERGTIN/IVNGTPIHERSRNI DNSALVTVLR
25900	56268	A	26041	1	2851	MKTLIARHKAGEHIGICSVCSA HPLVIEAALAFDRNSTRKVLIEA TSNQVNQFGGYTGMTPADFRE FVFTIADKVGFARERIILGGDHL GPNCWQQENADAAMEKSVEL AVVIDLWSRAVIGWSMSPRMT AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK RHNLRGSMSAKGCCYDNACVE SFFHSLKVECIHGEHFISREIMR ATVFNYIECDYNRWRRHSWINS LLSQKRNTQGRIEDGRQH
25901	56269	B	26042	1	1048	
25902	56270	A	26043	323	1290	GTSMNTVGTPLLWGGFAVVVA IMLAIDLLLQGRRGAHAMTMK QAAAWSLVWVTLSLLFNAAF WWYLVQTE\GRAVADPQALAF LTGYLIEKSLAVDNVFVWLML FSYFSVPAALQRRVLVYGVLG AIVLRTIMIFTGSWLISQFDWIL YIFGAFLLFTGVKMALAHEDES GIGDK\RWCAGYA/VHLRMTDT IDNEHFFVRKNGLLYATPLMLV LILVELSDVIFAVDSIPAIFAVTT DPFIVLTSNLFAILGLRAMYFLL AGVTKRFSMLKYGLAGILVFIG IKRLIVNFNLLQTRACLGGGWA FGETLIIKPGEYRMKTAGG
25903	56271	A	26044	28	96	
25904	56272	A	26045	1	777	

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25905	56273	A	26046	77	532	KPSRPEISKGKSVKPAASRRARE CAVQALYSWQLSQNDIADVEY QFLAEQDVKDVDVLYFRELLA GVATNTA\YLDGLMKPYLSRLL EELGQVEKAVLRIALYELSKRS DVPYKVAIKEAIELAKSFGAED SHKFVNGVLDKAAPVIRPNKK
25906	56274	A	26047	3	175	
25907	56275	A	26048	85	440	YSSSSLWAARKRRQMVLSARR FATSDRVCRCVLVWSAGTSRA KSKSTGWLSMASKAIGVSS*TK TPTARRVSSSSLPCGMAIPLPIP VLPIFSRVRIASKTT*GSSLSCFA ARSLMTS
25908	56276	A	26049	80	706	KLIQVAVVIGGGQPLGAFLCHG LAAEGYRFPVVDIQSDK\AANV AQEINAEYGESMAYGFGADAT SEQSVLALSRGVDEIFGRVDLL VYSAGIAKAAFISDFQLGDFDR SLQVNLVGYFLCAREFSRLMIR DGIQGRIIQINSKSGKVGSKHNS GYSAAKFGGVGLTQSLALDLA EYGITVHSLMLGNLLKSPMFQS LLPQ*KTKLGIK
25909	56277	A	26050	741	893	TGCSGKRSLQQRREERRRNPVQ KIRCTV*RVRNGRIRYCSPRAGF YSRYR
25910	56278	A	26051	269	987	
25911	56279	A	26052	1	1268	MDAKCDRSRFPWLWPTKRPRG CFATFVPIGIPYDQTKTHLHTLS LVAKRLADKTICRRLRAAQSDE ELYQIITDTEGTPDEARCEEKQY MVLMIVSGRSGSGKSVALRAL EDMGFYCVDNLPVVLLPDLAR TLADREISAAVSIDVRNMPESPE IFEQAMSNLPDAFSPQLLFLDA DRNTLIRRYSDTRRLHPLSSKN LSLESAIDKESDLLEPLHGFPDY DTVGFSCKRRIDYVCRIKHSRRI RQVVLLNFAKSGAFSTTRGTDD KTRRSLLVTL/VAYFLCAR/EFS RM/MIRDGIHVRIIQINSKSGKV GSKHNSGYSAAKFGGVGLTQS LALDLAEYGITVHSLMLGNLLK SPMFQSLLPQYATKLGIKPDQV EQYYIDKVPFKRGCDYQDVLN MLLFYASPKA\SY\CTGQSINVT
25912	56280	A	26053	1	168	LKVFILVIFTLSRE*EHAMFGFL FLC*FAENDGFQLHPCPCKGHE LILFYGCIVFH
25913	56281	A	26054	2	253	

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25914	56282	B	26055	319	3780	
25915	56283	A	26056	513	762	
25916	56284	A	26057	375	550	GVGLCGRSSIRRNM*CK**G*/L SPKIALMACGRRHTRSLFMTSK DLSRMMRLQKEIRL
25917	56285	A	26058	662	1033	EPKRASGCMWPVGAHCHHPLL LLACQQKLGPPSHQASSRS*NIQ TLDRLCMSSWIPQEHSSSQSWH RSCFLNVTRPWSFYSPVGKNR WMGPFWSFSLDALLLFFTLHSY VAWPVEMMALNLLG
25918	56286	B	26059	1	2034	
25919	56287	A	26060	369	515	HAKPPGGLGHCSLCPSHYSCIH G*KGPRYVSVSCSRGWKPEAT KAFMW
25920	56288	A	26061	352	2631	
25921	56289	B	26062	10	351	
25922	56290	A	26063	321	537	EPLDTGRGTSHTRACHGVGYW GRDSVRRYT*CK*RINGYSTPT WHMHEYVTNLHIVHMYPRTYS IIIKKMSD
25923	56291	A	26064	788	912	VHTHLSERTRKCLPPPAPS*WV TCHHGDCCLPTRLRAPQGP
25924	56292	A	26065	1348	1799	
25925	56293	A	26066	606	2219	ATYPSAHYPDHNRGEFLWPSL GLGKELDTFWSSLRVFGSPVSA VSRELVRKFSLGGTVDSTGSLP VCGDISPVSDVA/ACTREPLRFR LQVGDRYITLMDLPGVGESGA RDTEYAALYREQLPRLDLVLW LIKADDRALTVDEHFYHQVIGE VYRHKVLFVISQSDKAEPTSGG GQLSTAQKQNISRKICLLHELFQ PVHPVCAVSVRLQWGLKVMA ERMIKCLPREATSPVVSQLHPSF RTTVVREQARSDFGETVGAVL DSISAFPLIPAPVRAVIQAVRTT VVSFAASVTLLLLPLRSTPVEKS PTCILPASETFPLLVVMLNPVAS LLTLTSPVLDTSCPTHSLSAAQP NLIQLSGNNNISFVVNRAVVTN VLNTMRTACNSQATIQIYNADI ARDFGTRGIFSINSGFSTVYSRRI GHQSPEVTGEAMALTLSSQPSC IDDGLVAVNLDTDGLRIGDARQ KAITAGYPVVDTDDKCRIRRLR RIRHEQCADENSYQAYNYCRP VGRIRHLCRIRQSMPDATLSRLI
25926	56294	A	26067	543	741	

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25927	56295	A	26068	3	373	VYTGLKPRTIDAQYTPINVV/W KFLSLTHHAYSPLLVVINKAKF DGLSPEFQQALVSSAQEAGNY QRKLVAEDQQKIIDGMKEAGV EVITDLDRKAFSDALGNQVRD MFVKDVPQGADLLKAVDE
25928	56296	A	26069	1	1107	MGAFTGKTVLILGGSRGIGAAI VRRFVTDGANVRFTYAGSKDA AKRLAQETGATAVFTDSADRD AVIDVVRKSGA*ILILKRRSISSA FNSRASPKTPIPAFTTRISNAPLL RTTSMTASLSALSVNTAVAPVS CARRLAASFDPA
25929	56297	A	26070	39	254	
25930	56298	A	26071	1432	1845	
25931	56299	A	26072	674	1614	AVIVVAILVSKSTGAWVAFSIR MPSITFSHNSVVAGVASARKDS SPSYGDPLESAIPKLNVKRSRSG LSKSLLTLTSCSTIWINWITGQT PLKPCSVTGSVVPKAWRSPSTL TTMTTR*PFTLPA/LDTFISRPAG CTYANECHAPESATIRNDVAAR PCNCAQCAALDCVSVFVTIRHS CSSVYSAPGILVAALQAGHKPV ALVGGATGLIGDPSFKAAERKL NTEETVQEWVDKIRKQVAPLP DRKNISPADSRLSPDGRYRGYV HPAPPIPDSHLIRHHRCVIYQWR QCLAQFRLNGWAASRSQSICRI GCD
25932	56300	A	26073	1	3476	MSSSCIEEVSVPDDNWYRIANE LLSRAGIAINGSAPADIRVKNPD FFKRVLQEGSLGLGESYMDGW WECDRLDMFFSKVLRAGLENQ LPHHFKDTLRIAGARLFNLQSK KRAWIVGKEHYDLGNDLFSRM LDPFMQYSCAYWKDADNLESA QQAKLKMICEKLQLKPGMRVL DIGCGWGGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGL DVTILLQDYRDLNDQFDRIVSV GMFEHVGPKNYDTYFAVVDR
25933	56301	A	26074	200	1100	
25934	56302	A	26075	1	2061	
25935	56303	A	26076	1	3294	

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25936	56304	A	26077	1	2064	MNYSLKQLKVFVTVAQEKSFS RAGERIGLSQSAVSHSVKELEN HTGVRLLDRTTREVVLTDAGQ QLAFRLERLLDELNNTLRDTGR YGATTERSARYSASLPAPTSGR SEPAALVQNSSSQPSSLKENIM KLRSVTYALFIAGLAAFSTFFLA \AQSIRCGYETSQADSQHSGAK KFNDLLQERPKGELKLKLFPDS TLGNAQAMISGVRGGTID\MEM SGSNYFAGLSPVMNLLDVPFLF RDTAHAHKTLDGKVGDDLKAS LEGKGLKVLAYWENGWRDVT NSRAPVKTPADLKGLKIRTNNS PMNIAAFKVFGA\NPI\PMPFAE VYTGLETRTIDAQEHPINVVWS AKFFEVQKFLSLTHHAYSPLLV VINKAKFDGLSPEFQQALVSSA QEAGNYQRKLVAEDQQKIIDG MKEAGVEVITDLDRKAFSDAL GNQVRDMFVKDVPQGADLLK AVDEPGWAERDIWAFAPAFFY PLFISDFNRVRLEFVGHYQDVC EKPASTTLWLDVGRSSGLDLTY QTLNVKNDLSHFPVPFFDPSDN RTNTLPMVFAGAPDVGLQQAS AIVASWFGSRSGWRGQNFPVL YNQLPDRNAIVFATNDKRPDFL RDHPAVKAPVIEMINHPQNPYV KLLVVFGRDDKDLLQAAKGIA QGNILFRGESVVVNEVKPLLPA GSQPVWSSSASESRCCFYA
25937	56305	A	26078	1	480	LGNTKTVKGWLAQLPAKYHQ RATCMFDRHGLLALLAGRFLA FVRTLLPTMAGISGLPNRRFQFF KAKLR\WLS*PTRIAAALAFMP/ FMDDHHPRLMQTVILQILQRRG TGDRLKIMVERRYAHVGFCRQ LLDAQVFGVFILNPFQHAANQT EVSLATDQRQ
25938	56306	A	26079	1	2184	

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25939	56307	A	26080	1429	2152	NLFREVVFPTHCPVCGSDVERV EGEAVARCTGALICGAQRKESL KHFVSRRAMDVDGMGDKIIDQ LVEKEYVHTPADLFKLTAGKLT GLERMGPKSAQNVVNALEKAK ETTFARFLYALGIREVGEATAA GLAAYFGTLEALEAASIEELQK VPDVGIVVASHVHNF\LPKKAT AMSSASCWRKVFTGLRRSLSTR KRLTARLLVKPWCLRAASGTP LKRASLLMFSGCFSHTSGLAMY
25940	56308	A	26081	1	2448	
25941	56309	A	26082	125	741	AHLNRTRWKVCWIR*RKISPW AKRNTKTVKG\WLAQLPAKYH QRATCMF\DRHGLLALLAGRFL AFVRTLLPTMAGISGLPNRRFQ FFNWLSGLLWVSVVTSFGYAL SMIPFVKRHEDQCRNGVFGKR KGGIAAALILTRLRRRFVSSWK RFRELRRKSSQADDMNVFGILE DFTHQFIGGAFLRADISGAAKM SCLAKAQASSSMH
25942	56310	A	26083	1066	1359	
25943	56311	A	26084	256	952	RLKRCSTGKSMAVIQDIIAALW QHDFAALADPHIVSVVYFVMF ATLFLENGLLPASFLPGDTLLIL AGALIAQGVMNFSGLRIAVLDP RNQVRGGGLSIFKGRWLGNPK TVKG\WLAQLPAKYHQRATCM FDRHGLLALLAGRFLAFVRTLL PTMAGISGLPNRRFQFFNWLSG LLWVSVVTSFGYALSMIPFVKR HEDQVMTFLMILPIALLTAGLL GTLFVVIKKKYCNA
25944	56312	B	26085	1	1290	

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25945	56313	A	26086	1	1839	MRCQNAWWIMQHSSGSERLSS VLLHFRRTNLADSNDRIQYHSL RFFDEDGAQWLVILGDVLNHG PRNALPDGYAPRKVAERLNEV AHKVIAVRGNLRQRVDQMLLI SRAINRLVASNWNRRSAQMRC PISGKNLAWIPVQLPVYWQNN CRRLLMRSHRKHGSGTNLPGE LMAIKLIAIDMDGTLLLPDHTIS PAVKNAIAAARARGVNVVLTT GRPYAGVHNYLKELHMEQPGD YCITYNGALVQKAAD/GYDDY/ RF/LEKLSREVGSHFHALDRTT\ LYTAN\RDISYY\TVHEFLRCHQ FPLVVCDGGRMTPRAMFLFSSA HILMPLNYHNSHINTLFPVAGT LMVEPTESESKVELDRFIDAML AIRAEIDQVKAGVWPLEDNPLV NAPHIQSELVAEWAHPYSREVA VFPAALVTGGSRGIGRATALLL AQEGYTVAVNYQQNLHAAQE VMNLITQAGGKAFVLQADISDE NQVVAMFTAIDQHDEPLAALV NNAGILFTQCTVENLTAERINR VLSTNVTGYFLCCREAVKRMA LKNGGSGGAIVNVSSVASRLGS PGEYVDYAASKGAIDTLTTGLS LEVAAQGIRVNCVRPGFIYTEM HASGGEAWTRRSR
25946	56314	A	26087	2	1275	VNFSPKSSQIHHALRTVAGRFA VKSIDYFWHDSCNASKRFHIWE SIMLELLFVIGYLVMLMVTGVS LLGIIAALVVATAIMFLGGMLA LMIKLLPWLLLAISVVWVIKAI KAPKVPKYQRYDRWQLAVRRS PLLPDHTISPAVKNAIAAARAR GVNVVLTTGRPYAGVHNYLKE LHMEQPGDYCITYNGAL/VYRK AAGWLAPLAAKLLLKLMDELI GFLEKLSREVGSHFHALDRTTL YTANRDISYYTVHESFVATIPLV FCEAEKMDPNTQFLKVMMIDE PAILDQAIARIPQEVKEKYPVLK APNLQQPHGSSGSSFHREIFFSS RSEDKRRGGLVVSGISLLVVSA GPWVRNANEPLGQLKTWFSLS HTLTLTYTRAPACRLTSTQTEP RARPCLSPLSSEPRDRSLTPRLG QRFIYLAVQ
25947	56315	B	26088	1	1509	
25948	56316	A	26089	1	1323	

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25949	56317	B	26090	1	5073	
25950	56318	A	26091	249	531	CWAMRMDSKVGVITPIRMWSA SGPFAMGTLVPTFAAVTDIPTK SVTTCLRQICERWQAPSTR*SRF ASLSQPAPRFTPSPITLALVLLP ARRC
25951	56319	A	26092	3	1038	LVLFGVAETYPVANDFAAGAG AYVRGRYAAGVRAWPTIITRK TMKTLVVALGGNALLQRGEAL TAENQYRNIASAVPALARLARS YRLAIVHGNGPQVGLLALQNL AWKEVEPYPLDVLVAESQGMI GYMLAQSLSAQPQMPPVTTVL TRIEVSPDDPAFLQPEKFIGPVY QPEEQEALEAAYGWQMKRDG KYLRRVVASPQPRKILDSEAIEL LLKEGHVVICSGGGGVPVT\ND GAGSESVIHKDLAAALLAEQIN ADGLVILTDADAVYENWGTPQ QRAIRHATPDELAPFAKADGSM GPNVTAVSGYVRSPVQMHHRQ FQPVIIHIATNQIDHHRRIIHHWL
25952	56320	A	26093	1	3639	MKRLIVGISGASGAIYGVRLLQ VLRDVTDIETHLVMSQAARQT LSLETDFSLREVQALADVTHDA RDIAASISSGSFQTLGMVILPCSI KTLSGIVHSYTDGLLTRAADVV LKERRPLVLCVRETPLHLGHLR LMTQAAEIGGNTGEIDEEELES LLYAIAKGNVFNFQTILHLPVA VQNDTIDFYQMFARIWSSHPQ WLTLYLAQHRAVIIPDDAKLHR NLLRWYSAGRLDIPELLDYAQS WRETEPDNEDAPY

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25953	56321	A	26094	1	1260	AWARQDRRLSVKQWGKPPVD ETIPAKEQVRILRKLFDRYYGE VAGRGDGFCSPHVARYVGRVA G*RPCRLGPGHPTNRTPFVAPL LEALDIAKYFSVVIGGDDVQNK KPHPDPLLLVAERMGIAPQQML FVGDSRNDIQAAKAAGCPSVG LTYGYNYGEAIDLSQPDVIYQSI NDLLPALGLPIAKIRNRKMTKPI VFSGAQPSGELTIGNYMGCTEA DRQFAFNFNNFVLIQLLTNGGP DRLGTTTPAGYTDLLVNYTYRI AFEGGGGQDFGLAAAIATLIFL LVAIMFPLLMVVAISLRQGNFA TGSLIPEQISWDHWKLALGFSV EQADGRITPPPFPVLLWLWNSV KVAGISAIGIVALSTTCAYAFAR MRFPGKATLLKGMLIFQMFPA VLSLVALYALFAPRVRAALCY
25954	56322	A	26095	1	3240	
25955	56323	A	26096	494	792	ATRLRHGVTSVGGDGGLQLTV MDKLDVILLMSV/NPGFGGQSFI PQTLDKL/REVRRRIDESGFDIR L/EVDGGVKVNNIGEIAA/AGA DMFVAGSAIFDQPDAR
25956	56324	A	26097	1624	2390	RTSERRWHAKALLKLFSAHHA GFVCCKEEEERLATGKVGWLP VETLLAQQHIEGHYQVDPSLFK PNADCPVRVSGMSMKDIGIMD GDLLAVHKTQDVRNDPLLVPL FTLIREGKLAANWPLEQDELLT RLQKSCDMTQVSADYNALFIG DECAVPPYRSAWVEGATEAEV RAFLSERGMPLADTPADHIGTL LLAASWLEDQSTEDESEALETL FKRGA/LPKSLCLWGKAPAPHG SPVGGFSKGPKTWAPHEGAS
25957	56325	B	26098	1	534	
25958	56326	A	26099	67	399	

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25959	56327	A	26100	8	1016	PESRRKAVMTQPVLDIQQLHLS FPGFNGDVHALNNVSLQINRGE IVGLVGESGSGKSVTAMLIMRL LPTGSYCVHRGQISLLGEDVLN AREKQLRQWRG/ARVAMIFQEP MTALNPTRRIALQMMDVIRHH QPISRREARAKAIDLLEEMQIPD AVEVMSRYPFELSGGMRQRVM IALAFSCEPQLIIADEPTTALDVT VQLQVLRLLKHKARASGTAVL FISHDMAVVSQLCDSVYVMYA GSVIESGVTADVIHHPRHPYTIG LLQCAPEHGVPRQLLPAIPGTV PNLTHLPDGCAFRDRCYAAGA QCENVPALTACGDNNQR\GAC WYPQQEVISV
25960	56328	A	26101	3	102	ISRLNTQQHFG*RTRQISPHSPQ GCSRCPLHS
25961	56329	A	26102	290	490	SSLNSCMAVWDKTRLIRQ*LV MWSY*SPSPCR*PAGYRHMKL RSTSLVLSTPSRLFLAVIPPVVVI
25962	56330	A	26103	1	3255	
25963	56331	A	26104	119	634	
25964	56332	A	26105	1640	1770	HLDSNRRVHDSTCNWCCNLS* QRLLWSG*WSELCCSVPRQKR A

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25965	56333	A	26106	281	2108	RESLKQKVGGRPQLSPFPPPDS WALDPGGGRARETPRGVSNAT KEPISVAQHGN/GGDKEIRRELK YYAHLGRRLKDWSGIPRYHGT VETDCGTGYVYDVIADFDGKP SITLTEFAEQCRYEEDIAQLRQL LKQLKRYLQDNRIVTMSLKPQ NILCHRISESEVIPVVCDNIGEST LIPLATWSKWCCLRKQERLWK RFIAQPALAIALQKDLQPQATE ASGAENMASIASGNIARTDPDM LSIPLSKKICCFGDRIIEIPETIDQ PVRFWVLTGPVVDMGIYACYL SSPQWGWYAERDAEIENETVR REVEELRQASETDLQPGTIEYE RHRLTRAQADAQELKNARDSA EVVETAFCTFVLSRIAGEIASIL DGIPLSVQRRFPELENRHVDFL KRDIIKAMNKAAALDELIPGLL SEYNRADRQYAGGSRVAARFA ASPRVAVLSVITGLIPRHVCAPY LLCGDPCCLSTPEDMTPRFRRY AVRSGNRSTPGLDHRCDACQR SAYELADLRCRPPPSTLFLLPEA DKNDFSDALPAVADAMYAAPP RRKAAPSKPEKAVVSPLRSVRK ARHGSVCSLRPDQYAVRNLPA YRSCSSPDLQFMVWCALA
25966	56334	A	26107	1	2880	
25967	56335	B	26108	61	5101	
25968	56336	A	26109	80	561	IRPLPPRFKTESRSLPGPCLQPGT FLWSRNRRVLGFPSMNGEDMG LLFLCSEWERSSEGWLCNREGG SGHSIEPHCCTFLHLTHRSLAFS LLAGVSCTCASSCKCKE\CKCTS CKKSECGAISRNLGLWLKVGR EPKAVPEVRASGEPAFLCPCRL SLPV
25969	56337	A	26110	1	277	
25970	56338	A	26111	902	1006	
25971	56339	A	26112	2	1265	
25972	56340	A	26113	409	525	
25973	56341	A	26114	91	431	NHKPGNIDVARRIQRGFAGDQI GHLRPVERQCSPDKRRFIAADG REIRGKQRAGHIFQLLSRCLLQI LNHCQRRAAHFRFQLSNQRHQ QLLPV/HYHAAEREYPAGACLV RWLL
25974	56342	A	26115	3	71	
25975	56343	A	26116	1	1212	

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25976	56344	A	26117	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVWDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGPGRLPFNRIGLIRRITRRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSGLKRVYHSPG APDIREFTRDAIP
25977	56345	A	26118	5	402	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI
25978	56346	A	26119	48	219	PETCGHLWAYVWPSCAAV\GL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25979	56347	A	26120	1	912	

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25980	56348	A	26121	1	1857	MRVCARACVRTRTRMCVYAH TCVCVRTYAYVRVRVRVHVRA RVRVCAYARTRVRNSLSILPFIQ LTLATPIHHIHQEEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLIRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPLALLLAFLCSTSPGF GDPDGLGVIAYQDTVRPNAAT AISELNALAVKGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL VTTLDDRVVAGSAGRYGGDGA GDSECVKIVAQEIRQTDRNIER DRSPRPSGERVRVRGKGGIEAN QPLSTAFTNQITIRQSIRLFSNQF VFHKGISRVVAGSSAIISNVSPG CILRTPNCRRGFPISCTGEGKAA YGWQRDGGHAEYLLAEEKDLI LLPDALSYEDGAFISCGVGTAY EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDVY/V*IGVARVSWMNGRID SELRTRVRAYAHTRTRARTCTR TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
25981	56349	A	26122	3	1180	SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFVDL LPAQQRMKGENWYRGTADAV TQNLDIIRRYKAEYVVILAGDHI YKQDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN DKIIEFVEKPANPPSMPNDPSKS LASMGIYVFDADYLYELLEEDD RDENSSHDFGKDLIPKITEAGLA YAHPFPLSCVQSDPDAEPYLAR CGYAGNFMESEPRSGLIRVSCM PAGPPLPLPAARSEAPKAAGTV ASVPSIAPARLRPVPDPVELVLV AAEFITPGDPTPRLHGSGFIDIR QIHHQTRSHLEGVKTGIRFLNH FSGNPQGGIAHVNGVARFQVK QCHQAWGQQYAARLRFQARGI SLQIAIHRVDIIHRFDVRQL
25982	56350	A	26123	16	543	
25983	56351	A	26124	1	3387	

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25984	56352	A	26125	1688	2234	LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTPFGVC TSASMNVPVLTLRIRTRVTGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/WVAGTFD*SVWF GHDTDVVTLYRFHEALCYSVT LRTPHRRVLRFKSQHPGELACFI SPVA
25985	56353	A	26126	905	4761	PPHNWMPSNATPGIAFVWCAY GAI/LPGDAPVPVVDDYRKVVR KDTKGLIARWKYFWMSVIALG VAFALYLAGKDTPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTDGLDGLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAVLLRQEFLLVIM GGVFVVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
25986	56354	A	26127	1056	1373	
25987	56355	A	26128	1	301	SSGTDAGRRYRPRQRPSKSRNN RRVNRQPAPQQSSRN/SLRPSTT SSPFSLPAVKLPSAP/V*SAGMR LAEVRRVDSAISTVDSR*CPTAS SFSTGSITVTL
25988	56356	A	26129	362	595	
25989	56357	B	26130	1	1305	
25990	56358	A	26131	1	2022	MISKRSERSFGYGVGLVRRQDF SSSEGFFNLHSLRIDINKCLGVRI STATSTMGIVLPEQIKLACNGIQ RVALCGGDDYLTSVDSFDVMF CSRFGWQVRPSSFCSPVFTWVT ENQQHLHRGKDNLSLKNNNSA CGAACGSLRGEKSDPPSARNNP SSQQGGKKESGQQPSLKDPHIL RHDSAHRPRKEKPRQPVNASLV VKFWRVKCVCVHNDHKRPACS VVCVDGDTYCWTEAYPAMGL PTLRGPDSALGERPE
25991	56359	A	26132	3	236	
25992	56360	B	26133	1	4638	
25993	56361	A	26134	1501	1914	SAFSRALTGRQHFNNCAFTRFS NGAECLLYHVCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
25994	56362	A	26135	561	698	

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25995	56363	B	26136	4	2040	
25996	56364	A	26137	804	947	LPCHCSCPWDGDVQPSPTPRQ WT*GERLH*QSEALPGVCCAPG HGPL
25997	56365	A	26138	1	734	SVHIGHQFFQFQSTSLNICPPLH RLFIAFQMNIRRNAAARHAKFQ RLQAQVSIFEDDMSRKIANRQA TAMLNAPPFEANIGIHNVPFIGF EAVIRQHFARRLNAFFALLLFR PFRLFCPFPGINANQRSQVRQPQ LPRLDITFQFWSWLSGGVDQRT VDIVCHQWRSALDRKEYYPAE TTMPTALHSRLCIIVGKIKRPVI VLFREANQARVGLFE/H*STAA RPFWSAAPAGPALPLRVANAPS
25998	56366	A	26139	2	309	
25999	56367	A	26140	472	885	SAFSRALTGRQHFNNCAFTRFS NGAECLLYHVCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
26000	56368	A	26141	1	2469	
26001	56369	A	26142	1175	1435	
26002	56370	A	26143	218	443	AMARWKMLCTKSPPCVCLPGY P\G*RLAGPHHHHEFPPPAGAAS TGPPIVQDHQSLAGRSRRHDDS RHLGRCHHH
26003	56371	A	26144	1	2031	
26004	56372	A	26145	1419	1875	TFCSPRSQPGSLKRRLRAGAGN CPLYSTGNGPLQRAICCAQPT*L HGRVPSHVPATFSSFQLWSFTV GACIHRSMYIISRSRCPFDPKTK TATMLGITSFVMERCQLFILSRA FTSGQPTCYYPTASSNTWFSST RHCQVINLHSNSMHISL
26005	56373	A	26146	218	441	AMARWKMLCTKSPPCVCLPGY P\G*RLAGPHHHHEFPPPAGAAS TGPPIVQDHQSLAGPRRHDDSR HLVRCHHH
26006	56374	A	26147	1196	1462	LNTLVVAVRDGLKMTTVIANN VTSVSVLKIARNVTRKTILPPAA AANVTPYWLIRTIC*KRRYD*K TRWYYAVAACLCNMGTTRKA NG

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26007	56375	A	26148	45	443	APSDPKRDFPLPHGADSAMAE YDRCHRAVLSQGGQWPTALSA GDHAAYSLHAALVQPERRCHG RCPVRNRLHAPVCPIIPG*RPAG SHHHHEFPPPARAASTGPSIVQ DHQSLAGRSRRHDDPRHFGGC HHH
26008	56376	A	26149	581	957	TSWISFSRTTPSTVSPYSTVDAN GIIWSARNRLASVNNIASWLSFF SNPLYLAITKPNCRLMMRNGCS TPGPGCWLSCIRC*WAVCSCVD AASRFLPCRGARRSASPHPPRQ APRRCGALW*PASAETNCSSPC SRLPS*LRGCCFKVLTLPGRSAI SQSTSTSASSSALWRPLVAGIG
26009	56377	B	26150	1	3924	
26010	56378	A	26151	597	856	
26011	56379	B	26152	1	2781	
26012	56380	A	26153	2809	2989	RCGYVRE*LAKSLQSNHFQWR MPQHQTAYCRS*AWYRHVAH ERLPAQTDNRHQHADRWNG
26013	56381	B	26154	1	2802	
26014	56382	A	26155	4493	5470	IQRRNHRRDGWCLASLPAGTD HAGARAEEAGSWHSGGPHRVR ARSVSTPFAPIV\NTATSLKPVR QLLDAALKIDHRRTLPKYSFGT FRRWYRSVAAQQAQYKDQVA FFHGCFVNYNHPQLGQDLIKVL NAMGTGVQLLSKEKCCGVPLI ANGFTDKARKQAITNVESIREA VGVKGIPVIATSSTCTFALRDEY PEVLNVDNKGLRDHIELANRW LWRKLDEGQ\TLPLKPMTLKVV YHTPCHME*MGWTLY/TLELLR NIPGLE/LTVLDSQ/CC/GIPPIRV VIHMFRQIEESGADLVVTDCET CKWQIEMSTSLRCEHPITLLAQ ALA
26015	56383	A	26156	2467	3465	

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26016	56384	A	26157	5758	7019	LKEGLLEPLAVTERLAIIRWRRP TMNDTSFENCIKCTVCTTACPV SRVNPGYPGPKQAGPDGERLRL KDGALYDEALKYCINCKRCEV ACPSDVKIGDIIQRARAKYDTT RPSLRNFVLSHTDLMGSVSTPF APIVNTATSLKPVRQLLDAALK IDHRRTLPKYSFGTFRRWYRSV AAQQAQYKDQVAFFHGCFVN YNHPQLGKDLIKVLNAMGTGV QLLSKEKCCGVPLIANG\FTDK ARKQAITNVESIREAVGVKGIP VIATSSTCTFALRDEYPEVLNV DNKGLRDHIELATRWLWRKLD EGKTLPLKPLPLKVVYHTPCHM EKMGWTLYTLELLRNIPGLELT VLDSQCCGIAGTYGFKKENYPT SQAIGAPLFRQIEESGADLVVTD CETCKWQIEMSTSLRCEHPITLL
26017	56385	B	26158	1	2247	
26018	56386	A	26159	882	2372	HAVHESPPECRSNQQRPTRTCR TIIDIMEMYHALHVSWSNLQDQ QSIDERRVTFLGFDAATEARYL GYVRFMVNVEGRYTHFDAGTH GFNAQTPMWEKYQRMLNVWH ACPRFLFDLDGTLVDSLPAVER AWSNWARRHGLAPEEVLAFIH GKQAITSLRHFMAGKSEADIAA EFTRLEHIEATETEGITALPGAIA LLSHLNKAASGVTNKGFLTVD EIRRVTRAFARLGTEKVRLTGG EPSLRRDFTDIIAAVRENDAIRQ IAVTTNGYRLERDVASWRDAG LTGINVSVDSLDARQFHAITGQ DKFNQVMAGIDAAFEAGFEKV KVNTVLMRDVNHHQLDTFLN WIQHRPIQLRFIELMETGEGSEL FRKHHISGQVLRDELLRRGWIH QLRQRSDGPAQVFCHPDYAGEI GLIMPY\DKDF\CATCNRLRVSS IGKLHLCLFGEGGVNLRDLLED DTQQQALEARISAALREKKQTH FLHQNNTGITQNLSYIGG
26019	56387	A	26160	68	399	NKVKPRGDSV/PGSPHSPRLLSP PPLPGLLLWR/PLEEPFSPPLHC GSPFLGWPRPGGRGLGG/PPHSE QPASLSLPPTPRAPVRPEPPRRA PPPAPRRPVPSTTQGLRNASAP

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26020	56388	A	26161	207	479	PWSDGAGPLPSLPHPDGRG*SV NSPQVLL**GSGE/PRASDSPLP QLCGVSPHRPTWGSALWGGEQ CTSEMGETIDPPGPHTFSKNFCF ELQ
26021	56389	B	26162	1	453	
26022	56390	A	26163	1	379	
26023	56391	A	26164	1	1054	MFLQAAQKAWNPHLLLVRTQ AASTHGRRADPHVGRCGETPQ SWGKGESLALAPLSLTKAALED CSQISPSHQGTLLCLLILDLRTG KLSLEHTEEPSDVPSHLLYRWSI SSAITEVFQALASSDSTSQPVNV HTKEDMKVQDIALVLPSRKSR NACRTTTSTCKALLMRQLAAR VILQNCVSKSSRGIHVPQKNLT LPVRGDSVLAGSPHSPRSLSAPP LPGLPLWRHLKSPSAHRCTVGG PFLGWPRPEPAPSACREALAAF P/PGQGSGPAAR\QPEPPPPPWA PVQPESPRQAPPPAPRSPVPSTT QGLRSTGTKHRDWQAAPPAAP VRDPLGEASWAPESGGDVENL
26024	56392	A	26165	2	362	EMSRLYRSRDRD/GVCLQ/IEVK MVSRTEANIDDSLIGGNASAEA PEGEGTESTVITGVDIVMNHHL QETSFTKEAYKKYIKDYMKSIK GKLEEQRPDRVKPFMTGAAEQI KHILANFKNYQ
26025	56393	A	26166	35	359	
26026	56394	A	26167	22	459	
26027	56395	B	26168	102	431	
26028	56396	A	26169	85	674	RRRRLPSVAIMIILPGPSSSHDE MF\SDISKIR\EIADGVCAWKVE G\KMV\SRTE\GTID\DSLIGG\NA SAERPRGAKGTERHQLITGV\DI VMTP\HL\QETKFSQKEASKK\YI K\DYMKSIKRET*KNRRPEKSK TFL*PGAAEQIKHILANFKN\YQ FFI\GENMNP\DGMVALLDYP*D WVVTPYMIFF*GWV*KWEKC
26029	56397	A	26170	1	1640	
26030	56398	A	26171	1	1527	

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26031	56399	A	26172	61	2560	PGFCHPRKAYSSYGQRSKGSQK MKASSGRCGLVRWLQVLLPFL LSLFPGALPVQIRYSIPEELAKN SVVGNLAKDLGLSVRDLPARK LRVSAEKEYFTVNPESGDLLVS DRIDREQICGKQPLCVLDFDTV AENPLNIFYIAVIVQDINDNTPL FKQTKINLKIGESTKPGTTFPLD PALDSDVGPNSLQRYHLNDNE YFDLAEKQTPDGRKYPELILKH SLDREEHSLHQLVLTAVDGGDP PQSGTTQIRIKVTDANDNPPVFS QDVYRVTLREDVPPGFFVLQVT ATDRDEGINAEITYSFHNVDEQ VKHFFNLNEKTGEITTKDDLDF\ EIASSYTLSIEAKDPGDLAAHCS IQVEILDDNDCAPEVIVTSVSTP LPEDSPPGTVIALIKTRDRDSGE NGEVYCQVLGNAKFILKSSSKN YYKLVTDGALDREEIPEYNLTI TATDGGKPPLSSSIIVTLHISDV NDNAPVFQQTSYMVHVAENNP PGASIAQISASDPDLGPSGQVSY SIVASDLKPREILSYVSVSAQSG VVFAQRAFDHEQLRAFELTLQ ARDQGSPALSANVSLRVLVGD LNDNAPRVLYPALGPDGSALFD MVPRAAEPGYLVTKVVAVDA DSGHNAWLSYHVLQASEPGLF SLGLRTGEVRTARALGDRDAA RQRLLVAVRDGGQPPLSATATL HLIFADSLQEVLPDLSDRREPSD
26032	56400	A	26179	47	325	ATMRLSVCLLLLTLALCCYRA NAVVCQALGSEITGFLLAGKPV FK\FQLAQFKAPVEAVASNMEA INCVDTM\AYEKRVLITKTLGKI AEKCDR
26033	56401	A	26180	1	3747	
26034	56402	A	26181	2776	2874	
26035	56403	A	26182	89	369	
26036	56404	A	26183	382	555	
26037	56405	A	26184	2	67	
26038	56406	B	26185	1	444	
26039	56407	A	26186	1129	1275	
26040	56408	A	26187	61	313	WIPHQGYRWSCLPVPRCALAFL SPWVVDGTGHRGAGGGAGWG GFGRTGAHG\GVGGSGMAGCR SRAHSGGVGMTMTWQIIPEVP

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26041	56409	A	26188	61	433	WIPHRGCRWSCLPVPRGALAFL SPRVVSGTGRRGAEGGARRGG SGRTGAHGVGGRLRHGGLQVP SLAPREGSCTCGG\GSGAREEQ NLGFPREPRSGGGARGSDGICG MRVMFRKWILFCPSSR
26042	56410	A	26189	297	599	
26043	56411	A	26190	370	585	
26044	56412	A	26191	222	799	
26045	56413	A	26192	346	634	
26046	56414	B	26193	206	955	
26047	56415	A	26194	281	549	
26048	56416	A	26195	1981	2337	
26049	56417	A	26196	267	770	TRVDMIHYGLRKGPGETPS*SL RSFRAGQTGASRARGLTLLSSH SSALRKGSPKHFCTLCWQTFLA WCVWKVAFSPSRCQTQFDLGK STQWTLEILTDPKSHLFSRKQQ PQARAPAVFPAPLKGCHVGAR GSHCQGFQGCFRPSVAPLILGT DGFSLLEKLWTFKTC
26050	56418	A	26197	165	374	RVTVQWL*YLRPRMP*N*PRPR SGKPFIDSTHSSHR*RQRNAVSL FSPVMSALRRCSVHRRLPDGGV VA
26051	56419	A	26198	357	981	HWRGDVLRRSHRRTALQSRYF CGIYRSP/YKAR/MQIQFFDPQQ MEAAQKRLTEESDILNALENHQ FAIWLQPQVEMTSGKLRGISKQ LVGFTNRQNGATKLLVQYFTH RQIDCAGTADQPNPAGKVDDC GVTGNVTDRQQGKQHGQAKE NELQNACAFQRAEEHKQRKYA PQTQVDTKELCIWRIGQTQFRH QQNRNQRHAERTNHFGVR
26052	56420	A	26199	1	2601	

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26053	56421	A	26200	1	1236	MGPGDLPRGLATFWTELGLLS WARELARMPAVEMPPRSCPGR SRLSCSIGVAMFYGDLTAEQLY SRAISAAFTARHKGKNQIQFFD PQQMEAAQKRLTEESDILNALE NHQFAIWLQPQVEMTSGKLPG KSAAIMLPLSVNLSALQLMHPN MVADMLELLTRYRIQPGTLILE VTESRRIDDPHAAVAILRPLRN AGVRVALDDFGMGYAGLRQL QHMKSLVRLTKSEVSSETDQDE LPLAKVSEVDEAKRQWLQGMR HPVDTVTEPEPAEILAEFIRQHS AAGQLVARAVFLSPPYLVAEEE LSVLLESIKQNGDYADIACLTG SKDDYYYSTQAMSENYAAMSL QVVEQDIFSP\IAHAVRFECQTY PRPYKVAMLMQAPYYFQEAQI EAAIAAMDVAPEYADIRQGIVG
26054	56422	A	26201	1	1161	
26055	56423	A	26202	1	1038	
26056	56424	A	26203	1	1472	MVRLCIRLPIRVYAKVVDKNAL SLWMRERSDLWVQPKVDGVA VTLVYRDGKLNKAISRGNGLK GEDWTQKVSLISAVPQTVSGPL ANSTLQGEIFLQREGHIQQQMG GINARAKVAGLMMRQDDSDTL NSLGVFVWAWPDGPQLMSDRL KELATAGFTLTQTYTRAVKNA DEVARVRNEWWKAELPFVTD GVVVRAAKEPRIPPLATGPGRV AGGLEISTCSSGCRSEGNEPGKI SVVASLAPVMLDDKKVQRVNI GSVRRWQEWDIAPGDQILVSL AGQGIPRIDDVCPSDPAILSDIVP SW/VTTQW/LKKRAVSSRMMK NQ/VKKGSETGYFDKDEARFQK EGFRVVPPAALRQGAFIARNTE LRPSYVNIGAYVDEGTMVDTW ATVGSCAQIGKNVHLSAGVGIG GVLEPLQANPTIIEDNCFIGARS EVVEGVIVEEGSVISMGVYIGQ STRIYDRETGEIHYGRVP/AGKV DAKTRGKVGINELLRTID
26057	56425	A	26204	240	455	RLHPPYYRGWIFEEVPVISMGV YNGQSTRIYDR/ETGEIHYGRVP AGSVVVS\KVDAKTRGKVGINE LLRTID

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26058	56426	A	26205	197	1043	YEKSLTMQQLQNIIETAFERRA EITPANADTVTREAVNQVIALL DSGALRVAEKIDGQWVTHQWL KKAVLLSFRINDNQVIEGAESR YFDKVPMKFADYDEARFQKEG FRV\VPPAA\VRQGA\FIARNTVL MPSYVNIG\AYVDEGTMVDTW AT\VGSCAQIGKNVHLSGGVGI GGVLEPLQANPTIIEDNCFIGAR SEVVEGVIVEEGSVISMGVYIG QSTRIYDRETGEIHYGRVPAGS VVVSGNLPSKDGKYSLYCAVIV KKVDAKTRGKVGINELLRTID
26059	56427	A	26206	1	406	MGKKNWNTLGEGVCSCRMFL PDANTLAKNSACSAASAVQAA DRPDSQEAEALEHMAHSRCAL RCQTLVIVHVSLMRVSWYHSVI IVVPLTEPLLESLVRCRLRSRRD DVPVAPAVSATPRREP\SVLRIA ERTNA
26060	56428	A	26207	1	2574	MWAFRGKRPVTLKILHVPITNL RKNITSTRGLTKESSQGKLVRA QEEYTPAREIAKMG\GNPCRPG GIVFAGER*DVTSPYV*TSTRGL TKESSQGKLVRAQEEYTPAREI AKMGWQSLPARRYCLCWRKIR RYITLRLNIAYAGGYKAPVEDI ALWMETDGACDHVDFTWNIPS KCQGPMDIVSRPVFWHAHGIV LFAGARNLNPTLTRIPPYLWLL TLRTGYAAAGMQALALDSRGS PDAVVLSTQHSEEIDQ
26061	56429	A	26208	1	3771	
26062	56430	A	26209	239	451	LPPTAWMSTTNLTSAMLSVRG NVPMTLPARRRVNLPSSLICTCF HKPA*RISMPKPVW*KARIISGN STS
26063	56431	A	26210	1	2079	
26064	56432	A	26211	1573	2562	
26065	56433	A	26212	275	643	SSRTALFTGSAVPGCAPPSGRSL FPQCLQSKLARSFPIRCSRSGAA ILFRRLSFSPGTELILEDR/IVKRF MRENSRGPQVPAGLPMTEEQL KKLGGRQLRALGKLMPGEEE\S VLRIAERTNA

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26066	56434	A	26213	1	899	MGRTTRRDAAQAPGTRRSGDS RGYPYVTRPEGTDADDPQKDK AALGSHRVAGQPELFSIDELTR RDPHSASGAWTARYTVSTIAAF ALVIANRLYTIEEEATTPSGCGP ASSSTSSRGVDMCLRNLCMHG YDATIPLTLIAADSMDEYNKPD LSHVISQGQRADDLTRQTAGEF AEQFNLHLFPQTWVTDIDAEAR VVKSQNNQWQYDKLVLATGA SAFVPPVPGRELMLTLNSQQEY RACETQLRDARRVLIVGGGLIG SELAMDFCRAGKAVTLIDNAA SILASLMPPEVSSRLQHRLTEM GVHLLLKSQLQGLEKTDSGIQA TLDRQRNIEVDAVIAATGLRPE TALARRAGLTINRGVCVDSYLQ TSNTDIYALGDCAEINGQRD*SS ARRVVPGRFPGAVRWRQLPHP LRYCAGGPALPECQNPFFPAPV TEISTADERPSPSTDAASGCLLP VALTTPEYWQRCRLA
26067	56435	A	26214	1	1264	MDYMVPVGMDWLCRETAGM RVSIKKGSVVFPLNPELVMKVV RQRSTIVTPSGFKAGAFNFERFK EASNQTLGSTFLYSLSCPKPNL GSQPLDFDTKKSYTLKVEAAN VHIDPRFSGRGPFKDTATVKIV VEDADEPPVFSSPTYLLEVHEN AALNSVIGQVTARDPDITSSPIR LYRIPGDDAKCVQFNREGVKA LKAKPVEKAAPAPAAAAPKAA PTPAKPMGEQLALYRMAGSNA DRIQGRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPMTRTKELAEV VAAATPVKDKFKHPATRTFQA VRIWVNSELEKIEQALKSSLNV LAPGGRLSIISFHSLEDRIVKRF MRENSRGPQVPAGLPMTEEQL KKLGGRQLRALGKLMPGEEE\S VLRIAERTNA
26068	56436	B	26215	64	663	
26069	56437	A	26216	27	791	
26070	56438	B	26217	1	1638	
26071	56439	A	26218	1	375	STKKQRGEIHHPDGHGIAQDRH LPRTSVDQRPLRQTNHPAGL*Q ANG*GVFKRCRAHSATT**KDD E*NESAENAA*GGKVEGTDVT GDLLHENPAITPDKCEHNQATD CQWVALSCGRHERSSV

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26072	56440	A	26219	213	407	TTCCCTNLSIPLANKYRSLSPQS DWRLSMPR*NRYVQKAPARAN KTSPMKAPPANIALGVNVAR
26073	56441	A	26220	1	1179	
26074	56442	A	26221	176	569	WPMRHTFSEAHAAQRAGGKNP GHDTADYATNAVHTEDIAGIIH PQQAFEHGNAPQARQTSYHAD NQRAANPNVAAGWRHADQTG NRARTRPQQ*RLTTQRPFTEDP AKNCRRRCDHSIHKCQCRDFIR RAR
26075	56443	A	26222	1442	2309	
26076	56444	A	26223	155	2929	HLHWFVFSGWFTVTRLAFGEG NNFFGNINWLMLKNIELTAVM GSIYQYIHVAFQGSFACITVGLI VGALAERIRFSAVLIFVVVWLT LSYIPIAHMVWGGGLLASHGAL DFAGGTVVHINAAIAGLVGAY LIGKRVGFGKEAFKPHNLPMVF TGTAILYIGWFGFNAGSAGTAN EIAALAFVNTVVATAAAILGWI FGEWALRGKPSLLGACSGAIAG LVGVTPACGYIGVGGALIIGVV AGLAGLWGVTMLNAC
26077	56445	A	26224	2	1064	
26078	56446	A	26225	1849	2515	MEGHLWIRIDLSQSAVSHSVKE LENHTGVRLLDRTTREVVLTD AGQQLALRLERLLDELNSTLRD TGRMGQQLSGKVRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIVI DPGPVGDLQCEAILSEPFFLLCH RDSALAVEDYVP\ALPLPEGSPL VVKRITPVVERQLMLVRRKNR SLSTAAEALWDVVRDQGNAL MAAA

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26079	56447	A	26226	102	1655	RKQMNYSLKQLKVFVTVAQEK SFSRAGERIGLSQSAV\SHSVKE LENHTGVRLLDRTTRAVVLTD AGQPLALRLERLLDELNSTLRD TGRMGQQLSGK\VRVAASQTIS AHLIPQCIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIVI DPGPVGDLQCEAILSEPFFLLCH RDSALAVEDYVPWQALQGAKL VLQDYASGSRPLIDAALARNGI QANIVQEIGHPATLFPMVAAGI GISILPALALPLPEGSPLVVKRIT PVVERQLMLINVIQTLRFAFIFR LSRRQHFAKVTPLLHRHGDYF VFIGFDYGTANCSVAVMRDGK PHLLKMENDSTLLPSMLCAPTR EACGRVDVIEVSKSKVRKNTY AMRYVAGQPAERILPPGSFASI GQALPPGEPLSTEERIRILVWNI YKQQRAEWLSVLKNYGKDAH LVLLQEAQTTPELVQFATANYL AADHVPAFVLPQHTSGVMTLS AAHPVYCCPLRERKPILRLAKS ALVTVYPIFPYLSNS
26080	56448	A	26227	159	290	
26081	56449	A	26228	562	774	VLRMIT*SKSQFAQDMCRNVLL INNFGRIQHDPAIFHFQRNEAVP LWTVSAQEVKKDFTSGLRHGS VRGDL
26082	56450	A	26229	50	409	GYASQALILASIPAASRPSSARIS S*VPCGIKKSGRPMFSTGTGLR WAISTSFTPLPAPPIMAFSSTVTS ASWLAAISRINASSSGFTKRIST SVAFSDSATFAASSTNSRNAPPP VEM
26083	56451	A	26230	405	626	
26084	56452	A	26231	1	1528	
26085	56453	B	26232	1	1755	

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26086	56454	A	26233	152	2099	GNRLLVVSFIAFSKNSTHFKGIF AMRIILLGAPGAGKGTQAQFIM EKYGIPQISTGDMLRAAVKSGS ELGKQAKDIMDAGKL\VTDELV IALVKERIAQEDCRNGFLLDGF PRTIPQADAMKEAGINGHYVLE FDVPDELIVDRIVGRRVHAPSG RVYHVKFNPPKVEGKDDVTGE ELTTRKDDQEETVRKRLVEYH QMTAPLIGYYSKEAEAGNTKY AKVDGTKPQIYRGSLYVSDQIG HTIVNPDGVVCDCGRYGCLET VASLSALKKQARVWLKSQPVS TQLDPEKLTTAQLIAAWQSGEP WITSWVDRSANAIGLSLYNFLN ILNINQIWLYGRSCAFGENWLN TIIRQTGFNPFDRDEGPSVKATQ IGFGQLSRAQQGVDLGNMIITS GQIPVNPKTGEVPADVAAQAR QSLDNVKAIVEAAGLKVGDIV KTTVFVKDLNDFAPVNATYEA FFTEHNATFPARSCVEVARLPK DVKIEIEAIAMLYTGYHYNDAP SAVRYPRGNASGVELTPLEKLP IGKGIVKRRGEKLAILNFGTLM PEAAKVAESLNATLVDMRFVK PLDEALILEMAASHEALVTVEE NAIMGGAGSGVNEVLMAHRKP VPVLNIGLPDFFIPQGTQEEMRA ELGLDAAGMEAKIKAWLA
26087	56455	A	26234	935	1020	
26088	56456	A	26235	145	373	

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26089	56457	A	26236	530	1865	RGNKRLDLMFKQSHASMYIKQ PEQLDYQLNLKEVITAVFISMV VLNISPTLY/PDKPSPKDKYVAY AINIPDYELAADVYNINVTSPSG QQETFKILINLEHLRQTLERKSL TAVQKSQCEIITPKKPGEAILHA FNATYQQIRENMSEFARCHYG YIQIPPVTTFRADGPETPEEEKG YWFHAYQPEDLCTIHNPMGDL QDFIALVKDAKKFG\IDIIPDYTF NFMGIGGSGKNDLDYPSADIRA KISKDIEDPVTKERKQIHPEDIH LTAKDFEASKDNISKDEWENLH ALKEKRLNGMPKTTPKSDQVI MLQNQYVREMRKYGVRGLRY DAAKHSKHEQIERSITPPLKNY NERVHNTNLFNPKYHKKAVM NYMEYLVTCQLDEQQMSSLLY ERDDLSAIDFSLLMKTIKAFSFG GDLQTLASKPGSTISSIPSERRILI
26090	56458	A	26237	14	2031	LIVLS*QHG/DLRQNRSGAEHFG LQRLMLHASQLSLTHPFTGEPL TIHAGLDDTWMQALSQFGWRG LLPENERVEFSAPSGQDGDPTL GLIKEVACELSGMMRRSQPWE EAEESIPDRGESLLEVSGTPNAG WGAEGLAEREALLLCCCCGPM GPDPLGLGSPGSVRGRSRLIHH AISGEALWEVTSEGLDMAAAR QFAIEKGAPALRAMTFIERAAM LKAVAKHLLSEKERFYALSAQT GATRADSWVDIEGGIGTLFTYA SLGSRELPDDTLWPEDELIPLSK EGGFAARHLLTSKSGVAVHINA FNFPCWGMLEKLAPTWSGRNA SHHQTSYRDGPLTQAMEFEDK AQQRDVETARHFTFFRIIANED KKTGFPRFQTIVITASHKTIDRT RYTYGAWRCYRPLLTVEEYRA TGSLITQPKFPPHKSSEVHRVPR NQGRFVAVNSTLPTEPATVAPV RNGNASRDTAKTQTAERPSTTR PARQQAVIEPKKPQATVKTEPK PVAQTPKRTEPAAPVASTKAPA ATSTPAPKETATTAPVQTASPA QTTATPAAGAKTAGNVQSLKS APSSHYTLQLSSSSNYDNLNGW AKKENLKNYVVYETTRNGQP WYVLVSGVYASKEEAKKAVST LPADVQAKNPWAKPLRQRHRD LRGDERRDDRRSEYFNRQVIS

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26091	56459	A	26238	732	1025	HEAKRTGRSYWFTAV*WLRG WRRMVARQNAKNCWHGTFFR VARVSLPISAHASSTHLSGSAH YVPPSAYRNSRRYSRGLCRCRV SSCDAATGVVVPQ
26092	56460	A	26239	1905	3087	RVCSCDAGTLHWLQNLRCGLP VWCDGSGGTSGDPQQRRGSEC TG*QSRSQ*MRPVQPS*RRPGV YGGLPDS\WLICVDRNKLEQLT PEKRRQAKLRAMKPDEFAQIQ QAVITQMLQHPQTLGEEASKLS KDFDRGNMRFDSRDKIVAQIKL VTPQKLADFFHQAVVEPQGMA ILSQISGSQNGKAEYVHPEGWK VWENVSALQQTMPLMSEKNEQ NLYDCGALFAPVTWTSGSAAF PRPLTVEELLVVTFTEAATAEL RGRIRSNIHELRIACLRETTDNP LYERLLEEIDDKAQAAQWLLL AERQMDEAAVFTIHSFCQRML NLNTNECCFQRTTKTIHRDSFK STPRAAKSCSGLLPALAPSQISS NTPIQPLSRFKFSGVTSPTSAAS
26093	56461	A	26240	1	2235	
26094	56462	A	26241	166	416	CHVVGPFRVRRNLISAQH\PLTL NS\RHTTTRAARRLLRYFGTPR YRHSIDIHMQLDMTTSRSLSSL RDQLHCRWLLPAERQAI

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26095	56463	A	26242	1	2084	MLFPLATSGAMEPFPFLAGTAG ALVGGLQNIGSGVLASLSAMLP QTGQPGVVDDLNGIVDRAVLA AAGDADVASGAARLSARHRSI VISSMGERCCFIRSRITRICGHWI CPQGNEIPVVAVASHDTASAVI ASPLNGSRAAYLSSGTWSLMG FESQTPFTNDTALAANITNEGG AEGRYRVLKNIMGLWLLQRVL QEQQINDLPALISATQALPACRF IINPNDDRFINPETMCSEIQAAC RETAQPIPESDAELARCIFDSLA LLYADVLHELAQLRGEDFSQL HIVGGGCQNTLLNQLCADACGI RVIAGPVEASTLGNIGIQLMTLD ELNNVDDFRQVVSTTANLTTFT PNPDNSLYTTDKGALRMTTQL EQAWELAKQRFAAVGIDVEEA LRQLDRLPVSMHCWQGDDVSG FENPEGSLTGGIQATGNYPGKR VMPVSYVPIWNSTLSLSGSNWF NRKALGSPARYDVLPKWWRN VVKPTRTRLYIGIAFYKVGEPS KIEPDWMINGGVPELKKQLDL NDAVPEISGTILFREDYRNKPQT QQAADPPIRAKAAEIAVAHAH YLSIEFYRIVRIDPHAEEFLSNEQ VERQLKSAMERWIINVLSAQIR PQPAVT\HYRGLATVEMPVATG RYPTTRY\GLVELEPKTGRKHQ LRRHLAHLRHPIIGDSKHGDLR QNRSGAEHFGLQRMER
26096	56464	A	26243	1	2871	
26097	56465	A	26244	690	824	
26098	56466	A	26245	950	1484	

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26099	56467	A	26246	1	2625	MVAFYRHAGRMWPGIALSCSL GNIAASILLFSTSSLNMTWTTINI VEAVVGAVLLRKLLPWYNPLQ NLADWLRLALGSANSAGVNIS TATVCRQCEDAPCANVCPNGAI SRDKGFVHVMQERCIGCKTCV VACPYGAMEVVVRPVIRNSGA GLNVRADKAEANKCDLCNHRE DGPACMAACPTHALICVDRNK LEQLSAEKRRRIPGNIRRIRSGR YRRPVTAGCDAVVSGRAGYAI HDGGNNSMAKNTSCGVQLRIR GKVQGVGFRPFVWQLAQQLSH GSRMRDGTCNLKYDEYSRSGS MQYNPLGKTDLRVSRLCLGCM TFGEPDRGNHAWTLPEESSRPII KRALEGGINFFDTANSYSDGSS EEIVGRALRDFARREDVVVATK VFHRVGDLPEGLSRAQILRSIDD SLRRLGMDYVDILQIHRWDYN TPIEETLEALNDVVKAGKARYI GASSMHASQFAQALELQKQHG WAQFVKSDENDAPDRQSGSTG SQCKNCGADTEPQVAAGPGLS ELNPVHCPHLHYRAHFRADRH SVACSLLDTPVTGHQVAPTYRQ QVPRAGQVHDPSKHTRMPCEN IDPVRTIIRRISDPPVPASATLGA SKASRIRPRRSHSIPEITAKSRKP GGQPKWQVICWLDRDEKVVV MQTVRDQIGQHVFTAHRLDRP TSGVLLMGLSSEAGRLLAQQFE
26100	56468	A	26247	1	1833	
26101	56469	A	26248	1	517	MRNKLSFDLQLSARKAAIAERI AAHKIARSKVSVFLMAMSAGV FMAIGFTFYLSVIADAPSSQALT HLVGGLCFTLGFILLAVCGTSLF TSSVMTVMAKSRGVISWRTWL INALLVACGNLAGIACFSLLIWF SGLVMSENAMWGVAV\YTAPR AKCIIHLLNLSASALCAI
26102	56470	A	26249	3117	3527	EAVHRLARYRDAPRRS**SPLL CASVYP*LEQVPLQAQAVVPLR VLQAGKPVVPVAVLNAQAAAL ARPVAKLAAATAVQAAADRQ AAAPAALDAEHVAAVPALQAA AGPVDAAAQTHKAVGTGVAA TDEQPHAPER

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26103	56471	A	26250	2	563	STTSSTTAFSATTAGTPSTGNTP SASPIWRRPNFWARKVYLLHW FCHRQPSKEVLFHLALYRNNPR CKAVVHLHSTWSTALSCLQGL DSSNVIRPFTPYVVMRMGNVPL VPYYRPGDKRIAQDLAERETH\ NHAFLLANHGPVVCGESLQEA ANNMEELEETAKLIFILGDRPIR YLTAGEIAELRS
26104	56472	A	26251	2	1481	PENQINKLKQAIPADYRSHQKC VNQPSSPTITPRLFAITVITDERG YATGSAGNLSL/LLPDGNLLAT PT/GSCLGN/LDPQRFSKVAADG EWL/SGDKPSK/EVLFHLALYR/ NNPRCKAVVHL/HSTWST/ALS CLQGLDSSNVIRPF/TPYVVMR MGNVPLDLAELAA/DNQAFLL ANHGPVVCGE/SLQEAANNME ELEETAK/LIFILGDRPIRYLTAG VCPLAKMLNGTGQYLSIKRCT NNRSVRGTCSAPRAGPKGYGL MMMIDVLSASYSAYRSGDRTL LYSYHRASACADSTTLTVLISY TFHLVNSYSTVPPLEGSGTQPA SPSFPTRVSDDHNRDFFFLLSPC GLLQNLAQCIRQVGIQLDFGCV IISAQTETDGPLVCGRFEEGTPF SPQTPRDCDPNRSYSGNTQGVR GATSSPGSAISFEQTVNARSHVL RVTLTLGLTRPMLYVTGSLKWI NICILPISLKPLRYYIHLAAQFPT APISLGRSLHVVPHEEVAM
26105	56473	A	26252	1	413	
26106	56474	A	26253	3	247	
26107	56475	A	26254	300	665	
26108	56476	A	26255	1	1854	
26109	56477	A	26256	1	1611	
26110	56478	A	26257	942	1040	

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26111	56479	A	26258	1616	3678	PLAKTGRQREQLAGLAK/AHPS LTLHQDPVYVTRADAPVAGKV ALLSGGGTEHEPMHCGYIGQG MLSGACPGEIFTSPTPDKIFECA MQVDGGEGVLLIIKNYTGDILN FETATELLHDSGVKVTTVVIDD DVAVKDSLYTAGRRGVANTVL IEKLVGAAAERGDSLDACAELG RKLNNQGHSIGIALGACTVRSA GKPSFTLADNEMEFGVGIHAIL KGDIPEAEAILASIKPAGVVSRA DVVLPNQFQALRKSFIPERPVP VMVTRLFELPVQISLGVYSLER PANPQPIAYLVLQPRRKANNQN ASTSAIIRATIGEPISCSVPSRGC EGGISVAETVPAMIIAIGITISEG LDARYRHVNSEHDPSDRQAKF EWRYFGNLGKTVNDWRKNNK ADIKEDGNRRCRHTNQPHCRIE AVEYDDGRLCPLHGAHRGQSS DGELVKPTVKTQSLAVHYSIGK LRHRPNHGAVYYQRLRSGMGL MNAFDSQTEDSSPAIGRNLRSR LARKKLSEMVEEELEQMIRRRE FGEGEQLPSERELMAFFNVGRL RAGSVKTQRSGANKQRRTRCV SRPSADTIIGELSGMAKDFLSHP GGIAHFEQLRLFFESSLVRYAA EHATDSRDPRYRPKFYSISRSVP VSDNITLQQLLLSLNDQPARCK PSARCRLHGSHTSRYECNHRHG
26112	56480	A	26259	185	775	IPEIFSGETHLKVSTLSKPTFSISS LIRCTTRFSSQLSLGIATMSHRK RVISALKSLSRLSANSLVFANQ VERSSLTNLGCTRCSG*SLFWQ RPALR*PFGLCPTVALTYLIVSP EW*KAVSVKCWRNRRLTLMTS PICTNSGTLTTAPVDRVAQVTF QSPECLQHMRLTIALRYFRVAL SRRLLVYASVCFTFSG

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26113	56481	A	26260	301	1313	RLEHDGVCLHRANHRYPGCRL HLDYVEPQLQHDDALRAAVM MFKQYLQVTKPGIIFGNLISVIG GILLASKGSIDYPLVIYTLVGVS LVVASGCVFNNYIDRDIDRKME RTKNRVLVKGLISPAVSLVYAT LLGIAGFMLLWFGANPLACWL GVMGFVVYVGVYSLYMKRHS VYGTLIGSLSGAAPP\VIGYCAV TGEFDSNAAILLAIFSLWQMPH SYAIAIFRFKDYQAANIPVLPVV KGISVAKNHITLYIIAFAVATLM LSLGGYAGYKYLVVAAAVSV WWLGMALRGYKVADDRIWAA QSCSGFSIIPITALSVMMSVDFM VPDSHTLLAAVW
26114	56482	A	26261	3631	4078	CFLNFKTLLLVHLFRRVFLRIRL RHRKLHPVGLGGPVNKAAYAF CLGAMANGVYGPYAIFASVKM VSAFTVTASTMLAPR\WLLGLA GITEGAIPMAIEDPLRVIGSFVL GSMVTGAIVGAMNIINRTLRVE ASVTSAQIVQTIIRLRR
26115	56483	A	26262	814	2126	CTGCRKQRLPVVQGFAAGLAA NMIGSGFLGAVVGGLIAGYLM RWVKNHLRLSSKFNGFLTFYL YPVLGTLGAGSLMLFVVGEPV AWINNSLTAWLNGLSGSNALL LGAILGFMCSFDLGGPVNKAA YAFCLGAMANGVYGPYAIFAS VKMVSAFTVTASTML\APRLFK EFEIETGESTLLLGLADITEGAIP MAIEDPLRVIGSFVLGSMVTGA IVGAMNIGLSTPGAGIFSLFLLH DNGAGGVMAAIGWFGAALVG AAISEGKRIFRYRDLIIVNSNQL FLHDHRFPRWEGLESVFFLLAA FQQDVGIWPPLGAMLGLATAV VLGFLLYWGGIRLNLGAFFKW TSLFILFVAAGLAAGAIRAFHEA GLWNHFQEIAFDMSAVLSTHSL FGTLMEGIFGYQEAPSVSEVAV WFIYLIPALVAFALPPRAGATAS
26116	56484	A	26263	1	525	
26117	56485	A	26264	1	700	
26118	56486	A	26265	1	1428	
26119	56487	A	26266	254	475	RDQLVSELNQMLV*KSAFRMA ALITSRWPMVTHWFREVRRGN WRQFLPALTLLVRLSLMLMGR QAILRSRRNY

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26120	56488	A	26267	1	1657	MLIQRRRLAFDRAKHRRAEML AQRARGEEEAHHHSSPEGAIEV DESEVDLDAISAQSLRLVRSILM LIALLSVIVLWSEIHSAFGFLENI SLWDVTSTVQGVESLEPITLGA VLIAILVFIITTQLVRNLPALLEL AILQHLDLTPGTGYAITTITKYL LMLIGGLVGFSMIGIEWSKLQW LVAALGVGLGFGLQEIFANFIS GLIILFEKPIRIGDTVTIRDLTGS VTKINTRCHTHRRQQLLLQQA ATSSADVIYLGEAVCSKRRATK VGDWLEMAKSLAGSGKQIVLS TLALVQASSELGELKRYVENGE FLIEASDLGVVNMCAERKLPFV AGHALNCYNAVP\LKILLKQGM MRWCMPVELSRAWLVNLLNQ CDELGIRNQFEVEVLSYGHLPL AYSARCFTARSEDRPKDECETC CIKYPNGRNVLSQENQQVFVLN GIQTMSGYVYNLGNELASMQG LVDVVRLSPQGTDTFAMLDAF RVNENGAAPLPLTANSDCNGY WRRLAGLSLRQIKTCLIFLLCQP RGRRPYRTRAMPPILTMPANSP
26121	56489	A	26268	482	605	
26122	56490	A	26269	1	298	MWPGMVTHAVRIPLHNDTVTL SDNFQPFAGTDAMTITRPLEML RDGKCPQPDWISSEGACAGNA TDSPHPFELKAGKTITLEDGRQI NGADYLAAPVPGKALAIFGDT GPCDAALDLAKGVDVMVHEA TLDITMEAKANSRGHSSTRQAA TRESELFRYTVKHSLIFASVIGII TLLQASTKIYTPGRKEQGEPMT PRRTPARF*IKSGQNNHAGRWK AD*RRRLLSCSSAR

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26123	56491	A	26270	1	1707	MTRDGLANKALAVARTLADSP EIRQGLQKKPQESGIQAIAEAVR KRNDLLFIVVTDMQSLRYSHPE AQRIGQPFKGDDILKALNGEEN VAINRGFLAQALRVFTPIYDEN HKQIGVINDSRWSIIWSVLFGM LVGLIGTCILVKVLKKILFGLEP YEISTLFEQRQAMLQSIKEGVV AVDDRGEVTLINDAAQELLNY RKSQDDEKLSTLSHSWSQVVD VSEVLRDGTPRRDEEITIKDRLL LINTVPVRSNGVIIGAISTFRDKT EVRKLMQRLDGLV/NLC*RTS* TIPLRAHSPQSKSAIYHEIAP*NA PAFYRRKCHCADIFLPYF*TCR\ RDRAMSAYLRYIVQKADSSFL YDKYQNQSIAAHVMRALAAEQ SEVSPEQRRAICEAFESANNTH GLNLTAHKYPGLRGTLQTAST DCDTIVEAAALLPAFDQAVEGN RHQDDYGSGLGMAEEKFHYYL DLFRAVGDGHNSKEDATFGLG WRVNGNATMTPTFGTLASPQT YGHTGWTGTVTVIDPVNHMTI VMLSNKPHSPVADPQKNPNMF ESGQLPIATYGWVVDQVYAAL
26124	56492	A	26271	257	817	TSSRCISLRTSVLSLKVEMAPMI TPLLRTGTVLISNSRSLIVISSSR RGVPSRNTSETSTTCDHEWLSV DSFSIVLRLTVIQQFLCGIVDQR DLAAIVHGNDAFFDRLQHGLA LLKQRGDFVGFQAEKDFFQYL NQNAGANQSDQHAK*Y/LTR*C SSDCH*SVGSHGLTQGRSPPRQ FVYDFHRRWG
26125	56493	A	26272	1	2700	

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26126	56494	A	26273	1	1038	MGCLDLGDGRAGSVARYFRRY RPPCDAALDLAKGVDVMVHEA TLDITMEAKANSRGHSSTRQVL KKILFGLEPYEISTLFEQRQAML QSIKERSRRHRLPKEKKIMTPTI ELICGHRSIRHFTDEPISEAQRE AIINSARATSSSSFLQCSSIIRITD KALREELVTLTGGQKHVAQAA EFWVFCADFNRHLQICPDAQLG LAEQLLLGVVDTAMMAQNALI AAESLGLGGVYIGALRNNIEAV TKLLKLPQHVLPLFGLCLGWPA DNPDLKPR\LPASILVHENSYQP LDKAALAQYDEQLAEYYLTRG SNNRRDTWSDHIRRTIIKESRPFI LDYLHKQGWATR
26127	56495	A	26274	1	1338	
26128	56496	A	26275	2	375	HSDPEASGPLTRLRAMEQRRVT DFFARRRTPGSVPSTDRR*TIVR MIPCTSSGRRTKAMVILRTSLV NPASNE/CATELFNALDVSIQNP RMIISP*IQHRTELSGSPLVAVG RMCSLTPRVIFEH
26129	56497	A	26276	219	767	RFTQGKGPINNPAVIRPLDFPQN GSRPLANQ\IFTTSLKVGDYFGK RHKDVLRAIRNLKCSDDFTQRN FAPIDFIDKNGDVQPMYNITRD GCMMLVMGFTGKTAAAVKEC YINAFNWM\AEQLNRRMAMGE ELQHRYAIKETRSKLKGTIG\TR LMNERKKEKRVLELEHEHIMQ VTQPELLIG
26130	56498	A	26277	16	104	HICQSAPL*RGSSGLNGYGQYR PAGFLDG
26131	56499	A	26278	3	399	
26132	56500	A	26279	1112	1831	TGIRNCAPLSLTWKSKTANRKV RCGHIRYPLADGAKTSDGKDY LVVATTRPETLLGDTGRSRLTR KIRVTKELIGKYVILPAGTAPGV RQGPVWMPGDEVKKVTCKNG VVNEIWTRNHADIPLRPRFAVL ASGSFFSVGLVAERNGIREPILG LDVLQTATRGEWYKGDFFAPQ PWQQFGVTTDET/LRPSQAGQT IENLFAIGSVLGGFDPIAQGCGG GVCAVSALHAAQQIAQRAGGQ
26133	56501	A	26280	3	790	
26134	56502	A	26281	334	609	

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26135	56503	A	26282	1	1338	MTRHYGAEATNALLPGKASKH QIVGCGVNALSDLDPRRPDKTR SVASGIGAALLLRLIKTLADDL QNLTDLSVFNGERYKDAQHVV IRAAGEKNQAFIAGARHDLGGE LGVGLVWIPASKVNGIMGPSPV WLTFRVSNIAGESAEGLLVTKP KNYDQVPANKPIVDAIKAKKQ DPSGAFVWTTYAALQSLQAGL NQSDDPAEIAKYLKANSVDTV MGPLTWDEKGDLKGFEFGVFD WHANGTATDAKRYCANVKGV NPDTQEPSPSGVKVNDPKVDER LIRQEAGMVFQQFYLFPHLTAL ENVMFGPLRVRGANKEEAEKL ARELLAKVGLAERAHHYPSELS GGQQQRVAI\ARALAVKPKMM LFDDPTSALDPELRHEVLKVMQ DLAEEGMTMVIVTHEIGFAEKV RSRLIFIDKGRIAEDGNPQVLIK NPPSQRLQEFLQHVS
26136	56504	A	26283	1170	1575	DPPVLVQRDANSTVRFPHASAS ADPAGDIPPIF\AQAAGADLVY VGVEPPKPKAEVILVAEYSPIKT VADLGCPLHVQKVSRYPPEFTQ VITPVQCYVTIDALGQYAAWT RANMTYRPGSNIIQNLGNDIRL RTVQ
26137	56505	A	26284	3	1351	RTAPETPNQRPATLDSGILGGYI APDNLTITFIGGHSLFDERFCLA HRCQKAAEDDAFPHDSLDAAS LLEYAREKLNGLDVEVYHWNL QNFAPEDLLYARFDSPALKTFT EQLQQADGLIVATPVYKAAYS GALKTLLDLLPERALQGKVVLP LATGGTVAHLLAVDYALKPVL SALKAQEILHGVFADDSQVIDY HHRPQFTPNLQTRLDTALETFW QALHRRDVQVPDLLSLRAPKP KAEVILVAENSPIKTVADLKGH K/VAFQKGS/SSHNLLLRA/LRQ AGLKFTDIQPTYLTPADARAAF QQGNVDAWAIWDPYYSAALL QGGVRVLKDGTDLNQTGSFYL AARPYAEKNGAFIQGVLATFSE ADALTRSQREQSIALLAKTMGL PAPVIASYLDHRPPTTIKPVNAE VAALQQQTADLFYENRLVPKK VDIRQRIWQPTQLEGKQL

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26138	56506	A	26285	364	1937	KLSGRHCTAAMFRFLTFCLCEG MPMRNIIKLALAGLLSVSTFAD AAESSPEALRIGYQKGSIGMVL AKSHQLLEKRYPESKISWVEFP AGPQMLEALNVGSIDLGSTGDI PPIFAQAAGADLVYVGVEPPKP KAERILVAENSPIKTRTDLKGH KGAFQKGFSSHNLLLRALRQA\ GLKFTDI\QPTYLEPRWRPRAA\ FQTRGTVDA\WAIWDPYYSAA LLQGGVRVLKDGTDLNQTGSF YLAARPYAEKNGAFIQGVLATF SEADALTRSQREQSIALLAKTM GLPAPVIASYLDHRPPTTIKPVN AEVAALQQQTADLFYENRLHY SEYCRPMVSVGNWFLDGSHSV FSYDALDRLVQQGGFDGRTQR YHYDLTGKLTQKQWQYDGHG WLTDISHLSEGHRVAVHYGYD DKGRLTGECQTVENPETGELL WQHETKHAYNEQGLANRVTP DSLPPVEWLTYGSGYLAGMKL GGTPLVEYTRDRLHRETVRSFG SMAGSNAAYEMTSGTELIDLC
26139	56507	A	26286	511	1152	SVRFNIVFHFMRLLRFCCVLDH LICFTSPVNTFLRYNAFTLCNGE FGMSHPALTQLRALRYCKEIPA LDPQLLDWLLLEDSMTKRFEQ QGKTVSVTMIREGFVEQNEIPE ELPLLPKESRYWLREIL\LCADG EPRLAG\RTVVPVSTLSGPELAL QKLGKTPLGRYLFTSSTLTRDFI EIGRDAGLWGRRSRLRLSGKPL LLTELFLPASPLY
26140	56508	B	26287	184	415	
26141	56509	A	26288	15	87	
26142	56510	A	26289	78	157	CKRYGKARDTG*QPRTQKCTC CELDE

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26143	56511	A	26290	1	1817	MTSAISLGSRCSGRIPSDIIGSNL DITAFNWQPDLLTIWHRQLHLH LTRLDGGGHFYRQEVHLWRTD KSGDKRRPQGDPKTTGITAKVI NVRSTKLVGLPHRITATRWKR KRSRMLHTNTGKLVFNNRDQK RCTRKVMFDKALKLLDEAERL GSTSARSTIYQQCKRQGVITPHS ADFATTVRLLAHLSQERLGKLQ DSIYISLTDHCQFAIKRFQQNVL LPNPLLWDIQRLYPKEFQLGEE ALTIIDKRLGVQLPKDEVGFIA MHLVSAQMSGNMEDVAGVTQ LMREMLQLIKFQFSLNYQEESL SYQRL\VPHLKFLSWRILEHASI NDSDESLQQAVKQNYPQAWQ CAERIAIFIGLQYQQLGLTQPAV SKIINDIEDYFGVELVVRKNTG VTLTPAGQLLLSRSESITREMK NMVNEISGEKNPGEGSEKELET VYVQAVGAHWEGNQVWLILA GGALFAAWPRVYAAAFSGFYV AMILVLCSLFFRPLAFDYRGKIA DARWRKMWDAGLVIGSLVPPV VFGIAFGNLLLGVPFAFTPQLR VEYLGSFWQLLTPFPLLCGLLS LGMVILQGGVWLQLKTVGVIH LRSRVRIPCDLHIYAQMA
26144	56512	A	26291	557	808	
26145	56513	A	26292	8	274	
26146	56514	A	26293	523	1851	
26147	56515	A	26294	1	589	

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26148	56516	A	26295	1	1848	MDLSTPERGSPYPRLLPCGDPL GETIVAIDQEAKPSTEDLGNKK ETKYIKLKVIRWDNSDFNFLYS NYERIRARTTKKEDSATNVPVT FEKHGSHAVVYARRSATVLTD RNKEAPRVPQGGYMVSFVDIPE ALTQGETVAEAMEAAKDALLT AFDFYFEDNELIPLPSPLNSHDH FIEVPLSVASKVLLLNAFLQSEI TQQELARRIGKPKQEITRLFNLH HATKIDAVQLAAKALGKELSLE CLMDILNLNKHISGQFNAELESI RTQVMTLGGMVDKQLSDAITA IHNQDSDLAKRVIEGHKNLNM MEVAIDEAR/C*AIIAKHQS\TAS D\LRLVMVI/SKTIAEMERIG\DV GRNKICRTALEKLSQQHQP*VV S\LE\SLDRHTIQMLHDVVKAFA RMDIDETAKCQIFVEYVLKPKV IWLLCFANIFLYVVRIGIDQWST VYAFQELKLFKAVAIQGFTLFE AGALVGTLLWGWLSDLANGR RGLVACIALALIIATLGVYQHA SNEYIYLASLFALGFLVFGPQLL IGVAAVGFVPKKAIGAADGIKG TFAYLIGDSFAKLGLGMIADGT PVFGLTGWAGTFAALDIAAIGC ICLMAIVAVMEERKSAARKKFS
26149	56517	A	26296	395	1428	TSATATSTFALPRGGGYLVVSE WVVLRFTDIFLRIFPCDNGRTILI RFGIFRMLMIVAIETQQFPVTAI FRVIGMVVINVVNASEETNRRL HHRSLRLIQECVMDSLNLNKHI SGQFNAELESIRTQVMTMGGM VEQQLSDAITAMHNQDSDLAK RVIEGDKNVNMMEVAIDEACV RIIAKRQPTASDLRLVMVISKTI AELERIGDVADKICRTALEKFS QQHQPLLVSLESLGRHTIQMLH DVLDAFPRMDIDEAVRIYREDK KVDH\EYE\GIVRQLMTYMMED SRTIPSVLTALFCARSIERIGDRC QNICEFIFYYVKGQDFRHVGGD ELDKLLAGKDSDK
26150	56518	A	26297	667	1002	
26151	56519	B	26298	1	1716	

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26152	56520	A	26299	1001	2193	LMAATKPAFNPPGKKGDIIFSV LVKLAALIVLLMLGGIIVSLIISS WPSIQKFGLAFLWTKEWDAPN DIYGALVPIYGTLVTSFIALLIA VPVSFGIALFLTELAPGWLKRP LGIAIELLAAIPSIVYGMWGLFIF APLFAVYFQEPVGNIMSNIPIVG ALFSGPAFGIGILAAGVILAIMII PYIAAVMRDVFEQTPVMMKES AYGIGCTTWEVIWRIVLPFTKN GVIGGIMLGLGRALGETMAVTF IIGNTYQLDSASLYMPGNSITSA LANEFAEAESGLHVAALMELG LILF\VITFIVLAASKFMIMRRIA LTLSMATMAFGLFWLIWILMST ITRGIDGMSLALFTEMTPPPNTE GGGLANALAGSGLLILWATVY CGPLSDDRGGIRPTI
26153	56521	A	26300	1	1645	MPAFPYTADYFSGLTATTAALA ALHKVRETGKGESIDIAMYEV MLRMGQYFMMDYFNGGEMCP RMSKGKDPYYAGCGLYQCAD GLLSLDCVHRRLGAIDPILNECF KDIGLAHLLGTPEIPEGTQLIHRI ECPYGPLVEEKLDAWLATHTIA EVKERFAELNIACAKVLTVPEL ESNPQYVARESITQWQTMDGR TCKGPNIMPKFKNNPGQIWRG MPSHGMDTAAILKNIGYSENDI QELRPPNNKRTKMDRGAMDII GGQHLRQMWDDLADVYGHKT ALICESSGGVVNRYSYLELNQEI NRTANLFYTLGIRKGDKVALHL DNCPEFIFCWFGLAKIGAIMHE AVIALASPDNMNAFELTP*SGK LITTFPHLPLAISA*ASPACSSEK RWVMALRGHSFQSVRSWAHFS IWNRLVTQEPIIRR

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26154	56522	A	26301	2	1021	TPGNNVDSIFLAFFLNQFLTLGY IMGKTISIKVLFGIYLLLMAAKV FAFSCNVDGGIIVGAGTTSVYV NLDPVIQPGQNLGVDLAHHISC WNGDGGWYDTDHMNLVQGS AFAGSLQSYIGSLYWNNVTYPF PLTTNTNVLDIGDKTPMPLPFK LYITPVGAAGGVVIKAGEVIARI DMYKIATLGSGNPSNFTWNIIT NNNAVMPTGGCTVDSRNVTVD LPDFPGSAEIPLGVYCSSEQKLS FYLSGATTDSSRQVFANTAPDA TKASGVGVTLMQRQLAGINDS HLLHYLDDEVWDNDYLATPHF LLKSAILRSMNDALMTRVTGE KNGQVRLEEIER
26155	56523	A	26302	522	714	
26156	56524	A	26303	1	976	STCSSRSHLHLIQASPILPNYVA TAVAARIIADVQGISDTCVIAQP SPPHPGALRTLVFTTDEPETPQP PGAAGFQLVQKKQVQLHNVLY VMTPHAFAQGTVTIYLPGEQQT LSVAPLKNVVQLVTQQHLRDR LWWPGAFLTDFAAKVKALKD/ YPNHVMAQRASGEAEADDDV AATIKSVRQQLLNLNITGRLPV KLDPDFVRVDENSNPPLVGDYT LYTVQRPGTEQGSFKVKRARA RVRQTRAPLFGPKSPAPEHMES ELEFELIGPSKSTSGNPRGLRSE RPVLFCLYPEMPTAAARAILIAE EQSREVKIALVVLDRLQRE
26157	56525	A	26304	1	1701	
26158	56526	A	26305	1839	2038	ARSGCFVRQSCPRGRCSKNRR WRDPYDHYPARPAYCP*R/WC M*LSTLATPKKVSPCKPAPAAH RWR
26159	56527	A	26306	1	3270	
26160	56528	A	26307	1962	2049	
26161	56529	A	26308	94	942	
26162	56530	A	26309	1	4104	
26163	56531	A	26310	879	1367	TASELGKSCSRDHTPCTASVRA LYYARLRHAPANDPGEDGWAL AAKPPALPPRNSLNSQAIFRDKP NLPHRSPATYRQTERG*DTRSE FHA*TDAIPVATRARAGEFCRQ MFWGEDQADEQPA**ACCHRK *PVPK*DLAMLRAPPRMDSPPD ASRTSDLHN

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26164	56532	A	26311	1203	1911	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDH\K RPREALLDSLKKLQLDYIDLYL MHWPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQG GKGVFDQKVIRDLADKYGKTP AQIVIRWHLDSGLVVIPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDPDQFGG
26165	56533	A	26312	3	793	
26166	56534	A	26313	181	336	
26167	56535	B	26314	1	374	
26168	56536	A	26315	591	679	
26169	56537	A	26316	937	1395	YRLAAGSCGIRRRNRHCQRRPG RNSKRLIALISAIGMSIFLQNYV SLTEGSRDVAPSSVPLTPASLLI AGSPPH*TISRLSGPLLREIMLK QLYHCGKSLTNLPIREILRM*G* LTGEEIELARGDFHIRDIWHRA VTNTAHKTGITQAQHRH
26170	56538	A	26317	627	878	VVEWFEPLICVNGWESKWPVL LSE**PETVGTNCDSSN*IPASLN TSYTGLMAFDAIMVAVPTS*TC KIRRRVAGTKCGNPRA
26171	56539	A	26318	125	3078	IYTVEIQNLGFAFVTGENTTGIN SGTISLLQNGKDPAPSPIVLLAT NGGSATNAGTITGKVTEQHSVF NKYSTGTSNSFIFNNDVSSITGL VAQSNSTIINTDSGIIDLYGRGS VGMLAIADSTAENQGKITLDSM WVDANDTTAMRDIASNSAIDF GTGVGVGTDRYRGGRKNAPAF N\QLGGVITIYNAGAGMAAYG ASNTVINQGTINLEKNGNYDDS LAANTLVGMAVYEHGTAINDQ TGVININVGTGQA
26172	56540	A	26319	205	419	
26173	56541	A	26320	1829	2903	AWKVSHCAARPSFSRRWRGEK CTAGRRSQQFSARSTLKPMPSP R*SSMHRR**MPSASCALRLPIP PAAAQSSHQSKKLRTSDNASPV AAARPVRPIRWT

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26174	56542	A	26321	402	1781	QRTTGAERYVPHHQPCPPASSL SAGPRG\LHPAKVQEGVDIAIEN DVIVAIGDALTQRYPDASFKEM HGRIVMPGIVCSHNHFYSGLSR GIMANIAPCPDFISTLKNLWWR LDRALDEESLYYSGLICSLEAIK SGCTSVIDHHASPAYIGGSLSTL RDAFLKVGLRAMTCFETTDRN NGIKELQEGVEENIRFARLIDEA KKATSEPYLVEAHIGAHAPFTV PDAGLEMLREAVKATGRGLHI HAAEDLYDVSYSHHWYGKDL LARLAQFDLIDSKTLVAHGLYL SKDDITLLNQRDAFLVHNARSN MNNHVGYNHHLSDIRNLALGT DGIGSDMFEEMKFAFFKHRDA GGPLWPDSFAKALTNGNELMS RNFGAKFGLLEAGYKADLTICD YNSPTPLLADNIAGHIAFGMGS GSVHSVMVNGVMVYEDRQFN FDCDSIYAQARKAAASMWRRM
26175	56543	A	26322	284	340	
26176	56544	A	26323	113	646	WTLVPNWNNTQPYLGLFF*FIR DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQRSDSSLR EKKITKKHTKKRTASLILHAMI CCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT EQ
26177	56545	A	26324	1	582	
26178	56546	A	26325	3	947	QTQEWSGSATFTSDGKIRLFYT DYSGKHYGKQSLTTAQVNVSK SDDTLKINGVEDHKTIFDGDGK TYQNVQQFIDEGNYTSGDNHT LRDPHYVEDKGHKYLVFEANT GTENGYQGEESLFNKAYYGGG TNFFRKESQKLQQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGGATQA FAKENNQKAYKETYGVSHITR HDMLQIPKQQQNEKYQVPQFD QSTIKNIESAKGLDVWDSWPLQ NADGTVAEYNGYHVVFALAGS PKDA/G*HINLHVLSK

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26179	56547	A	26326	2	223	RIPIKNIESAKGLDVWDSWPLQ NADRTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNSID SWKNAGRVFKDSDKFDANDPI LKDQTQEWSGSATFTSDGKIRL FYTDYSGKHYGKQSLTTAQVN VSKSDDTLKINGVEDHKTIFDG DGKTYQNVQQFIDEGNYTSGD NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRGATQAFAKENNQK AYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDA/G*HI NLHVLSKGRRQLNRQLEKRGP
26180	56548	A	26327	1	803	MLEDPRKGLETPSPVSHNLHFQ FHLGPLLPGSPMKKWPALVVT GSKSPKLESYKHFQKIWDMHG EPSKREEGAGLTVNQHIPNGAS TCNEGPQRLEALGARIPMAAGF SSSKPTLVTPRRAYRADLRLEG YWGCQGVPGGPLVAQGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDA/G*HINLHVLSKGRRQ LNRQLEKRGPCL
26181	56549	A	26328	2	439	
26182	56550	A	26329	1	1084	MVIAAMETQLSNGPTCNNTAN GPTTINNNCSSPVDSGNTEDSK TNLIVNYLPQNMTQEELKSLFG SIGEIESCKLVRDKITGGATQAF AKENNQKAYKETYGVSHITRH DMLQIPKQQQNEKYQCDNLKT CHTSHGSVMAETAVINHKKRK NSPRIVQSNDLTEAAYSLSRDQ KRMLYLFVDQIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTPERR**HINLHVLSKG RRQLNRQLEKRGPCL

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26183	56551	A	26330	34	1949	MGYLNNVAGYREDLLANRAIV KHGNFALLTPDGVVKNIIPGYE NCDATILSTPKLGASFVDYLVT LHQNGGNQQGFGVEGIETFRY VISGNITAKAEGKTYALSEGGY LYCPPGSLMTFVNAQAEDSQIF LYKRRYVPVEGYAPWLVSGNA SELERIHYEGMDDVILLDFLPKE LGFDMNMHILSFAPGANHGYIE THVQ\EHGGATQAFAKENNHK AYKDTYGVSHITRHDMLQIPKQ QQYEKYQDTHDTPYCEPLPGET RLWGDTDVIGLFDAETDMNDV VAILENHPLLGAGFAHKIEQLE DKDWEREWMDNFHPMRFGER LWICPSWRDVPDENAVNVMLD PGLAFGTGTIQTLSVPAMLDSS THTRRMRSTLNLYEITRMSTVS TSEHSMTYTLVQVDMKEAQKP DTASYRTFNEFFVRPLRDEVRPI DTDPNVLVMPADGVISQLGKIE EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRD YHRVHMPCNGILREMIYVPGD LFSVNHLTAQNVPNLFARNERV ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPVG DFELLLCHGTVCVVGKMRDLIL QLSKSSIYSTKPPSRQVSVMLC
26184	56552	A	26331	1	145	LRLGLLYGRRFVPPP*YALLNK DSSPWYPFSVPVLASKTRYLWL LSPT
26185	56553	B	26332	1	3090	
26186	56554	A	26333	3	832	
26187	56555	A	26334	1	3258	

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26188	56556	A	26335	184	2324	ENRVRLFVLIVFQDLPTCYVNH NFVCTAADTFTTDITPKAGDAR LIGIAQTVRHLEDPMRAWKSIH KSCEILDPIHRAPVKENTHPARK INISDPAAGAVARIRYEGVLSVC RASASAYVSRSRTITVACWYVS NTGVTGATIGVKRQHRHARLFS GDGAPGFGTGKRDIRQLRRLVR IQIQRTFFAAVLHVPTPWSRAID AAALLTVIDVKVLTACACQAC RTLALRVAQVIDRCSNPGDIMS SVARRYWFISRWSAKRDCAVS YDQDPGQAQRSCRSCLVAVDR GLWLSAYCRSLMTQTLLPDDV PRILPNASSPSRLRCLQHLGNYR LLDLRKLIWLHRSQFSLCGWEK RLVKDLTRIQDTGRAKEILGAT ATLEFRLVNTNVDQAAAASGR VPGDSEVKQTREGQPVVLYKR VILTGDHITDSTSSQDEYNQPQ VNISLDSAGGNIMSNFTKDNIG KPMATLFVEYKDSGK\KDANG RAVLVKQEEVIIIANIQSRLGNS FRITGINNPNEARQLSLLLRAGA LIAPIQIVEERTIGPTLGMQNIEQ GLEACLAGLLVSILFMIIFYKKF GLIATSALIANLILIVGIMSLLPG ATLSMPGIAGIVLTLAVAVDAN VLINERIKEELSNGRTVQQAIDE GYRGAFSSIFDANITTLIKVIILY AVGTGAIKGFAITTGIGVATSM FTAIVGTRAIVNLLYGGKRVKK
26189	56557	A	26336	1	369	

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26190	56558	A	26337	1	1316	MNGLLDSDSDSLSSCQQRVKA RLHEILQKDRDFTAEDYEKVES RIYHFARLSVGGYTADSSLTLK VYLQLMKAPKKRRGEVNVGT VVAFIKGGFPVVKKDYFRPAA DGSSALCRFFPTGNVHDQSDPQ KVTDGAVVPVQPTDGPGLRCL RRARGCGAGRQGREQAQDCG AEIQAEAASRASRVQEGSYPRP PNGPFSTDLTGLMQFTKLLVLK VESQLTRRIRKCHNLREANIREE LRFFNCTNVALRTGVQFNRRPD SPGYSRGVLSPERHVRTRLYFT SESHVHSLLSILRYGALCNRGG TLCCRAIHTLHRHTIVLNGVTV TLNLVQLTFYGNVSEIIRHQCQ LTRHGNHPLPLTAIQGIALFSDN QAAYRFRADQRTLRPFGLPVAR QPVRRGGFHDIVIVFDFGTARQ QQE/LRLQLRVFSSFVLHEKKR
26191	56559	A	26338	2	1415	
26192	56560	A	26339	1434	1667	KRTDWRDRVAFRCRSIAESG*R QAIAKELELTASAEILLWDDYF APGYGVPNDEGMEAVKLLARL EGILLDPAVRLR
26193	56561	A	26340	1	1671	
26194	56562	A	26341	1067	3947	FCTVPNAVYIGGPGFGARHNAS NSLKDIAELVPFAHRYGAKIFV TLNTILHDDELEPAQRLITDLYQ TGVDALIVQDMGILELDIPPIEL HASTQCDIRTVEKAKFLSDVGF TQIVLARELNLDQIRAIHQATD ATIEFFIHGALCVAYSGQCYISH AQTGRSANRGDCSQACRLPYT LKDDQGRVVSYEKHLLSMKDN DQTANLGALIDAGVRSFKIEGR YKDMSYVKNITAHYRQMLDAI IEERGDLARASSG
26195	56563	A	26342	182	881	HAEPLPYRGLLLKLGESRGCLL PASLPFSLQEFFYSGPREELAQK TLLVSVWDYDLGTADDFIGGK CDPADQDVVHTALRE\TREELG LAVPEEHVWGLLRPVYDPQKA TVVPVLAGVGPLDPQSLRPNSE EVDEVFALPLAHLLQTQNQGY THFCRGGHFRYTLPVFLHGPHR VWGLTAVITEFALQLLAPGTYQ PRLAGLTCSGAEGLARPKQPLA SPCQASSTPGLNKGL
26196	56564	A	26343	237	338	

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26197	56565	A	26344	279	533	IHLRRILQRGQ*PRQRWRERCC ESGRGTSGPGSSQ*LTGSPQECC TPAGETGPRAHSPQ*SCWCHCC TPQGRQSICTRTSHRTA
26198	56566	A	26345	126	303	LLLSYGVGASHQSLECHHRSNH GSLWMHSKRCAGGKIRVGTPE CQ*SALERPGLPPLC
26199	56567	A	26346	368	746	SLLHTTSRAPEGPSRYPGPGPPS AATKGQRTRRPLCARPP/PGLPD APL/SPAAPTPTLPLPCPRVAQP AHGPPSASALSSWENRPCCRHE LAAKPPEQAARRGHARTPTAG PAPPGRRAALSGSQFP
26200	56568	A	26347	79	159	SFLGVSRRGGFGRVTGQ*WRE GQQINK
26201	56569	A	26348	1	3369	
26202	56570	A	26349	3	529	MELAKVVKSHPSAKMVLCIAT DDSHSLSCLSLKFGVSLKSCR\T LLENAKKHHVEVVGVSFHIGR GCPDPQAYAQSIADARLVFEM GTELGHKMHVLDLGGGFPGTE GAKVRFEEIASVINSALDLYFPE GCGVDIFAELGRYYVTSAFTVA VSIIAKKEVLLDQPGMEEENCS
26203	56571	A	26350	146	502	

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26204	56572	A	26351	3	2212	MKRSRCRDRPQPPPPDRREDGV QRAAELSQSLPPRRRAPPGRQR LEERTGPAGPEGKEQPPALASQ SAEIAASARLPPRLGRLLGFQK ACRCWSLNPHILMALLRSLVPP DKKHPQVWRGRPPLHLAPNVG LFSRVKVRSSVVIEDKSMRDSR RGLSQRRRRKKKKRGSSSKK KKRRKKRKKKRKKRKRRKN RKKKKKRKNKRKKKRKKEEK KEEEEERRKKEEEDEEGRGRGR RKRKRKKRKKRRSRKKKETAA AAAAGERLGKWWPGECPVEC VAYFLRRRLQQRLHPARQLLL QGMAGYLSESDFVMVEEGFST RDLLKELTLGASQATTDEVAAF FVADLGAIVRKHFCFLKCLPRV RPFYAVKCNSSPGVLKVLAQL GLGFSCANKAEMELVQHIGIPA SKIICANPCKQI\SQIKYAAKHGI QLLSFDNEMELAKVVKSHPSA NFHIGSGCPDPQAYAQSIANAR LVFEMGTELGHKMHVLDLGGG FPGTEGAKVRFEEIASVINSAL\ DLYFPEGCGVDIFAELG\RYYV TSAFTVAVSIIAKKEVLLDQPGR EEENGSTSKTIVYHLDEGVYGIF NSVLFDNICPTPILQKSSTKSLR TTIGEAFERLHRLLRERQKAML EELEADTARTLTDIEQKVQRYS QQLRKVQEGAQILQERLAETDR HTFLAGVASLSERLKGKIHETN
26205	56573	A	26352	1	860	MKKEDAFLKAFYIVHGKWNCV KGSLTRTPCCCTNCLAGGIWC MRVQIFQLENKVLPGFPWACR VDLYGQIGFDAAAQCLSLSVSK AEPLVKKAPPELREQLARKTLS SDNLKYLFDNKDIMKVKQSKK KKEHSFRKNNGCIKIIAFSDHAE DFRKLGCEVLGISVDSQFTHLA WINNPQREGDLGPLNIPLLAEV ASGLSEDYAVLKTDAGIAYRG RFISDGKGVL/SQITVNDLPVGR SVDEALRLVQAFQYAEEHAEV CPAGWKPGTDTIKLNVGDSKE

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26206	56574	A	26353	70	745	ERGSTRVIVRASSLCPRSFQSWP PVTRASESQPLTSRPQRWSDGA FKEVKLSDYKGKYVVLFFYPL DFTFVCPTEIIAFSNRAEDFRKL GCEVLGVSVDSQFTHLAW\ITT PRKEG\GLGPL\NIPLLADVT\RR\ LSEDYGVLETDEG\IAYRGL\FII DG\KGVLRQITV\NDLPVGRS\V DE\ALRLVQAF\QYT\DEHGEVC PAGWKPG\SDTIKPN\VDDSKE\ YFSKHN
26207	56575	A	26354	1	689	MAAEDELLLPRLPMLLETGKQ LLDEVELAAETTGYQIVQEKRA REHFINYLTQCHYYHIAKFELL KTKNNSAENHTANSSMAYPSL VAMASQRQAKIERYKQKKELD HRLSAMKSAVESGQADDEHER PPVKSFILTRNTAQAKLFGASYP SLATMTVSDWYEQHRKYGALP DQGIATATPEKFRKAAQQQKY QEVKEGEDDE/ALYRVREWDN WKDTHPGGYGNRQNMG
26208	56576	A	26355	1	810	NYLTQCHCYHVAEFELPKTMN NSAENHTANSSMAYPSLVAMA SQRQAKIQRYKQKKELEHRLSA MKSAVESGQADDERVREYYLL HLQRWIDISLEEIESIDQEIKILR ERDSSREASTSNSSRQERPPVKP FILTRNMAQAKVFGAGYPSLPT MTVSDWYEQHRKYGALPDQGI AKAASSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSS/PSSQEFR KAAQQQEEQEEKEEEDDEQTL HRAREWDDWKDTHPRGYGNR QNMG
26209	56577	A	26356	223	359	RKQQDEPCGHLQSPGKPFLTLS CRDPWGGLPV*LEKDHRKKKS
26210	56578	A	26357	1	3855	
26211	56579	A	26358	1005	1293	SDRRYEWDPCPR*LNGALLCLL LLEHPEGCPWHSVWSTGHSLEP MHFRFPSSQDLQLLLPLPGKLG YRARIRNHGHSCFLQRRKTVYQ GDGPLREP
26212	56580	A	26359	763	978	

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26213	56581	A	26360	1	1217	MQRRLKRRNAGLPCCEVPGYY REDASSPLLPKYKTNFSQCLVH FFDELRHHLVKTRHVLFIPLNH DIMQAFTLHARVIVGKVPGIFS RHPHAVLHLGHSQIGLLMEYPD ELLWECKEDALALIRRDAPMLT DFTHNLLNAPLLDKQAEWCEV FDRGRTTSLLLFEHVHAESRDR GQAMVDLLAEYEKVGLQLDCR ELPDYLPLYLEYLSVLPDDQAK EGLLNVAPILALLGGRLKQREA PWDALLDALV\QLGGSSLSSDN VKKQVNSEERDDTRQALDAV WEEEQVKFIEDNATACDSSPLN QYQRRFSQDVAPQYVDISAGE GQSSFQLVSYWEKDVQTCLEFL PSGGFVVSLASGVKLQTFTETD NLVKDITFFGKISTRSLKTYLKD VTEKREQSCVNLELK
26214	56582	A	26361	1	783	
26215	56583	A	26362	2	1646	PGSTISFRRVTQREKKQPEAELC QGSTSNLFQFIHPSLLSAQTVEL GLSKFVPKKMIITQTSH\CYMTS LGILFLINILPGTTGQGESRRQEP GDFVKQDIGGLSPKHAPDIPDD STDNITIFTRILDRLLDGYDNRL RPGLGDAVTEVKTDIYVTSFGP VSDTDMEYTIDVFFRQTWHDE RLKFDGPMKILPLNNLLASKIW TPDTFFHNGKKSVAHNMTTPN KLLRLVDNGTLLYTMRLTIHAE CPMHLEDFPMDVHACPLKFGS YAYTTAEVVYSWTLGKNKSVE VAQDGSRLNQYDLLGHVVGTE IIRSSTGEYVVMTTHFHLKRKIG YFVIQTYLPCIMTVILSQVSFWL NRESVPARTVFGVTTVLTMTTL SISARNSLPKVAYATAMDWFIA VCYAFVFSALIEFATVNYFTKR SWAWEGKKVPEALEMKKKTP AAPAKKTSTTFNIVGTT\YPINL AKDTEFSTISKGAAPSASSTPTII ASPKATYVQDSPTETKTYNSVS KVDKISRIIFPVLFAIFNLVYWA TYVNRESAIKGMIRKQ
26216	56584	A	26363	217	559	MKKALQVAMFSLFTVIGFNAQ ANEHPHETMSEAQPQINSATGV VKGI\DL\ESKKITIHHDP\IAAVN WPEMTMRFTITPQTKMSEIKTG DKVAFNFVQQGTLSLLQVIKVR KPAQ

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26217	56585	A	26364	72	157	ERRKF**SQSS\QKKNKERLQNA VIYLEL
26218	56586	A	26365	3	620	VSGGGWEPSGTLTAFKTASAIT TEMASRS\QGIQQLLQAEKRAA EKVADARKRKARRLKQAKEEA QME\VEQYRREREHEFQSKQQA AMGFQGNLYAEVEQATRRQV QGMQSSQQRNRERVLAQLLGM VCDVRPQRPSDLQKEEMTTFSP SLIIPARACRFLVRAQQSSGHLH YRAKDPVGTRSLRHTRSSRIHG GVPTEKTCVAKT
26219	56587	A	26366	28	187	TGTESGQYHCKRRKMGPEPIIK SLWARSDEPVFWG/LFGAGGM WSAIIAPVMIR
26220	56588	A	26367	1	870	MAVWPTGALALTPSPAGDAGA CSTAGGPCQGARGPRGSGPPA WGPDAVLEPLRGQRKPYVRPM TSTWWKKLPFYRFYMLREGTA VPAVWFSIELIFGLFALKNGPEA WAGFVDFLQNPVIVIINLITLAA ALLHTKTWFELAPKAANIIVKD EKMGPEPIIKSLWAEPEMINPNP KRSDEPVFWGLFGAGGMWSAI IAPVMILLVGILLPLGLFPGDAL SYERVLAFAQSFI\GRVFLFLMI VLPLWCGLHRMHHAMHDLKI HVPAGKWV\FYGLAAILTVVTL IGVCTI
26221	56589	A	26368	741	894	
26222	56590	A	26369	504	558	
26223	56591	A	26370	897	1097	RKWSQSTRLPWETGPSSETSPS GPIVSPTRSHLASPRRPPPTPP*S SPRRLLGAIPPGIGVPPLNE
26224	56592	A	26371	200	657	GPRRLSFVTGHKAYRGLGIVSG PTVPLVCAVCCSYWDPGVPRV VRLVVRLWPLCRCGGRSGDAS VAAAPLVCGGGI*DWDHCPFV CGPSLCALRPSCGCGSGMACRV VLLLRCPLAMFAFTSFFSVTEV GKFSPFPLPEFFFSGFALDLSLP
26225	56593	A	26372	196	404	
26226	56594	A	26373	1	3162	
26227	56595	C	26374	287	349	
26228	56596	B	26375	366	1637	
26229	56597	A	26376	365	604	VLAVSYPSLCLLL*KPIGPEDAI YALSSDFTCGSPTAAGRKQIRG EVCPRERCSVETCLSPNFHSLVS SFPFSLLQGFK

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26230	56598	A	26377	1	1404	TLVRCFPPLKLIFSIFKKKAASL GSSQSSRTYAGGTASATKVSAS SGATSKSSSMNPTETKAIPVSQ QMEGPHLPNKKKHKKQAVKTE PEKKSQSTKLSVVHEKKSQEGK PKEHTEPKSLPKQASDTGSNDA HNKKAVSRSAEQQPSEKSTEPK TKPQDMISAGGESVAGITAISG KPGDKKKEKKSLTPAVPVESKP DKPSGKSGMDAALDDLIDTLG GPEETEEENTTYTGPEVSDPMS STYIEELGKREVTIPPKYRELLA KKEGITGPPADSSKPIGPDDAID ALSSDFTCGSPTAAGKK\TEKEE STEVLKAQSAGTVRSAAPPQEK KRKVEKDTMSDQALEALSASL GTRQAEPELDLRSIKEVDEAKA KEEKLEKCGEDDETIPSEYRLK PATDKDGKPLLPEPEEKPKPRS ESELIDELSEDFDRSECKEKPSK PTEKTEESKAAAPGSCVGGCVS
26231	56599	A	26378	1	688	ITAISGKPGDKKKEKKSLTPAVP \VES\KPDKPSGKSGMDA\ALDD LIDTLGGPEETEEENTTYTGPEV SD\PMSSTY\IEELGKR\EVTIPPK \YRELLAKPIGPDDAIDALSSDF TCGSPTAAGKKTEKEESTEVLK AQSAGTVRSAAPPQEKKRKVE KDTMSDQALEALSASLGTRQA EPELDLRSIKEVDEGSLPDFQQQ SLSLGLPWPKMGQFLSSTFLEG SPATQRK
26232	56600	A	26379	199	384	VYKECR*GFSHESPPSKPQS/HIE *KFCMCGENGQGLRKKSSSKN SFFGTSFTWVGRENVKHI

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26233	56601	A	26380	166	2172	TYILRNLYKEVMLENYRNLLSL GKAVFFPFLH*FSRDLLIT*YVP QSQQFLSQHVLQIFLGLCAENH FHPGNSSPGHWKQQGQQYSHV SCWFENAEGQERGGGSKPWSA RTEERETSRAFPSPLQRQSASPR KGNMVVETEPSSAQRPNPVQL DKGLKELETLRFGAINCREYEP DHNLESNFITNPRTLLGKKPYIC SDCGRSFKDRSTLIRHHRIHSME KPYVCSECGRGFSQKSNLSRHQ RTHSEEKPYLCRECGQSFRSKSI LNRHQWTHSEEKPYVCSECGR GFSEKSSFIRHQRTHSGEKPYVC LECGRSFCDKSTLRKHQRIHSG EKPYVCRECGRGFSQNSDLIKH QRTHLDEKPYVCRECGRGFCD KSTLIIHERTHSGEKPYVCGECG RGFSRKSLLLVHQRTHSGEKHY VCRECRRGFSQKSNLIRHQRTH SNEKPYICRECGRGFCDKSTLIV HERTHSGEKPYVCSECGRGFSR KSLLLVHQRTHSGEKPQMTFSG VTPQLLERTVLLLAEMHSRDAL RSGTHSQPQGAACTTGAMHLC RGTFWPQPLTQRGQLQKVIPDP EIPIELKDHWVADTLQVSFFLCP VLPSLPSESSIFCLVVCSINYAV APQSGLMREKDVHVWECGPPP FARTAPITPTSDQNWRPLREKY
26234	56602	A	26381	434	946	NTFCLTAMKILCMWFSRWHSR WVGMQGPSC*PQRTLWMATLS STGRSCVPAACTPAPCGRISAA GRLRCSQLLPHAPAPAACCSCP SVHISFQPL*QLRTSLWTVQMK SQVTQTQVGSHSSTSQARALQG HQQVQKPGSRIRTGGVKPQLEG PGRWLKIRLEGHSWTCRQ
26235	56603	A	26382	3	2119	

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26236	56604	A	26383	3	2237	NRRKFSVSIGFYTVMDAQYKII TKTAHLITKESPQEEGKEMFAT MSKLKEQLTKVRK*FNALLYES QQLLIPLEELEKQMTSFYDSLG KINEIITVLEREAQSSALFKQKH QVRTILFKWCNSSQKMTLCLVL GSMISMLSTAKITIAGYKSEVEV SVSHHCI*NCKKTLTLIEKGSQS VQKFVTLSNVLKHFDQTRLQR QIADIHVAFQVICSPC*DWKKH VETNSRLMKKFEESRAELEKVL RIAQEGLEEKGDPEELLRRHTV SPPFRDQRVLNAFLKACDELTD ILPEQEQQGLQEAVRKLHKQW KVSQDRTAYHLLHLKIDVEKN RFLASVEECRTELDRETKLMPQ EGSEKIIKEHRVRLPHHSPHHLC EKRLQLIEELCVKLPVRDPVRD TPGTCHVTLKELRAAIDSTYRK LMEDPDKWKDYTSR*PQNGLW ISTNETQLKGIKGEAIDTANHGE VKRAVEVSSGSLSKRGETLSWL KSRLKVLTEVSSENEAQKQGDE LAKLSSSFKALVTLLSEVQHLL THFGDCVQYKEIVKNSLEELIS GSKEVQEQAEKILDTENLFEAQ QLLLHHQVKMPLSSAKKRDVQ QQIAQAQQGEGGLPDRGHEEL RKLESTLDGLERSRERQERRIQ VGAGS*ERFETNKETVVRYLFQ TGSSHERFLSFSSLESLSSELEQT KVYYGSLESIAVQAENLVKEAS
26237	56605	A	26384	1	390	GTSLFDEEGAKIVKDLMSKAEK NGVKITLPVDFVTADDFDENAK TGQATVASGIPAGWMGLDCG/P ESSKKYAEAVTRAKQIVWNGP VGVFEWEAFARGTKALMDEV VKATSRGCITIIGKRSYTKLIPI

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26238	56606	A	26385	1125	2228	NVMSHLGRPDGVPMPDKYSLE PVAVELKSLLGK*VPGSGAGRL CGGGSCQARCYAGSVILLENLR FHVEEEGKGKDASGNKVGPVIL TLLGVRA*VCKRLWLNVNDAF GTAHRAHRYQEPCRLPH*EQYS YLLE*PKYFAKALESPERPFLAI LGGYEELFKIML*VLFAW**AIT WIGGGMAFTFLKVLNNMEVGN KCQVDVK*LSMIIAGCINEKNG VKITLPVDFVTADKFDENAKTG QATVASGIPAGWMVSHLSGLV V*VNRNSVVSFIHFVWNGPVG VFEWEAFARGTKALMDEVVK ATSRGCITIIGKRSYTKLIPI*AG RILIRGRCTGGGASLELLEGEGL LFFGLFGIRVDCAVRGG
26239	56607	A	26386	2	482	TRQAWHEGPRGVPHSASLRSA RRQSAPSLTESPTSVPSCISKMA LSNKLTLDKLD\VKGKRVVMR VDFNVPMKNNQITNNQRIKAA VPSI\KFCL\DNGAKSVVLM\SHL G\RPDG\VPMP*QVTPLEPVA/V VELKSLLGQGMFCS*RDCVSPE VEKACANPPG
26240	56608	A	26387	3	378	
26241	56609	A	26388	311	578	LGIRGQTLGFLSRARCGGSRRS LEMQNNAGEFVDL*VPRKCSA SNRIIGAKDHASIQMNVAEADK VTGRFNGQFKTYAISYFLNLFL HH
26242	56610	A	26389	3	333	DAWDLCRVTSCFLSLSRAVWW QQAQPSLEMQNDAGEFVDLYV PRKCSASNRIIGAKDHASIQMN VAEVDKVTGRFNGQFKTYAIC GAI\RRMGESHDSFLRMAKADG IVSK
26243	56611	A	26390	23	389	LAASFLSRARCGGSRRTQALEM QNDAG\EFV\DLY\VPRKN\SAS NRIIGAKDHASIQMN\VAEVDK VTGRFNGQFKTYAICG\AI\RRM GESDDSIL\RLAKADGIV\SKNFL TGEESQDVGIFCHK
26244	56612	A	26391	206	354	
26245	56613	A	26392	1227	1430	GSSSPRDPQEEDLKLLKFAFSR GPPLSLVHPPPLLSYPSARR*PQ TPPRPPPRHPSLHPLHPPSAQP
26246	56614	C	26393	17	319	

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26247	56615	A	26394	1	645	MIHEQNENIKKNTKTIKKNQTEI LELKNTVTEWKNLLEVFNNSFR QNEESVNLQTSYLKSLSRGEKR KKKCEEMIRDLGQYQPGPYMH DGYSRRESGPNVPRRAQVDGG DARKGTHRRKRVLERGLWLKR EDKKAQGYKGR*KGPRV*GTD PQEEDLQRLSAETWLVL*PEPR P*KAPAKKGEKVP*GRKGKAD AGKEGNNPAENGDVKTDQAQ KAEGAGDAK
26248	56616	B	26395	1	663	
26249	56617	A	26396	265	735	VMWLRYDTLSETHMHQLLGL NLLFLLSQD*VAEFHMELEWLP ATDTQTNAYIKRPVSLEPYLME GGYNKVFLAKGNIPAKSYTFIHI LLDTIRDEMAGCIEKAYEKILFT KATWILFLNTPKQMMDNTKK* GWVLGPNNYYSFASQQQKLED TTIPS
26250	56618	A	26397	215	386	
26251	56619	A	26398	3	515	QLPESAYMHQLLGLNLLFLLSQ NRVAEFHTELERLPAKDIQTNV YIKHPVSLEQYLMEGSYNKVFL AKGNIPAESYTFFIDILLDTIRDE IAGCIEKAYEKILFTEATRILFFN TPKKMTDYAKKRGWVLGPNN YYSFASQQQKPEDTTIPSTELAK QVIEYARQ\LEMIV
26252	56620	A	26399	423	4482	KLVWILFDFICLAFL*FFSTYMY SCE*ILVKLTLYFSFHVYLLIYC ECENLTGTLDLVFI*KCKSLLIW IA*TVYKKIHMEGEVKG
26253	56621	A	26400	173	174	AVSLLKHSNNDLCSS/GFPTSRT ADPTSCGSH\WPWGPQSLKQ*P ELYIGPF*PRLELKQLGCRAPSP
26254	56622	A	26401	135	699	RDLVPCAPAAPAMAKRGQDTV WAMASEGASPNPCQLPQGVEP AGQCRRKMWG*SPHTEPPLGT A*WESLELPRDLLNGFDQNAD NDMDNEIQAEVVSDGDEELVG NQSKGTWCPVPQLLQLWLKGA KIQFGPWLQRVQAPILASFHKV LSLQGSAEGKCGVEAPTQSPH WALPSGAVRRGPPSSRPQNGRS TNCLHCEPGKAADTQCQPVKA ARREVVPCKAKGAELPKTMGT DLLHQCDLGVRHGVKGDHFGA LRFDCPTGFWTYMGPVAPLVW PIFPIWNSCIYPMPVPPIVSRR

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26255	56623	A	26402	27	264	RLVEWL*PRDLLNGFDQNADN DMDNEIQAEVVSDGDEELVGN QSKGTWCPVPQLLQLWLKGAK IQFGPWLQRVQAPILASFHKVL SLQ
26256	56624	A	26403	624	955	VPSLGSFHVVLVLSVHRRQELR FGNLHLDFRRCMEMPGFPGRSL LQR*SPHGEPLLGQCRREMWG QSPHTESPLGH*LMEL*HPPSPR MIDPPTACAVPLEKLQALNASH
26257	56625	A	26404	851	1387	PKIVELLKYSGDQLERKLKKDK ALMGHFQDGLSYSVFKTITDQV LMGVDPRGESEVKAQGFKAAL VIDVTAKLTAIDNHPMNRVLGF GTKYLKENFSPWIQQHGGWEK ILGISHEEVD*NIRFVIRNTLCLL WSCARWPSDGPTGDYNVQGR WSIDVFKTIIPVTGEASGEVSFV
26258	56626	A	26405	1	229	LRRLGITHVLNASHSRWRGTPE AYEGLGIRYLGVEAHDSPAFD MSIHFQTAADFIHQNKRAISAL HLCRKSGIRQA*MSIHFQTAAD FIHQNKRAISALHLCRKSGIRQA
26259	56627	A	26406	2	594	SVLGLTLPAPRFKTLRRRWVQG QKVLRKAPFGKKPRGSLTFWR ASTRVRDMANNRRELRRLGIT HVLNASHSRWRGTPEAYEGLGI RYLGVEAHDSPAFDMSIHFQTA ADFIHRALSQPGGKILVHCAVG VSRSATLVLA*PHAVPPPLPFVE AIKKVKDHRGIIPNRGFLRQLL GLGPQLAAGSGSMRGGGEKLR
26260	56628	A	26407	605	1231	NCSNSGVWRISHKKERSIPDSK RRRSRGNTKSSSPRPTTRSLEKL LTSGSPRIWPVRMS*LHDKARR ASFSSSSSAIKKAFSSASRSSNES VSSLSNSSLEGQSKSMSISSSST GVGSRLALGLYTSSEMVKGSSF ILSSSSLGGSSYSRAAFTGELEIK GAEMFSSLGNGTPVLRAVTLEP SLSRRTNTLLLQWFPMCNWRL RRVWI
26261	56629	A	26408	771	1121	FSPKLLPRREGRKPCEAPARTQ TPRSKSSTPPSQV**SVDSDPQP KGKQDRSRGGPLQERAQRESG PNLLAATVVPRPRAERHPAISTE GPTGPPEGSAPSATSSVAAAGP APHSR

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26262	56630	A	26409	3777	4343	DQEEPFSGNSSIIQSLFTIKLNPQ SSLQEVCSLDTHNSPVRVFKNS CSAKFHFKFVWNVILLLQLSSE ELILSFVIPGVGHCWSSYCYILQ PRIFPLWSFYIVIYVEDSSICVSS LFPSWR*RP*IIGSIK*CLSSQMG WNFQSW/NLPR/CVVLVLWSIK KGL/HIWCMPDFPAFRKESLLN FRWLGHLLA
26263	56631	A	26410	473	667	PCSDWGWRSPWNLQLEETWAL *CCSHSHKVSQEGTWMKLETII LSKLLQGQKTKHPMFSLTGGN
26264	56632	A	26411	1416	2108	QRANIQNLQRTQTNLQEKRNPI NKWVKDMNRHFSKEDIYAAN RHMKKCSSSLAIREMQIKTTMR YHLTPVRMVIIRKSGNDRCWR GCGEIGTLLHCWWDCKLVQPL WKTVWRFLRDLQLEIPFDPATP \LLGIYPKDYKSCCYKDTCTRM FIAALFTIAKTWNPTPKCPS\MI DWIKKMWHIYT\MEYYAAIKK DEFMSFVGTWMNLETIILSKLL QRQKTKHRMFSLIGGN
26265	56633	A	26412	1	278	FRCSSYYYFKYFFCFFLFSLLLF *IFFLFLSLLFASLLFLASPLCVC YFFFIVVAQFLNSLFHFFSLFVL CFSGLEVSIDISSSVEILSSAMSIT LMGLSKAFLIT
26266	56634	A	26413	181	742	PLLKSGCISFLLLRLLVKLYRFL VRRNNSTFNQVVLKRLFMSRT NRPPLSLSWMIQNIKLPDRENR KAVAVGTITDDVRVQEVPKLK VCALRMTSQARSGILGAGGKIL TFDQLAPDAPKGCGTVLLSGPR KG*EVYRHFGKAPGTPYSHTKP YIRSKGRKFERTRGRLASRGYK NYRSYPLIKDCL
26267	56635	A	26414	368	675	SLSTLLSSRDCPLATISKQLRVL ARGCVVNNCFCKHLLNTCSLA GTVPG*GASSGRQKFKLLAKFK VLARLCSSGGSRGEPFSCLFLFL GATGILRLMASSS
26268	56636	A	26415	40	355	LLGNPSPVVKGRPCRHDGSEI/A PRVYFRGCS*SSHSWVSHFLSA PSHPRMLPTSRHRPPLRPLT*ER RGKRRDD*PLHHP*P/CWSTCSP STSARATPTPPSGSGW

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26269	56637	A	26416	347	725	EAKRRRPLSTLMEKRCFQPLWT RPSRKKPRGRTWRPPALNPTRI AGPPSPPAVSPGFGPIPP*SISCFP KGPGFSMGFLRLRCFSAVQKVL APGSPA*PCLSCGPFRTALGDL ARTPEKLCWLERS
26270	56638	A	26417	525	708	IVAELIQHHQLPCSHPLSGGKIK DQQVVFLSLSP*SSHNKTLY*AP KTNQRPQDYPEGCNA
26271	56639	C	26418	1	1050	
26272	56640	A	26419	934	1708	PQRGVWVLSVILHFPWLGSGPL PNSAGD*AARYSWNQILKPDC* WKLSSAAGISFQRS*VNFHYGE FCPKIPSGMYESKLGSHTDKTP HFLPAQKTRSTPSPATAPLPGAT SPRPPRGRRRRRRCPEQQPPPPL QAGPTAAARHRQDPLPRFSPLC FHSHPRASGAGSRPAPARVSPW TRRPAAPVSSGRGRLAPKRSLS PRPPRPGQQGGRVPARRELPLA PRGLCVRLVYSLCSSLCGSLPSF SLGSLVFSSSDQG
26273	56641	A	26420	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCRR*PYSRGT
26274	56642	C	26421	4	90	
26275	56643	A	26422	216	305	ICWKYFCAG*CGKYFTLGPRSH SYRRSDY
26276	56644	A	26423	859	1248	CVISVFRASRKSKHNVIAVVFS YCSVSVGQRPAVP/QHQVLLQT QGISGYPGRAGTLTGLHPMQV CRCRR*PYSRGT**/REPS*LREG GSAPPKSVCWPVGACIKRLSSM SSSFSSFPFIKHAHACCRVLS
26277	56645	A	26424	132	548	SSGFSWGFFSGYQRCRESR/CD YPPPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEVWDHGPTR IVGLIISLGPRSHSYRRSDNQTG TTVPLVSSV
26278	56646	A	26425	382	697	YAVKQAKTTFEDMTGRRASLL LHKGYLEFELFLQTAAYQSGSP APQGTWSGTGSVCHCCSLAE*T PFRTTGACCGLMARTGHARAA SICPPDAVAPLSPSPNAWF
26279	56647	A	26426	167	412	SYVKYFPHQPAQKYFQQIHCAI GLHNAGYPGRAGTLTGLHPMQ VCRCRR*PYTILSLQEQTDVVSL N

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26280	56648	A	26427	3794	4021	RGLCAPLPPLTPCFSPPLRRRAA SHLAPPTPLPTPQTPTRTRALPS SPGLGRGA*RTVLPSAPPEVPLA WGCRRA
26281	56649	A	26428	65	564	PHPDSGPQ*LQ*PHPDSGPR*LQ *PHPDSGPR*LQ*LQ*PHPDSGP Q*LQ*PHPDSGPQ*LQ*PHPDSG PR*LQ*PHPDSGPR*LQ*PHPDS GPR*LQ*PHPDSGPR*LQ*LQ*P HPDSGPQ*SDSGPRGHR*LQ*L Q*PHPDSGPQ*LQ*PHPDSGPR* LQ*PHPDSGPR*LQ*PHPDSGPQ *LQ*PHPDSGPQ
26282	56650	A	26429	184	438	DPAVDLCDLSSRRLLFS*RYVL VMLFSISLVSFVFISVHVICNYPF ALFFVCASFCGGAGGLVEFVL MIVGDASAALLCMPRCEC
26283	56651	A	26430	524	1995	
26284	56652	A	26431	601	1058	LPSSGGRCRSPKTR*SACLVSGS PRTPAMIRSGAGQPLARSPPTPT PPFCRPLTRAPQASSMTWTGTS TTTWTLCAMRTDCTGLPSTSPT WCFCTRSSSWPAATSGSNSRAP ARSWSTLCLSC*SASTRPGPRGP CRRQWWRRATPSRPSAR
26285	56653	A	26432	1	371	
26286	56654	A	26433	71	335	
26287	56655	A	26434	2	416	
26288	56656	A	26435	60	370	
26289	56657	A	26436	466	1454	PCVFQIGPRRIHTVRVRGGNKK YRALRLDVGNFSWGSECE*GPL GVGGKTHLNGFKIHRARPALIF LNSAA*EIGAGKDCGLPNITRN VG*GVVEDELMPHGL*RLRVPF ISP*GPHGAEEPGGVCQGHLSSS LLDAKFLL*AGCTRKTRIIDVV YNASNNELVRTKTLVKNCIVLI DSTPYRQWYESHYALALGRKK GAKLVRVTSL*GLWGGQPDSS LLVMKTLSSSATEGREMRAF*A EEGQHWGVQGSRKLPGPAFLP* AHIFVSPFQTPEEEEILNKKRSK KIQKKYDERKKNAKISSLLEEQ FQQGKLLGEKADELEVGSRRD

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26290	56658	A	26437	2	787	SQWLKLPSPLPHAGISRY\NWD QAP*KTGGPRESPYHKKREVM KLGRPSCPN/NPKIGPPAGIQHSP VCRGGYQEIPVPLRLDRGEFLP GGSECCTS*NKGSSIVVLQCHL NNGAGFVPKTPGWKEFCIVASS DQQQPYRPVVTSSHLCACPLGP QRKGAQAGLLEERRDF*TKKRS \KKLRKEI*LKRKKNCQNSAVL PGREQFPARGKLSCRA/SRFQGP GQLWAEQDGFCA*EGQKSLEF LSLGKSKARKGQIKSFVLSSPM
26291	56659	A	26438	62	872	ANWTEPDDTKTMWRLSVPLDR SPQTQNCTGEPLMPTGRQELPQ RGPEPMEAPAPARPQSRRVPAA GPVARQPHMRPPHSKQGEKQK MPGSRWPGQRGRGRWGSPLES A**TRKIFTGIPILPLLPGTPGRP APEEGMQSADKNRVKRRGGTQ RNSALALEFCELLFVSSKWFCA LPSTLRLKALSAAVALLAGDPE FGVRNVWVWVAGGVRCKRVA HRTTEAGAFFPDWFVWVFAAT KRGDGETSGCEHSEPVSGSSGG SPPRGQYLPGM
26292	56660	B	26439	1	606	
26293	56661	B	26440	48	381	
26294	56662	A	26441	16	209	
26295	56663	B	26442	466	1275	
26296	56664	A	26443	2	252	
26297	56665	A	26444	95	266	
26298	56666	A	26445	119	343	CTLRQESKLSRGDLTAPPVSSPR GHRSSKKGGNT*LGSMQL*AES CRAEPPRPALLCPGRSVSACQW GPEGPFF
26299	56667	A	26446	1	383	NTGLGRGKAMTPSMSCRISML LQRPGGVLVGWDPDAAHPVGT *RHSVAQHN*MPW*GAEGMGQ PC*WHGMGTSDGPGLSDSERPE LS/HADSEGRVSKAKQSELAGP GQKR*GQKPPKGYRFQERTQR
26300	56668	B	26447	430	540	
26301	56669	A	26448	111	591	PGAPSSHSGPRLLAWEPIVLAP VASLGLGEAEDCSFLGRKAGV GPRHPR/ARRVHGSGSRETCRG *QEPRPMLREPVCSAFLRTVKK LSGRVFPPLAVKQVLSAAPAVP ALLRTAPKTPWDGPESAESQPP SLGPAVVLDISDRRKQETIKAT GGPGRLRR

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26302	56670	A	26449	1041	1410	QEERGKVEE*ELEGRRREEKRR GRGRRGSGLEEGRRRRRRGGG DETKDKR*RKRGGHRKEKKEE RRRRRRGGGAAKKEEEEDRLP TRAFSCVEQQSASKSPLVELHP GPIPQGPPLAAAGAC
26303	56671	A	26450	288	424	KRPAEGAPNP*GRPGIRPQA*K RPAEGAPNPRGPRRKEGRSGAK GSLDTGDGGEAWWAGSPHPS WP
26304	56672	A	26451	111	540	LPLALSNPKQEVVSGRGGQVDS QAGLTMTGRAVCCLQLCLNAS GAGDAEAMSAGPPGPGPARAD TEQLPSPSLPQVS*HWRGSASTS ATRTWPLRRRCSSMARSTCRAS ASASAGPWPWPGAPVPWRHSA EPSCSQLPGPSA
26305	56673	B	26452	57	558	
26306	56674	A	26453	804	1524	ARETSHGDFLHFPLIWLFSLKG NVPAARINIMNWNQGLISHVGE GNVNRKHDVIGFNFPWNCLFN VSDLVTMIGSPRQRNHFGLVM VLTGIHTFHRHVGHCRCGPWS NQASHQKGDDLEHEQNPTNNA QLLGAHVFYNCPRPFLRPPFFFS P*NKCFRGELFAPSSHHSPSFLA SFLGAAKLQRCWSAARMGPGR KAPARIPPAQPARVPPMPGAVI VAAPPPVDAPIVRICVHVCLHH
26307	56675	A	26454	2	330	SCSRSGTALGVPVLAGPVRSAL TYLPAHSAGQRHQHDAGPTRG LGAI*DLPPVVTPGEQPSPCRGQ DQVPIVAAGE/PRCAPSLGSPPG LE/PVSLSSMSSPPRPPSCPLSG
26308	56676	B	26455	1	969	
26309	56677	A	26456	43	568	RSRLVFPLYFHASQGPGTASRE VPGGWAWGPVAQRINGICLLH STGPEAPSTMPPPTRLCGGPCGP ALPFSSQLAARGNPRSLPAAQL RALLSKISPPVVTPREQPSPCRG QDQGADCGKQVNKMCSQAWG SPPGLELCPCHQ*AGPPRPPSCP LSG*FVLRTGAPGAAPPSGTV
26310	56678	A	26457	1	456	HEDAASSFQADVSLGNDAAVP LSGRGGINTYIPLIIPGFPYPTAA TTAAAFRGAHLRGRGRTVYGA VRAVPPTAIPAY\PGVDMQPTD MHSLLLQPQPPLLQPLQPLTVT VMAGCTQPTPTMPLPLPLAME LALWRVYTEVATADLPPTEVT

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26311	56679	A	26458	609	1031	VCKSYPGHQGSSCLPDGQIQLW LHGYGQEFCGQETHPFLDG*RG AESL*GHNSGHDQWCLGDGCC WGWLLTYERHEQLPAELEAPG GWGKDGDSRGTESTC*EAGAG AGPAHPAPPAPAAEGEPDLFQL PGQGCSRIPCG
26312	56680	A	26459	1	393	
26313	56681	A	26460	357	843	QTEGGAQTDGQQSQTQSSENSE SKSTPEDNKICG*KPDHK*TFLF YQEISISI*RCACFPPFSRCMQGF GFVTFEKCNFMFPNVVHFFPAL FSPCYDMH*SSLSSNSLKCLPSI VVTVHLLLNAS*NFCHILGLPL VPGFPYPTAATTAAAFRGAHLR VFV
26314	56682	A	26461	3	1172	GRAHGEAAADGGGGMQNEPL TPGYHGFPARDSQGNQEPTTTP DAMVQPFTTIPFPPPP*NGIPTEY GVPHTQDYAGQTG\EHNLTLY GSTQAHGEQS\SNSPSTQNGSLT QTEGGAQT\DGQQSQTQSSENS ESKSYPRNGLHVSYYFLSGFRD P\DFRQMFG\QFGKILDVGIIFN* RGSKVNNATARVMTNKKMVT PYANGWKLSPVVGAVYGPELY AASS\FQADVSLGNDAAVPLSG RGGINTYIPLIIPGFPYPTAATTA AAFRGAHLRGRGRTVYGAVRA VPPTAIPAYPGV/DLPGTDFTVL TSMVDMQPTDMHSLLLQPQPP LLQPLQPLTVTVMAGCTQPTPT MPLPLPLAMELALWRVYTEVA TADLPPTEVTVKPLQMGQPPSS
26315	56683	A	26462	1196	1459	KQCQRRCLETEVWKLSKLQIST KASNRQDRSTFSAPPRKSQLM W*TSLLSYFQKLPQSPQPSATT ALISQQPSTLNPQPWPGSCPGG
26316	56684	A	26463	2234	2702	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTACRRAFGTKSIG*GPTI PESSRWQQKGGVSGDGRSSCR RAVAPLEPVPRAPEAA\ARPRPP SHGRDPPPGPDPPPLRTPASAM DKSAGTSCRLSPLKALGSARAE QTMGRPAAERSYPLLRAQYSSR
26317	56685	A	26464	70	398	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTACRRAFGTKSIG*GPTI PESSRWQQKGGVSGDGRSSCR RAVAPLEPVPRAPEAA\ARPRPP SHGRDPPPGPDPPPLRTPAS

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26318	56686	B	26465	18	123	
26319	56687	A	26466	19	347	
26320	56688	A	26467	3	746	SRKLLSKSVP*LNP*SR
26321	56689	A	26468	1705	2031	CDAPGDPQPGLRDISWLGTTDR SASPQRLAAAALTAGNGRRCSS GPRRRPPP*PLARPRQRRQPPER QPVVWPPAFPARWAEHTCPLA PWQPRSPTTPSQPAAVTARAS
26322	56690	A	26469	1	420	
26323	56691	A	26470	65	330	RDCEARCARGPFWSWLSPRRK GKRQKSQLISQRLERHFLSGKN RQKRPSKMAGPDGAAPLEPGA VAAPMGPKSSRGSPGRAGKAA ETS*SPGRAGKAAETS
26324	56692	A	26471	327	981	ASYQKFFQLLPDCNLAPSPHPQ VPATPSTSWGHLSKPPGAFRKR HSSSRCPKAGHQWGGGQRNTP TAAHFRRLSAGSLQLCPQLRVS PLTTGSLPPRSREPPRTPAPPSPY PNCRPLPKSTRTPSVGWSGPPSC GTRLQSHPQEAPAG*GSVRRPF LGP*RMPS*ALL*KHTGGL*GPP HPPMPTMCQPKQASKLQLLNC PQPSPSQGAGATMGNVG
26325	56693	A	26472	336	923	LKNIFLSLPRSINIRFATLLDTPG VENLVIACLQKHS*PYF*GS*NI CLSFQDGTLYHKMHAVCLKCL *KPSLLSLL*DIEYIRSHYNIEDFI YFSHHQREEHGHMHHFALNPIF RHYTKFFLKVYL*SCTQTSVLS LSDILSPKI*IAVFQFQNPYAHSL TSALHYLVPVRPRLLPGLDDQC PGHNTFPVVSIN
26326	56694	A	26473	97	298	DNLTLLPRLECGGMIMAHCSLN LTFSSDPAASAS*VAGTTGT*H HAWIFVFLCNWLRNRGVTVKK RS

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26327	56695	A	26474	1958	3269	KFTMSILKIHARELFDSRGNPTV EVDLFTSEGLFRAAVPSGASTGI YEVLELQDNDKTRYMGKGVSK PVEPINKTIAPVLVSKKLNVTEQ EKIDKLMIEMDGTENKSKFGAN AILGVSLAACKASAVEKGVPLY HHIADLSGNSKVILPVPVFNVIN GSSHAVTKLAMQEFMVLPVGA ANFREAMPIGAEVYHSLKNVIK EKYGKDATGVGDGGAFAPNIL ENKEGLELLKTAIGKAGYTDK VIVSMDVEASEFFRSGKYDLEF KFLDDPTRYISPDCLADLYKSFI KNYPVVSTEDPFDQDDWGAW QKFTASAGIQVVEDDLRVTNPK RTASAVNEKKCNCLLLKVNQIR SVTESLQACKLAQANGWCVM VPHHSGETENTFITDLVVGL*PG QLKTGAPC*SERLAKYNQLLRI EEELGSKAKFAGRNFRNPPAK
26328	56696	A	26475	2	684	HSGSSLLHFPILLINRKGFSPTG MISLMCNRIVLSTHAKLQSCTP SNLPSQLPIGLSMSTPTKYRKLS FPGKTSQNITVPDSIVSPTFKETL EFISKGGSSTCIVSPGPA*SLSNA VSSSSMSSSLSNATNTPQSSSH* KSCFPWYTPSVKP*PRPSSSNST PKNIPETVLSANRGPLKRTTPG NFSSPDLSCTFTGQPPSIWRPLL KLVSGFKQAEPLLTIGNCQK
26329	56697	A	26476	1284	2339	APPSARGACAASRRAAVPALPT PPSVCSGSHMSTYWPAAPR**T PGSSTAASPSPAASRAPRAASPV LTASPPLPAASPSPAASHAPPAA SPVLTASPPLPAASPSPAASPAP PAASPVLTASPPLPAASPALAAS PVHTASPPVHVASPPVHTASPP VHVASPPVHTASPHVHVASPPV HTASPHVHVASPPVHTASPPVH VASPPVHVASPPVHIASPPVHT ASPHVHVASPPVHTASPPVHVA SPPVHTASPHVHVASPPVHTAS PPVHTASPPVHVASPPVHVAYP PVHVASPPVHVASPPVHVASPP VSCSGDSTSDCFPPQPGAVFPHS LAPSLGGWSHLVAALP

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26330	56698	A	26477	131	544	TGRPLPRPLKTQEIPSGCGVMG RATPGTSGLGDSVRRVRGAIPA PRSSLGRGFTCV*LTTGAQLAPS LVPAAPRLPAALMDIQPEPLAS AAPAATGPAQVTAATPLTTASA TPLTTETACSLGSSAASPLAPRA HCV
26331	56699	A	26478	1440	1877	PFQNLFQRNERTSCLCCLCMGA TWASLRALCCSPSP*HGWISW WWSTPTPFANGSVTSCSALTRS RWRPTWSEASGLWHAPAALL WKLRPLTPCFRSPISLSDLDLTS HHQQGAPTMHTCLGVGSSSWE LQAIFVLSYWFSPLHC
26332	56700	A	26479	56	345	ITWHLGLMMLSRSLGL*SGISFI NFPM\K*EMIPY*KLS*IQNLFQF PKVRPKGSQFGQVKH
26333	56701	A	26480	392	634	
26334	56702	A	26481	416	601	FLITDPRIWKASSDPSAKLFTFP SGFLM*AGTWMKLETIVLSKLT QEQKTKHCMFSLISGS
26335	56703	C	26482	34	279	
26336	56704	A	26483	173	307	
26337	56705	A	26484	196	527	SAVAAACSRPEEDAMELVLVF LCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFS VGILLILSRRCKCSFNQKPSGPR R*GSPGGRTSSPPMQQKPQKAE
26338	56706	A	26485	597	797	PSENELKALGYTSSAWKRFSEQ QWGLSLGSSAPSWRLPW*GDW ELPGEPGGDSSHRPFPGPIPRAP
26339	56707	A	26486	3	184	
26340	56708	A	26487	256	635	GCVAPQIREQHAQSTENAAKPT RRIHSRQSEKPGRWRHGWRAG GWRRSKRAPARHRPRCPAVCP RDGEDCSREAAGA*GLSGSSAC PTSSTGASCCFCVPGQLNSVGF AVLGSKVLWTPGESPFCQ
26341	56709	A	26488	1	378	
26342	56710	A	26489	1	571	

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26343	56711	A	26490	105	849	RRQDSGQSPAWPAGALLLTLLT HCAVPGSWAQSVLTQAPSASG TPGQRVTISCSGSSSNIGNNPVN WYQQLPGTAPKLLIYRNNQRPS GVPDRFSGSKSGTSASLAISGLQ SEDEAQYYCAAWDDSLNGSYV FGTGTKVTVLGQPKANPTVTLF PPSSEELQANKATLVCLISDFYP GAVTVAWKADGSPVKAG\VET NKPSKQSNNKYAASSYLSLTPE QWKSHRSYSCQVTHEGSTVEK TVAPTECS
26344	56712	A	26491	129	1191	RSRPQCLGPQGRRVTISCTGSSS DIGAGYDVHWYQQLPGTAPKL LIFRNSNRPSGVPDRFSGSKSGT SASLGHHWGSRVEDEADYYLP VPIDSSLSGSTVLQARGELRQEP TSSSARRSMKKGRDLGEAQLQ LRVEKTGLRTISSMAWSPLFLT LITHCAGSWAQSVLTQPPSVSE APRQRVTISCSGSSSNIGNNAVN WYQQLPGKAPKLLIYYDDLLPS GVSDRFSGSKSGTSASLAISGLQ SEDEADYYCAAWDDSLNGYVF GAGTKVTVLGQPKAAPSATLF WPSFEDASDDEAEL*CAIRDYY PKAVMVA*KTNITPLKQGKDTP SPSLLTPSSDEVKSYKNLLPGFP
26345	56713	A	26492	283	840	TLPAGFTDVISIHKTGENFCLIC GINGRFAVHCITLEEAKYKLCK VRKIWFHDAHTIHYLDSFVKVN DTV*TGKITDFIKFDTGNLGRIG VITNRKKHRGSFDVVHVKDAN GNRFAPWLSNIFVTGKCNKPWI SLPRGKGIRLTIAFHSDKWFCSD ISVQNLCKRFSQGDTGIKNSEA RRCSNLQV
26346	56714	A	26493	1	843	MARGPKKHLKRVAAPKHWML DKLTGVFAPRPSTGPHKWRECL PFIIF\LRNRLKYALTGDEVKKIC MQRFIKIDGQVR\TDITYPAGFM DVISIDKTGENFRLI*LTPKGSAF AV\HRITPEEGQVQSCAK**RYI VGTKRNPFI*VTHDAR\TIR\YPR NPLIQGEMDTPFQIEFKKTWPR LT*FPSKVPNTG*PCVMVTWRC LTLGRI\GVIT\NRERHP\GSFNV VHVKD\ANVNRFA\TRLSNIFVI GKGN\KPWISLPRGKGIRLTIAE ERDKRLAAKQSSG

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26347	56715	A	26494	375	1327	QPYFPMETVMTLEGGQKPVME SYTLHYLPCLLCLPWRNPESSE WQRQLLDFPLASAPGSGLTQH MAAPKSGQNLEAKPKGQASLV LSSRKICGVLSGACAACPGGPA R*VDPAIPFPLAGEAGLEGRPRP QRCAAKWQSRDLIPGLPGSTGL PFPPY/PPCSPGALLSQSPPQAAG SLLARTPHAQGCPPPRLRPARIL PWPASSARRYTPQPSRKGTQRT PLFSLNLLETTTASYSLDFLLTA PEGFSPLFTASQEHDQNQQEHD FLLQDEGLRSPVKTRARLPLGL HGDKVEKAGPWSLGARESNLC SATSQRSAVAAGVPRAQPLPPK GKGWLDPPTWQGRRDTQRTLR SIHHRFYGYSARGWPGPLALLQ GFVRSLELPCAGSDQNRGQRLK GNPGAAFAIPKTLDFSKAGKED KGGNGVCTTPSQAFDPLPRSSQ SPLGNMAVSGSSSSGSWKSSGT QEKKSLNQKRKVDEAEKKEEK EKKKEPEPNFQLLDNPARVMP AQLKVLTMPETCRYQPFKPLSI GGIIILKDTSEDIEELVEPVAAH GPKIEEEEQEPEPPEPFEYIDD
26348	56716	B	26495	1919	2074	
26349	56717	A	26496	179	431	PPTSLIRVSCTSTSTSLCTSWLCS SLSWLYSWAGPFFSGKMTASC RGSGQINREIVLMLLLRS*VFVV ISPLEGGSETSPFMDL
26350	56718	A	26497	37	199	DGLPGLALGLDAQASWSASVV TGHRPPAPPGLALGGCHGPAAP P*SGPAGSPCH
26351	56719	A	26498	3	224	TGHRPPAPPGLALGGCHGPAAP P*SGPAGSPCH*TAPRGAGTPLP GSRRTGTSPWPHPPGLPHIPDVT GGHRH
26352	56720	A	26499	151	403	MPRHRRSASVVTGHRPPAPPGL ALGGCHGPAAPP*SGPAGSPCH *TAPRGAGTPLPGSRRTGTSPW PHPPGLPHIPDVTGGHRH

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26353	56721	A	26500	1	465	VSPKLLPSYASRPYLVPNALSSP SVPPALSASSAPPRPATRRRPPP RGLSASWPLRRRSRQDAGAGS RRLRERQNRGRRRSDLAPTLGA GLRRDRPGRQPRPGKALAPFAV PRPRTNFRGRS*KSGSQRTRTPP RREICRTHSRDRPRKLVRGRGT ANGARALPGRGWRPGRSRRSP APSVGARSERRRPRFWRSLRRR EPAPASCRLRLLSGHEADRPRG GGLRRVAGRGGAEEAESAGGT LGDERALGTR
26354	56722	A	26501	1	1344	
26355	56723	A	26502	548	689	LGKFAPGLTASKAEATAAELCL KYPLEICTFL*GCVCVCVCVCV CVL
26356	56724	A	26503	154	476	TLA*AAAASTSCSPRPPPPSPAS TTTRWRAPWRTR*EPPESLCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVLCMTVDL
26357	56725	A	26504	920	1420	TLA*AAAASTSCSPRPPPPSPAS TTTRWRAPWRTR*EPPESLCTG MRSWPSGMTACTQTPSTAPPSP HPPSLSDSSALCSSASVRRMWI MKRLKPSMMHVLCMTVDL*LI PTSTPTT*PSELLAPSPNSPIDTT QMSGLTATSVPKKLAFSWQQL CYISLIQPLSL
26358	56726	A	26505	1118	1403	AGWDPSFLISFSGLSNAISSSSSS LSSQ*ESNASA*YSSATSGSSGIS WYPRSDVASSTIDSSSWRSMEG IG*DSGRFSKVGSSDSSSLPCHL SS
26359	56727	C	26506	29	379	
26360	56728	A	26507	3	948	GVSLCCPGWSAVVGSWLTAAS TFRAQAILSSSWAYREPPVRVG RRPQPPLLLTRAQGRVISSSFRH LHDFVWRTAGKESTSGANETG PLPERGRRPGGRGPGSRSPRSH AVQREGAAGSVPAAGRDGGRA GHDVPHEGQRAEAAAGEAGGE FPLLLSDRRGRARRSPAAGALQ SRPGRARHLLHQLH*GP*EEVS L*VQQRGAVSGVDGGSASGQL RVHAEKAHLLQERNPEG*RAK DPLGTVSALSEEARFQLRWLAG VSAGHGGQRAAGRDWPCPAM NRLAMPGSVLFWFLVFGSGFH CVAQARVQWCHSSL

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26361	56729	A	26508	31	202	ILITYIIKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQFL
26362	56730	A	26509	471	1716	FKRGQYGQLLRPRFHHGQILYA RRQGADAAGDSDFCTEWPAAL DSDEKCEKHFPIEIDSTDYV\HH GPSVRNPRARVVVLRWLRITLH ESAAVEGLAVFPPARRHREPEY SIPSPSQAFTPAVLATRVTGQLG GHTQIQNPTVAPTILGNTPTFHL TCFRIFSLPRHLFPKDKWRTLG APFLRTLLLVGTESSVHLSGIDP DLLVFEQSPTYLNTRSSSNRWD RLRILKAMNLDKQTTTINGMLP STEAPSSTTHQDLVVNTNSTSY SKELTTDFWARFTSLNESITTKI NKVSPSTDFISNPDNKTISPFFEP IDTKLSHMPVPPGLNSSKQLLN KTKGYNSRNHTSANEDEVSVT SKTWLVSVALCTSVIFLGCCIVI LASGCCGKQQGQYKPGQRKSG SLQIKNRNHMKENSS
26363	56731	A	26510	410	867	LLTLSRTTPLMSLGFPGIPKMIN RPRQSSPIKLQNSSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRVWTAS*SFICLSDPQKVQ IQSAPNRKAWCLVILVVVSHSS TPFSWQKVMKWIKKISFRVFAA GQGLLGGYSNPRYSFSF
26364	56732	A	26511	135	756	VITILTPMLADRTRRIERPPKKK GTTSLGQRKWLLTQDWPSVYP VA\HPFKPSAVP\LPVPNGLSSK KRACPWQ*EGN\LELLKI\PNFS GF*LPVGN*KSTCEALKDF/CAL SGPAALGQWTRKC*GR/PFSI*I* QH*LWFHQDHPVRNPRARVSS LKSKAFSV*I*HDHAKKTLITLV GERYCKTPDVLTIKQNRWPLRS QITIMPVYL

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26365	56733	A	26512	161	2150	YLDAEKMGQKASQQLALKDSK EVPVVCEVVSEAIVHAAQKLKE YLGFEYPPSKLCPAANTLNEIFL IHFITFCQEKGVDEWLTTTKMT KHQAFLFGADWIWTFWGSNKQ IKLQLAVQTLQMSSPPPVESKP CDLSNPESRVEESSWKKSRFDK LEEFCNLIGEDCLGLFIIFGMPG KPKDIRGVVLDSVKSQMVRSH LPGGKAVAQFVLETEDCVFIKE LLRNCLSKKDGLREGGASPGSL RLAAPGPPLTLNAACPLRLAVL AAMAAAALPAWLSLQSRARTL RAFSTAVYSATPVPTPSLRVDD LHLTEIVGMLDSVLTPEDSSGK YRFISGEVLCRITGCFTGVRVEA KDLFGGCCSNPNEVMVTWIKVI VEKEVWLYLRYILKALPPRTEK MAVDQDWPSVYPVAAPFKPSA VPLPVRMGYPVKKGVPMAKEG NLELLKIPNFLHLTPVAIKKHCE ALKDFCTEWPAALDSDEKCEK HFPIEIDSTDYVSSGPSVRNPRA RVVVLRVKLSSLNLDDHAKKK LIKLVGERYCKTTDVLTIKTDR CPLRRQNYDYAVYLLTVLYHE SWEYWKEWGKK*D*SRHGKSI YGENSSSERKYPGKRFSR*KLL RKNMGN*LKKSSLGTKEIEEYK KSVVSLKNEEENENSISQYKES
26366	56734	A	26513	3	1186	PASTMSIRVTQKSYKVSTSGPW FFSSCSYLSGPSAHISSLSFSRAG SSSFQGGLGRGYGGASGMEVIT AVMVNQSLLSPFIDKVQFLEQQ NKMLENKWSLLQQQKMAQSN LDNMFESYINNLRWQLETLGR KKLKLEAELGNMQGLVEDFKN KYEDEINKYTEMENEFVLIKKD VDEAYMNKVELEYRLEGPTDEI NFLRKLYEQEIRELQSQILDMS VVLSMDNSHSLDMDSIIAEVKV QYEEIANRSWAEAERMYQN*Y AKLSQLEAALQRAKQDMALQL HEYQELMNFKLAQDIVITTYRK LLESEGSWLESGMQSMSIHMK TTSGYAGSLSSAYGGLTSPSLS YSLGSSFGSGAGSSSFSHTSSTR AAVVKKIEAQNGKLVSKSSDV
26367	56735	B	26514	361	1215	

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26368	56736	A	26515	230	561	VRTRHLFCEAAAEETPVFTMA NEKPTEEVKTENNNHINLKVAG QDGSVVQFKIKRQTPLSKLMK AYCEPRGLSVKQIRFRFGGQPIS GTQRNLS*KKESVDAASFIVVL
26369	56737	A	26516	1242	1415	NSPSDSSLVWAWRRPQSRSWS ERGGGANNRGGGRLLGNSVFG RK*LPHRRVSRVPNTK
26370	56738	B	26517	1	585	
26371	56739	B	26518	258	1081	
26372	56740	A	26519	42	275	TFAWSEEGTSPPSIQSSWDPRCP HRNTPAQTGKPPKRAWPRHPV HH*EPHGDQQDDGPAVSPP*SY SQYPWPEGLDV
26373	56741	A	26520	646	1905	
26374	56742	A	26521	6510	7361	
26375	56743	A	26522	1	879	DCQDKVPRRKEPSMCSGLLRV KSWVSLQTYWKPRATQGVYV LPLTEERMVVLGASRVGKSSIV SRFLNGRFEDQYTPTIEDFHRK VYNIRGDMYQLDILDTSGNHPF PAMRRLSILTGEAHWCLGWGG RARAWVRSVLGT*QILEVKSCL KNKTKEAAELPMVICGNKNDH GELCRQVPTTEAELLVSGDENC AYFEVSAKKNTNVDEMFYVLF SMAKLPHEMSPALHRKISVQY GDAFHPRPFCMRRVKEMDAYG MVSPFARRPSVNSDLKYIKAKV LREGQARERDKCTIQ
26376	56744	A	26523	2	478	
26377	56745	A	26524	120	1167	GHVGHMCTGQHMASAYVGRV NVLRKEVDRACFGEKAKQ*VG S*EELWAIWGQGREVCLGIEEA GAIISTRHCNSQNGVRVWAPYL WALEAAPV*VQDRSSPGSQACS LPSPCALTMGTGIMPLYQEAK WKPRQRPGTSGGTVSSEPHC*D AGSGCWLCQPGLREVAHVSAE ITYTSKHSVEVQVNVMSENILT GTSGSDSVDWSSKGRGYTAAS LLRAEDAPGPGPKVLEVPPVVV RCPFYFSLGGRWQRSGHLT*LE TKWRNGDIVQPVLNPGKSRGH QQQVPLLTGDA*EAGALHGFV HGGKKEAPWPLHSCPLAHCCFS GRYNRPGAVAHACNPSTLGDG
26378	56746	A	26525	225	438	
26379	56747	A	26526	216	364	

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26380	56748	A	26527	2	397	SCCSDWSAMA*SQLTAISASWV QAMLLPRRPE*LGGSNPEGTG* SERRLCHYA/HSLGDRARIHLH KKGRQEGSKEMSRAQTRRVW HATMETEQKQNYGRL*CCSPST NTRRRTSMRKNKAIAREIERYS KGI
26381	56749	A	26528	312	1061	QQTLYSFGVSFYFSSYCLIFSHG CSSSSICRRARLYHWAAPFRPP GRKRRDCTGQRKTSAGEPEIPP PLHHHHHHYSHHHHRHRHHH HHHHGLQRSSKNFLLWPE*ILF CGSRRLGRAALFLLRSFSHPAK QGAESLLGKQS*KHLASTQCGP RGRGS*EKWPRAQLGRKQPSES AAGAAGLAHGPQDSLVLERAG EK*SGLRGEGNRPFGGSSSLGG HPLLQRSPAESSPAGTGVRTSH LEGRPASFR
26382	56750	A	26529	161	453	SSSLPCSPSSCPHTSFFLDARQEP RTCRVVGLKEL*QKQGLPHCR* QEREKSCSPSGSPDLGAPQPRA VTPSLGLCSSWHLQASRRHCTP RCPQWKR
26383	56751	A	26530	301	630	RWKPKIRGSEGSAS*PQGR*LLP SGRRG\ATGSAESTLPKAESSAG DGPVPYSQGSSSLIMPRPNSVA ATSSTKLEDLSYLDGQRNAPLR TSIRLPWHNTAGGRAQEVKA
26384	56752	A	26531	1	1394	
26385	56753	A	26532	240	1150	LLLHVPSPSPASTGPPSCGPCWP PRSAPAAGRGSSSGCLAGEDPA TTHKSAGTGECHRGPVGHCGQ AHTGPSYPSGPPASCGPAASAV TRGQSCRSLTFRPGRHQIPGAE* QLPRGQGETGRTGLGHYLTLLS CSSRWPLPKSGDGSPSRWEYRD S*ERPGRRTAPRCCSRSTGLGD GLKKFPSSY*GP*KCAPSGCGG QAPWSAGGSTCPPDART*MPR ARARSWAHTGRPCFPRLLSIQA TP*RTGGRTCGFCLAS**GSRRG RPSSAESLPIPAPPGCGQH**PER SARLSWGGGMRGPR
26386	56754	A	26533	1463	1627	

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26387	56755	A	26534	1	1758	MHKYVRYSTVHNSEDMESTQ MSINDRLDKENIIHIHRGILCSH KKKQDHVLCKNIGEAGNHYPQ QRNTGTEKQIQCVLTYKWKLN NKNTWTQSEEQYAVGPVGGRI GRLTNNRHTQDSESWVRGVTA FWSRGANNALDIPAFIIKFSEGR GSLHTHDGPPGPTSSLKLSFSHS FDSTGLCRPHDLVLGLIIPTMVN ITSQLDWLEDAQMAGEALFLE GKLTTRKDIYTENPSLHHHHQR PKVDKTTKMGKKQNRKTGNS KTQSASPPPKERSSSPATEQSW MENDFDELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERVSAMED EMNEMKREGKFRDKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DVENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKGRVTLKGKPIRLTADLS AETLQARR/DVGANIQHS*RKE FSTQNFISSQTKLHK*RRNKILY RQANAERFCHHQACPKRAPEG SAKHGKEQPVPAAAKSCQNV
26388	56756	A	26535	620	886	INGVILSKPPLPPISTTPIAGALLL PLTKEQRGDF*KPSRNMRTSCW KTPESRANFLKFRPRSHCLTRM GSSCLLPSKTCLSSSSTFHH
26389	56757	A	26536	237	415	RCLQRPSAGTAGHPPSAGRPPL AAGLAG*RARHRSDLPGSAASS QESWCLRAALPEAPA
26390	56758	A	26537	373	691	
26391	56759	A	26538	2	233	
26392	56760	A	26539	5	68	ALQWEEKHEL*EQSLHRKPGG
26393	56761	A	26540	184	434	GGRRGCTVGEAAVTQSLSLCS HEGRAIRHQRDSASIVLLDQ*Y TRHPVLDKLLAWI*ALAEDKAT LGSAIAAEWKITPAFSFP
26394	56762	A	26541	466	683	GRPHSLPHPHADSSELTTDCS* WRWIFKHKTDHIRHQRVHTGQ KPFKC*Q*GKAFRHSFDVTKHQ RTDAVGLHQTCCLGGVLLWGA HWRGHPSYSLWSAHCCQHGGE GASGGGLSLHLDRLSLDAAGRP QPVLPPTGQNILVGPLPQISLCS RSLCVLRLDGLSQLSPGEEGSH SQKWTSQEVKLFRSRHQSTSDV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26395	56763	A	26542	194	558	GCDRPSRPRPGAPRPPAATASC PPRSCWPLVPSPHCP*PCRKRRY PGERRTSPAPPVPPGPGRPAG*T PPCELRPSSTHVALLGLALPGSE GTGLRTSVRARDRLHRRTRERA AAGTAPGP
26396	56764	A	26543	1	248	MVAIHNADDAKCWGDVEQLE LSFTAALPVLPHPSLPGERPLQE AVAFLCWLLVDVLLKATVSKV GGGSALASVARVMKAQAFSPL LRILHKASTSSFRARKDSAHTPS CLLTPSGPERAGPLTQDSCQPSP HDSFRAPALLEPSSALSTAVASL RRREERLEPEQRVGELGSLGER QHEPSDNHDFQPKSKQEQLQK TLQPSGGPHCSSLLLMVFWWK QWRKTEPLKAERTGYKEKEIST KCSSSPSGQLSQSSAAGPAWPE DARPEATWSATLLSFDPRCKND SIEEPCSVHISCTAYSDPLKIHNS YRECGLCPEVNLEVADPSSSSR ELWFRAGAQGAGAMQGVTEL RPPEFVKSRKPQVGSGHMGNC LSKGKRFLGHCQYKQGLPQRH QLQAEERESGMRHTTGGAYAV LTTGVSPWWIWIWERRWPCAF PGKNEEPAGKVPFPSELVLTLQ RC**CQMLGGCGAIGALIHCCS ACAASPFSPWRKAPPRGCCFSL LASGRCAPEGNCLKGGRRQRT CQCGSGYESTGF
26397	56765	A	26544	423	621	LPSRGAGLGTCSPPCLSLPSPPW APVRPEPPR*SPPPAPQRPVPSTT QGLNCAGAGHGTGRQLHR
26398	56766	A	26545	1162	2027	MTPEPEWSLS*VGNYKRTVKRI DDGHRLCSDLMNCLHERARGV SRADPTMAGAE*PAASLPCTGP QYGTVEKAWMAFMSEAERVS ELHLEVKASLMNDDFEKIKNW QKEAFHKQMMGGFKETKEAE DGFRKAQKPWAKKLKE
26399	56767	A	26546	1	504	

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26400	56768	A	26547	3	1215	QTMYFLTPILVAILCILVVWIFK NADRSMEKKKGEPRTRAEARP WVDEDLKDSSDLHQAGAGGN AVEGVDQSKVNGRATGFASKL DIGKRRREGELETGSYPPKTHA YALKKSGPWNPGTWQHRKIVR GLQFYTVFFPHSSVLAFLAPVID PSVASSSSLRSSTTDNELAELSE FADADEWQESEENVEHIPFSHN HYPEKEMVKRSQEFYELLNKR RSVRFISNEQVPMEVIDNVIRVT GTAPSGAHTEPWTFVVVKDPD VKHKIRKIIEEEEEEINYMKRMG HRWVTDLKLHRTNWIKEYLDT APILILIFKQVHGFAANGKKKV HYYNEISVSIACGILLAVF*NAG LVTVTTTPLNCGPRLRVLLGRP AHEKLLMLLPVGYPSKEATVP DLKRKPLDQIMV
26401	56769	A	26548	3	263	RPGEMACKYPLRCSGARVERL AKKKAHACLLWTATIKVITNSV KLRRSS*GNRLKPSILC*DMKA LRQYPMPLRAWLLPMVVWVM
26402	56770	A	26549	82	318	SGEAGKEEGTRMVRIRPEPKRS LLWTATIKVITNSVKLRRSS*GN RLKPSILC*DMKALRQYPMPLR AWLLPMVVRVMV
26403	56771	A	26550	91	714	SESLVLVWCGRVSCVLFCVCD VCVLVGGSGVAVRCFGGRGCG PRRVGRRWSCWCGWCGAVLIR RVCLAVMFGLALCVHPLLYPR TLLLRGQKVDRFKTNLSSGESL VTLVIFPAHGLARSRFLNLDVL FGVHFIAVEFWHAVGLIVNKQ VKGKILAKRINALIEHIKHSKSQ DSFLHCANEQRQT*QCAGPCM GPEPRQACLNTCIRS
26404	56772	A	26551	29	363	FAKMTNTKGKRRGTRYMFSRP FRKHGVVPLATYMRIYKKGDI VDIKGMGTVQKGMPHKCYHG KTGRVYNVTQHAVGIVVNKQV KGKILAKRINVRIEHI\KHSKSR DSFLKR

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26405	56773	A	26552	186	512	FHLSKHRAPPYPVTAPPRTSWG SLVKQVNESNGSRLLRTSLVHE DLEGVSVVSGMNCDSALARYII ILETLIIYLISPRCWIIDSSGACSG LAMYLPLLGDDGVLLCTPNFM AWRSNRTQFMMRSSSHMVDAS PRGRHMSPREEAFGYSSRASHM LLSLLAPPWPQLMGRGLGCQQ QERPQECVPLGMTRSPYSEIHF GSSRALGSSPGSCAHEVLGPSIL TVNPFIPGSSVHVWPSNGNETN KLPHTRAGSCGSATCSVKRWG PQKPRPLPKPPLVPQALLLVRG PAAAREEAVQPPKEEVTQRPGG HSSPGVFAHLKGPRSVVEIRME YGEE*PPGRCVTSSFGGWTASS LAAAGPLTSRRAWGTSGGFGR GRGFWGPQRLTEQVAEPQDPA LVCGSLLVSLPLLGQTCTEDPGI KGFTVRMLGPKTSWAQDPGED PRAREEPKWISL
26406	56774	A	26553	1	382	FRTSCRQLSAAPPPARSPLRPPG GG/EPAPGRTSRGHRPQM*SGT PAPRPPARSTVSPASPLPKPRAG RCGSRPRSACSTFRPC*SLASVS SAKTQGWKMWQPATERLQHF QTMLKSKLNVLTLKKEPLPAVI FHEPEAIELCTTTPLMKTRTHSG CKV
26407	56775	A	26554	797	1213	AWLKFLLGTRRFLRFSKYSFSID SARSLVPGRWPAPGRTSRGHRP QM*SGTPAPRPPARSTVSPASPL PKPRAGRCGSRPRSACR*GAPG SRGPAFPRRTPSVTRWALGLPW LQGLRTAFCWQILSRVTAATLP DKIH
26408	56776	A	26555	1002	1655	KEFCIYNRNPNACSYGVAVGV LAFLTCLLYLALDVYFPQISSVK DRKKAVLSDIGVSGEPHPAGTP CTESTEGCPGHRRRKDNPLNEG TDAARAAIAFSFFSIFTWVSTAT AHQPTLVPFPH*APGWVVFPAS AQP*ASPACRGRQPCITPGSEVA GAPSTLGGQGRHYMDPSQDSS MPYAPYVEPTGPDPAGMGGTY QQPANTFDTEPQGYQSQGY

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26409	56777	A	26556	262	628	QHFQTPWPWPLCAAAGTSAGT SHSGSSSGAFSSWPCWTAAEPA ARKRGRPAGSWSSPATGAPGR CRHRILSRGAGGSAGFVCSGLR GIGPLGI*LSGTFPGLTAGPETPA TERAPGASQHFR
26410	56778	A	26557	1098	1599	RIRKSHHCINTVTLGRGNSLGK DFVRESPGGDRLNVGQTHKHR GLGRFAQPHGTSAGTSHCGSSS GAFSSWPCWTAAEPAARKRGR PAGSWSSPATGAPGRCRHRILS RGAGGSAGFVCSGLAESGL*ES SSPGRSQG*PQGQRHPQPNGLP APPSTSVSVLVRISR
26411	56779	A	26558	440	698	IKLWAATFIKVCRLSFSCGMSIL *RCTGSKSCCCCCRRPLWAGPT SCAGGCGCCWGPGPPAELGPD TPAAEEAAEACCWDAAIFLA
26412	56780	A	26559	448	576	
26413	56781	A	26560	513	782	EIWWWAWTKWCGCWVVSCF HLCGRHC*GTCWSSETWR*MC GTSGTAPPCECWREGKDDCGR DRPMETHGCCSSFSISSPRAGKD ATTGT
26414	56782	A	26561	798	1505	FLRATSPSGHHFSYHLWIWISLR SFLCNECSESCCLLNSSMWQAP GLSHYSLLLIWLWLVFQTLNPR HLLHLLPSPLNVVDRLCSCQHH HHQ*CHHLHHNLH*NHSHHRH HHHQ*RLPLHYHLHQHHHHHQ NHCQQHHHRYHQHHYQHHDH HYRHHHPWLAGARALCDSND AGCPGSTGDGWRPYSADSDSL DALSFPRPLPFPDCQSLRGLASA VIQGYNWLVLTENHILFHLF

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26415	56783	A	26562	1	1073	MHATNSSSVPQEIQVEALCPLL TQPQKSPSITSAMLCQLKKPQPS RSKEREADPISCGPECQGNWDL CVEAATGLYGDGHLRDSSRTR VLMTTGTYRDLQGLEGRAGHV AELHVLPVWAIQDRGYVLWC WTASLHPRDVAREQGFPNDCT WALGCTLTAESTHTHSAALAR QAYSQLSKKPTLLNEPEHITEK KFINLARFEALNSRTWLGVLY WIAQIQDVPVTVESTTGQRAAR ISPREADRTLVKGQVQGIRQTVI MSVPGRKEGDKLKEVSDGREA ANQAGMKWGKECKSSSGTEN AMSGKEVGILQEEKGDWSHGV VRGWQEKWMTYNFWACGRG KNATCRLEMTRTSENDLKHNQ EGLWHGRERAMLGDTHTLAW REEEMEQKQALRIHSLYGKTSG QRALGSWWVERFMGMRSGSSS DCNGLVTEG*TLQSACIPEPTCS H*GSPAP*LHP*GAEKQSSTTEH SPCPGLPRQAERGAQPRVPPCP QDPADPCKFQWS
26416	56784	A	26563	1	387	MESTEIGPHIYEQFTLTKMTRKF NKEQLVLISLALLDSGHTSNSL AWPSCLIVSGVGSCRWVCGLT D/CQE*SLRPSQSAGVCRRSTPD PVCLGVTRGGCRTEKIAACSFL WKLRPRGAPARCQPELSCM
26417	56785	A	26564	47	472	LLRLHFWQEERLKPSRKKITKK HTKKRTASLILHAMICCRSLNSS KTKNTKCLNSINQRLKILSLQK GDPLESTCRH*CCHVHRRTKAP GQRRVGRQHVVSAGNHRHPHK GDPLESTCRHATVTGQGLLEFA GGPLQTLFA
26418	56786	A	26565	329	615	TKTEIGTRSINELRQQLFATTNT FFFPSIFGESNTTSTSLTLKNSAI WCPTGTKLPEGRTGSNLCCSAA SAGDTQANRVWSGPSAN/C*QT CRRRSC

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26419	56787	A	26566	525	716	PTCLLTPPSKGRQTPYATGELR LASDGCPSGTKLPEEGAGSNTQ ANRVWSGPSANSSRPAEEGPDC CRTTCCRTTCWKPTTVTTCSST PCCQPACCVSSCCQPCCRPTCC VTSCCQPSCCSTPCCQPTCCGSS CCGQTSCGSSCGQSSSCAPVYC VSSCCQPSCC*SGPSSAGLLEFA EGPLQTLFAWVLLPAPSSGSFV PDGHPSDASRSSPVA
26420	56788	A	26567	3	390	EGPCCKGWCC/RSPDTML/CPT VFITCRPGDSLRCLHHQGPRFQ AQN\CQPFGQTSS*LQEFFPIPQ WCLECRRALAGIWQVPLWDEA SLPEEGAGSNLCCSAASTGDTQ ANRVWNGPPANSSRPAGEEAD
26421	56789	A	26568	658	1005	NSKYWTPSGPPPRLASGAIYGN SLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGPGSGPHL GPDG*MVGSQVQHDNELYFC/ APAGSYPLWVKALPQPPSQPFL KPVASM
26422	56790	A	26569	1149	1715	VLQLNLPGPVASWCSRDVGPPL ARPIPPPAPHTPLSSAGPSAAAP GPARQLPHPRGDSRTARLLPGQ GSS*SWR*GAWQSGCQSYRKP GLSV*AAGAPYRNAGPLQPGCF PPS*SLPNGGIHPGPGPGSGPHL GPDG*MVGVGPSGAGAAPEPA PGLWDPPGHCSQASTPPGACKE RETLPTALPRLS
26423	56791	A	26570	32	335	LWSLFDHHVQRAVCDSRAKYR EGRRPRAVKVYTINLESQYLLI QGVPAVGVMKELVERFALYGA IEQYNALDEYPARRLY*SLSY*I YELTKCKDSQEKNG
26424	56792	A	26571	407	842	TEPLITINRLQRRRRSAPVAAAG PAGTLARRAPAVTAERAAGPG PASVHRRPGWRRAQSGPAAAQ ALRPPPPR*PRDSASPLSRKELL KLLGTKHYGRLTATEAQAPQG QHKLLCRETGELVPHWAGSHY RGISNPINNIQDHIL
26425	56793	A	26572	409	614	GLPPPAVGDRQRCLPVRH*RPS QTIRAEQEPRSAAPRKRRPKEG CRRSRGSSPLADNLGDLGSGGQ GG

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26426	56794	A	26573	3	266	GNHCRRQYRDAQ*WP*EAGRY SSCAGSARLGKAKG\RGPQGV MGNE/MRSRRAQEFKKYLHSK TSR*KSHTGPEAELTSPGAKKE GCSQ
26427	56795	A	26574	36	384	GWYCSSRSDVCSGGNSSAHSQ LPHQPLPRLRPGGSCHPRESSSP SKQRGGPVGDRQRCLPVRH*RP SQTIRAEQEPRSAAPRKRRAKE GTRRSRGSSPHPEKLGDLGSGG QEVRP
26428	56796	A	26575	101	334	CSTSKEKWQCGLRAECSPVFPA TEVPEYSC*GRKPSHLSCHRAP TLEEAANRKWPCTQYDAIQNA CYYNDSLVLRLS
26429	56797	A	26576	435	761	QGTNTWVPHWVLRLGLLHTSP PEGIAELPRSLPSLTEHQACQLD CVLVAIGTAILVAQTATTSPPIC GEADAHPASTPLPPSWPPQGRQ LSC*NPPLGPWPSGRVQTP
26430	56798	A	26577	38	236	RLLPLENCCLSSASGTCAHQAP LLLCSCPNC*SCCCCHHCCCPC GCCCWHCHRPSTKGNSATFTA
26431	56799	A	26578	1316	1548	FFSITGLSSVAGGQFVNLYLKR LNSNFIYLSGYVIVYINIYVFIYC I*KFVLHVTLRTDCCKTIVKKH VFRLFLKAM
26432	56800	A	26579	1	272	RPVNSRLDDFVAACAAMAKIK ARDLRGKKKEELLKQLDDLKV ELSQLRVAKVTGGAASKLSKM *VRRPDHSPRGWGARVHRDRR RISKLA
26433	56801	A	26580	1	363	
26434	56802	A	26581	286	867	IYALSLGAGGAAASAGLCSNEP RFKARDLRGK\KKEELL\KQLD\ DLKGGSCPQLTRSPKVTERCGP PKLSKIR\VVRKSIC/RVFSPVIYP DFRKENLQGNSYKG\KKYKPLG PCGP*GRTRAMRPPGSNKARRE NLEGPKEAGSGKGAAFTRCGK *RGSRALRGRLCQLKHKENLKT KKQQRKERLYPLRKYAVKA
26435	56803	A	26582	164	346	LHPGRRPGLTHLGVPSPGPGPT EKLAPGKPSSAACAPSPPALD* HIAFGVDALCPTFGLN

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26436	56804	A	26583	316	723	LVGGWGGLWGGLHGPLYGQA QGASPLLPPPPPAHRPPPHRHST EHGVEHPLVT*TAPLSPCPLGFR LGQLALHRGASTKGLLTGGVW GLHSWPIGDGRATIHEAVVRAS PWPSRLGTIHGVRGGRDVQEG AELPAV
26437	56805	A	26584	177	418	RNPVVAQGLLCACRMFKVGNR TPSSSAEWPSSFAPPKKGPLPKA TSEPLFPHPKRR/PLASVPSHREC RPPLGASKTAPRD
26438	56806	C	26585	149	277	
26439	56807	A	26586	1037	1455	EESYGLLSVPSVTGSLLLQDLH KLGCHQFGHSKKRRVSGIWMA VLPFPFRCQPHLLLLLENPRAN GPARQPTNHQPP*KAGTQLPNS VAPVQSQTGFPPTPARKARAPT WPGAARPPGTASNKSPARSPCS SPSFSILP
26440	56808	A	26587	175	450	
26441	56809	A	26588	77	337	RDHEPTRRKKVRTHPNVRRNK LRTRRL*EL*HSLRGSAASFLKE GRPWRSGGGAQRR*KYWRKG KYSGKMQSWSRVYCSLAKVRA
26442	56810	A	26589	1043	1555	ALRQGPEGARAPNMDSSVSRC QVPGPQVCRAVPTEILASPAVE RAPAAALSSTTIWMPMSLCPW RPVLAACTSMTVRGRSTMYLP TTTGNAGCTWPKASLATRWLS SPMGRQARSLMLGAQVTLSWD RSMPWRRRGRSSGRNLSTI*WR LDWSLRRTWRSGRAWMSGIST
26443	56811	A	26591	313	462	VCFTPEPARPRIRQTRPDRRNSE HIRT/RRRKKLRTHLNIRRNKL WTRHL
26444	56812	A	26592	630	777	KERRGREKKKEEEKRRRGRRG GRRRKRRRRRGRGRGRGRGR* KERRGREKKKEEEKRRRGRRG GRRRKRRRRRGRGRGRGRGRR RGSRRFL
26445	56813	A	26593	284	461	HSPGGSAASFLKSVRRRTHQFR TH*FHIHKNRTFTSR*SH*RMRQ WDQREVKVLFL
26446	56814	A	26594	573	968	AQRFCHSQWRCSSSRAVLEENP APLDTTPLSGRSKSSGRGCLVS LGL**PPSTRRSSHL*QPSSP*AS TFLQVRMTAPSGL*PQRPA*KL RSSPLLLTKNPFPEAAAF*SRGP PVSLKDTASLQAAFLGWP

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26447	56815	A	26595	3	699	RGRSRANSPQLLLEGGADPTVG DIGHLSVGVGPVHNAVGACQP DQTTPKHLADNPGPWTLDALT YQPHAANSCHKRGIAAS*SLMII MVIIFLVLLFWENEVNDEAVMS TLEHLHVDYPQNDVPVPARYC NHMIIQRVIREPDHTCKKEHVFI HERPRKINGICISPKKVACQNLS AIFCFQSETKFKMTVCQLIEGTR YPACRYHYSPTEGFVLVTCDDL RPDSFLGYVK
26448	56816	A	26596	2	483	
26449	56817	A	26597	2	1041	WPQDGSCTWLAVAMGCWLAT QQGSLTRVPVATSGIQGCQAAP SPMWAAWTHGWASCYFRAAL QLPLPPGSTGNGSMSTSTAYSA SSPGFM/YTKAQGERSDHKENV FYVQHQKYVGGATQAFAKEN NQKAYKETYGVSHITRHDMLQ IPKQQQNEKYQVPQFDQSTIKNI ESAKGLDVWDSWPLQNADGT VAEYNGYHVVFALAGSPKDAD DTSIYMFYQKVGDNSIDSWKN AGRVFKDSDKFDANDPILKDQT QEWSGSATFTSDGKIRLFYTDY SGKHYGKQSLTTAQHLQQYLT YKRSFSIVVDAIIALPPLKRAAW PKSRHPPQVGLMEVQHLFPIPN NFEEHV
26450	56818	A	26598	116	338	

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26451	56819	A	26599	971	2485	FISSCFVRACGTLNPGVTMFYVI LGKFCDFAEPWFPHVMQEQLR VVGKGLWGFVRVSLSGFRIHGP HQKTASLAQVHKAVLHDGRTV AVKVQHPKVRAQSSKDILLME VRALPFSFLCPQSTFMWLVDEA KKNLPLELDFLNEGRNAEKVSQ MLRHFDFLKVGGTMQCRVWW SGGLMEFVDGGQVNDRDYME RNKIDVNEVRSRAQGCCAGER GVNGFVHCDPHPGNVLVRKHP GTGKAEIVLLDHGLYQVEEAFV TQPWGLWGQSLIWTDMKRVK EYSQRLGAGDLYPLFACMLTA RSWDSVNRGISQAPVTATEVG GPSRPCLFLNAEISHLLNHVPRQ MLLILKTNDLLRGIEAALGTRA SASSFLNMSRCCIRALAE*VWA PPSPPLLAP*ISFSEAFNLWQINL HELILRVKGLKLADRVLALICW LFPAPLCTVHVTILLLLWNPLRT LWPLSQGPQAELWHSSLFFSKK TQQPTFPFLVCAIGLDVPTTSVK
26452	56820	A	26600	831	1205	RKEGQGPSVHPLGSGCFPPGHA FWEALEANTWVPCVRL*RTPV SAELLGLAPGGRWRAVNRDRG RVAAASSLGEPCYSSPADASFP RSDSGGLDRQGGSCRYPKELFG SHPQRARCTEGSLQVL
26453	56821	A	26601	377	962	LFSIFITQDPKLRELLDVGNIGR LEQRMITVVLKACV**LCSI*AN ASVIYIFQEWTNDHLLVL*SMC HLNLSPLLCSLHSIYRNREGGS WGRKKTIC*LRCFISQNDSIPQE DFTPEMQILE*NLV*KILIAWFFI VFSGAKSKPYLTVDQMMDFIN LKQRDPRLNEILYPPLKQEQVQ VLIEKYEPNNSLARK
26454	56822	A	26602	1	810	MDAKKRKLYKYASTDSPAFAI TFIIMPYMENQAAKLAFERLSL NELVFSSEALTHSETFLPQPDNR HQNMSSTIHTAPIDTALGGNPA FLYLFLQDFQPTQDNSLASVTP SAGVSARLAPPPTPGPFTDVVV LDVLDEVGQGGEVESAAPESA GIGEEGGGGDACHGATSRAP*Q ASPPPPSSPIPADSGAADSTSPP WPTSSSTSRTTTSVNGPGVGGG ARRAETPAEGVTDASELSCVG

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26455	56823	A	26603	28	457	GGIPDSTARLSILTPRHHLQRSC SCNGTATRFSGQSYVRYRAPAA RNWHIHFYLKTLQPQAILLFTN ETASVSLKGFEGCLDAVVVNEE ALDLLAPG/NDGGRLAGDTSPH PVLPPQ*LLQPEHMPQWWEVL MDPRGRLCLQMS
26456	56824	B	26604	205	1722	
26457	56825	A	26605	11	374	VSPSRSGIPGSTHASGQL*TGDR S/GPMGPPITAT\Q*DGDSDAYH GLATLHALLPALPGAAGF/PSGT SEPCPSSPC\GQHHHAGQLGHD LPVHCSEDPRPQPPPLGGPLEDL PSLLWHSDFFI
26458	56826	A	26606	69	551	QSGRSPQHVFPSVRGSGARSRG WILVHPSQYHHNPQRIYSACGR SGEHISPGYPCS\DGHDAYDQQ ADGTHHDACIFH\PRGSPRSP\G QCCLLTGGSRSGT\SGASATPG GRRGG\PAQGGE\PASRNSSVEE LTARVLAPAPAPALASAQPTLP GFSISPSTK
26459	56827	A	26607	476	1016	CLWLLSCLYCSLGDCCLWWAV SVLCQVSAPRQALCFAPGENGD GGQQGLRGAPPGPGPRGPAPQP GPGYPGARQRGSPQQP*LSSEP GPYLRLSRSGGR*GPGRCCSRSP PGR*PVQAGDEDGQDAGSHI*T QPRVSEEGGTDEDQWSLPQEVP SASVPYQPLSHCQTVPASLQPH CLFS
26460	56828	A	26609	247	342	RSIMPWLPKGSGWEVSSIPP*RC LHQLWSTSRNMAL/HVRVLQT EQAVKEYNALVAQGVRVGGV FHSTC*WSLKRRINH
26461	56829	A	26610	129	272	NDTVSGLGRLESPTLMRQRNV CSHCYPGSAK*GYMIYKDALPR RTSL
26462	56830	A	26611	133	453	QVDPNTVLRNAVHTNTYLQGL THPSANHKSLYTLLNNFLHICR LHTRRMHGKTGRVYGITQRAV GIVVNK*VTGQILAKRIVPIEHI KHTKSQ*SFL*ELRPSPVAS
26463	56831	A	26612	352	543	VPSINCGVPQGNMALMCRVLQ TEQAVKEYNALVAQGVRVGG VFHST\SDGSLKRRINH*VPKKK

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26464	56832	A	26613	576	927	FAERTRTHH*PKPRWKGALGC RARTAVTSRGCLAPSRRRRRLP GRRAASQPGPNADPKACRPWN PRGSQVHAKRNALCFSRASDAP PRPDASPGQIFPGRRRKECQTC KTRVRLGCL
26465	56833	A	26614	67	415	ALARKLPTNFQWVKKIDASPGS PIPLNAP*PSPSVQTTPTTGHPG RALSTVSEVPGAGARLTYRVPF TRCKRSLILPSPVWVSRIPSTAK SPILISSPGGAHAASVSALTLVS GYE
26466	56834	A	26615	87	347	GIRY*LCHGFYHAYLGFRRRTS SPLQVSRPPPPRGTQSEP*AQSP RSPELELGLHTASHSRAANAAS SFHLRFGFPGFHPRPSPLF
26467	56835	A	26616	3	175	GFVTSSFFLGCLSFPDAYDLVFL LARE*HWKH*TQSILTLIAQCVF PEQPKRLCWVS
26468	56836	A	26617	539	788	EKEVPTLLDCCAALGQ*KCKMI QLLWKMV*SFSTKLNILLPNNP AVVLLGIHLKELKTYVLTETCT LMFIAGSQRNLRDYFRP
26469	56837	A	26618	843	1136	VKEQVYRRIAASRSVRRCSYQS RPGLLPTAGHHPQFHLYSDCHG NDIYSVYYQCEHGHAASSSETG VPRFPCPWWSETAQ*TGCASHP GPSAQRSAL
26470	56838	A	26619	2073	2329	LVQTSRPPDPSWA*SATVTRPE QASWARNLSRFPLLGMATVSG RGLPSGPGPRAMSPAGEPAPGA AEPAPPGSAAIPHRRPLLGQ
26471	56839	A	26620	723	1023	ITLLGLSLIPLISRLPWTQSWGPL SFLSTPTSLLISSTPLILNTINSLM TLRFLPPGGAFP*TPEPCIPPTQH PHLDVSLTGISNLPRPQSCFHCL HLS
26472	56840	A	26621	99	288	CLCQNKLGEGRDDNFTSWQSS AC*TFCFLLAVDSAETTAAES*C CCCCCCCSAAGGWRRLVH
26473	56841	A	26622	130	450	RQLKLTAGCAKSPWLFWLKSY HSLYLAAACLLGLTYTRLGRSQ SSPPIHSHEFPPATSL*QQLHGQ PA*WLYDGPATP/SIAPPAHLLP PPWRGGTPSPWLPPSPLQE
26474	56842	C	26623	1	672	
26475	56843	A	26624	408	581	LIKDESAPRTPQTVLASAQFCLL CR*ARCCRGGSCCCCCCCCCCC WWWCCCCYFGND
26476	56844	C	26625	66	264	

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26477	56845	A	26626	70	551	AAEDVWVYPSELYWPGPHGHC ETPRAGVFVVTSHEEGPGAGTA SSSSKGPSWARWGLEVSPLRWP SGQVGGAGSAESGQPLGSGFTF KAMGNLGESRARQAQLIHDRN TASHTAAAARTQAPPTPDKVQ MTWTREKLIAEKYRSRDTSLSG FKDLFSMKP*VSPLRWPSGQVG GAGSAESGQPLGSGFTFKAMG NLGESRARQAQLIHDRNTASHT AAAARTQAPPTPDKVQMTWTR EKLIAEKYRSRDTSLSGFKDLFS MKP
26478	56846	A	26627	479	961	PQSSLQGNLQMPWGSCLDSST HYRPSLVGVDFQLPSFWLVICG TCKHCHRMLHSVALFWVPLHC GWSIPRPRCPHPHHPPPLRGPSC HPPSPPWACPPRTGVQSATCPF A*RPTWSFTCDPTTKRSMRGLT HILRSGEKRPLPALCARSTSGSA TTSPGT
26479	56847	A	26628	1	223	MGAVQKAYNLQKKRRRRRGR RGRIRGRRGRGRRRRGRRRRK KKKKEEEEEEEEEEEEEEEEE EEEEEEEEE*EVEEEEEEEEEEE EEERRRRRKKKKKKKKKKKKK KKRKKKKKRKKKKKKE
26480	56848	A	26629	1	341	
26481	56849	A	26630	78	354	ENDSFYNDL*ATQRRRRRRRKK KKKGEERRRKEKKGEERRRRR RRRRRRRRRRRRRRRRRGRG RGRGRGRGRRRRRRRRRRRR RRRRRRRRRR
26482	56850	A	26631	1	327	
26483	56851	A	26632	41	246	
26484	56852	A	26633	1	170	RKRRKRKKRKKKKKKKKKE KEKEKEK\RRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRR RRRRRRRRRNTNNETGE
26485	56853	A	26634	1	282	MCIESEREEEEEEEEEEEEEE EEEERRRGRGRRRRKKKRKKK KKEEEEEERRRKKKRKKKEEEE EEEEERR/MRKKKKKKKRKKK KKKKRQSL
26486	56854	A	26635	1	396	
26487	56855	A	26636	1	255	MLWLPQPALGTRAAETLACSR RRRRQLYNCCLYLRRRKKEEE KEKEEEKGKEKEKEKKEE\KRR RRRRRRRRRRRRRRRRRRRRR RRRRN

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26488	56856	A	26637	1	290	MKKKKEGRRRKKEEEGEEEGE E/DRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRTTT TTTTTTT
26489	56857	A	26638	2	423	
26490	56858	A	26639	3	167	QQKEDEEKEKEEEKEEEDEEEE /ERRRRRERRRRRRRRRRRRR RRRRRETQEAETI
26491	56859	A	26640	1	325	MEKNEKEQEEEEKKEKNSKKK EEEEEEEGGGEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRGRRRRKKKKKK
26492	56860	A	26641	1	618	
26493	56861	A	26642	1	291	
26494	56862	A	26643	3	155	YRHLPKKKEEKEEEEKEEEEEE EEEEEEEE/ERRRRRRRRRRRR KYEKKCL
26495	56863	A	26644	1	1410	
26496	56864	A	26645	578	842	TQEAELAVSRDHATALQPGQQ SKTPSEEEERRKKEKEEERRRR KKKKEEEEG/MKKEEEGRRRRR RRRRRRRRRRRRRRRRRRRR KKKEEEEE
26497	56865	A	26646	215	471	
26498	56866	A	26647	432	761	
26499	56867	A	26648	1	357	
26500	56868	A	26649	2	281	
26501	56869	A	26650	533	758	EQKKKKKEKKKKEKEKEKEEE EEEEE\ERRRRRKRRTRRRRRR RRSRRRRRRRRRRRRRRRRRR RRRRRNTEK
26502	56870	A	26651	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEETLFSNM
26503	56871	A	26652	1	279	
26504	56872	A	26653	1	795	
26505	56873	A	26654	1	642	MKKCKTSVIGIATFYLSIPHIYT PPNQTSSFMACAIAIEVQLTSAE PASIGFPVQKSPCGHLQLNGYK SSSKQGFPTPLLKQESWNSSVKI TTCNVGDKKNINDRRSANMMH VNNFPFRRHSWICLDRVQSETL PQEKKEEEEERRRRRKKKEEE ERRRRKKKKKEEEEEEEEEE/ RRGRRRRRRRRRRRRRRRR RRRRRRRRRRKKERISSL

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26506	56874	A	26655	1	1167	MAPRPQAARLPSCGTRSQGAA RPPPLGTAAAYRPLSSRLLTGPP PASSSWLAIHFRIRVGSSGQGN QRIKYLGIQLTRDVKDLFKENY KRLLNEIKEDTNKWKNIPCSWV GRISIVKMAILPKVQAILMLVLF LHLFCKYNIVGMENAGNGHD WSLDRHLMQASANQQATQLAI SRPSNQSKAQDFLRLLRKEKQT ALDTFAPLKEQAQKWNEDGIR SSVIPGIQHQSLLLAVLTFNSSK TSLGDRARPVSKKKKEESRKK KKKKKKKKKKKKKKKKKKKK RKRNKNKKKNKKNKKKNKEN KKKNKKKKEKKKKERKKKKR KR/MEEEEEEDEEEEAEAEEKE RKERKRKKEKGRREGRKEGKR EGKGRRGRGRRKNKEERRRSR
26507	56875	A	26656	342	616	RILHKSFRKLLCKGSFCSTRSPT REIRSKKKEEEEEEEEEEEE/ERR RRRRRRRRRRRRRRKKRKRK RKRKKKTKTKTKKKKKKKKK KKKK
26508	56876	A	26657	1	705	

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26509	56877	A	26658	1	2267	MKVELMGFAEGLAVRVREQEE VRLNWKVELLWTDLRDVPKG ANSFRVSGSSGVEVFMVYNRT RVKEPIGKARWPLDTDADMVV SVGTASKELKDFKVRVSYFGEQ EDQALGRSVLYLTGVDISLEVD TGRTGKVKRSQGDKKTWRWG PEGYGAILLVNCDRDNHRSAEP DLTHSWLMSLADLQDMSPMLL SCNGPDKLFDSHKLVLNVPFSD SKRVRVFCARGPEDVCEAYRH VLGQNKVSYEVPRLHGDEERFF VEGLSFPDAGFTGLISFHVTLLD DSNEDFSASPIFTDTVVFRVAP WIMTPSTLPPLEVYVCRVRNNT CFVDAVAELARKAGCKLTICPQ AENRNDRWIQDEMELGYVQAP HKTLPVVFDSPRNGELQDFPYK RILGPDFGYVTREPRDRSVSGL DSFGNLEVSPPVVANGKEYPLG RILIGGNLPGSSGRRVTQVVRD FLHAQKVQPPVELFVDWLAVG HVDEFLSFVPAPDGKGFRMLLA SPGACFKLFQEKQKCGHGRAL LFQGVVDDEQVKTISINQVLSN KDLINYNKFVQSCIDWNREVLK RELGLAECDIIDIPQLFKTERKK ATAFFPDLVNMLVLGKHLGIPK PFGPIINGCCCLEEKVRSLLEPL GLHCTFIDDFTPYHMLHGEAYS LECRQHWGKNLYFRVGLKKK KKKKKKEKEEGQEEEEEEEEEE
26510	56878	A	26659	1	990	
26511	56879	A	26660	1	235	MTAKCVCGWGVGERERERKER EEEEEEEEEEEEE/ERRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRKI
26512	56880	A	26661	1	1101	
26513	56881	A	26662	348	806	
26514	56882	A	26663	39	684	LRCENPISSHVGHVGVSLAHTR GLFSRLILADREDISENWCSLVC CVCVCVCVCVWWLCISLFPGD MMTLLMKKDTLTEEET\QFYIS ETVLAIDSIHQLGFIHRDIKPDN LLLDSKGHVKLSDFGLCTGLKK AHRTEFYRNLNHSLPSDFTFQN MNSKRKAETWKRNRRQLAFST VGTPDYIAPEVFMQTGYNKLC DWWSLGVIMYEMLIGKLHG

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26515	56883	A	26664	3	276	IKSIDDTSNFDEFPESDILKPTVL SSAP*AVHWRQGSESTLTSISFP VATSNHPETDYKNKDWVFINY TYKRFEGLTARGAIPSYMKAA K
26516	56884	A	26665	95	405	
26517	56885	A	26666	3	349	GPGGWLSLSPLVL*ALES*KEEE EEEEEEEEEEEEEEEEEEEEE/ ERRRRRRRRRRRRRRRRRRK KREKKKSWVDCTEEVAKYVGL ASLRISRVPPTDSTKEKTIEKVN RRK
26518	56886	A	26667	1	370	MHVAWSCPTAQSSQATVDSGK TLAETESPIGLSSKVGGKNIRAG EWDELKYDRFPGQKPKKKKRK RKEEEEEEEEEEEEE\KKKKKK KKKKKKKKRRRRRRGRRRMQ QSHPNPTSAILAPWA
26519	56887	A	26668	1	430	MTFFPFDKRETDILLILNFSMEH CTRGQDPLGYQTTKKGFKDTE TPEKESLESKAECLGRRRKKKN KEEKEEKEKKEKEKKEKEKEK KRKKKRKKKKKKKKKKKKKK KKKKKKKKEEEEEEE\GMRKR RRRRRRRRRRRRRR*RRRRRR RRRRRRRRRRRGRRRGRRRR RRRRRRRRRRRRRRRRRRRR RRRRMRKRRRRRRRRRRRRR
26520	56888	A	26669	1	708	
26521	56889	A	26670	1	1233	
26522	56890	A	26671	1	366	MSYVAAVMFFCSVLGKFQMNL EEEVEKRRRKKKDKKKEKEEE EEK/DERRRRRRRRRRRRRRR RRRRRRRRRRRREEEEEEGEE EEEEEEEKKKKRRRTLYCM*IA CKLKYLWTVSGHILCPNTN
26523	56891	A	26672	1	667	MSKEGNNRHWDRLEGGGWRR VRVEKRLFRDYPSSHPRGAEAF TSPDSIGRCTLRFPGLQMGLHQ PALIAILRSGADLSHLEGPMLEA GASACAPAVSPGDQALQQHPG EGRKVPGKRRRRKEEEEEEEE KRKKKKKKEEEEEEEEEEEE\ KKKRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRNKQTKGP PCKNLMLVFCPQNKAPSPCLQI AAEFSWAWAR
26524	56892	A	26673	365	670	
26525	56893	A	26674	29	370	

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26526	56894	A	26675	1	1364	MEMIWPSKGMPFTSTSYSNKES SLLSVVQTSSYSHTHTRGSSEE VESLNRPITGSEIVAIINSLPTKK SPGPDGFTAEFYQRYKEELRIK YLGIQLTRDVKDLFKENYKPPL NEIKEDTKKWKNIPCSWVGRIN IVKMAILPKIIVEDALQIYYDMV LVCVGVGVSCRIVISSLEVLESR RGQRIFFLVQAEQVLWAFKEVS SNCNDKSTLRGSVVKLQCTSGT SAFDIFQVGSRVLGEHRLPSVH SATYMSLTYFELAGLLEKSSQL VGSTGVEDIVAIMIPEPKGKEIV SLLERNITVTMYITIGTRNLQKY ERWKKKRTKGLEYQEFGFDDV KFRSLLDIEAEMPDLHRLPRNM HASSPSKRTARGRNKNKSSRLT MFGVEIQEEEEEEEEEEKKKR RKEEEEEEEEEE/ERRRRRRRRR RRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRGGRRRRRKH
26527	56895	B	26676	1	499	
26528	56896	A	26677	1	1684	
26529	56897	A	26678	2	297	
26530	56898	A	26679	68	319	IQHITS*TKKKRKRKKEEEEEEE EEEERRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRR RRSHTSIPKESTLLQSQSVGLG
26531	56899	A	26680	1	1617	
26532	56900	A	26681	92	338	LEKEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEN*NVERY KKEGQW*KQRRQEKGLILPDG
26533	56901	A	26682	1	548	MVDQRHLVLTSSTKKNQNNNF QVFVIENVGREPQTDKIASPGA GQSCTASVTADLLSRDLHFTKV PSWSSDGPPYYPPACHLMSEPY FWGSCCYDTPIKTKTTNEEEEG EGEEEEEEEEEEEDEEEEEEKEE EEEEEEEGEGEE/ERRRRRRRRR RRRRRRRRRRRRRGRRGRRR RKPRGGR
26534	56902	A	26683	1	1215	
26535	56903	A	26684	1	571	
26536	56904	A	26685	1022	1365	TSLLPPSSSIPSRLPSVVLSVRILS LWILACLAPWRWDLLRKASCL PAFSLLLSGANGSFSLGFQALL GRKEEEKEEEE*EKEKEKEKKK KKKKKKKKKKKKKKKKKKK KKKKKKKNF
26537	56905	A	26686	24	355	

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26538	56906	A	26687	120	594	
26539	56907	A	26688	117	487	
26540	56908	A	26689	2	2482	
26541	56909	A	26690	2	654	KGDVGEWLSAGKGESSAMFAS EQEISKDEQGTPVLGSFYWEVD SPRKESSQAWAPGQEWIKLERD TTEEKMFEQLKPIEPVQKTLPW VGEVAATLQEAMKRDCWREA RVKKKPVTFEDVAVNFTQEEW DCLDASQRVLYQDVMSETFKN LTSVAWVRKKEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEE\KRKRKRKRERK KKKKKKKERTTWLWGNPLT
26542	56910	A	26691	789	1072	
26543	56911	A	26692	1246	2367	
26544	56912	A	26693	579	1214	
26545	56913	A	26694	119	1870	SCSRNRLLPPVSESLTRPLPSLA RWLPPPGLRQPSSRDYWPKGRL RLSAVPSPASPWALVSCLLPPSS SQEKAGKILKKRVEKQQPEEKV GKGLEESLCPCSSMSNHTKERV TMTKVTLENFYSNLIAQHEERE MR*RILFEKIEEEGLKDEEVINIG NVFLRKETEFLRLKRTRLGLED FESLKVIGRGAFGEVKITATCQ VGHVYAMKILRKADMLEKEQ VKHSCSSAFILVEADSLWVVK MFYSFQDKLNLYLIMEFLPGGN YLTMKGHKDTLTEEETQFYIAE TVLAIDSIHQLGFIHRDIKPDNL LLDSKVLGGHWHELPFQEPRLR GFLSQCCDTPFRALRFLASPSFQ VPLHSPRPDLCTGLKKAHRTEF YRNLNHSLPSDFSKW*QLR*PK AETWKRNRRQLVSNICGF*KN AENVSLGQVRWLTPVIPYIAPE VFMQTGYNKLCDWWSLGVIM YEMLIGKLHGFRGLPQETYKK VMNWKETLTFPPEVPISEKAKD LILRY*RTSLHLQIKSIDDTSNFD EFPESDILKPTGNTTSIVSCDYK NKDWVFINYTYKRFEGLTARG
26546	56914	A	26695	271	446	YLVHILDALPRDPTALRRRQRC LGS*RKHQTRLRSGRPSSGPGG TDISVTAVSAPAQK
26547	56915	A	26696	1	171	WGVIWRENGRCFSGLLRAGLG AAWEPRVGEIKILVS*LGTC*IK LICQSWVGANPRA

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26548	56916	A	26697	1	179	MWKGPKGLDMYGKSSVSPKTS DILGRD/NSPAGLEGANSGVAN CLWRGPCGRKLWEASRN
26549	56917	A	26698	2	140	DN*KGVHKRILSKLAPELGSFK GFRSLAVNTHNSYGGKGNRPL KIR
26550	56918	A	26699	3	601	
26551	56919	A	26700	232	1809	
26552	56920	A	26701	1	851	MQQEDPEESTKSPNPTTNKKQE KKLSLFGGLFTWTRVKFGAVT QIGGPPLGDQSPVLLLLQRLFSK GYRVSPSKAQISSPSVTYLNSVS LIKTLLKTTLLPKEAGVIHCKG HQKASDPIALGNTSADKGLFRP PPFPSHQARGFAPAQDWQIDFT QH/RP/GVRKQKYLLV*VDTFT G*VKAFPTRSEKATAVISSLLSD IIPRFGLPTSIQSNSRLAFISQISQ AFFQALSIQ*NLYIPYSPQSSGK VEQTNGLLKTHLTKLSLQLKK DWTVLLPLALLRIRACP
26553	56921	A	26702	434	867	RLILPNRLGSPLLVWVDTFTG* VEVFPTGSEKVTAVISSLLSDIIL RFGLPTSI*SDSRPATKSSFSLISP TLGSHDAPNPTRSSPEKHRPLSL HTIPQNFRCPDTLPLFRFIFFAFF SNTLHIMGKMAAEGPKSTLYC QFTEK
26554	56922	A	26703	96	415	
26555	56923	B	26704	1	933	
26556	56924	A	26705	1422	1774	DCPPSPIAFPQCTHQHHHHQYH YHHRHHHRHHHYQR*K*NPGL PLFVYCYFQNH*ACHCSWGNS EHMTIASESQAVPLQPPQDSQG FFEDLELHYFFGDPSETRPGKQP KVSVQQIL
26557	56925	A	26706	355	1014	RHLRPQERAPAPSGSVPSRPGCS QAPGGLLRVGRGGMLLPGCAA VADLQEEVPGFSWDAWAVKG EQRQGGGGVVKH*DAIPGQRV SDPGPPEPLASAPGQLSPSTPEY RRPPGESRRHRRPDLAQDQRGA AVLLLAGARGLSPLPRIPALGA ASFPPTLQFFLQLPSSGASTTSA GFFLLVLHQPLWLLLLDFLFDN LLLLRHSLFIPHGFLKCVSIPAF
26558	56926	A	26708	95	298	GSTQVLWAAWGGAGWTPRWP VFATWPWVQDMWPQQAWPLP QGVDIP*ACPPPPLRT*WL*ENR KAGS
26559	56927	A	26709	110	195	

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26560	56928	A	26710	241	957	KSPQIGLQGSWGAVGVGMRDP KERATEASKPDLLAQRQGEGHI FILFFSDYIPIFSSYLSLQRSSRGP SFFGPFSSPHNIPCEGRQNSETPP WPSLGKRSKKSSLYPLPKAPQP KSRAPSPISNNLKNFPQPSEKKD GPQPLWPQKWPLAPLFSRSPS* DDSGPCTEYCRRARRFKSFEDM AHIGPPKKVLYKIALGKFWELA DAKKKRKKGTSETETCLLSRAT ELLPKGKRHCRGIL
26561	56929	A	26711	496	708	GMLFRGSGACRRGGRTGGSGH A*PEPPVLPPLLHAPEPLNSMPH GLPAPPASPCHFPNLDSCVHSHS DTPLSVLPLPHLKSPLSSSDFCS YEVKKDAILSPMLSWWAGHRS AAGED
26562	56930	A	26712	302	561	TFLLQLAAVWSADRVREALRP ALWDWRSAVPHPSPQGPTG*R GVGVHPAAASRGGESSHPTAF DRSPPPPKPLRI*PEPSARSGLP
26563	56931	A	26713	1	411	LLVFQVHQCLHCKLL*/PSYVPL GYTEAFLATQNIGRVSLWAKH GHPDPFPLARADFRAQESPSPN DPSWLL*YFER*WSQATTKG*N RCC*RCD*LQAPSRRPEAVHTN DPR*REVREEHMVLQVLTR
26564	56932	C	26714	361	642	
26565	56933	A	26715	1805	2260	
26566	56934	A	26716	472	1667	AIHLLSLQTEFLVAERSSAAGRT TPATRAAFLAASCGPLHSCPTL LCSQLCCFSRSRSRVSGPKASLG IKEIASVDRVNTRRPACSTSSWL HNSGFTLSLANRDGGKRIRSET AKKGMSGDRSMKSWEVRRGY RWSSRAVRRPRACSSDGGTHF ALPMAARGSSGPSPGSPANSVR QSLKSESSISAIWVAEQAAGNV PRTSAQFGTGSESANTAARLIE KLLRAELDKPEIRDERIVGWWT TFGRPQLGSRVGFCACSLAARM SSTSQNLEAAFGGKFCFLWALL LGLDDTFESRISDTGSAGLMLV EFFAPW*VHSESANTAARLIEK LLTAELDKPEIRDERIVGWWTT FGRPQLGSRVGFCACSLAARMS STSQNLEAAFGGKFCFLWALLL GL

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26567	56935	A	26717	2	237	SVRQTTATSPAHKNSKRLIRSC QGF/HPEPPPTGACYKCPQPRIP HEPCPI/S/SQDPTENWTVQLTW QPLPEPLELWPKAV
26568	56936	A	26718	1	313	MESAQKEAVEIFGQPHAASSSG DVKPLLFIDFYKCSGEKVVCME HALRACYMCRKSGHWAKECP QPGIPPKLCPIC\GDPTGNQTVQ LTWQPLPEPLELWPKAL
26569	56937	A	26719	377	583	
26570	56938	A	26720	1221	1394	VASFYSLLQPPYPSTSFSFQSWR HTSISPFS*FQFLSFSGIFWQPLP EPLELWPKAL
26571	56939	A	26721	160	234	
26572	56940	A	26722	163	414	
26573	56941	A	26723	212	399	YSLKDCWPLSLSLNHFLLSILAS PFNLSLLLISVPFLFW*RTETRFI WQPLSEPLELWPKAL
26574	56942	A	26724	809	874	
26575	56943	A	26725	49	220	
26576	56944	A	26726	71	375	LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQT\TSPRNISPILNPEL ATSARNLATRPRNACSPGFLLS RVPSVRDPTGNRTFQLT\WQPL PEPLELWPKAL
26577	56945	A	26727	1	1011	CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGDSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKKNGEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQT\TSPRNISPISNPRQRRQV LSMDPKLRHRSRTGKAAFPWC LIIAGTPL
26578	56946	A	26728	150	211	
26579	56947	A	26729	445	549	
26580	56948	A	26730	193	249	
26581	56949	A	26731	372	564	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT\TSPRNISPILN/PEK KETRFIRGPKTPAPVMD
26582	56950	C	26732	185	640	
26583	56951	A	26733	1662	1774	
26584	56952	A	26734	233	527	

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26585	56953	A	26735	380	731	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQT\TSPRNISPILNQEL ATSTRNLATRPRNACSPGFLLS CVPSVRDPTGNQTVQLTWQPL PEPLELWPKALCLTDSFPDLLG LTAED
26586	56954	A	26736	2	182	
26587	56955	A	26737	2	89	
26588	56956	A	26738	2	89	
26589	56957	A	26739	161	460	KMKEFMKKSSRTKDTRQQEQV LEPLFTIAKTWNQPKCPSTID*I KKMWYIYTMEYYAAIKRNKIV FFAGTWMQLEAIILSKLIQEQKT KHHMFSLIRGR
26590	56958	A	26740	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDYFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTMEYYAVTRRNKIVSFA ET*MELEVIIVSKLTQEQKTKHC MFSLTSGS
26591	56959	A	26741	902	1065	
26592	56960	A	26742	326	484	WYSWDCQLVTPWRPRIIPGPLG TWMELEAIILSKLTQEQKTKHH MFSL*SGS
26593	56961	A	26743	527	825	QPLWGQLH*EVPSCWRFSA*IC YSSGLTVMLSSWLDLIRPPWTL R*PREWRQCMGENHIGRGLGF* RPWTWMELEAIILSKPTREQKT KHYMFSLISGS
26594	56962	A	26744	398	557	HYWLGTVVHTCNPSTLGS*GR QIT*AQELETSLGNKNVGCSELI LLSTLGNRV
26595	56963	A	26745	3	359	HRPGIPGTTISSWMDAWGRLEA RYMSYLHSRRGDHA*DKLQRD NRFASQTHSHWAKSSCHCRFES RPFFLPSPSWSYNRSWGGESAE RTWMKQRGTCLSHSPLDLLHP GLCQHKVGAR
26596	56964	C	26746	127	216	
26597	56965	A	26747	135	197	
26598	56966	A	26748	84	202	VLIHIRRDIMIPETVD*WEY**P* RLVPGQVQWVKPAIP
26599	56967	A	26749	483	669	
26600	56968	A	26750	1	274	EIRNKIHVSENSQIKTVKEKPSIS SSVSRLKGVNKVRASFPEDRKD YTGSKAPKGS*GYTIN*LK*NN KRKKKQNKKLMPKTEQGQKN SIR

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26601	56969	A	26751	63	398	TPLRQPCSIRNVQQEPVGRFSGT GLPLSVARSSPWEAWPQCKWR FQNAGD*DIRQPDRGQGPRPAE PEKREPYLRSQQGAFLGSHSSGI QSQLLGLGESCSYGATGKPVHP
26602	56970	A	26752	3	231	SVHEEEKMALPLGQSHCGLLY LYY**RCFKCYSFYCILFIKNAFI Y*NI*IYINTHTHTHTHTHIYIYI YNCLYI
26603	56971	A	26753	4266	4944	TDEIGASRLSRVESLAPEVKQN TTASGCELMHTEMQALRADW KQWEDSVFQTQSCLENLVSQM ALSEQEFSGQVAQLEQALEQFS ALLKTWAQQLTLLEGKNTDEEI VECWHKGQVSWLPV*KAEPRT EDLKSQLNELCRFSRDLSTYSG KVSGLIKEYNW*A*TLLKGCQN KEQILQQRFRKAFRDFQQWLV NAKITTAKCFDIPQNISEVSTSL QKIQVRVLSI
26604	56972	A	26754	3	556	
26605	56973	A	26755	143	724	GWIPSDNSICVQEDCRIPQIEDA EIHNKTYRHGEKLIITCHEGFKI RYPDLHNMVSLCRDDGTWNN LPICQGCLRPLASSNGYVNIYEL QTSFPVGTVISYRCFPGFKLDGS AYLECLQNLIW\RPAHPGALLW KEEDLNIFSLSFISHTSGWQLLC FIFALC*SPLPPQHLPVPQLAPPH LCSKCCSPAIKDV
26606	56974	A	26756	3	1393	CLRPLASSNGYVNISELQTSFPV GTVISYRCFPGFKLDGSAYLEC LQNLIWSSSPPRCLALEVKIPVS GAVRVTITLPVTLGHPNVVTQR WKAGASDKGELVVLKLLFSPT AQVCPLPPMVSHGDFVCHPRPC ERYNHGTVVEFYCDPGYSLTSD YKYITCQYGEWFPSYQVYCIKS EQTWPSTHETLLTTWKIVAFTA TSVLLVLLLVILARMFQTKFKA HFPPRGPPRSSSSDPDFVVVDG VPVMLPSYDEAVSGGLSALGP GYMASVGQGCPLPVDDHSPPA YPGSGDTDTGPGES*TCDSVSG SSELLQRLYSPPRCQESTHPASD NPDIIASTAEEVASTNPGIDIAD VDSSNIKLPDWQTKYRVASPAR STCEDRSGAPVGTHESLFFSIPS SARQDWAPLDSQLESPQCRLPT LQRDFLVDPQAERPVPLDPELT EIWCPNKNRIERHMEHSGIEA

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26607	56975	A	26758	1	500	
26608	56976	B	26759	19	148	
26609	56977	A	26760	184	539	LPAKEEEGHSKKSGPLLGPRRA LPGTALGARGAEQGDPEADH* GADTTKRCPGLGPAPVPRKGIP AEGPRRGSRAGLGMWGPGLGA HRTAAPSPAEAPSPCQHPSSHSC PVACFEPVF
26610	56978	A	26761	1	441	DENRELLG\ELDGIDVLLQQLSV FKRHNPSTAEEQEMMENLFDSL CSCLMLSSNRERFLKGEGLQLM NLMLREKKISRSSAL\KVL\DHA MIGPEGTDNCH*VCLTFLALR\T IFPLFMKSPRKIKKVGTTEKEHE EQCCSILASLLRN
26611	56979	A	26762	1	2403	
26612	56980	A	26763	17	751	AKMPFDANKLYCSEVLAILFFS PLENRELLGELDGIDVLVFA*Q VFKRHNPSTAEEQEMMENLFD SLCSCLMLSSNRERFLKGEGLQ LTLL*LSHSSDSCEMPTWRGGS MEQGGRMGLGLVSVGLEHALL LTYGLYQRLPPQPQNAQPSFVH REKKISRSSALKVLDHAMIGPE GTDNCHKFVDILGLRTIFPLFM KSPRKIKKVGTTLPPLPAAATPT NRPSAMNGRVRMEAEQSSAHC

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26613	56981	A	26764	1	1914	MAEGERGADVPH/GPRGLAGR RGVGGAARGRAG/PGGT/EGGG GPESLSGGSGVGDSGGGCAPGP SAPPARRRVPLAMGPRNLLIDW IWIMDTTLGLGTEGGGHSPPVL PLCASVSLLGGLTFGYELAVISG ALLPLQLDFGLSCLEQEFLVGS LLLGALLASLVGGFLIDCYGRK QAILGSNLVLLAGSLTLGLAGS LAWLVLGRAVVGFAISLSSMA CCIYVSELVGPRQRGVLVSLYE AGITVGILLSYALNYALAGTPW GWRHMFGWATAPAVLQSLSLL FLPAGTDETATHKDLIPLQGGE APKLGPGRPRYSFLDLFRARDN MRGRTTVGLGLVLFQQLTGQP NVLCYASTIFSSVGFHGGSSAV LASVGLGAVKVAATLTAMGLV DRAGRRALLLAGCALMALSVS GIGLVSFAVPMDSGPSCLAVPN ATGQTGLPGDSGLLQDSSLPPIP RTNEDQREPILSTAKKTKPHPRS GDPSAPPRLALSSALPGPPLPAR GHALLRWTALLCLMVFVSAFS FGFGPVTWLVLSEIYPVEIRGRA FAFCNSFNWAANLFISLSFLDLI GTIGLSWTFLLYGLTAVLGLGFI YLFVPETKGQSLAEIDQQFQKR RFTLSFGHRQNSTGIPYSRIEISA
26614	56982	A	26765	201	632	NLLLCPLSAESRPEEGVRLFCSQ FRSRQRPQAHKSAWGTTALSES MNCFASFGASISSSADQEQLHL PGAVGSGRPGECLGPSGRCSK* GATFPGQKGRWKEARPSPVPAP AAGLQSRAGHPRGGIRPGRPHG ERDSAACWGR
26615	56983	A	26766	197	777	LPSRGAGLRTCSPPCLSLPPTPW TPVRPEPPQRAPPPTPRRPVPST TQGLRNASARRGTGR/PAPP/VS PGAGSTR\EASWAPESAARAGL WGPSNSVQRAAESASRPHGFG QPPKAPARPGWLTGKFPASVPS ASRRAPPAAVTSARHYYLRQPP PRPSSCPECNKIRLWPAFQLTPL CQGPAASERDRRKPQKRR

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26616	56984	A	26767	178	697	ATLFIQKHQSGVKSTNP*IGRRS LTPEITAELGLERLNPRRCSSCL LGLKFEYHNSNLPLQLHGQAC GDPTNSVQRAAESASRPHGFGQ PPKAPARPGWLTGKFPASVPSA SRRAPPAAVTSARHYYLRQPPP RPSSCPECNTIRLWPAFQLTPLC QGPAASERDRRKPQKRR
26617	56985	A	26768	1	858	
26618	56986	A	26769	10	1332	
26619	56987	A	26770	1	1086	
26620	56988	A	26771	1	1392	
26621	56989	A	26772	1	987	
26622	56990	A	26773	1	336	
26623	56991	A	26774	46	302	APGAVKKTWFGKKGREREKQE RR*RQLGKENENIVALQLIRTD QEYWRHHSWHFFLSAAACQPE LFLLKHTAKNNRRIRVSQKWK
26624	56992	A	26775	1	1839	
26625	56993	A	26776	284	816	APGAVKKTWFGKKGRERGETR EKNNQPTVRTNSQTRDTFFKT* DLF*RMPSWELPSPASS*ASKTI KYLGIQLTRDVKDLFKEKYKTL LNKIKEDTNKWKNIPCSRIGIINI MKMAILPKSGPSAARLLEFAGG PLQTLFAWVSPEEAAEQQILPN SQSCYLILPLEASSQRGSWLY

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26626	56994	A	26777	1	2547	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSKEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIREELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITTDPTEIQT TIREYYKHLYANKLENLEEMD TFLDTYTLPRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGLT AEFYQRYKEELVPFLLKLFQSIE KEGILPNSFYEASIILIPKPGRDT TKKENFRPISLMNIDTKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDNIQQPFML KTLNKLGIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELP\FTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIMK
26627	56995	A	26778	1	489	SISWKLWFTEFTLFRFFQPSVSA VPVSTLAVVLGLKTLSLLFSHSF PGRHSWALRAISLLPSFLYTSSL MNSFSYTVHLYLGGLLRLCGSR DPHACGFPEGSPLPSGSAA*PFI WGMRKPSCVLAPSCSRRDSFG CLSFSGHQCLHKSHVGSPSGPQ ERLYNG
26628	56996	A	26779	354	685	YRGYLRGECFP*KALCCEPAAY LQTCPNPFSGPACSGHALHSLN VGDCVYLICPRYPPLRRAGKPR DTGIEGRTLSSGGPSVHSSFHSA VLFPYTSKLLWIERRRPAGQS
26629	56997	C	26780	1	867	
26630	56998	A	26781	139	513	
26631	56999	C	26782	1	948	
26632	57000	A	26783	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCRR*PYSRGT

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26633	57001	A	26784	1	224	SRAGYDHVVEPVERGTSGVRW YACCGLMVCPANPQHFAHGY/ VGKIPGYPARAGTLTGLHPMQ VCRCRRCPVYEI
26634	57002	A	26785	112	254	
26635	57003	C	26786	1	567	
26636	57004	C	26787	1	543	
26637	57005	A	26788	165	633	RIPGLLLCPAYPQHFAHGYVDK IPGYPGR\GTLTGLHPMQVCRC RRQAPCMKSNNALIVILGTVTL DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWIYPLVNS
26638	57006	A	26789	264	800	ISNFELCSRSIHLLCSSTGYPGR AGTLTGLHPMQVCRCRR*PAV
26639	57007	A	26790	1	738	
26640	57008	A	26791	84	162	AVLDLGPPTGRDPPQGSPDPYS GAFLLASCGAPLGQRSQRKEQ AAIFAVLQLLLVIPPGVGGTQT NRVWSGFPANHGNPGYPGRAG TLTGLHPMQVCRCRR*PPYRVI PQCGTPLGQGQPEVFVKQFWIL GLRLGETPHRGHQILIQGHSC
26641	57009	C	26792	1	531	
26642	57010	A	26793	216	519	QRESTIPSRPVERSNLGVRLYAC CGLLLCPAYRQHFARGYVDKIP GYPGRAGTLTGLHPMQVCRCR R*PDRRGTERVSARKHVCFVVV SLFVAACRPPLRA
26643	57011	C	26794	1	606	
26644	57012	C	26795	1	1059	
26645	57013	A	26796	1	3285	
26646	57014	C	26797	1	1390	
26647	57015	A	26798	211	679	RIFKCKADLLLYDMLVYVTLWI HRAVTYTHRVPNHSYRRSNIKS ETTVPTRIVGPVERSNLGVRLY ACCGLLLCPAYPQHFAHGYVD KIPGYPGRAGTLTGLHPMQVCR CRR*PKPAPLPGSPQHLCSHQPH LAQRKTGQCFLQGHCFPEKNW GTV
26648	57016	C	26799	1	774	

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26649	57017	A	26800	542	1269	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQRKYP GCRLYASCELLLCPVNPQHFAH GYVDKI\PGY\PAGAGTLTGLHP MQVCRCRRQAPCMKSNNALIV ILGTVTLDAVGIGLVMPVLPGL LRDIVHSDSIASHYGVLLALYA LMQFLCAPVLGALSDRFGRRPV LLASLLGATIDYAIMATTPVLW
26650	57018	B	26801	1	1531	
26651	57019	A	26802	1889	2154	
26652	57020	A	26803	147	162	APSLHLKDTVDRSNLGVRLYA CCGLLLCPAYPQHFAHGYVDKI PGYPGRAGTLTGLHPMQVCRC RR*PGAHTVVDIRPREDHLGSA GQPNCPENGCLQGFHTGLAYPE HHPCI
26653	57021	A	26804	2381	3641	
26654	57022	A	26805	1	2367	
26655	57023	A	26806	1	488	MDLLYMAAAVMMGLAAIGAA IGIGILGGKFLEGAARQPDLIPLL RTQFFIVMGLVDAIPMIAAIAFV LFVLFCMKYVWPPLMAAIEKR QKEIADGLSSAERAHKDLVLAK ASATDQLKKAKAEAQVIIEQAN KRRSQILDEAKA*GRQEPLVQV FLESARKR

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26656	57024	A	26807	2125	2435	VSPRQKSARPDLT*IRTLLCKVL GVLFSVAGGKKGPTCILQILKG QRRQEA*CISVMAERVWASGQ A*WEVWLHWAKSIDWFLFWK QHVHALRVRLDTCLFSLEEGSS FWNQGLTWKVVRRTFSESINH TPRITLGVPYSVHGIQLPGLLNF GEFKVCFVLSPRIFNLTHENFLS SEGPERRGLLGATFNCLNKRLA KYRMRNVHPKPKLVRYLHSRL PPEPAAAP*AWCGPRHLSRRQM SSSSQIGNDSFQLQVTPVHLLPL SHTTRKNPEMYDLPLLIFNPQES AILQLFHQDGECLHCSPIVGDW CHLGHSQACPSFHVPSGLFVPS LLCGAAFGRLVANVLKRYSVC VRVCAHVHVCARVRVYACVC VRMTISLTVILIESTNEITYGLPI MVTLMVSTLPPGPCQAQGHVR PTGPIFRSLLEWETEVEMDK*G HDFAHVLVSECISSEA*GMLLL GGGPDRSLFSTFRAVWSLSRLL DSVIAAGKQ*A*RT*SVGYSLL CPDLKGDPSAVFILRTTVHHAF PVVTENRGNEKEFMKGNQLISN NIKFKVKKTA*EERQVRDKRSR LTRLSALPIRNMCDEHIASEEPA EKEDLLQQMLERR*EPGGAPTA RRATQRWGEPLAQML*LTFHG LILRSQLVTLLVRGVCYSESQS VSLSEAEISQARPDEARGVGRC RRADLTLLNPRMIVVRRAAPAC
26657	57025	A	26808	24	369	
26658	57026	A	26809	4	371	
26659	57027	A	26810	82	703	
26660	57028	A	26812	1	1692	
26661	57029	A	26813	293	563	NVWPSSSVRGRNE*GREGGRR RTQQAAGLGPAPSDLWWLWLS WCLQKNMSQGGENLPAGPGSC CGREAQEGAGTSLEDAPFFEAQ LLQLH
26662	57030	A	26814	1	488	VARLYWKRPSLHACHFRDPRA GLSENPRLLQCSPSSSSGNVWG PHLYAVPCL*NGRIIPSPWNYRS LNSTTSSTCSSFAVVSSPSCPWV QLPGSCLLSRSLLQRVAWSQAP VPMRSEQDQLQKPPPPSAGLPA SVHANL*PGDRKGSVWTPAGV AQIPSPWP
26663	57031	B	26815	51	90	

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26664	57032	A	26816	299	707	RPPCRISCHPHTRCEGGRLRSRS PLLS*MPLSHPQGPSQPPAGSMS SSPPATTSTCSCSPPAAGCTRGR TTGRPFWTASGPAELDWASGSS VGL*SQGSQLGACGASYAGLG VPPRLLGPMTSCCMSLPFPSPAR P
26665	57033	A	26817	146	330	TVARRMELTPALLRALLNGILPI SEPPSNRIFACWGKPAWTACCN SLRARR*RAISCCPSH
26666	57034	A	26818	1326	1694	IFGWFGACCSLGSCCVVFTAST CTTVCGGCAIKVGSCLSLATMG CCVCCTSGLGCACSCWRGVSF* CLMESWGICGSLCWSWSACRW MVCFCLVWKHCRVFTCS*VCS SGGWLSFCCLADCD
26667	57035	A	26819	1	1407	
26668	57036	A	26820	75	1397	SRGSGREKFPAQLSYQTLLGKG PIEGTSLSNLAQQRCKEHHCHF LREQGPNCLIIERFMDRYTGKYI HMASHTTRCRPHVSRRPKARLL APATRSRSARARLRETRVRRGS PSCLWLNRRSRLPAEHSVRSPP RDMVFESLGLPSTKSSEFRSAA PEAAERAQPGDPCGLQTPAPLR PGFRRNQDPASAAAAAEEVRS GGGRGRILATTLWGCNTLCITQ YTRIRKLTLVYCGVESKQEWG EYHEGVQAGLTRPGRSPKLISK FLEKELTDRNWDQEDEAEEVK SSFPKND*VLKNRAIKKAKRRN VGFEVSAPLQLLLFKGLVVPSG GGRFSGFGSGAGGKPLEGLSNG NNITSAPPFASAKAAADPKVAF GK*LPSPSRLLVDKVSNPKTNG DSQQPSSSGLASSKACVGNAYH KQLAALNCSVRDWIVKHVNTN
26669	57037	A	26821	3	89	AASGRSFRGYSRRHCYHRR*QL HACHCP
26670	57038	A	26822	150	383	LCLGEVWKGSFFLTGTKRPGVF LSLHKKACYHHNHHRYHHHH HHQTKP*QQELNSLLLHFPPHQI QGDQFHHHLYYL
26671	57039	A	26823	105	417	LCLGEVWKGSFFLTGTKRPGVF LSLHKKACYHHNHHRYHHHH HHQTKP*QQELNCENMPQYNF QNGSQSYQTLLL/SLSTKFM*YS KFFVVISVMFIASSPETDF

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26672	57040	A	26824	89	554	AMNSCVTGDRYSPCGGFGFAF LYSSVSVSSSSEYQLSPLPPAKR PLAAQQSCSIPIASVFQQTIHSLF AKDKKEFSSNLLDSKVNMCHE AHQLISHS*ANFRSICHIPQRW* NLIFEKFSDVSMGSGTFG**AEN WS*TLSIAASLVYSLLHKIQ
26673	57041	A	26825	84	239	ACTKKACYHHNHHRYHHHHH HQTKP*QQELNSFRFSLSQPSLL AVFLFLRP
26674	57042	A	26826	2	245	
26675	57043	A	26827	154	546	LIVTVHVNHLGVLINHRFRISGC GVCGTDCISHKFPGAADATGPS WTTHCAVITFSLTTGSATKKTE DNNTFVFNVDVKAN*HQITRA VKKLCDIDVPEVNTLPNVSISFR FLLCSTVFCTLTVFFLRENG
26676	57044	A	26828	331	612	NHRGLPFPDYIPGTYFLFFFFLF FSFSSFSSSSFSFPASGNHNSTLY FYGINFFSFHIGMRMGGIFLCLT CFT*HDVLQAHPHREGRQDLLF HD
26677	57045	B	26829	928	1617	
26678	57046	A	26830	95	929	
26679	57047	A	26831	3	1128	LYNRRRRRRCSHCRHRCRRLSS GLRKEEVISLGASLGRVFVPCSP PTVSAARGPTGAPGGPNSKPLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNLVEILP AIFSSFLNLQHVNLWFLAAAM KAVTEQGHELSNEERNLLSVA YKNVVGARRSSWRVISSIEQKT ERNEKKQQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKCRLSNYFRYLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFLTILIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTLC DI*P*QNSACVINFILFLNILRDN LTVSTTSTGFIVSFLFTYLIIHCY LQEVCSVSLCTLNIYPLCDKKK
26680	57048	A	26832	139	601	EGRGHLAQELLSERVFVPCSPP TGMTMDKSELVQKAKLAEQAE RYDDMACSSERHVTEQGHE\LS NEEKKSCSLVAYKECW*APRR\ SSW\RVISSIEQ\KTERNVEGSSR WGKEYREKI\EAELQDIC\NDVL ELLDKYLIPNATQPESKVFYLK MK
26681	57049	A	26833	70	122	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26682	57050	A	26834	179	876	CIVILFFFSQFNFVGRILGPRGLT ANVNRYLELHTLYGYMNLFIV SIMKDVLSL*RE*F*SCTL*IF*E EQNRGKPNWEHLNEDLHVLIT VEGV*I*LLYLWTVSNAFISCVF HV*AEGEDRYCCLYTSF*ISLLT VAALAFSLAATAQAAPRIITGP APVLPPAALRTPTPAGPTIMPLI RQIQTAVMPNGTPHPTAAIVPP GPEAGLIYTPYIYIISKYLWLLSS CSPEP
26683	57051	A	26835	3	915	AEAHPRLPDAADERQEAHDSLP NFCGIFNHLERLLDEEISRVRKD MYNDTLNGSTEKRSAELPDAV GPIVQLQEKLYVPVKEYPDFNF VGRILGPRGLTAKQLEAETGCK IMVRGKGSMRDKKKEEQNRG\ KPNW\EHL\NEDLHVLITV/EKV LQEQGQEIKLKRAVEEVKKLLV PAAEGEDSLKKMHLMELAILN GTYRDANIKSPSLAFFLAGTAQ AAPRIITGPAPGLPPAALGTPTP AGPTIMALIRQIQTGGMPNGTP HPTAAIVPAGPEAGLRYTPYEY PYTL\APATSILEYPI\EPSGCI
26684	57052	A	26836	1182	1360	KLSICVYIYICMFIYTHVSV*FYI YIYTHRHTENHYFCNSVQFVLY LFTFFCYYFIWPA
26685	57053	A	26837	3	348	RNSKHVCRAEP*GHFCYK*HF WNHTEHTAVLEI/EQINARDET DF\YLGNRCTYVCKEQHSGPGS KSNTTIVIWGKVTCAQGKNSV VCAKFQSHPPAKAIGHRIHVML YHWRIQIH
26686	57054	A	26838	264	527	NSKHVCRAVP*GHFC*K*HFW NQREHTTVLEIEGVYARDETEF YLGNRCTYVCKEQHSGPGSKS NKTRVIWGKERGSGWCRLSGR
26687	57055	B	26839	26	515	
26688	57056	A	26840	92	341	
26689	57057	A	26841	224	1111	
26690	57058	A	26842	2	592	HSLTGRCIFFLITGTSPGSPEMST TLKIMSSKEPSISPEIRSTVRNSP WKTPETTVPMETTVEPVTFSPQ LVFARLMTGVGLGAALPNLIAL TSEAAGPRFRGTAVSLMYCGV PIGAALAATLGFAGANLAWQT VFWVGGVVPLILVPLLMRWLP ESAVFAWRSISNKRA*FRDCRC CSAAIIW*RRFPFKSKPVM
26691	57059	A	26843	2	141	

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26692	57060	A	26844	1	978	
26693	57061	A	26845	144	647	
26694	57062	A	26846	1642	2652	FGILVLLALIVIWYNNFFGAETE AILPYDQYMHRFAAYFQQGNM ESNGKYVDRNGNVVDYQTGPII WGEPGTNGQHAFYQLIHQGTK MVPCDFIAPAITHNPLSDHHQK LLSNFFAQTEALAFGKSREVVE QEYRDQGKDPATLDYVVPFKV FEGNRPTK*ILLREITPFSKLNEV KAISDTICVIRDGQHIGTRDGIE HLTAWHPVNRHIKRVNDVSFS LKRGEILGIAGLVGAGRTETIQC LFGVWPGQWEGKIYIDGKQVD IRNCQQAIAQGIAMVPEDRKRD GIVPVMAVGKNITLAALNKFTG GISQLDDAAEQKCILSHPRCSW QGRHLLH
26695	57063	A	26847	52	137	
26696	57064	A	26848	1	1858	MGLKVDDKVPLFAVVSRLTSQ KGLDLVLEALPGLLEQGGQLA LLGAGDPVLQEGFLAAAAEYP GQVGVQIGYHEAFSHRIMGGA DVILVPSRFEPCGLTQLYGLKY GTLPLVRRTGGLADTVSDCSLE NLADGVASGFVFEDSNAWSLL RAIRRAFVLCQGQFHHRTTDVE YKGDPKAVKIEESEINYLLNVY NTHFKKQLSRDDIVWTYSGVR PLCDDESDSPQAITRDYTLDIHD ENGKAPLLSVFGGKLTTYRKLA EHALEKLTPYYQGIGPAWTKES VLPGGAIEGDRDDYAARLRRR YPFLTESLARHYARTYGSNQRA ACSAMREREARTLPQKLAGTL GMLSKVMRIPRQQEVTALRTY LQIRIGLHAAFNACEEMCQRVA LERQLDSEERALLIERSQTVIRQ GRDLLHAWDATWNSAQALDN ALQPDRAGQFADALEKYAADE SFFAQLDKYDIPVVVIGKVEGQ YAHVYSVDTDNFGDSIALTDAL IESGHQNIACLHAPLDVHVSVD RVNGYKQSLAAHNIAVRDEWI VDGGYTHETALKAARQLLSQS PLPEAVFATDSLKLMSIYRAAA EKNI\AIPQQLAVRILFGLHL*IV LSTRAGFGNLAHY

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26697	57065	A	26849	136	3261	PMSPTIYDIARVAGVSKSTVSR VLNKQTNISPEAREKVLRAIEEL QYQPNKLARALTSSGFDAIMVI STRSTKTTAGNPFLLEVAQAFP AKAE*KGFQVLVRTSHNPAEDL QKCESKIKQKMIKGIIMLSSPAD ESFFAQLDKYDIPVVVIGKVEG QYAHVYSVDTDNFGDSIALTD ALIESGHQNIACLHAPLDVHVS VDRVNGYKQSLGAHNIAVRDE WIVDGGYTHETALKAARQLLS QSVSLSVAVSWSAC
26698	57066	A	26850	73	174	
26699	57067	A	26851	252	575	PGFPRGPPPPPGFAPFHVSIWDT DLSDPAARAGLGVRWTPDPPR RAARSPVLPRGLSAGQRPAARL LGGMEEGRFRQVAVFSES*SAV CPPPSPPPLSPLAPWTETA
26700	57068	A	26852	1	462	AQSVNSQTFSELRATQTFYKTT SHNSPGVFHTSTKR\FIDGNPPGI FSAITA*RLMMP*RSSIFSASASI LSVSFSGSTCNNDQRPARFGVL *DTRGETGCA*TGRPRRAR*LR RVEVRAV*LLRVRARNGAQMA LVKTPCQTSAHNAPCRGRE
26701	57069	A	26853	692	918	
26702	57070	A	26854	1	2427	
26703	57071	A	26855	1347	1978	LPHCVANHGCALR*QKWVHD KEQTTQTLKMVAENGRWVIDD IVSNHGSVLQAVNSENEKTLAA LASLQKEQPEAFVAELFEHIAD YSWPWTWVVSDSYRQAVNAF YKTTFKTANNPDEDMQIERQFI YDNPICFGEESLFSRVDEIRVLE KTADSARIHVRFTLTNGNNEEQ ELVLQRREGKWEIADFIRPNSG SLLKQIEAKTAARLKQ
26704	57072	A	26856	1	733	LSEVDVDVRQSIHSAHAKTLDT QGLRNEFLVEKVFVADEYTMV YSHIDRIIVGGIMPITKTVSVGG EVGKQLGVSYFLTSNRRTINKY LVPDVLETCQSSMGLTELAPGN *WNTMPCHTHERRMEVYFYFN MDDDACVFHMMGQPQETRHI VMHNEQAVISPSWSIHSGVGTK AYTFIWGMVGENQVFDDMDH VAVKDLRANHHQRFIISQRSDI HLTTQWIKRAAQTIHPPVSIIQQ IVAFFE
26705	57073	A	26857	2	255	
26706	57074	A	26858	1	597	

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26707	57075	A	26859	2	640	EARGRQPQLHHLPHPPRASSPP LALQPLGRSRRCPPPPGAAAPD PRPDMGDLPGLVRLSIALRIQPN DGPVFYKVDGQRFGQNRTIKLL TGSSYKVEVKIKPSTLQVENISI GGVLGPLELKSKEPDGDRAVY TGTYDTEGV\TPTKSGER\QPIQI TMPFTDIGTFETVWQVKFYNY HKRDHCQWGSPFSVIEYECKPN ETRSLMWVNKESFL
26708	57076	A	26860	218	426	TQPRVWSQAQ/RALQPDTELPQ PPQTPKSDTDQMLSVKKKKKR KKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKLYFQT
26709	57077	A	26861	1	423	
26710	57078	B	26862	1	252	
26711	57079	A	26863	1	171	
26712	57080	A	26864	5	254	
26713	57081	A	26865	16	220	ILDTSPMRWTQKNFSMILAQPE QQCKTLSQNKNKDRRIKKKEE KKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKKKEKE EEKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKK KKK
26714	57082	A	26866	32	286	
26715	57083	A	26867	1	847	EVKDLYDKTFKSLKKEIKEDLR RWKDLPCSWIGRINIVKMAILP KAIYRFNAIPIKIPTQFFNELEGA ICKFIWNNKKPRIAKTLLKDKR TSGGITMPDLKLYYRAIVIKTA WYWYRDRQVDQWNRIEDPEM NPHTYGHLIFDKGAKTIQWKK DSIFNNWCWHNWLLSCRRMRI DPYLSPCTKVKSKWIKELHIKP ETLKLIEEKVGKSLEDMGTGER FLNRTAMACSKKKEKKEEEED EEEKEKEKEKEEKEKEEEE\KK KKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKK
26716	57084	A	26868	1	376	MLMKDPQWNSSIFISTHLALQQ KRRQAEYGAQEPSRRIVGGKGS GAQVDEEEEEEEEEEEKEE\KK KKKEKKRKKKKKKKKKKKK KKKKKKKKKKKKKKKKKMLL LSLPMIRPRLPHPRWASSPSSMV AKP
26717	57085	A	26869	1	2031	
26718	57086	A	26870	1	957	

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26719	57087	A	26871	171	495	SQLLDMRKPFQKPGLRQLKTLP QYLNTR/CILDYLDNISPQQIRK LFYVLSTLAFSKQNEASSHIQD DMHLVIRKQLSSTVFKYKLIGII GAVTMAGIMAADRSESPSL
26720	57088	A	26872	1	3114	
26721	57089	A	26873	173	397	
26722	57090	A	26875	823	1194	
26723	57091	A	26876	1	1263	MESNAVQLTRMEYAMKSLSLL YPKSLSRHVSVRTSVVTQQLLS EPSPKAPRARPCRVSTADRSVR KGIMAYSLEDLLLKVRDTLML ADKPFFLVLEEDGTTVETEEYF QALAGDTVFMVLQKGQKWQP PSEQGT*WRRTQRKDSPVSRPC STHGLQEIQL
26724	57092	A	26877	128	317	
26725	57093	A	26878	431	574	
26726	57094	A	26879	112	482	EGPEAKPKRSNCAPEKRSSPIPD WEPAFSEDGRARTVARLQHPPL GGPTHRYHHFLRRHDPPLRVHP AAERQEAHPGTSI*QSSPNSKQS PQGKWKITFPNSLSLTRKYYFQ QPRGWDFFKKT
26727	57095	A	26880	3	179	
26728	57096	A	26881	977	1127	
26729	57097	A	26882	121	708	
26730	57098	A	26883	38	828	GSRLRRLQAAAARPALPLPLPP WEWKHLPHVPEAKWWLTTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESLDLAEFAK KQPWWRKLFGQESGPSAEKYS VATQLFIGGVTGWCTGFIFQKV GKLAATACGEVDF/LLLQLANH TWVHQSLTGNEWEKDIEESPKS SLKIRKSQSDYLLRSGAKAAGR WCHFVKKNVLVTWGIFPEAFC LAWHPKEDDLHVPLFPGFFPSQ QPFTLHHRDIESLLLFFPWPSFP GHWEN
26731	57099	A	26884	1	642	
26732	57100	A	26885	1183	1349	

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26733	57101	A	26886	1	1371	MSFLIDSSIMITSQILFFGFGWLF FMRQLFKDYEIRQYVVQVIFSV TFAFSCTMFELIIFEILGVLNSSS RYFHWKMNLCVILLIL/VFPMV PFLQLAYFIVSNIRLL\HKQRLLF SCLLWLTFMYFFWKLGDPFPIL SPKHGILSIEQLISRVGVIGVTL MALLSGFGAVNCPYTYMSYFL RNVTDTDILALERRLLQTMDMI ISKKKRMAMARRTMFQKGEVH NKPSGFWGMIKSVTTSASGSEN LTLIQQEVDALEELSRQLFLETA DLYATKERIEYSKTFKGKYFNF LGYFFSIYCVWKIFMATINIVFD RVGKTDPVTRGIEITVNYLGIQF DVKFWSQHISFILVGIIIVTSIRG LLITLTKFFYAISSSKSSNVIVLL LAQIMGMYFVSSVLLIRMSMPL EYRTIITEVLGELQFNFYHRWF DVIFLVSALSSILFLYLAHKQAP
26734	57102	A	26887	1738	2140	
26735	57103	A	26888	81	733	
26736	57104	A	26889	1061	1154	
26737	57105	A	26890	1	3207	
26738	57106	A	26891	113	367	
26739	57107	A	26892	2	1391	
26740	57108	A	26893	154	647	
26741	57109	A	26894	40	747	
26742	57110	A	26895	1	3186	
26743	57111	A	26896	271	491	
26744	57112	A	26897	304	1836	
26745	57113	A	26898	1	2343	
26746	57114	A	26899	1	765	
26747	57115	A	26900	318	473	
26748	57116	A	26901	2	426	
26749	57117	A	26902	1	433	
26750	57118	A	26903	2	1004	
26751	57119	A	26904	125	199	
26752	57120	A	26905	3	156	
26753	57121	A	26906	2	397	VDGMGWSQDLFRALGRSLSRE GKEHVGTDQFGNKYY*SRSTK TGEVRWRRGQRLRGQ*LRGQT IREKRIVEAANKKEVDYEAGDI PTEWEAWIKRTRKTPPFMEEIL KNEKHREEIKIKSQDFYEKEKL
26754	57122	A	26907	1	1350	
26755	57123	A	26908	1	582	

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26756	57124	A	26909	2	687	GARQVLPGESPCFSSS\AKIVKP NGEKP\DEFESG/LSPQALLEL\E MNSD\LKA\QLREPELLRPA*GK LKVGGCSENLSI/ILLFPVPSN*K SFPENPQVRA*YRELEKK\FQW GSHVGLYRPQRRILP*AQLRKK PVQKNKQKASPRARTLTAVHD A\ILEDLGLPQAKIVGARESRVK L\DGSRL\IKVHLDK\AQQNNVE HKV\ETFSGVYK\KLTGKDVNF EFPRSFNCKQK
26757	57125	C	26910	164	208	
26758	57126	A	26911	2288	2625	GSEGHLPITKRWSSLWEWRKG LSEVGSCKRNLVRCLRTAI/LM GGEAGVIHCKGHQKASDPIALG NAYADKVARQAASSPTSVPHG QFFSFTLVTPTYSPAETSTYQSL PTQGK
26759	57127	A	26912	1	400	
26760	57128	A	26913	3	277	
26761	57129	A	26914	1	630	CEIKNRKAAEKVNKTKGKFFEI NTYPGPIKTGEPSGQTQKWLDI VRNTLVEEDTSSWSWRAHQPK STLTGTGRPSTNGTMSSLARTV REEPGNQPNYRGKPSPFWFPHL VRAASTQPVITRLLQHGRLKPI NSPYNFPILPVLKPDKPYKLVQ DLHLINQIVLPIHPVVPNPYTLL SSIPASTTHYSVLDLKHAFFTIPL HP*FQPLFTF
26762	57130	A	26915	1	384	
26763	57131	A	26916	1113	1319	GRDPVSAFYIWLASFPNTIY*IG NPFPIACFSQVCQRSDSCRYAA LFLRALFCSIDLYLCFGTSTMLF
26764	57132	A	26917	2	2144	
26765	57133	A	26918	99	470	
26766	57134	A	26919	636	1220	GPGFQAQNCAAIWADTKLAAG IFSHTPVAPGTPVRQNHLLPWD APAWSGEECLPLLRLVYVVFPS QCKQSCQEV*TGQSPPQLGKAF VARLPL*IPSLWAGHLFLEHPV YCCGCVTAGRQGSWKGQRRH GHPFPLPLLLLQMVCCSISYQY DYPESSFLLLFLSSLCSAGKSTG SHAILLGSAFVLPHLVALRS
26767	57135	A	26920	10	161	RLRMVRDIKVLLNTRSLRNCLG DLTNKGRSIIGPPL*ELSKASVM VPVGF
26768	57136	A	26921	1	855	
26769	57137	A	26922	5	1442	
26770	57138	A	26923	1061	2332	

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26771	57139	A	26924	804	1100	SPKGGPPDPSHGTKFHSRPCEET TKQAFCEQHGCLFHLGTLGALL G*QRWLHQLSRPSLGCNESKSL FQ*PPLP*E*KEIQCKVPPNLGL GVRSGKGF
26772	57140	A	26925	3	1186	
26773	57141	A	26926	126	363	SRSKDQGLDPSGTWCKRAFSPG PWPIIPVAAGGGGHSGGGKSET PAHLQKGLHKVKNC*PSTYSVC QTPDAEHPVSNK
26774	57142	A	26927	1	1125	
26775	57143	A	26928	401	446	
26776	57144	A	26929	332	499	
26777	57145	A	26930	74	200	
26778	57146	A	26931	300	416	
26779	57147	A	26932	324	430	
26780	57148	A	26933	60	381	
26781	57149	A	26934	2344	2453	
26782	57150	A	26935	131	274	
26783	57151	A	26936	144	444	GGGENFSYPWYLLVGCGWFSS SPIVPDVPPFSLLLPAQKKKPAP PK\PEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK
26784	57152	A	26937	540	811	
26785	57153	A	26938	69	375	QHLRPAAVAAATMPKRKAEGD AKGDKAKVKDEPQRRSARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKADAGKEGNNPAEN GDAKTDQAQKAEGAGDAK
26786	57154	A	26939	9294	9486	SLLYQPRCMAFRIKASS*RGMP GGSASAARKPTG/SPGREGAGR RGQWGPRNCCAGRLPGGESTV
26787	57155	A	26940	248	613	
26788	57156	C	26941	94	234	
26789	57157	A	26942	2157	2408	
26790	57158	A	26943	547	815	
26791	57159	A	26944	254	467	VFLISVYNGLAISLYLGIHIRQK PVMPRNPLNCFGVLG*G*AGIG *IRSSLRTLVPLDNFSPKYLTFC EQS
26792	57160	A	26945	238	391	
26793	57161	A	26946	232	1659	
26794	57162	A	26947	1	951	
26795	57163	A	26948	1	2046	
26796	57164	A	26949	3	97	SVR/SKFYVREPPNAKPDWLKV GFTLSVEL*M
26797	57165	A	26950	1	828	

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26798	57166	A	26951	224	475	AGPRKMAPSALLRPLSRLLAPA R\LPSGPSVR/STKFYVREPPNAK P\DWLKVGFT\LGTT\VFLWIY\L IKQH\NEDILEYKRRNGLE
26799	57167	A	26952	1	411	
26800	57168	A	26953	442	2490	
26801	57169	A	26954	3	1592	
26802	57170	A	26955	9	308	
26803	57171	A	26956	153	227	
26804	57172	A	26957	1	411	
26805	57173	A	26958	517	825	
26806	57174	A	26959	6	646	
26807	57175	A	26960	1	275	
26808	57176	A	26961	3	272	
26809	57177	A	26962	1	1002	
26810	57178	A	26963	1	1791	
26811	57179	A	26964	2	160	HMTTSLLAQSGFQKTSALNKIT TKGSH*VQFTSLLPPPERVLVS MAERPWGG
26812	57180	A	26965	1	892	
26813	57181	A	26966	1	549	
26814	57182	A	26967	234	387	SCLEVCDEQGPEK\TRQRALRG VSSVTEDTLNICRLCWQPLPEPL ELWPKAL
26815	57183	A	26968	269	501	RARSEGAGLWSVVAPSAVSVFF VSDPRCAPFHRSPSCCSP/RRPC LSLSA*SRPRASGVGACLLWQP LPEPLELWPKAV
26816	57184	A	26969	210	296	
26817	57185	A	26970	71	283	LRLGDLPSEINPLSSCSLLREKD PPTTSGPQT\TSPRNISPISNPDST GNRTVQLTWQPLPEPLELWPK AL
26818	57186	A	26971	1112	1180	
26819	57187	A	26972	71	284	LILGDLPSEIKPLPSCSLLREKEP PTTSGPQT\TSPRNISPISNPDSTG NRTVQLTWQPLPEPLELWPKA
26820	57188	B	26973	1	663	
26821	57189	A	26974	1	502	MLLTQSLFGGLFTRTHMKFGA VTQIRGPPLGDKSPVLLLFALER QRRHVLSMDPKLRCWSRTGKA AFPWCLIIAEMPDYSPTFQRCQ TTQGRLPWSFTLSSKSRFSGEG ARACYKCQKSDHQAKECPQPG IPPKPCPICAGP\TGNRTVQLTW QPLPEPLELWPKAL
26822	57190	A	26975	233	496	
26823	57191	A	26976	226	543	
26824	57192	A	26977	1478	1744	

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26825	57193	A	26978	3	450	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLIS LRPNPLCPHPDLVSLCPDPFPAF LEAHKNFQTTEPQQPGVPPEPP PTGACYTCRKSGHWAKECPQP GIPP\NHVPSVWDPTENLTVQLT WQPLPEPLELWPKAL
26826	57194	A	26979	615	724	
26827	57195	A	26980	1	1968	
26828	57196	A	26981	227	556	
26829	57197	A	26982	400	548	
26830	57198	A	26983	1	1968	
26831	57199	A	26984	65	741	
26832	57200	A	26985	1	658	
26833	57201	A	26986	1	666	
26834	57202	A	26987	67	608	NPGKGGCFVL/VLDGLLRDRKA V\IREETFDGWHPQDRPLPAHA\ LVAG\IDRPTPPQK*TA\AMGKK KDRPKRSKIKSFCGKCYNY\NH\ LMPHKGTLWDIPLGQNLFVQL RDVF\RDPGSLNRKA\RREGPRF KFE/EREYETGQETKWVLPRKL AGFKNAFGFDSLKIIKKKKKKK KKTTKKGRP
26835	57203	A	26988	1	352	
26836	57204	A	26989	1	1419	
26837	57205	A	26990	2	878	
26838	57206	B	26991	75	2931	
26839	57207	A	26992	229	724	IIFIVYSSQLTYVKISDSFQTFKF CLDFCLFFSEMS\FLSLNISSCS* YSAKVNSCGKFGLTKGSFSAPL TPLFFLCFGSELVEGV*ELLAVG GLHLARIFLCLSISSLC*FTHSCC FTRVTPINLASNNSCLLGFRLQS SSIAPSLGLLDGGVCFIRDLAAA
26840	57208	A	26993	737	1048	KKYNIQLEKPYFKHLYKNKLL KLSN*NMTSVQQFTIELEGNLS LSCIELVC/ILVTHCHLF/CMNK AW*QKKNT/WLSILTC*KHWQ YYNLVNSTDFNTSSSFLSKV
26841	57209	A	26994	1	1209	
26842	57210	A	26995	2	1683	
26843	57211	A	26996	1	1386	
26844	57212	A	26997	1	471	

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26845	57213	A	26998	2	514	VTARRRGTRWLRFRRASRVQK WLWLADFYLRYYVGHKGKFG HEFLEFEFRPDGKLRYANNH\N YKNDVMIRKEAYVHKSVMEEL KRIIDDSEITK\EDDALWPPPDR VGRQELEIVIGDEHISFTT\SKIG SLIDVNQSKDPEGLRVFYYLVQ DLKCLVFSLIGLHFKIKPI
26846	57214	A	26999	1	570	
26847	57215	A	27000	1	980	
26848	57216	A	27001	270	356	
26849	57217	A	27002	1	1032	
26850	57218	A	27003	1	1017	
26851	57219	A	27004	1	450	
26852	57220	A	27005	1	637	APIECGGIPSLPVLCQSRANDQE GVRLLEPSEAMPKSKELVSSSSS GSDSDSEVDKKLKRKK\QV\AS ENPVKK\QKTGETS\RALSS\SKQ SQPAARDDN\MFQIGKM\RYVS V\RDFKRQKCLI\DIREYWMDPE GEMKPGRKGISLNP\QQWEPSL KEQISGPLIDASKKTCKISEPILI KPCTVPVVLIWLFSIGFCFLNVL RSYCMFGLQKNL
26853	57221	A	27006	20	412	RFSPLSFLLAGDSCTCAGSCKC KECKCTSCKKSKWDPLFPLPLP CPPACPLSTILRGIKAVWGCPIA RKLLPPQ*SLSGRAGILIPGVAS THLCRLLSAPR\CCSCCPVGCAK CAQGCICKGASDKCSCCA
26854	57222	C	27007	32	505	
26855	57223	A	27008	854	1021	ALGGVAEYDLKEGLLLKH*AL VQSLVATEVRLVLCITSHTDML QICFFVYATVTQ
26856	57224	A	27009	1	726	
26857	57225	A	27010	99	537	
26858	57226	A	27011	1	963	
26859	57227	A	27012	146	609	VYLRCTGGEVGATSALAPKIGP LGLSPKKVGDDIAKATGDWKG LRITVKLTIQNRQAQIEVVPSAS ALIIKALK\EPPRDRKKQKNIKH SGNITFDEIVNIARQMRHRSLAR ELSGTIKEILGTAQSVGCNVDG RHPHDIIDDINSGAVECPAS
26860	57228	A	27013	3	501	
26861	57229	A	27014	1	1623	

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26862	57230	A	27015	53	1227	QPPVHTTPASSPCDD\DIAAL\V VDN\GSGMCK\AGFAGDDAPRA VFPSIVGRPRHQGVMVGMGQK DSYVGDEAQSKRGILTLKYPIE HGIVTNWDDMEKIWHHTFYNE LRVAPEEHPVLLTEAPLDP\RAT REKMTQIMFETFNTPAMYVAIQ \AVLSL\YASG/RVTTGIVMDSG DGVTHT\VPIYEG\YALPHAILR LDLAGRDLTDYLMKILTERGYS FTTTAEREIVRDIKEKLCYVAL DFEQEMATAASSSSLEKSYQLP DGQVITIGNERFRCPEALFQPSF LGMESCGIHETTFNSIMKCDVD IRKDLYANTVLSGGT\NMYPGI ADRMQKEITALAPSTMKIKIIAP PERKYSVWIGGSILASLSTFQQ MWISKQEYDESGPSIVHRKCF
26863	57231	A	27016	2	438	ADLLQVSNCVVSSCQPPAFLVL FSSSRLPAGEGRGRPGQTQRPSS LEGAWHSVTLERRCLVSHLINL REAGMYPSRPCHHLFPDQLV*T EGGF*RPRLGWQRCHGTPQQA PSQPAFRSKHPRKGMPALQQQP GSGLCRPLPCRCR
26864	57232	A	27017	112	493	AHSRTPARPENRAAASAPRKPR RAMSSPPEGKLETKAGHPPAVK AGGMRIVQKHPHTGDTKEEKD KDDQEWESPSPPKPTVFISGV\I ARGDKDFRPADAQVAHQKPHA S\MDKHPSPRTQHIQQPRK
26865	57233	A	27018	1	1176	
26866	57234	A	27019	3	307	
26867	57235	A	27020	86	179	SVKRRC*SLLTWIGMRLQRQHR ECLAEQVGS
26868	57236	A	27021	1	948	
26869	57237	A	27022	3	534	EGAHFRAAHHPRSTGSRCPGSL QPSRPLVANWLQSLPEMPVDFT GYWKMLVNENFEEYLRALDV NVALRKI/APTLLKPDKEIVQDG DHMIIRTLSTFRKLTSWNF\QVG KEFEEDLT\GIDDRKVHDKQ*A WDGDKL\QCVQKGEKEGRGW TQ\WIEGDELHLEMRVEGL\VC KQVFKKVQ
26870	57238	A	27026	1	2400	
26871	57239	A	27027	294	425	
26872	57240	A	27028	1	797	
26873	57241	A	27029	1	173	
26874	57242	A	27030	1	1047	

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26875	57243	A	27031	2	1019	PTSAPHSLSPRAVIERRSRALDW NASPSLSDPQGLDASLPFPSHKR SRTASPEPAEHPVMDKNE\LVH\ KAKLAE\QAERYDDMAACMKS VT\EQGAELSNEERNL\LSVAYK N\VVG\ARRSSW\RVVS\SIEQKT\ EGA\EKKQQMAR\EYREEIETEL R\DI\CNDVLSLVGKSSLIPNAFT SRRSKVF/YILENGKGDYLPFTL GWRVAAGWMDQERGLFDPVH NKAYPRKAFWKSAKKGNGNPT HP\IRLGL\ALNFSVFYYEILNSP EKACSLAKTAFDEAIAELDTLS EESYKDSTLIMQLLRDNFDIVG HRDTQGRRKLEGREEGRGENL TGPFPTFCSWPHS
26876	57244	A	27032	177	477	
26877	57245	A	27033	1	1290	
26878	57246	B	27034	49	1112	
26879	57247	A	27035	98	245	
26880	57248	A	27036	1	351	
26881	57249	A	27037	3	471	
26882	57250	A	27038	1	440	MKMRVGCMLTAESLSDGGNS HQRTLSLFEESKESQCEARGEV SKAGVWLVPLEPSSDALPKITS LVRPAVPWRPSSEAGLCEVRGG VLGKASKAPIKEPQLDRGMGL GAQRRGSSGTEVQSGETLGASG SPRGLLEPRPDWVSNNGAGSLG FQQLPIVDKIRTIAQAVCGAKDI ELCPEAQVKIDRYTQQYYSC*N PKLPAPLFETQSGLGSKSPLGLP LAPRVSPDCTSVP/GAP/SAAGP RAPCPDPAVAPLWGLCWPFPEL
26883	57251	A	27039	1	1113	MHQEDLRAWYLDLGLPSHQN AQPTAWKCQRAPSPYTHQDMA LIPSPTARWLSPEKEPKQGEVG EKSLLPDPTLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRLLADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIILCTLVNKLQPGSVP KIN\ASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANNLFESG NNMQVRVSLLALAGKAKTKGL RSGVDIRDKYSEKQNFDDTTM KASQCVIRLQITNKCASQSGMT AYGTRRHLYDPKNRILPPMDNS TISLQMGTNKCASQVGMTAPG TQRHIYDTKLGIDKCENSSMSL

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26884	57252	A	27040	347	1061	
26885	57253	A	27041	212	386	LQGSWVTSGLERICGSILGTIPL AHEVTDTQHGRMVYQVATAG F*SSLGAASIGTQGL
26886	57254	A	27042	1	1017	MHSRRERARGLRGAHHPLVDN GPPQSLRAPPLLSPLKTAGAKSI WEPLASARRPETPERTPLQKTP EQVPTNFMGALHMKTSAPLSS RNGEGRRGGTSVASCPWVVGA VCSAERQPCTQRVREALMGGW RAGAQNNRAEDQVDEFTEVGF RRWVIKNYDELKEHVLTQCKE VKNLDKSIHPEISRLHEFITTTHT LPVIGGKVSLLSKCQDNAEQKQ SQGCSQEGHEVYDPRLNSSSSS SSSGGGQSPGLRRCSTSAAAAA ALEGAALKPMPVHAGLVGSGE GGGAGAVAGPCSRWGATTAA ASSAQPAQPVRGGSSGAQGHR GGRRRQAGKGGPAG*TAAAAA AP\GRGAEPGAAALLNLGGGSG GAG\SAALKPMPVHAGLVGSG EGGGAGAVAGPCSRWGATTA AASSAQPAQPVRGGSSGAQGH RGGRRRQAGKGGPAGSS
26887	57255	A	27043	644	949	
26888	57256	A	27044	811	1886	
26889	57257	A	27045	1	410	HAHSLNSIILPTPLEIHKV*IQIY A*GCKRISNNCWHCHQHLLSIS PDLRINEGKECGPSPWIGVEAR/ MGGELSSAVGLTSLLLYQQVPF HPHFQSPTFIPRESILLQHASCW RQHHLHTGIYSSYLPGWKQEFS
26890	57258	A	27047	1	2445	
26891	57259	A	27048	1	457	
26892	57260	A	27049	1	873	
26893	57261	A	27050	2549	2728	ATSRSSALITSSKYPGKF*LILI* RSTLETANSISARLNNPFLRKYP SYFSLFMGTTRI
26894	57262	A	27051	277	394	
26895	57263	A	27052	2	1394	
26896	57264	A	27053	1	1091	
26897	57265	A	27054	1	1404	
26898	57266	A	27055	2457	2674	ANHCYLLSELQHWSDCPVVLQ SAG*RH*DRN*DGNQY*SR/SLS *SR*STTK*RNTPCSQVSSLSRLS TRSAP

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26899	57267	A	27056	716	1455	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGNYTSGDNHTLR/DPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG YVSNSLTGPYKPLNKTGLVLQ MVLIPNDVTFTYS\HFAVPQAK GNNVGIHQATLTN\RGFFEIKKA TFAPSFL
26900	57268	A	27057	66	197	
26901	57269	A	27058	379	905	AGNFVHITVRKMLWIRRDQQQ S/DKQDIQTAHRSYSVLKGYND MYYGWPCCKVNEISGQLASEP A*SLVLPAAG*QAPASGSPWLS GGPQQVEDAGAGYGFAPGQPP PPPRTQPRSACSRRAAGSQFHG RPLLPRQAAKARAPRSLGCGSL GRFSTGVRPDKCIFPPETENAA
26902	57270	A	27059	1	1608	
26903	57271	B	27060	1	1974	
26904	57272	A	27061	2712	3216	KTGRGPTDKFG\ANDPILKDQT\ QEWS\GSAPFTS\DGKFRLFYTD YSGKHYGKQSLTTAQNVQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTPFFRKESQK LQQSAKKRDAELANGALGIIEL NNDYTLKKVMKPLITSNT
26905	57273	A	27062	1	3066	
26906	57274	A	27063	1	972	
26907	57275	A	27064	14	273	
26908	57276	A	27065	42	302	
26909	57277	A	27066	1	487	MGLSLKGPESAPIPKTPQFNKIL FKPIAVYNRFTQFRLSETKEITN PYAMRLYESLCQYQRYQLPQS YQR\SLTSAAASCRSVLMRSTA ELQCASHTLRKRKAARRLISLS EMPRKQGDYRTRIWKFEDGLS NVLVIQLNKLIICVMCLVRDCD VLKTYFHR
26910	57278	B	27067	1	1035	
26911	57279	A	27068	132	230	CHYFACMWSGCEVYS*SAPG** C*EDLSGMVR
26912	57280	A	27069	1	2784	
26913	57281	A	27070	855	980	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26914	57282	B	27071	85	863	
26915	57283	A	27072	345	500	

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26916	57284	B	27073	1	1116	
26917	57285	A	27074	1	1173	
26918	57286	A	27075	1	999	
26919	57287	A	27076	771	908	
26920	57288	A	27077	104	547	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLFKFLKNGLNFLLHSVGTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDADDVLSTEVKRVITS SASNITPAFFCS
26921	57289	A	27078	34	1353	
26922	57290	A	27079	213	338	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26923	57291	A	27080	1	1246	MVKVGTSYVPINVSFSPKVGPG LPGINRDTRIYLFCEVIFRHRKD RESADLGSDGQNGPRPWIGEA VAAAAADGVTFSVPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRNRFTQFRLSETKEITNPYAM RLYESLCQYRKPDGSCIVSLKID WIIERYQLPQSYQLYYFELAIPV GYFYPGSFSTASRILLLHPRGLR AITIAVFGKQNTYIRLEPFKINV LEQITKHIEKLQCGGVVKQLSR RGNNQHISSTYDINRADYPG*A RDPHLMLRLAIETVAHDYDVIV IDSAPNLGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPWMEEQNSGCRGKTS RVEVPHRDSQFKVIKLVTLRQL VTLYDPVDFQRDDA
26924	57292	B	27081	1	1041	
26925	57293	A	27082	1	1011	
26926	57294	A	27083	2	1007	
26927	57295	A	27084	1	738	

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26928	57296	A	27085	1	1439	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRV WTPGINCPEPCPGVWTPGINCP GAWGIHGPHGSAENTGPLHPG QTSAQLETSLLPSLRSARELELA QLSPRRKQNRSLQNIGVTPSLR VPWPKASNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSAKK RDAELANGALGIIELNNDYTLK KVMKPLITSNTVTDEIERANVF KMNGKWYLFTDSRGSKMTIDV PQAKSNNVGITSYMTNRSFFED/ KKATFAPGFLWNIKAIKTS
26929	57297	A	27086	345	563	
26930	57298	A	27087	1	1188	
26931	57299	B	27088	1	1186	
26932	57300	B	27089	1	1090	
26933	57301	A	27090	183	410	
26934	57302	A	27091	1	1557	
26935	57303	A	27092	888	1165	CTRERRIKARGPPAGKRWLLLS GSSGRKHHL*QDPRPGSQTAGD LPEPAR\PIIVIGEGSQMGLDECQ FQFRNGRWNCSALGERTVFGK ELKV
26936	57304	B	27093	1	1027	
26937	57305	B	27094	1	1117	
26938	57306	B	27095	1	1377	
26939	57307	B	27096	1	1014	
26940	57308	A	27097	1040	1285	
26941	57309	A	27098	901	2277	
26942	57310	A	27099	1	1122	
26943	57311	A	27100	1	1137	
26944	57312	A	27101	1	1881	
26945	57313	B	27102	1	1211	
26946	57314	A	27103	294	506	NRRPGSAATVWAAAAEPSERG NNPALENR*SSGFSWGFFSGYQ RCRESRATTAPGYGNSRTG*AT CWLYN
26947	57315	B	27104	1	1073	
26948	57316	A	27105	1	1809	

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26949	57317	A	27106	1688	2187	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVA\RKDRES ADLGSDGQNGQDLDWGGG\AA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS INSTEVYTKVFALDVAARHRV QFAMPESDAVAMLSF
26950	57318	A	27107	782	1402	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLIKLLFYKIPSMLV SSVLLLEVKSHIVGPGLPGINRD TRIYLFCEVIFRHRYLFAISSWS GVTVA\RKDRESADLGSDGQN GQDLDWGGG\AAAAADGVTFS VPVTPHTFRHSYAMHMLYAGI PLKVLQSLMGHKSISSTEVYTK VFALDVAARHRVQFAMPESDA VAMLKQLS
26951	57319	A	27108	197	421	LAMPGAGFSSSLRMASIFSIHSV GTRDLSRVSTILSPLYNTVAPG AN*CRELKLVLDADDVLSTEVI RVITSSA
26952	57320	B	27109	1	934	

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26953	57321	A	27110	1	2047	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKTVDLKGFEPDVRILLTKYS NSNGSQSPWMEEQIRDAWGSM VLKNVVRETDEVGKGQIRMRT VFEQAIDQRSSTDTSLSTPAAP MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFSHPGELSARSGDALQ KAFTDKEELLKQQASNLHEQK KAGVIFEAEEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMALNLDRSRVPAYIIRSYIR CGRKGFASAGVGGCRGWLNY AASEQIVLRVHHMRCEIPHRCV
26954	57322	A	27111	1175	1298	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26955	57323	B	27112	1	1056	
26956	57324	A	27113	1979	2217	WLSVRVDGGANSGCLGKHGSK KCCT*NG*SW*RSDPDENCF*T EQ*STLFN\GAWRNALSIWEPV CN/GNFRSSD*TTLGD
26957	57325	B	27114	320	1633	
26958	57326	A	27115	606	705	
26959	57327	B	27116	1	4118	
26960	57328	A	27117	4048	4051	
26961	57329	A	27118	1791	1884	ADGCIIQIG*RLSPNKCL*TWSA LCKPIAE
26962	57330	B	27119	1	2436	
26963	57331	A	27120	1	2449	
26964	57332	B	27121	173	4112	

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26965	57333	A	27122	916	1568	HHSHEQQFQWPVGASGVDRW AGYLHQFRSLTQFQYGAEPDR KE*CQIFIFMQKTLSCLSILGKR TMSLMQ
26966	57334	A	27123	1268	1773	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVA\RKDRES ADLGSDGQNGQDLDWGGG\AA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEVYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
26967	57335	A	27124	606	852	HQILFDRTPVSVDQSVEKKG*D HSVRPQ*AAPGHVHYLTIPEKS SQHYHPRTTSE*TSGRYESSGG LSFSQCMRGALEFCC
26968	57336	A	27125	1	2680	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGTA SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCLALHRIETELMGKFDEGKL PTDPHLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEPDAETSQGAL GTLANVVTSLANLSESLNNGDT SEIQPEDQSASEITRAFDTLAKA LNTTDSSSSPSLADGIDTSGGGS IHVISRDQSTPIIEVEGPLLSDTH VTFKSIREDRNGRSQKTVHTEG DMNMNIKKIVKQATVLTFTTA LLAGGATQAFAKENNQKAYKE TYGVSHITRHDMLQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTVAEYNGY HVVFALAGSPKDADDTSIYMF YQKVGDNSIDSWKNAGRVFKD SDKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYLVFEANTGTENGYQGEE
26969	57337	A	27126	2014	2138	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCNPTAE
26970	57338	B	27127	1	7616	

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26971	57339	A	27128	240	719	HSKKLVTLSHGSVMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LPEHDGFCYIHVAQSAEITGLTS \GNPVRIYGRH*RVSRGRKVVL YRPEEDAGDEKGYESFPWVIKR AHRPSRGLFSGHIPPISHSLLYR
26972	57340	A	27129	1505	3812	
26973	57341	A	27130	471	566	
26974	57342	A	27131	1	229	
26975	57343	A	27132	121	303	
26976	57344	A	27133	183	524	MSTPRPPFVPAFVGRRPSLLFVP AARLTDVRGRKVRACGLLSPR LRSPSSSSATRVARHSIGRPRVA RLSTVFVAVCVESPSRQRRWCL FALAATPRAPGTLA*SCLTDSFS A
26977	57345	A	27134	1	1025	MIFVLQIRVRGHDDSFLKNHLV FLVIYGTNGTFNQTLVTDNNGL APFTLETSGWNGTDVSLEGKFQ MEDLVYNPEQVPRYYQNAYLH LRPFYSTTRSFLGIHRLNGPLKC GQPQEVLVDYYIDPADASPDQE ISFSYYLIGKGSLVMEGQKHLN SKKKGLKASFSLSLTFTSRLAPD PSLVIYAIFPSGGVVADKIQFSV EMCFDNQGTDLTSTVRVTRSSA SVMVYGASEAIGQRQSSAAKP RRSQSDSLGPEFQGLWERLPGL RINGELITAYPQVVVVRVPTPW VQSDSDITVLRHLEKMGCRLM NRPQAILNCVNKFWTFQELAG HGVPLPDTFSYGGHENFAKMID EAEVLEFPMVVKNTRGHRGMY ELLVSTMGCSNSGMVTTPIKWL SMISVQCLANGTFLSPSLTKCPK GIRASVPLSGGPRSLKARTFSAF SGPVRSDEQAEALPEAYEPIEV NEFGEIDLLAMVEDEIILALPVV PVHDSEHCEVSEADMVFGELPE EAQKPNPFAVLASLKRVRSMA VQQNKPTRSKRGMRRSHDALT AVTSLSVDKTSGEKHLRHH*SA DLAAAPRAPGTLAQGCLTDSFS
26978	57346	A	27135	79	306	SGDLPWEINPLSSCSLLREKDPP MTSGPQTNQPKKHLINFKSGPH WKSDCSTHLAATPKAP\GTLAQ GSLTDSFSA
26979	57347	A	27136	159	254	
26980	57348	C	27137	63	370	
26981	57349	C	27138	107	408	

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26982	57350	A	27139	210	291	
26983	57351	A	27140	395	680	
26984	57352	A	27141	157	485	
26985	57353	A	27142	1	507	
26986	57354	A	27143	1	1041	
26987	57355	A	27144	1	671	GASGAAAYGADMAKSKNHTT HNQSRKWHRNGIKKPRSQRYE SLKGVDPKFLRNMRFAKKHNK KGLKKMQANNAKAMSARAEA IKALVKPKEVKPKIPKGVSRKL\ DRLAYIAHPKLGKRARARIAKG LRLCRPKAKAKDQTKAQAAAP PSVPAQAPKDKDTSNIFISNRKR GCDFTKKETNIPKVLTISMAPSL MSLYSVTRNQTTKPPSRHKNLT KGQLEPLY
26988	57356	A	27145	6	448	
26989	57357	A	27146	930	1307	
26990	57358	A	27147	1	675	
26991	57359	A	27148	142	456	
26992	57360	A	27149	3	175	
26993	57361	C	27150	378	434	
26994	57362	A	27151	1	792	
26995	57363	A	27152	1	578	MVRCVRLVEAGSVVRYLSTSIC RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAYVRARELHTLEVTGLET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRLGASL/HTSASKHTM VRALTYCSSREETFTAI
26996	57364	A	27153	1239	1905	SAAAAPATGVPACRAGAWVSA APPAEGRPARARRHPGRCLEAA GPRGQRGAAHGH*ARAGSPQP GAPPCHPLGIPARQPLGLPRRTR CFGGIAQRGRAARHCLLSRPSA KAKRNSSYREPGMGGWRSPQA LGEYGKGSQAGSARLSGAASQ GRRARHLRGKAPAWNPAPPPSP PPPALGLPLRTQREATRKPRRE EARRPRPRPLRPGGANGSPGPP RAARA
26997	57365	A	27154	1	1275	
26998	57366	A	27155	3	92	EAVDPHSECYSS*RWCVRSFFIL VGLWSH
26999	57367	A	27156	2	367	
27000	57368	A	27157	98	293	GQTFATASISLLRYATGCGVFP RV*IRSPRAIPALSGDWPAPFSV LSEPPRFVCLRAMTKAAAFL
27001	57369	A	27158	3	211	

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27002	57370	A	27159	1	519	GQLI/LKDTFITQSAADIRRKFQ KQALGPEHNLEALLNLAILVFY NRDQEEQAQKEKRDQRKAAPL IMALRQTLVVQRGQKMEQANH LIPGYSEIARPLYTLIKEIQRANT HQVEWEPEAETAFKPLKQALV QAPALSLPTGQNFSLYITERAGI ALGVLTQTHGTTPQLVAYL
27003	57371	A	27160	72	381	DSHTRSGTTRWGIRCRSGSSPSR RARWGRWGGLAAVALRRPAP AAGGTAPRGCLPAA*GSPPAPP SGS*SGSSDRPARMPLVVGLSH EFE*GLAGVDGEVLPPSRCVAL LLLRVERLHVAVYLPREALHQL HPLALDLDLLIARLVCHWLWG CPTSLSKDSKSYSCSLCDV
27004	57372	A	27161	515	747	SHGNSGNFQGTRDTISLS*AQLT TSTKDPWTDPPALWPRVFPSGG HYNCRAPSSP/TIQQEVARAVIT QFPTAAGVSCL
27005	57373	A	27162	1	663	
27006	57374	A	27163	1	1980	
27007	57375	A	27164	1	672	
27008	57376	A	27165	1	691	
27009	57377	C	27166	1	1491	
27010	57378	A	27167	830	2592	
27011	57379	A	27168	1	3744	
27012	57380	A	27175	2	365	QWDWAPWSRGWCSSGRLGPH RSPRSGGGSG\RRAAGPKPCPSP RSDAPAQPRGRSRRVLPLPQVQ AEPPEPWPVLPAAPKPLARPEA GMAGPGGRRTTSLPRRRGCGC CCPASSCFSSLSC
27013	57381	B	27176	1	1392	
27014	57382	A	27177	79	1241	
27015	57383	A	27178	3	299	

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27016	57384	A	27179	1	812	MPTVLACPAFDSRGSPICRFDPP ELTSGVRALEESPNAITLPVCGR DVKFTLEVLRGDSVEKTSRVW SGNERDQELLTEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLVGEL DDEQMAALSRLGNDYRPTSAY ERGQRYASRLQNEFAGNISALA DAENISRKIITRCINTAKLPKSV VALFSHPGELSARSGDALQKAF TDKEELLKQQASNLHEQKKAG KRSRRLHHTLLRVVAEIDKPDP RDELAGLLQFAGGPLQTLFAW VSPVEAAEQQRLLLAPSSGSFIP EG*DHPVRPQ*AAPGHVHYLTI PERSSQHYHPGALQE
27017	57385	A	27180	306	701	
27018	57386	A	27181	1	396	
27019	57387	A	27182	1	1263	
27020	57388	A	27183	1	873	
27021	57389	A	27184	149	421	
27022	57390	B	27185	23	268	
27023	57391	A	27186	1	363	
27024	57392	A	27187	2	398	TKFAARRPALAACAAISKIKAR DLRGKKKEEL\LKQ\LDDLKVE LSQLRVAKV/TQGGAASKLSKI RVVRKSIARVLTVINQTSGKKT FREILTRGKKYKPLGPCGP*GRT RAMRRRFKPSTEGEP*RTQGSR
27025	57393	A	27188	224	547	
27026	57394	A	27189	1	888	
27027	57395	A	27190	280	1170	
27028	57396	A	27191	1	191	
27029	57397	A	27192	438	1240	
27030	57398	A	27193	168	378	
27031	57399	A	27194	1	1362	
27032	57400	A	27195	2	918	
27033	57401	A	27196	38	397	RRCRPTMPRP\WCTCRGYQGPR KAQGG*AQDPKGCQPQARSTC LHCPPQAWE/RVLVPVLPRGSG CAGQ/MAKAKAKAKDQTKAQ AAAPASVPAQAPKRTQAPTKA SE*ISLPT*GQKDWCDP
27034	57402	A	27197	1	1206	
27035	57403	A	27198	734	913	
27036	57404	A	27199	3	778	
27037	57405	C	27200	164	274	
27038	57406	A	27201	1	2700	
27039	57407	A	27202	1	747	
27040	57408	A	27203	164	409	
27041	57409	A	27204	152	380	

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27042	57410	A	27205	230	2579	
27043	57411	A	27206	1	2433	
27044	57412	A	27207	1	528	NHQIRNDFTISPGVKADSRTSPI PQQPASSFDITEAAVSFAKDSLA GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP\ TQALNFTFKDKYKQIFLDGVDK RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVGK AGAERELRGFGDCLVKIYKSDG IK
27045	57413	A	27208	1	292	MTSKDKTSRGTIRQQHSRFKKI RCSAATTAGTQANRVWSGPLA NSNRPAAEAGVSTAAAPDGPPP PSVPTVDSDSLESAQFKCDNLK TCHTSHGSVMAETAVINHKKR KNSPRIVQSNDLTEAAYSLSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDEKGYESFPWFIKRAHSP SRGLYSVHINPYLIPFFIGL*PDK EGNEIWVDMYTVKPSGWTVRT FDKPRKRFIAFFIAGILFRAIKNH FLPRETLQCLPYILTGFRRGQSE YFSIFSNMDLADTVMFL
27046	57414	A	27209	1	1452	
27047	57415	B	27210	53	844	
27048	57416	A	27211	281	624	ACSDVWSKFRLRWSPNPRCQE RPSAEKMSPHPPSAARHQASWS ARRLTQWPRPCHTQ*GQSEEH GHRSGLMPAG\THQLPDEHAIT PHLQSTAPIIPEPKTLSHKDSSLQ GTGK
27049	57417	A	27212	3	411	
27050	57418	A	27213	265	480	LDTILTASDGRPTYTPP*FLLLS/ CFCYGFFCYIFGCSCRALARAR AGGGGVPAAHRAAGRGSRAPE RIPPH
27051	57419	A	27214	294	620	
27052	57420	A	27215	1	420	
27053	57421	A	27216	1	342	
27054	57422	A	27217	175	244	DLLIEMGSFFVQCRTAIL*RKQN
27055	57423	A	27218	11	951	

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27056	57424	A	27219	20	1654	ELRFPAACSQLQFSDGLHRVDQ PPSSMCVSAADLWLC\EAGKLL VVPMDGSHWFTMRSVVEKLIL RGHEVVVVMPEVSWQLGRSLN CTVKTYSTSYTLEDLDREFKAF AHAQWKAQVRSLFSLFLSSSNG FFNLFFSHCRSLFNDRKLVEYL KESSFDAVFLDPFDACALIVAK YFSLPSVVFARGIGCHYLEEGA QCPAPLSYVPRILLGFSDAMTF KERVRNHIMHLEEHLFCQYFSK NALEIASEILQTPVTAYDLYSHT SIWLLRTDFVLDYPKPVMPNMI FIGGINCHQGKPLPMEFEAYINA SGEHGIVVFSLGSMVSEIPEKKA MAIADALGKIPQTVLWRYTGT RPSNLANNTILVKWLPQNDLLG HPMTRAFITHAGSHGVYESICN GVPMVMMPLFGDQMDNAKR METKGAGVTLNVLEMTSEDLE NALKAVINDKSYKENIMRLSSL HKDRPVEPLDLAVFWVEFVMR HKGAPHLRPAAHDLTWYQYHS LDVIGFLLAVVLTVAFITFKCCA YGYRKCLGKKGRVKKAHKSK
27057	57425	A	27220	1	2022	
27058	57426	A	27221	124	205	
27059	57427	A	27222	248	443	
27060	57428	A	27223	263	415	
27061	57429	C	27224	1	717	
27062	57430	A	27225	349	1125	
27063	57431	A	27226	629	796	
27064	57432	B	27227	1	388	
27065	57433	A	27228	2	346	
27066	57434	A	27229	448	555	
27067	57435	A	27230	2	423	CEPIKVYVVGN\GAVGKTCLL\I SYTTNAFPGEYIPTVFDNYSAN VMVDGKPVNLGLWDTAGQED YDRLRPLSYPQTDVFLICFSLVS PASFENV/LCKGAVKYLECSAL TQRGLKTVFDEAIRAVLCPPPV KKRKRKCLLL
27068	57436	A	27231	1	1503	
27069	57437	A	27232	1	635	

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27070	57438	A	27233	3	1107	AVFLSFGWWPLPGIGFQSAEGE AAWTAAPAPSAPPPSKPRARPP RPEPAASYLSALPPPPRPSERPS MQAIKCVVVGDGAVG\KT\CLL I\SYTTQCHFLGEYIPTVFDN\YS A\NVMVDGKTGEIWGLWDTAG QEDYD\RLRPL\SYPANRMCS*I CFS\LVSPA\SFENV/LVQKWYPE VR\HH\CPNTPI\IPVGT\KLDLRD DKRHDSRNLKEKKLT\PITYPA GS*AMAK/ERLGAVKYLG/CAP AAHTSEGLKTVFDEAIRA\VLCP PPVKERGRENCLPVVNVSAPSF LGSCPLGTFCRLCSKKNKKKKQ KKKNNGGAFALNANFLLQINFS IKPFFEPISNFKVLFVLNVRVQT HILLKFSPKMTSLLKALFFK
27071	57439	A	27234	3	203	
27072	57440	A	27235	1	112	LGNTWG*QPCKRLKIWLSLEFT KINVIRHMWKKFKRL
27073	57441	A	27236	1	513	QHWGRYLKRAFEQWQVPRFG HMPDPGPVKPLQPVEVETRGN DYKFLLFHFWDEWLYKFSADE FFIPGKLCAIVF*KRL*RPGAVA YACNPSTLGSRGRWIT*GQEFE TSLTNKEVKVLSIDQRNFKLRSI GWGEEFSLSKHPQGTEVKAITY SAMQVYNEENPEVFVIIDI
27074	57442	B	27237	125	302	
27075	57443	A	27238	93	432	
27076	57444	A	27239	3	279	
27077	57445	A	27240	263	446	
27078	57446	A	27241	237	369	
27079	57447	A	27242	389	836	
27080	57448	A	27243	1422	1580	
27081	57449	A	27244	103	444	RSLTCPGDMFPVVLVINIQLLLT YANFCSWLESLPRKWDFLFYCI VRLQIFQTFMLCFLLNTLPLRNF FYQIP*IISLKFKVPQISKAEAKC HQSLCIGRVTFIPVPNKFFISI
27082	57450	A	27245	3	242	MHRNAQHHVKTAKPWGLHPL KPQPK*YSGPF*PPLEQLRCKAT GP*GCTQQGGPGPGPQNNFSLL GLQACDGRDCHEGL
27083	57451	A	27246	506	664	
27084	57452	A	27247	1	1515	
27085	57453	A	27248	269	541	RFPNLNS*LLYTRGLTPHESCQ GLGLAPSEAMAQTIPWPLLATA RLAVTGNQILMQISAAGLNFSS ENGAFISIALSGCKFFKLLCSAS
27086	57454	A	27249	1	564	

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27087	57455	A	27250	2	235	
27088	57456	A	27251	3	1393	
27089	57457	A	27252	28	271	
27090	57458	A	27253	12	485	RMAFCRASQADQDRFICIYPAY LNNKKTIAEGRRIPISKAVENPT ATEIQDVCSAVGL\NVILRKIKM YF*EWNRDVQYR\GRVRVQLK QEDGSLCLVQFPS/RLYTKPNF WFLGKSVMLYAAEMIPKLKTR TQKTGGADQVFQQGEGS*KGK GKQKEVT
27091	57459	A	27254	1689	2176	APPGMGAASLCAFGLLVTFAT ASPRYAMVQPSFRLGTKLGQA EADEPFVSSGSVPPSFLSPLLPA APGARRG*LQRGDLGRQAPPPA PGCAPGLA*GRPPAPHL*RLCSR PTFFPPPANSSRLALADSPPPRQ LQGARP*PVPGRLLTSTGTPRPL PRPLGP
27092	57460	A	27255	263	439	
27093	57461	A	27256	1	499	MSELPFTIATKRIKHLGIQLTRD VKDLFKKNYKPLFNEIKDDTNK WKNIPCLWIGRINILKMAILPKV IYRFNAIPIKLLMTFFTEMENTT FKFMWNQKR/CPHCQDNPKPK EQSWRHHAT*LQTILQGYSNQN SMG/TWMKLETIILSKLSQGQK TKHRMFSLIGGN
27094	57462	A	27257	1940	2062	
27095	57463	A	27258	1232	1432	
27096	57464	A	27259	168	1189	
27097	57465	A	27260	1	1760	
27098	57466	A	27261	453	543	
27099	57467	A	27262	873	962	
27100	57468	A	27263	8	411	FSRCRCSGR/YLCMASCL\CFHH CWWMASHHWPI*RTQV*CAC WEGRHLG\CAPKCLSLLGFTRL LACVLWLPILQSVIPIHIQVSITV RVLFAAAHDEARASEATFQESG GPYPLLSTPLILLKAVVVLMLD AHAS
27101	57469	A	27264	1	552	
27102	57470	A	27265	828	1211	
27103	57471	A	27266	428	655	DQKVPPLEMYFGIEVKSLKQLR SISA*SLFSSRALKEDSGLLKLK QPRSSGVIPRRFIVSWPWKMVR QPVLFSVG
27104	57472	A	27267	1	855	
27105	57473	A	27268	1	1261	
27106	57474	A	27269	164	260	

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27107	57475	A	27270	147	224	RLTLPDHLGSLLDHHR\ALGNS YSGG
27108	57476	A	27271	1	837	
27109	57477	B	27272	184	288	
27110	57478	A	27273	1	286	
27111	57479	A	27274	1	699	
27112	57480	A	27275	1	3660	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCLRVDGQQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAAATSNVHMVKKISI TERSCDGAAEMKWEDQNIGD
27113	57481	A	27276	1059	1229	
27114	57482	A	27277	2	4735	
27115	57483	A	27278	415	825	SCADFQDYWDQREYTYNRPHT ASRRIVLDFLLFPEW/PTFVAFW APLFNPSKRASLYRFSLCISSLSF GSHWGSVPGNWVLTYSWG/SL VISRCMFL*PLSCCLEHSPPFICV KEEHEQLVAISPSGVMGLDNSL EQIN
27116	57484	A	27279	1	1326	
27117	57485	A	27280	2976	3068	VWTALTNRLGQQVSICG*PGTE DSKGDWLL
27118	57486	A	27281	78	220	APTSLHS*SYFKNCGHGRLRWV ITHIRLVISWATYLVQNNIIQTR LF
27119	57487	A	27282	1	1077	
27120	57488	A	27283	307	922	QVVPSSLSAISQSPAPCG/CSP*G PSPGAT
27121	57489	A	27284	1	4560	
27122	57490	A	27285	87	237	LLFFQLGGDAFSFKFSSGVNF\R NSLICQAWGKRVFSALLCIILSE YTSPL
27123	57491	A	27286	1	246	
27124	57492	A	27287	46	396	
27125	57493	A	27288	1	552	
27126	57494	A	27289	3	418	AEKCPCLGAFGFGWDHPRRPG SWGAWSEGSGSPPARIVKMSLR KQTP\SDFLKQIIGRPVVVKLNS GVDY\RGVLACL\DGYMNIALE QTEEYVNGQL\KNKYGDAFI\R GNNVLYI\STQKRPDVRTPKRA TLFIVGYIFL
27127	57495	A	27290	202	450	

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27128	57496	A	27291	304	642	
27129	57497	A	27292	75	393	
27130	57498	A	27293	1	678	VFGLGSVAHMLLNKTFGSYLG VNLGFGFGVTMGVHMAGRTS GAHMNAAVSLTNCALGRVPW RKFPVYVLGQFLGSFLAAATIY SLFYTAILHFSGGQLMVTGPVA TAGIFATYLPDHMTLWRGFLNE AWLTGMLQLCLFAITDQENNP ALPGTEALVIGILVVIIGVSLGM NTGYAINPSRDLPP\RIFTFIAGW GKQVFRWHHLPGLHWLHHPT GAPEIGGFCGV
27131	57499	A	27294	2	1694	
27132	57500	A	27295	1	356	GIFVTYLPDHMTLWRGFLNEA WLTGMLQLCLFAITDQENNPA LPGTEALVIGILVVIIGVSLGMN TGYAINPSRDLPP\RIFTFIAGWG KQVFRYFPCPGPIPLSFSVGPLC VEGWGVM
27133	57501	A	27296	1	544	
27134	57502	A	27297	320	610	LREYTINIHTAHPMEWASKKRA PRALKEIRKFAMKEMGTPDVRI DTRLNKAVWAKGIRNVPYRIR VRLSRK\RNEDEDSPNKLYTLV TYVPVYHFQK
27135	57503	A	27298	1	303	
27136	57504	A	27299	1	1311	
27137	57505	A	27300	1	3126	
27138	57506	A	27301	2	779	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKGPRGTA*FSLL* ATGEKGFGL*GVPCFHRIIPGFM \CQG\GDFTRH\NGT\GGKSHLW GRNLKDENFI\LKHTGPGILSHG KMLDPNTNGSQFFICTA\KT\EW LDGK\HVVFGKVKERHEILWEA MGALLGPRNGKTQQEESPIVPG GQLRIKFDLVFYSLTTKIIPFCSF KESTPPPHLLASILESLCSRLQFP FGFHVFLVPCHA
27139	57507	A	27302	143	390	
27140	57508	A	27303	249	1516	

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27141	57509	A	27304	2	645	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKGPRGTA*FSCL* SIEEKGFGL*GVPCFHRIIPGFM\ CQG\GDFTRH\NGT\GGKSHPM GKKFE\DENFI\LKHTG\PG\ILSH GKCLDPNTNGSQFFICTA\KTEV VGMAKHVVFWQK*KKGMKYC GRPWERFG\SR\NGKTQQRKITI C*LVGQLRNKVLTWWF
27142	57510	A	27305	72	387	VCLQHGPWSSLKHVQGWRDD CHGLSLGPRTHVQAGTLPKPTL WAEPGSVITQGSA\VTLWCQGI LQTQEYRLYREKKTAPWITRIP QEIVKKGHDPIPSITWEHTG
27143	57511	A	27306	1	322	
27144	57512	A	27307	1	1125	
27145	57513	A	27308	1	1419	
27146	57514	A	27309	198	1634	
27147	57515	A	27310	78	216	
27148	57516	A	27311	1	489	
27149	57517	A	27312	18	463	AEGVEPGSPRVVLLESEQFLTE LTRLFQKCRTSGSVYITLKKYD GRTKPIPKKGTVEGFEPA\DNKC LLRATDGKKKISTVVSSKEVN* VFRWLISNLPLGANMDGLKKR DKKNKTKKTKAAAAAAAAGP AAAATAATTAATTAATAAQ
27150	57518	A	27313	1	1242	
27151	57519	A	27314	147	965	DPPSPVPAPPSSPRDGHFLVPDA TMAEEQPQVELFVKAGSDGAK IGNCPFSQRLFMVLWLKGVTFN VTTVDTKRRTETVQKLCPGGEL PFLLYGTEVHTDTNKIEEFLEA VLCPPRYPKLAALNPESNTAGL DIFAKFSAYIKNSNP\ALN\DNLE EGTPGKP*RFLDNYLTSPLPEEV DET\SAEDERCLSDGTFLDGNEL TLADCNLLPK\LHIVQVVCKKY RGFHHPPRPFRGVAFGYL\SNA\ YARENFRFPPVPDDEEIELAYE QVAKALK
27152	57520	A	27315	1	933	

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27153	57521	A	27316	63	641	FAKMTDHKGERGEATRYMFSR PFKKTMGVVPCGHNN*RFYK\K GDIVD\IKGMGYCVQNGMP\HK CY\HG\KTGRSLTIVTPACLLPLL *TNQF*GKVFS\KRINVRIEHIKH \SKSRDSFLKRVKENDQKKKEA QEEGT\WVQLKRQPAPPREAHF V\RTNGKEPEL\LEPIPYEFHGIN RCPKKKIKDLWATKKKKK
27154	57522	A	27317	1	390	
27155	57523	A	27318	75	394	IWGDVEKGKK\IFIMECSQCHT VEKGGKHKTGPNLHGLFGRKT GQAPWDTPYTAANKNKGIIWG EDTLMEYLENPKK\YIP\GTKMI F\AGIKKKEERADLIAYLKKSY
27156	57524	A	27319	2	529	ERQTRHAGGVRRGPRPKLQRD KAAAAAVLGAVRKRPSVVPM AGQDPALSTSHPFYDVARHGIL QVAGDDRFGRRVVTFSCCRMP PSHELDHQR\LLEYLKYTLDQY VENDYTIVYFHYGL\NSRNKPS LGWLQSAYKEFDRKYKKNLKA LYVVHPTSFIKVLWNILKPLISH KFGKK
27157	57525	A	27320	287	445	
27158	57526	A	27321	2	362	
27159	57527	A	27322	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRLLARAEKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLV\CRKMGVP YCIIKGKARLGRLVHRKTCTTV AFTQVN
27160	57528	A	27323	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
27161	57529	C	27324	62	217	
27162	57530	A	27325	1	1545	

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27163	57531	A	27326	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRAILYKRLKVPPAINQFTQAL DRQTATQLLKLAHKYRPETKQ EKKQRLLARAEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVDPIELVVFLPA L\CRKMGVPYCIIKGKARLGRL VHRKTCTTVAFTQVNSEDKGA LAKLVEAIRTNYNDRYDEIRRH WGGNVLGPKSVARIAKLEKAK AKELATKLG
27164	57532	A	27327	550	827	DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLLQQL PQEHTRKTLPLQQTSAWTYRLF HTSCEI
27165	57533	A	27328	908	1331	GDMRGRREGGFGLGRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLTMPLAPATFL RVNCWAG/RGR/C*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPEKRDLPL RVKDQGRHPCVV
27166	57534	A	27329	1	1134	
27167	57535	A	27330	62	310	
27168	57536	A	27331	243	578	
27169	57537	A	27332	324	995	NLVPRPGTWIRGLPLGDHSPVL LLFAP*ERSTYDLRSSDRPAQET SHQFQIRERQRRHVLSVDPKLR RRSRTGKAAFPWCLIIAGTPL*L YTHVSRVSDHAGMPALVLHP* R/LSPTFLGKGQHALKGLKPVIT RLLQHGLLKPINSPFPSPILPVLK PDKAYKLVQNLRLINQIVLPIHP VVPNPYTLLSSIPPSTTHYSVLD LKHAFFTIPLHPSSQPLFAFT
27170	57538	A	27333	1	1860	
27171	57539	A	27334	1	957	
27172	57540	A	27335	97	826	
27173	57541	A	27336	245	392	
27174	57542	A	27337	736	1300	
27175	57543	A	27338	590	891	
27176	57544	A	27339	1256	1654	VQPVRLVSGMQHPGSGWRRL WGQHSTSLTSKEHLHISKRGNI DNLVQRNMP\SNEKPKCPELPP FPSCLSTVHFIIFVVVQTVLFIGY IMYRSQQEAAAKKILLTTIFLCT SSICVQNDVVLREFKYLNCFIV
27177	57545	A	27340	295	852	

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27178	57546	A	27341	3	446	ILAWFGSIAEAPSAAWLCGSSQ GRYCSSFNRVVRQNSSDAKVV NVPKTRITFCKK\CGKHQPHKV TQYKKGKDSLYAQGRRRYDRK QSGYGGQTKPIFRKKAKTTKKI VLRLECVEPNCRSKRMLAIKRC KHFELGGDKKRKGQVIQF
27179	57547	A	27342	1	565	
27180	57548	A	27343	1	1050	
27181	57549	B	27344	1	2109	
27182	57550	A	27345	2916	3229	
27183	57551	A	27346	3	671	AGILAAIREANMGAYKYIQEL W/RKKPSDVHAFFLRV\RCGQT RSFFVFTGVPRPTRPDKARRLG YKAKQGYVIYRIRVRRGGRKRP VPKGATYGKPVHHGV\NPA*KF ASKALQVPLPEGTEAGR\HCGG S*ESLNSYWVGEDS\TYKFFEVI LIDP/YSHKAIRRNPDTQ\WIT\K PVHKHREMRGLTSAGRKSRGL GKGHKFHHTIGGSRRAAWRRR NTLQLHRYR
27184	57552	A	27347	1	1646	
27185	57553	A	27348	2	2600	
27186	57554	A	27349	1	2403	
27187	57555	A	27350	100	520	
27188	57556	A	27351	1	570	
27189	57557	B	27352	1	837	
27190	57558	B	27353	1	1434	
27191	57559	A	27354	1	2379	
27192	57560	A	27355	3	952	IDWAPKSDRIVTCGADRNAYV WSQKDGVWKPTLVILRINRAA TFVKWSPLENKFAVGSGARLIS VCYFESENDWWVSKHIKKPIRS TVLSLDWHPNNVLLAAGSCDF KCRVFSAYIKEVDEKPASTPWG SKMPFGQLMSEFGGSGTGGWV HGVSFSASGSRLAWVSHDSTVS VA\DASKS\VQVSTLKTEFLPLL SVSFVSENSVVAAGHDCCPMLF NYDDRGCLTFVSKLDIPKQSIQ RNMSA/LWERFR\NMDKRATTE DRNTALETLHQNSITQVSIYEV D\KQDCRKFCTTGI\DGAMTIW DFKTF\ESSIQGLRIM
27193	57561	A	27356	3	134	
27194	57562	A	27357	1	478	
27195	57563	A	27358	1	623	
27196	57564	A	27359	425	667	
27197	57565	A	27360	121	401	
27198	57566	A	27361	1	1818	

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27199	57567	A	27362	552	2325	
27200	57568	A	27363	693	1270	
27201	57569	A	27364	18	146	
27202	57570	A	27365	270	683	
27203	57571	A	27366	1	1398	
27204	57572	B	27367	1	1152	
27205	57573	A	27368	40	538	SPSPKDSPGVRVGISCYIGGPCQ QRLLSPVRASKMTKKRRNNGR A\KKGPRHVRGPSPLKFLPPSSC HLTVPRCRAQGTRPIKKF\VISK P*VEAAAV\RDISEASVFDAYL\ LPKLYVKLHYCVSCAIHKQK*S GNRS\REA\RKTRTPPPRFR\PGG *LPHGPPTKSP
27206	57574	A	27369	204	401	
27207	57575	A	27370	3	980	
27208	57576	A	27371	2124	2836	
27209	57577	A	27372	139	8892	
27210	57578	A	27373	1	2592	MAGLGASLHVWGWLMLGSCL LARAQVRASAPRHLFSRSLRRG LSFSDTEARCARELIHVHTSTN APARTEAYPAGSAEPPRRPRAG REHSFFSQRYVPLPPLGGALGS GPAKLPPPRAPCPVRFCADLET LCGALDCYKVRGGAAPARPAP RPAGGIQVSSLSGFGTESLPGGN PFPHRDHRESGTMDSPSLTVAT PLSLTPPIPRELACGDWRRVGG GAGGGGLRRRGLGGDKAGKR KSSDLPCGPGFLQSLLQKRRHW ESGLGLPGCGCESELVSGCGAP TLRQHIIPAEGRNGVKEKSADL GCGGSQGLRAKKGTNPGIENG KRKGKEGMLDAWICRRSAFGP GREKLGGEEVGCNDKGKIRFIE VKMSKKISGGSVVEMQGDEMT RIIWELIKEKLIFPYVELDLHSY DLGIENRD/ATNDQVTKDAAEA DKKHNV\GVKCATITPDEKRVE EFKLKQMWKSPNGTIRNILGGT VFREAIICKNIPRLVSGWVKPIII GRHAYGDQGFGSNMQNAIMK KLKWLHLARVGKFSDANAKFY CRLYYAGEFHKMREVILDSSEE DFIRSLSHSSPWQARGGKSGAA FYATEDDRFILKQMPRLEVQSF LDFAPHYFNYITNAVQQKRPTA LAKILGVYRIGYKNSQNNTEKK LDLLVMENLFYGRKMAQVFDL KGSLRNRNVKTDTGKESCDVV
27211	57579	A	27374	2	2138	

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27212	57580	A	27375	1	2355	
27213	57581	A	27376	249	1544	EIYSLSRFIEVKMSKKISGGSVV EMQGDEMTRIIWELIKEKLIFPY VELDLHSYDLGIENRDATNDQ VTKDAAEAIKKHNVGVKCATI TPDEKRVEEFKLKQMWKSPNG TIRNILGGTVFREAIICKNIPRLV SGWVKPIIIGRHAYGDQYRATD FVVPGPGKVEITYTPSDGTQKV TYL\VHNFEEGGGVAMGMYNQ DKSIEDFAHSSFQMALSKGWPL YLSTKNTILKKYDGRFKDIFQE M\YDKQYKSQFEAQKIWYEHR L\ID\DMVAQAMKSEGGFIWAC KNYDGDVQSDSVAQGYGSLG MMTSVLV\CPDGKTVEA\EAAH GTVTRHYRMYQ\KGQGDVHPIP LASIFAWGPEGL\AHRAKLDNN KELAFFANALEESFYETHE\AGF MTKDLAACIKGLPNVQRSDYL NTFEF\MDKLGENLKIKLAQAK
27214	57582	A	27377	1	692	
27215	57583	A	27378	251	2150	
27216	57584	C	27379	93	293	
27217	57585	A	27380	308	534	
27218	57586	A	27381	2	856	
27219	57587	A	27382	3	327	AQELHTFEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCGVEALTTLEVAGRM LGG\AKQEKKKKKTGRAKRRM QYNRRFVNVVPTFGKKKGPNA
27220	57588	A	27383	150	456	
27221	57589	A	27384	651	835	
27222	57590	B	27385	1	2193	
27223	57591	B	27386	109	714	
27224	57592	A	27387	150	458	
27225	57593	A	27388	1	2055	
27226	57594	A	27389	1	804	
27227	57595	A	27390	645	1828	
27228	57596	A	27391	899	1216	
27229	57597	A	27392	79	156	
27230	57598	A	27393	1796	2215	
27231	57599	A	27394	107	724	
27232	57600	A	27395	854	926	PLEIPHEPPPGRG*HAPQLPRGQ
27233	57601	A	27396	2	413	
27234	57602	A	27397	54	442	FAKMTNTNLNRRGTRYMFSRP FRKHGVVPLATYMRIYKKGDI VHIKGMGTVQKGMPHKCYHG KTGRVYNVTQHAVGIVVNKQG KGKILAKRINVRIEHITHSKSRH SFLKRAKENDPEYE\EALENGT

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27235	57603	A	27398	1	490	
27236	57604	A	27399	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLRA L*G*DLTHHIIILFPFFFL**PAPP REAHFVRTNGKEPELL
27237	57605	A	27400	336	928	
27238	57606	A	27401	13	724	INPPPPPFRPEPPSSSKFAKNDGP QRGKRRGTPIIMFS/RGPFKKTM GVVPLAHIFMR\IYKQRCDFVDI QGEWGTLFQKGNCPHKVVTHG QNLEGVLPMVTPAMLVGHLL* NKQV*GQRFLPKRNLMWRI*A HLRHF*GARD/RASLKTCGREN GSRKKERKPKGGKVTWGFQLK RRHLGFPPQEEATFLLKEPIGGR EP*ACLEPYFPYWISWGINRVF KKKIKGPSGLQKKKKKVD
27239	57607	A	27402	1	759	
27240	57608	B	27403	1	372	
27241	57609	A	27404	1746	2966	DMKNGAKEGESYLLLQCLPPSP LPSPPPSPSPPPPPPPPSPSSPSPP PSPPPPPSPSPPPSPSPSPPPPTSPP SPSSPSPSPPPSPPSPSPLSPTPPPP PSPSLPPLPSPSLPPPPSPSPSPPPP PSPPPSPPPSPSPPPSPSPSPPPPPS PPPSPPPSPSPSLPPSPSPPPSPSPP PSPSPLPSPSPSLSPSLPPSPSPSPP HHHHHHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHYHHHC HHHHHHHHHCHHHHHHCHHH HHRHCHHHRHHHHRQHHHHH HHHHHHQHHHPQTLH*PSESQ HIVGAQ*MLHCHSLCVYIQGSH SVRKFLVLKQKLSMGMVLPPG GDLEHCGACLDCDQDWRCAM PSHKYPPKHAHCCEGCLC
27242	57610	A	27405	150	462	ICEGRTCIFEEPCNCSSLYVRSN GGNHSHSTTTFKYNGSNWIPR WQGPSGSTQPSKARRPVAFSQG NCAMEKGN*SDILGTTEHWL*A DIDSRGPKMSLQSSS

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27243	57611	A	27406	142	1285	SRMSKAFGLLRQICQSILAESSQ SPADLEEKKEEDSN\MKREQPR ERPRAWD\YPHGLVG\LHNIWT DLACLNSLIQVFVMNVDFTRIL KRITVPRGADEQRRSVPF\QML LLLEKMQDSRQKAVRPLELAY CLQKCNVPLFVQHDAAQLYLK LWNLIKDQITDVHLVERLQALY TIRVKDSLICVDCAMESSRNSS MLTLPLSLFDVDSKPLKTL\EDG LHCFFQPRELSSKSKCFCENCG KKTRGKQVLKLTHLPQTLTIHL MRFSIRNSQTEKDLATPLYFPQS LDFKPRSFQLKRESC\DA\EEQS GGQYELFAVIAHVGMADSGHY \CVYIRNAVDGKW\FCFNDSNIC LVSWEDIQCTYGNPNYHWQET AYLLVYMK\MEC
27244	57612	A	27407	1	1077	
27245	57613	A	27408	3	242	
27246	57614	A	27409	213	928	EGPARQRLLSPVRASKMTKKR RNNGRAQKRAAAHVRGPSPLK/ CFPSGPLPPNCAR\CVPQGTRPI KKF\VIR\NIVGGRSRQGHISEAS RLRMPISLPKL\YVKLH\YC\VSC AIHKQK*FR\NRS\RESPAKTRTP PPRF*DLAGGCPTVPPPKAHDL GPEYCRHQTCVNWVCCRQATI LGKELCGQIRKLPSQQMSPGWL PSGYSCWLYKYKTEATTALQS RGEVYHPLQALWSRPPGRDPL
27247	57615	A	27410	1	267	
27248	57616	A	27411	257	322	
27249	57617	A	27412	2	176	
27250	57618	A	27413	218	923	
27251	57619	A	27414	2	429	TKFAARRPALAACAAISKIKAR DLRGKKKEELLKQ\LDDLK\VE LSQLRVA*VTGGAASKLSKIRV VRKSIARVLTDINQTSGKKTFR EILTRGKKYKPLGPCGP*GRTR AMRRRLNKHEENLKTKKQQRK ERLYPLRKYAVKA
27252	57620	A	27415	1	1146	

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27253	57621	A	27416	2	670	IAGEITRRGSRARPRPGPQCPPG PPGTAMIKAILIFNNHGKPRLSK FYQPYSEDTQQQIIRETFHLVSK RDENVCNFLEGGLLIGGSDNK\ LIYRHYATLYFVFCVDSSESEL GILDLIQVFVETLDKCFENVCEL DLIFHVDKVHNILAEMVMGGM VLETNMNEIVTQIDAQNKLEKS EAGLAGAPA\RAVSAVKNMNL P\EIPRNINIG\DISIK\VPNLPSFK
27254	57622	A	27417	5	379	
27255	57623	A	27418	536	675	LEWSSAKFPTAVGVSLLLSSVC RSQ*FLMDAMSRMDLVRYTSA RVS
27256	57624	A	27419	2	1220	
27257	57625	A	27420	435	552	
27258	57626	A	27421	5	379	
27259	57627	A	27422	1	1062	
27260	57628	A	27423	17	467	
27261	57629	A	27424	105	355	
27262	57630	A	27425	283	466	APRSARPIVHGVKATRPKPRNL LDKDMFSKSDPLCVMYTQGME NKQWR\EFGRTEVIDNTLN
27263	57631	C	27426	167	379	
27264	57632	A	27427	164	1185	
27265	57633	A	27428	1	873	
27266	57634	B	27429	20	523	
27267	57635	A	27430	3	1225	
27268	57636	A	27431	1	884	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAENFRALSTGEKGF GL*GVPCFHRIIPGFM\CQG\GDF T\RH\NGTGGKSIYGEK\FEDENF I\LKHTGPGILS\MANAGP\NTNG SQFFICTAKT\EWLDGKP\VVFG KVKE\GMNIVEAMERF\GS\RNG KT\SKKITIADCGQLRIKFDLVF YSLTTKIIPSGSPRESTPPTHLLA SILESLCSRLQFPFGFHVFLVPS
27269	57637	A	27432	27	410	LQDEATGCQKLIEVDDERKLRT FYEKRMATEVAADALGEEWK GYVVRISGGNDKQGFPMKQGV LTHGRVRLLLSKGHSCYRPRRT GERKRKSV\RGCIVDANL\SVLN LVIVKKGEKDIPGLTDTTVPR

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27270	57638	A	27433	93	866	TVSFPATGC\QKLIEV\DDERKL RTFYEKRMATEVA\ADA\LGEE WKGYVVRISGGNDKQGFPMK QGVLTHG\RVRLLL\SKGHSCY RPRRT\GERK\RKSSSVGCI\VDS KSWSVLQLGLLLKKKKK*RRIF PG\LTDTTVPRRLGPQK/RASRIR KLFNLSK\EDDVRQYVVRKPLN KEGKKPRTKAPKIQRLVTPRVL QHKRRRIALKKQRTKKNKEEA AEYAKLL\AKRMKEAKEKRQE QIAKRRRLSSL\RASTSKSESSQ
27271	57639	A	27434	2	401	
27272	57640	A	27435	1373	1838	
27273	57641	A	27436	1	257	MNRQLSDSYTEDTKEPSDVTTS ERTRSPPGSAKTTMIDTLKKLQ DV\QKLRTPKIPQSQQQICWNN MSRLRDQS*RSSKKRQRLWK
27274	57642	A	27437	247	831	
27275	57643	A	27438	1	993	
27276	57644	A	27439	267	281	CNCPNIFEARWVNLKSLSKIHE* RPFQP
27277	57645	A	27440	274	482	
27278	57646	A	27441	1	219	
27279	57647	A	27442	1	681	
27280	57648	A	27443	11	1094	
27281	57649	A	27444	51	65	NNTFLKYC*IDFND*DCGGEDIS PN*LGLPIPLSMVLCEIIHF
27282	57650	A	27445	1	1563	
27283	57651	A	27446	3	318	
27284	57652	A	27447	1	294	
27285	57653	A	27448	7	259	
27286	57654	A	27449	29	191	
27287	57655	A	27450	2	519	KSQDYKSLNATCAGGTSFSGC ARRLLLSTCSSGWRSGGLSLRG GKMELEA\MSRYTQPSEPQLSS PHLTVVLLAIGMFFT\AWFFVY EVTSTKY\TRDIYKEAPHPP*VA LTPSMGFGVLF\LLL\WVGIYRV SHPRVTTQNGFHWKPAFCKINF FFYLFAWEVFPPAAHNKVQML
27288	57656	A	27451	144	386	VCECKMPKVQPNFTHWSRS*N DDLNRSSLWQA*PQAASVEIIIL RS
27289	57657	A	27452	462	672	
27290	57658	A	27453	1	475	
27291	57659	A	27454	1	741	
27292	57660	A	27455	62	390	
27293	57661	A	27456	549	641	
27294	57662	A	27457	456	774	
27295	57663	A	27458	2852	2935	

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27296	57664	A	27459	699	761	
27297	57665	A	27460	399	434	
27298	57666	A	27461	683	1661	
27299	57667	A	27462	1	95	
27300	57668	A	27463	3	517	
27301	57669	A	27464	6	401	RGLTEVPETSGGRVSVGAMAK HHPDLIFCRKQAGVAIGRLCEK CEGKCVICDSYERPCTLVRICDE RNYGSYQGRCVICGGPGVSDA YYCKEVHHPGERTRDGC\SKIV NLGSSKTDLFL*TAKNTGFQER
27302	57670	A	27465	1	321	
27303	57671	A	27466	67	348	
27304	57672	A	27467	1	642	
27305	57673	B	27468	193	445	
27306	57674	A	27469	32	216	AGPSQPTNQTTGKSPQLQQDYF PRRSYRCSHRLIICLNVIGDAV* STVQLKALMLRGRNYK
27307	57675	A	27470	214	440	QDRWGLAPHPPAPGLPLPGPTN QTTGKSPQLQQDYFPRRSYRCS HRLIICLNVIGNAL*STVQLKAL MLRGRNYK
27308	57676	A	27471	35	3801	
27309	57677	A	27472	1	2901	
27310	57678	A	27473	1	1317	
27311	57679	A	27474	1698	3255	RVACPCVVWLCWAHWELWRT EEVEGGIAGTDVAR/EASDFILT DAIFSSIVKAVMASLQRRGSRE L*LPAAGVWKLQTDF*AQSI/AE EGIECKSIKPVLAKYLVWTRLF VGLLAELRDESAPETTPAGRRR QPQVWSGARQTCGQRTERLAG GLGEMQACSGNLGAEKEKQSK KLAGGWPMSPTSLHALGPKLV PAKSQRHRAEHMSTWQVGVVS SSYFTGNLVGTLLTGYVIKRIGF NRSYYLASFIFAAGCAGLGLMI GFWSWLAWRFVAGVGCAMIW VVVESALMCSGTSRNRGRLLA AYMMVYYVGTFLGQLLVSKVS TELMSVLPWVTGLTLAGILPLL FTRVLNQQAENHDSTSITSMLK LRQARLGVNGCIISGIVLGSLYG LMPLYLNYKGGKSSPTPAVRPA RHNSLPGPEAKKYRPGFIIGLTS CIAFSVQAANVDEYITQLPAGA NLALMVQKVGASAPAIDYHSQ QMALPASTQKVITALAALIQLG PDFRFTTTLETKGNVENGVLKG

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27312	57680	A	27475	152	468	GLGIQ*LLCCSSFCFQLLPEKKE GRLAGDAGAARPAKSGRFLGL TSGLPSEWSARTGPEPPKSLSG GGELNGSSLGFGTQDGRGTRE GRDRGLHPARPPQYQHSP
27313	57681	A	27476	541	4172	
27314	57682	A	27477	3	1110	
27315	57683	A	27478	340	1032	
27316	57684	A	27479	2	779	
27317	57685	A	27480	3	281	
27318	57686	A	27481	519	737	VPDLLLQLPNAGLCGHFCDPGD SLQCLCHQGPGFQAQNWAAV WADTKPAAGAEAREPGDLA*L VPPTWSPTR
27319	57687	B	27482	1	915	
27320	57688	A	27483	68	145	
27321	57689	A	27484	1281	1433	
27322	57690	A	27485	171	708	
27323	57691	A	27486	1	270	
27324	57692	A	27487	278	588	VYIKRMPKKKV/SEGTIKEEPKR RLAQLSAKPAPAKVEAKLKKA AAKDKSSGKNVQTKGKRRAK GKQAKVANQETKEDLPAENGE MKTEESPASDEAGEKETKSD
27325	57693	A	27488	304	513	PVRHGAFFQDKSSDKK\VQTKG KRGAKGKQA\EVAN\QETKEDL PVD\SGETKT\EESPSLLIEAGEK EAKS
27326	57694	A	27489	1	435	
27327	57695	A	27490	3	273	
27328	57696	A	27491	9	293	
27329	57697	A	27492	1	504	
27330	57698	A	27493	1	529	IPPPRLFLPVATEVARVRLLPPP PPQNAARDALTSPSYLAWASPR KQTPSPPAAKDIK\KILEQRGYP KADDDR\LNKVI\SEAEWKYTL KDVIAPGVLASLPSVP\AGGAV AVSACPQALAAPCCLGSAPA\A AEGEEKMKKKEEVLKES\DDD\ MGFGPFELKSLPPLQIKGLFYTS R
27331	57699	A	27494	1	396	
27332	57700	A	27495	2	398	
27333	57701	A	27496	1	702	
27334	57702	A	27497	1060	1446	
27335	57703	A	27498	46	216	HPLQLSVIPFLPVK*HVDQMGF AD/CVLSN*VNCLASRFLAVSV ALRSSRFIFTMVP
27336	57704	A	27499	1	1152	
27337	57705	A	27500	126	184	
27338	57706	A	27501	238	498	

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27339	57707	A	27502	1	852	
27340	57708	A	27503	3	171	
27341	57709	A	27504	1064	1302	
27342	57710	A	27505	449	668	SPGDYFISLMAAMGRPQVGYW APELLQKMMRKRMNR/VKKLI QNYKQLK/CSLTLNNHVKLVRT NLRFHLAGLLG
27343	57711	A	27506	1	2454	
27344	57712	A	27507	2	408	
27345	57713	A	27508	205	715	
27346	57714	A	27509	1	813	
27347	57715	A	27510	1	864	
27348	57716	A	27511	17	396	
27349	57717	A	27512	3	428	LTNYAAAYCTGLLLARRLLNR LGMDKIYEGQVEVPGNEYNVE SIDGQPGAFTCYLVADLARTTT GNKVFGAPEGAVDGGLSNPHS SKRFLGLSIPHSTK*ILGYDSEN KEFNAEVRRKHIMGQKFADDL HCLIEEDENASKK
27350	57718	A	27513	164	431	EFFFSTSNIGVYLQIIHIVGKPI*H /YLV*ILSY*HLAARTISSKIKSN SLVPCASNRGDVGSTRRPRVTR RSVRYSAPAAPLRSPLFAR
27351	57719	A	27514	1307	1947	TNEGSGNSAPLFSGARNQTRMI VRGTNR/DIICQIAYARTEGDMI VCTAYVHELPKYGVKVDLTNY AAAYCTGLLLDRRLLNRFDMD KIYEGQVEATGDDYNVVSIDG QPEVHRKHIMGHNVADYMCY LMEEDEDGYKKQFSQYMKNSV TPDMMEEMCKKAHAAIRESPV CEKKPKKEVKKKKWNRPKMS LAQKKDWVAQKKASFLRAQE RAAES
27352	57720	A	27515	1	987	
27353	57721	A	27516	1521	1641	
27354	57722	A	27517	2	614	ILSRVVEFPLTAEVPPELLAAAG FFHTGHQDKVRCFFCYGGLQS WKRGDDPWTEHAKWFPSCQFL LRSKGRDFVHSVQETHSQLLGS WDPWEEPED\EPLWPPPSLPLG TLSCPHPGERSSLKVPRSQEGSV QPRPRGRGGFLSPQ/DARDVEA QLRRLQEERTCKVCLDRAVSIV FVPCGHLVC\AECAPGLQLCPI WQKPPSRSR
27355	57723	A	27518	3	89	

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27356	57724	A	27519	1	1618	ASSHVETRAHAEERLLKKLFSG YNKWSRPVANISDVVLVRFGLS IAQLIDVDEKNQMMTTNVWVK QEWHDYKLRWDPADYENVTSI RIPSELIWRPDIVLYNNADGDFA VTHLTKAHLFHDGRVQWTPPA IYKSSCSIDVTFFPFDQQNCTMK FGSWTYDKAKIDLVNMHSRVD QLDFWESGEWVIVDAVGTYNT RKYECCAEIYPDITYAFVIRRLP LFYTINLIIPCLLISCLTVLVFYLP SECGEKITLCISVLLSLTVFLLLI TEIIPSTSLVIPLIGEYLLFTMIFV TLSIVITVFVLNVHHRSPRTHTM PTWVRRVFLDIVPRLLLMKRPS VVKDNCRRLIESMHKMASAPR FWPEPEGEPPATSGTQSLHPPSP SFCVPLDVPAEPGPSCKSPSDQL PPQQPLEAEKASPHPSPGPCRPP HGTQAPGLAKARSLSVQHMSS PGEAVEGGVRCRSRSIQYCVPR DDAAPE\QMARLPAPWPLATPT RLSSHPQTSPLRANAHARRSPL RCPRVPRSRPAAPKHRPRTCPC
27357	57725	A	27520	1	3158	
27358	57726	A	27521	2	237	
27359	57727	A	27522	76	254	PLHITFFSRACFPSLHNCCEY*Q PGF*TS\KTPQLWCQLRQYSFK HSFLVVPTCPVPLLG
27360	57728	A	27523	86	376	SLEGRLSDYTPTFQGCQTTQGR LPWSFTLSGKSRFSGEGARACY KCQKSDHQ\ARNACSPGFLLSRI PSVRDPTGNRTVQLTWQPLPEP LELWPKAL
27361	57729	A	27524	1	167	MPEPQRPGVPPEPPPPGACYAC RKSGHWA\RNARSPGFLLSRVP SPPGPSRTPSFG
27362	57730	C	27525	1	381	
27363	57731	A	27526	243	437	VTSTVRQTPATSPAHKNFQMPE PQRPGVTPEPSPPGACYKCQKS DYQA\RNACSPGFLLSRVPSV
27364	57732	B	27527	88	1485	
27365	57733	A	27528	1	3759	
27366	57734	A	27529	36	438	RNDRVRPHRDVYSLQGRLSDH SPTFQGCQTTQGRLPWSFTLSG KFRFSGEGATTSPAHKNFQTPE PQWPGIPPEPPPTGACYTCRKSG HWA\RNARRPGFLLSRIPSVWD PTENRTVQLTWQPLPEPLELWP KAL

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27367	57735	A	27530	314	691	SLQGHLSDYTLTFQGCQTTQGH LPWSFTLSGKSRFSEEGTKGDV SGSQDNCGERVSRQTREQRSLH HRQGACYTCRKSGHWA\RNAR CPGFLLSCVPSVWDPTENRTVR LTWQPLPEPLELWPKAL
27368	57736	A	27531	383	2907	RSPTSKTKDICHRSWRRGL/WV NKASEDGEDLDRDVSVASNIEP WTGWCRAAPLQADLGPNSSSA SAPPPYNPFITSPPHTWSGLQFR SVTSPPPPAQQFTLKKVAGAKG IVKHALKRLKPVITRLLQHGLL KPINSPYNSPILPVLKPDKPYKL VQDLRLINQIVLPIHPVLGIIGLT SSVRRDAGQDLKRDRAEFLLG DEVHHPHRRRIAEARRLLLGQH FDPLHRLIGQVLELGEARYAPP VEQHHRLAPARRTGQRLHPLE QFGQAGRAQRRNRLGIEHRDR LDRPDDGAGNALAGDGDFRRG CLFAGIGIRPRYCRYRQSQDDR RPSHAAPRPRALPIPHRPATPIA DVMVMFSVAIMSQLRLVLRHI DGISRWPPAVVFITDVKIWLVY PSDDCRIRSNDRDDMQGEAPA MSMNAAARVGDPIGHSFSQGL FGEALDGLFFARRSEVDMRAG NLGRLIARGLSGGRWTPADGQ LTLGSRDVFINGPPATMTIRSTG QCRQHSGLRTVTRTETDSIGPIE VPADAYWGAQTERSLENFPFG AREQMPIGIVHALAIVKKAAAR INRGHGLAGEKADAIESAAHDV IEGRHDDQFPLVIWQTGSGTQS NMNANESSNDTFPTALHVAAA LAVTKQLFSALDRLHAALDAK AKEWDSIVKIGRTHLQDATPLT LGQEFSGYVQQLANARDRIEGT
27369	57737	A	27532	929	1227	PENGTFEFSILQVLDNSCHKMG KWS/RGA*RPGILLHIGPSLVSA PNVTHPKSFFFLSFLFLRSPPQV PSPLNPSFLWTHLTSPLLPRLLL ARLSQVPILT
27370	57738	A	27533	98	412	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ACYMCRK\SGHWA/RANARSPG FLLSRIPSVWDPT*KFGLVQLTL GKPLPEPLELRP\RLSD
27371	57739	A	27534	14	249	
27372	57740	A	27535	49	341	
27373	57741	A	27536	392	571	

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27374	57742	A	27537	1	1590	MPNGTNESHRYNASERSQTQK DEQTGKTVGPPEWTPLVRRNG GDSGLDFHFFAEKLKIIVDSAG RAGTGHMRPPAVHFGHRGQA MITLSPLRAKQKAVLQKPPPLT STYSLMLPLFLPDKRPPTTEWF LPVMEDAHELTLAWLMLALYR KPNASVQGSAQEETLCVFRVKE PLEWQALFADVHSGVNDKGPN INCSLYEHIKNVSEIVLNLAQTQ KNPAHSDPSSTPAGCM\PGTTA GGSAVMSACCPSPAAPGPLPGP ATGSC/SPSAAPRPPDPPPGHPE GIMAIRAAPSCLGACITLQDEET CEQTHTHSRIYMIYLFARCLLH AIARGRSRKCAASAGGTCPHVR VPGGGSYFRVSLQGQQTHWMR PENGFSTCVRTKSRRCPIIREQH PTKIPKALTANANQAFFLLVNG HSMVASPHQSQRRADLGGFWR DASSSLLANSQVQVCGSLRKRP HGWVVPFSLRCVAPLTADDSR LRTASLEMSTPPMHVQDDWQL RRGLPAGNTAVTVSELIYLNAN GRLQVEKFLF
27375	57743	A	27538	279	759	
27376	57744	A	27539	443	696	
27377	57745	A	27540	1	179	
27378	57746	A	27541	3	1237	
27379	57747	A	27542	4	152	
27380	57748	A	27543	760	908	
27381	57749	A	27544	203	570	
27382	57750	A	27545	312	500	
27383	57751	A	27546	1	441	
27384	57752	A	27547	1	630	
27385	57753	A	27548	1	1254	
27386	57754	C	27549	236	408	
27387	57755	C	27550	220	398	
27388	57756	C	27551	254	445	
27389	57757	A	27552	1	2742	
27390	57758	A	27553	1	744	
27391	57759	A	27554	1135	1751	RPGSTLQVRQNYHQGLRRPPIN R\QINLE\LYAS\YVYLSMSY\YF DRD\DVALKNFAKYFLH\QSHE E\REHAEKT**KL\QNQRRLAEF FLQDYQRNQD\CDDWGRAGLN \A\MECALAFWKKNVESSHYW NLHKL\AT\DKN*PPIWCDFHW RHIYLE*AG*KAIKRIWGDHVN QTFA/RKMGSAPNLGFGEYLF* QSTPWGDSDNESSPWG

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27392	57760	A	27555	224	547	
27393	57761	B	27556	22	130	
27394	57762	A	27557	1	408	
27395	57763	A	27558	1	1011	
27396	57764	A	27559	56	822	
27397	57765	A	27560	146	411	
27398	57766	A	27561	1	885	
27399	57767	A	27562	115	1200	
27400	57768	A	27563	791	1114	
27401	57769	A	27564	67	401	RLGSSGREVIHPGERGLENNVC/H*SSGNQENELEMNKTANGDCRRDPRERSRSPIERAVAPTMSLHGSHLYTSLPSLGLEQPLALTKNSLDASRPAGLSPTL\TPGERQQN
27402	57770	A	27565	109	345	HPLFIFPDPLPPPTFHPLIGPRMCFSPGLALCPHPNLILNCSSHNSYVLWEGPGGK*FESWGRFPHDTVLVIVNKSHKI
27403	57771	C	27566	63	167	
27404	57772	A	27567	231	314	
27405	57773	C	27568	99	323	
27406	57774	A	27569	1	1347	
27407	57775	A	27570	192	269	WFYKGEFLCTHS/HCLLPRKTCLLPAAM*YCDSQFSMAGETSQSWQKAKEEQRHILHGGRQKARLTWQQAGECVHRNSPL
27408	57776	A	27571	107	797	AQWRRAAPPAAGVTCPFRLQPGMETPLDVLSRAASLVHADDEKREAALRGEPRMQTLPVAS\ALSSHRTGPPPISPSKRKF\SMEP\GDEDLDCDNDHVSKMS\RIFQPPILNKTANGRLARRDPRERSRSPIERAVAPTMSLHGSHL\YTSLPSLGL\EQPLALTKNSLDASRPAGLSPTLTPGERQQNRPSVITCASAGARNCNLSHCPIAHSGCAAPGPASYRRPPSATCV
27409	57777	A	27572	1	1686	
27410	57778	A	27573	1	1614	
27411	57779	B	27574	208	366	
27412	57780	A	27575	15	1729	
27413	57781	A	27578	1	1614	
27414	57782	A	27579	308	464	KAHHHWSLEKCKSEPQ*DTISWTWMKLETIILSKLPQEQKTRNCMFSLISGS
27415	57783	A	27580	291	378	
27416	57784	A	27581	2	91	
27417	57785	A	27582	439	519	
27418	57786	A	27583	2	91	
27419	57787	A	27584	2	91	
27420	57788	A	27585	2	91	

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27421	57789	A	27586	50	394	
27422	57790	A	27587	1	666	
27423	57791	A	27588	2	91	
27424	57792	A	27589	5	91	
27425	57793	A	27590	884	991	
27426	57794	A	27591	290	460	
27427	57795	A	27592	86	349	
27428	57796	A	27593	2	89	
27429	57797	A	27594	723	882	
27430	57798	A	27595	255	352	TGTWMKLETIILSKLTQE\QKTK HCMFSLISGS
27431	57799	A	27596	1	1685	
27432	57800	B	27597	82	263	
27433	57801	A	27598	491	816	RHRGAQRKAFLQRVNCGLCCT WNLCPQKLRGRKWPVQVS\PA AGRDPGGPLL*PEGTLWGAPFC LGAPPPLLTAACAPAAGRAGGT RGAAPACPEDRTNAHSQHHHP HV
27434	57802	A	27599	645	1142	
27435	57803	A	27600	218	326	
27436	57804	A	27601	181	2316	
27437	57805	A	27602	2	238	
27438	57806	A	27603	709	1416	
27439	57807	A	27604	3	501	SSRALRLLGVVVRIRQAGTMA VTKELLQMDLYALLGIEEKAA DKEVKKAYRQKALSCHPDKNP DNPRAAELFHQLSQALEVLTDA AARAAYDKVRKAKKQAAERT QKLDEKRKKVKLDLEARERQA QGQGE*GGRRESRSTRTLEQEIE RLREKGSRQLEEQQRLI
27440	57808	A	27605	1	963	
27441	57809	A	27606	135	384	
27442	57810	A	27607	349	679	SETYWFFPRESQHLDLDVWPPR SEHHSQSTGTHSGVSESLSPRYF QRCNAHSPSQGHEEQYLAPWK HRLYQRMSDLPLNDIR*FQYSK GHHRCQSNEAVQNPKQLQSLL
27443	57811	A	27608	1590	2758	
27444	57812	A	27609	123	2312	
27445	57813	A	27610	1	1809	
27446	57814	C	27611	79	309	
27447	57815	C	27612	77	325	
27448	57816	A	27613	1	606	

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27449	57817	A	27614	2	686	SQCAELSASPLSPAPGLPRHSRL HALLGLAMPVDLSKWSGPLSL QEVDEQPQHPLHVTYAGAAVD ELGKVLTPTQVKNRPTSISWDG LDSGKLYTLVLTDPDAPSRKDP KYREW\HHFL\VVNMKG\NDISS GTVLSGIVG\SGP\PKGTGLHRY VWLVYEQG\RPLKCDEPIL\SN\ RSGDHRGKIQRWASLPVKK\YE APGPPVAGHRVTPSPKWDEPM CPQTVTKQLSWGK
27450	57818	A	27615	446	1300	
27451	57819	A	27616	2	346	
27452	57820	A	27617	1	305	MAISTSGSSVPWPSA/PSGPHGR GS\PWGFCLATCWQSIRGQGGD PWSAGSGHPGTKGASAPGPGE GQSGGDSGSA/GR*GSHHLPGP ASFRAGSGQAWDGKGK
27453	57821	A	27618	287	475	
27454	57822	A	27619	37	314	
27455	57823	A	27620	1	367	
27456	57824	C	27621	360	610	
27457	57825	A	27622	604	980	
27458	57826	B	27623	8	442	
27459	57827	A	27624	1	2268	
27460	57828	A	27625	296	398	APPGPTLPWASTPSRGCT*APPG PTLPWASTPSRGCTSSWFMLPA MRRCGAPC
27461	57829	A	27626	1	3633	
27462	57830	A	27627	1853	3809	
27463	57831	A	27628	1	656	MTHNQEKNKSTNTEMTMMMK LADKDDKTAMINMLQVVKKV EEAMSMMRRNKDVKNIHGRA RWVKPMIPALWEAKEVEGKYS AHNFWGSWKFKSSSRSSSSGPE SPARTHASFCQPDGGPTNKLGT KAFRVSPASSLLVDLNTQEVEII NVRKATPTCSLELGRKRRDGA AERAALDVVVVIYQLAPAAAP NCLNPVTSRR/PPQTPAPEGQGR RQSFEE
27464	57832	A	27629	127	273	
27465	57833	A	27630	3	405	AAFHARGHRAGLSASSCSWRC CPSSSAPCAPYAAPAARMLQTC LKQSPAGMPPASPSSPAAHSWG STSFSKYSPRSTSTSCCPCISSCW ESWPCPTPSSPL*NKFFPASFPN RQYQLLFTQGSGENKEKDHQL
27466	57834	A	27631	689	987	
27467	57835	A	27632	228	527	

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27468	57836	A	27633	108	441	
27469	57837	C	27634	156	287	
27470	57838	A	27635	2	363	RFTKVEMKEK\MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAKL
27471	57839	A	27636	2	367	
27472	57840	A	27637	1	936	
27473	57841	A	27638	1	865	
27474	57842	A	27639	1	1287	
27475	57843	A	27640	1	2565	MGPGARLAALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLLRRYLRGEEARLRDL TRCNDETITYLLDKRLTVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLRSRWAVGGATG SWVLSKGDRASLGERVVTGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLSPTSTRQRGQ SERSQDANGRRKQKTKSEPERF EDAVLLAGFKVEEEPVQRPRRK EWFQGPSPGHCCPAQPQDSAPC ILATHAPARAQNAPGTAWAAA LEGTSTVSLDHFHVVGVVVVS GGEIILLLSFRFYDKVLSLHEDS TTPVANPLLAFTLIKRLQSDWR NVVHSLEASENIRALKDGYEKV EQDLPAFEDLEGAARALMRLQ DVYMLNVKGLARGVFQRVTGS AITDLYSPKRLFSLTGDDCFQV GKVAYDMGDYYHAIPWLEEA VSLFRGSYGEWKTEDEASLED ALDHLAFAYFREQSSSPATEQS WMENDFDELREEGFRRSNYSE LQEEIRTNGKEVKSFEKKLDEW ITRITNAEKSLKDLMELKTKAR ELRDECRSLSSRCNQLEERVSV MEDEMNETKRGEKFREKRIKR NEQSIQEIWDYVKRPNLRLIGV LESDRENGTKLENTLQDIIQENF
27476	57844	A	27641	219	451	APAAEGAGRIS/PCSRHSPAGLE/ WLCPHLCALF*QCPP/PTCHQSA SPR\WP*G/RPAAGPHPPAATVA PKRKGKTKSSTRE
27477	57845	A	27642	237	561	

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27478	57846	A	27643	3	461	TRTRRGSRTAEAR*CTPGWRPA GRRSALCSRGHLGP*RPPRTRS GAAPGPHSPCGRPDGAPCSRLP PHRSRSPPHGSHVPAAGWLSAG PHQRWPAAAAGPGTDQCRVVG PERASPHIWKGSTVPFLPSWTFL RVLSVPGCSLPRCCWLGHCQ
27479	57847	A	27644	2	159	
27480	57848	A	27645	1	243	
27481	57849	A	27646	219	462	
27482	57850	A	27647	256	427	
27483	57851	A	27648	1	954	
27484	57852	A	27649	2	4690	
27485	57853	A	27650	1	1275	
27486	57854	A	27651	1	867	
27487	57855	A	27652	1	472	
27488	57856	A	27653	2	1215	
27489	57857	A	27654	3	401	
27490	57858	A	27655	712	1245	
27491	57859	A	27656	2	1178	
27492	57860	A	27657	278	339	
27493	57861	A	27658	1	1407	
27494	57862	A	27659	1	687	
27495	57863	A	27660	484	776	
27496	57864	A	27661	299	1318	
27497	57865	A	27662	1	960	
27498	57866	A	27663	122	282	
27499	57867	A	27664	1	600	
27500	57868	B	27665	1	375	
27501	57869	A	27667	356	439	
27502	57870	A	27668	49	360	
27503	57871	A	27669	2	580	GRVGCGGPWAARVGERIPNMA GRKLAS*KPTD*VAFARD/IIPQ NPKAPLPSFLKS\WNGDPSPSRL\ AALP*ESHPAI\DWA*LPRPNVA QGLAWVDDFE\KKFNAAERFPC PEDK\YTAQVDA\EEK\EDVKSL C/AEWVSLSKA\RIVEYEKEME KMKNLIP\FDQMT\IEDLNEAFP ETKLDKKKYPYWAHQP\IENL
27504	57872	A	27670	1	675	
27505	57873	C	27671	137	1357	
27506	57874	A	27672	1	1032	

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27507	57875	A	27673	3	938	MANNPGANGQ\PGGPGGPGMG KPRCF/RGEVFGIVIRGRGSRP/R GRGRGR\GRGARGSKGRG*RD W\VPVHQVGAALVKDH*RSKF PWKEIYLFSLPH/IKESEIIDF\FL GGLLSKDEGFE*LCPVQEQ\TRA GPAATR\FKAFCCYPGTTNG\HV G\LGVKCSQE\VAHRPFRGA\IL AKL\SIVPVR\RGYWGNKIRKP\ HTVP\CKVT\GRCGSVLVRLIP/S QPRGTGIVSAPVPNKL\LMMAG IDDCYT\SARG\CTATLG\NFAK AT\FD\AISKTYSYLTPDLWKET VFTKSPYQEFTDQLVKDHTRVS VQRTQAPAVATT
27508	57876	A	27674	1	864	
27509	57877	A	27675	2	752	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFMCQGGDCE/RHHNGTG GKSIYTEKFEDENFILKHTGPGI LSMANAGPNTNGSQFFICTAKT EWLDGKHVLFGKVKEGTNIVE AMERFGSRNGKTSKKITIADCG QLLISLTCVLS
27510	57878	A	27676	3	327	AQELHTFEVTGQETVAQIKAHV ASLEGIAPEDQVVLLAGAPLED EATLGQCGVEALTTLEVAGRM LGG\AKQEKKKKKTGRAKRRM QYNRRFVNVVPTFGKKKGPNA
27511	57879	A	27677	567	838	

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27512	57880	A	27678	3	1923	ATMAQGLEVALTDLQSSRNNV RHHTEEITVDHLLVRRGQAFNL TLYFRNRSFQPGLDNIIFVVETE DAVYLDSEPQRQEYVMNDYGF IYQGSKNWIRPCPWNYGQFED KIIDICLKLLDKSLHFQTDPATD CALRGSPVYVSRVVCAMINSN DDNGVLNGNWSENYTDGANP AEWTGSVAILKQWNATGCQPV RYGQCWVFAAVMCTVMRCLG IPTRVITNFDSGHDTDGNLIIDE YYDNTGRILGNKKKDTIWNFH VWNECWMARKDLPPAYGGWQ VLDATPQEMSNGVYCCGPASV RAIKEGEVDLNYDTPFVFSMVN ADCMSWLVQGGKEQKLHQDT SSVGNFISTKSIQSDERDDITEN YKYEEGSLQERQVFLKALQKL KARSFHGSQRGAELQPSRPTSL SQDSPRSLHTPSLRPSDVVQVSL KFKLLDPPNMGQDICFVLLALN MSSQFKDLKVNLSAQSLLHDG SPLSPFWQDTAFITLSPKEAKTY PCKISYSQYSQYLSTDKLIRISA LGEEKSSPEKILVNKIITLSYPSI TINVLGAAVVNQPLSIQVIFSNP\ LSEQVEDCVLTVEGSGLFKKQQ KVFLGVLKPQHQASIILETVPFK SGQRQIQANMRSNKFKDIKGY
27513	57881	A	27679	1	756	
27514	57882	A	27680	1	2601	

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27515	57883	A	27681	1	1677	MARKDLPPAYGGWQVLDATP QEMSNGVYCCGPASVRAIKEG EVDLNYDTPFVFSMVNADCMS WLVQGGKEQKLHQDTSSVGNF ISTKSIQSDERDDITENYKYEEE HFEAFQSVAQ\LPITRPFSWILRP F*RP*RKISTSFIRPLFTFL/LRLM NAHPEFRMAMKDAKTYPGKIS YSQDSQDLSTDKLIRISALGEEK SSPEKILVNKIITLSYPSITINLLA RVLSPSLPGPAGLASRSEYGPA KPTPTGNSSWPASAARSPGSRP CLSLHTSPQAEGAGSGLDQPRE RLPQCSGELKGSSSAARMGAE NEEAPRASEGCQGCQQAVTSQ QDGGPLLQNRFFWDCGDENGA DAVYLDSEPQRQEYVMNDYGF IYQGSKNWIRPCPWNYGQAASP WRYGQWWVFAAVMCTALGIK SCDFQAARNNEEHHTKALSSRR LFVRRGQPFTIILYFRAPVRAFL PALKKANKGKLESFSYICFFSIV FGSKNSYAKVAYLEVAYPATL QNGALRKYLVLGAAVVNQPLS IQVIFSNPLSEQVEDCVLTVEGS GLFKKQQKVLIP
27516	57884	A	27682	1	1653	
27517	57885	A	27683	3	2170	
27518	57886	A	27684	2	244	ACPSTSTSHCRGATCSCSRTS\C SGVLQHSLRHCASGRGFSSRCP ACCGSPGLGLPAALPPAAWGL QIAPSPQGTPGNSQS
27519	57887	A	27685	618	851	
27520	57888	A	27686	78	240	
27521	57889	A	27687	860	1246	
27522	57890	B	27688	1	2301	

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27523	57891	A	27689	1	1719	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNREHGKKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTLTSQLKELEKQEQ THSKAGRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL HINRAKDKNHMIISIDAEKAFD KIQQPFMLKTLNKLVLEVLARA IRQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNIPCSWV\GRINI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA KSILSQKNKAGGITLP

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27524	57892	A	27690	1	1902	MNAKALPTLSPLPQATTESVSL TQERSSSPATEQSWTENDFDEL REEGFRRSNYSELREDIRTKGK EVENFEKNLEECITRIINTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSAMEDEMNEMK REGKFREKRIKRNEQSLQEIWD YVKRPNVRLIGVPESHGENGTK LENTLQDIIQENFPNLARQANIQ IQEIQRTPQRYSSRRATPRHIIVR FTKVEMKERMLRAAREKEIQT TIREYYKHLYANKLENLEEMD KFLDTYTLRRLNQEEVESLNRPI TGAGIEAIINSLPTKKIPGPDGFT AEFYQRYKEELRIKYLGIQFTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTEPSEI MPHIYNYLIFDKPEKNKQRGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIDMGKDFMS KTPKAMATKAKIDKWDLIKLK ELLTAKETTIRVNRQPTKWEKI FTTYSSDKGLISRIYNEL/KQIYK KKTNNPIKKWAKDM
27525	57893	A	27691	1	2781	MGKKQNRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMNEMN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRDLD
27526	57894	B	27692	1	756	
27527	57895	B	27693	1	1743	
27528	57896	A	27694	1	1407	
27529	57897	A	27695	3	391	
27530	57898	A	27696	604	955	SSVFLGDPPILIGNKEMCLSSVL LINGSINFLHPFREDKGAVDVP GVATQQLILLNDPVLTASEILG\ LVSSLSK*TSPPIPGPGGNA*AR QPSCP*KGELSWRSAPSLVQFSS

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27531	57899	A	27697	1	1783	MGARAGGSCSCLMWLLLASG HFMGCVAAGDTVGPEKFRSCY TITLLQSKLSYSFGKNNKNFQL RKCLQTVDNLFVPNQNGYYCH SQTSLDRAQIDLNGRIRNGSVY SAHSTNSLNNPQPYLQPSPMSS NPSITGSDVMRPDYLPSHRHSA VIPPSYRPTPDYETVMKQLNRG LVHAERQSHSLRNLNIGSSYAY SRPAALVYSQPEIREHAQLPSPA AAHCPFSLSYSFHSPSPYPYPAE RRPVVGAVSVPELTNAQLQAQ DYPSPNIMRTQVYRPPPPYPPPR PANSTPDLSRHLYISSSNPDLITR RVHHSVQTFQEDSLPVAHSLQE ERSSSPATEQSWTENDFDELRE EGFRRSNYSELREDIQTKGKEV ENFEKSLEECITRITNTEKYLKE LMELKTKARELCEECRSLRSQC DQLEERVSAMEDEMNEMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLAKQANVQI QEIQRTPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKGRVT LKG/ITHQT/RQRISRQKLYKPEE SGGQYSTFLKKRIFNPEFHIQPN
27532	57900	A	27698	3	1046	
27533	57901	A	27699	1	3585	
27534	57902	A	27700	937	1119	

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27535	57903	A	27701	1	2231	MGKKQSRKTGNSKKQSASPPP KERSSTPATEQSWSENDFDELR EEGFRRSNYSKLQEEIQTKGKE VKHFEKNLDECITRITNREKCL KELMELKAKARELREECRSLRS QCDQVEERTLARLIKKKREKN QIDAIKIDKGDITTNPTETQTTIR EYYKHLYTNKLENLEEMDKFL DTYTLPRLNQDDVESLNRPITG SEIEAINHSLPTKKSPGPDRFTA KFYQSLPSSCDYGHAPAHPDVF RVSSFWWVRGLAGSGVKLQTF AVSVTALKAARLELFIPPDSGA QLASPSGSLTRTGGGAACQSHA VCPHSSAFGWSMGLGAMEQG AALIGEARASREPMEEVGGSG MAACRSQALPRGQLRPSEKSRA APEHSSSPAMEQSWMENDFDE LREEGFRRSNYSELREDIQTKG KEVENFEKNLEECITRITNTEKC LKELMELKTKARELREECRSLR SRCDQLEERVSAMEDEMNEMK QEGKFREKRIKRNEQSLQEIWD YVKRPNLHLIGVPESDGENGTK LENTLQDIIQENFPNLARQANIQ IQEIQRTPQTYSSRRATPRHIIVR FTKVEMKEKMLRAAREKGDSV ERSFSNKAELLFQLHGHQRESL SKKEAQVWRDKGLYFRKGLLD QAQSWSRQVASILGAQIQVEGS PEQRLENVELAGGHLNTLKAIP MVAVAGGISFKCGAVLLLGAA
27536	57904	A	27702	596	1593	KPRLENYVKNAEASGANAINW KKGY/LVMEDEMNEMKQEGKF REKRLKRNEQSLQEIWDYVKR PNLRLIGVPESDGENGTKLENT LQDIIQENFPNLARQATVHIREI QRTPQRFSLRRSTPRHIVRFSKV ETKEKMLRAAREKEIQTTIREY YKHLYTTKLENLEEMEKFLDT YTLPRLNQKEVESMKRPITSSEI EAVINILPIKRSPGPDGLTATFY QRYKEELERSSSPATEQSWMEN DFDELREEGFRRSNYSELREDIQ TKVKEVENFEKNLEECITRITNT EKCLKELMELKTKARELREECR SLRSRCDQLEERVSAMEDEMN

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27537	57905	A	27703	717	1803	STGRKAPHHTYSKIDHILGSKA LPSKCKRT/E/IITNCLSDHSAIKL ELRIKKPTQNPSTTWKLNNLLL NDYWVNKEMKSEIKMFFETNE NKNTTYQNLWDAFKAVCRGK FIALNAHKGKQERSKIDTLTSQ LRELEKQEQTHSKVSRRQEITKI RAEPKEIETQKTLQKINESRSWF FERINKIDRRLARLIKKKREKNQ RDAIKNDEGDITTDPTEIQTTIR EYYKHLYANKLENLKEMDKFL NTYTLPRLNQEEAESLNRPIAGS EIVAIINSLPTKKSPGPDGFTAEF YQRYKEKLVFGAGYFGMWAL AALPSNLLKLSQLCQEAAEVNV LVQFVCICPAQEPTEIDVLFSVL PPLSLILN
27538	57906	A	27704	407	1696	NILRNAVPHQQQNKA*RRMTL TS*EKKASDDQTTPSYRRKFKA KAKKLNT/YEKNLDECITRITNR EKCLKELMELKAKARELREEC RSLRSQCDRLEERVSVMEDEM NEMKREGKFREKGIKRNEQSL QEIWDYVKRPNLHLIGVPESDR ENGTKLENTLQDIIQENFPNLAR QANIQIQEIQRMPQRYSSRRATP RHIIVRYTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLLAET LQARREWGPIFNILKEKNFQPRI SYPDKLRFISEGEIKYFTDKQML RDFVTTRPALIEALKEVLNMER NNRSPSSSPATEQSWMENDFDE LREEGFRRSNYSELREDIQTKG KEVENFEKNLEECITRITNTEKC LKELMELKTKARELREECRSLR SRCDQLEERVSAMEDEMNEMK REGKFREKNNKKK
27539	57907	A	27705	2597	5904	
27540	57908	A	27706	1	675	
27541	57909	C	27707	137	1357	
27542	57910	A	27708	1	1032	

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27543	57911	A	27709	3	959	MANNPGANGQ\PGGPGGPGMG KPRCF/RGEVFGIVIRGRGSRP/R GRGRGR\GRGARGSKGRG*RE WNAVHQVGAALVKDH*RSKFP WKEIYLFSLPH*RNQRIIDF\FLG GLLSKDEGFE*LCPVQKQTRA\ GQPHPGFKA\FVAIGDY\NGHV GLG\VKCSKE\VATGHPVGAII\L AKLSIRPRCAEGYLGNKVLAKP \HTVPLQGDKGRCG\SVLVRLH PLHPRG\TGI\VSAPVA\KKLLM MA\GIDDCYTLS/ARGCTATLG QIWPRAT\FDAISKTYKLP*PPD LWKETVFTKV\PYQ\EFT\DHLV KDPHPESSVQQDSELQLVATT
27544	57912	B	27710	50	1598	
27545	57913	A	27711	1	3916	
27546	57914	A	27712	334	462	PAFITVNKCSSARKLIQV*GPVA CRVHILPLVVRCPPKPGTTG
27547	57915	A	27713	256	654	
27548	57916	A	27714	1	855	
27549	57917	A	27715	211	436	
27550	57918	A	27716	19	319	
27551	57919	A	27717	987	1392	RHCLCSPSRSSESLQPTASSSSA RSSPSPPASQPVPPGPAGAAAAP HPPCCPPESTCWTWPC*SPLCH WAVA*ARSGPGPLGECFETHGP HGCPPGQSPRPPQ*APSAWWTE VQPR*PRPAPEGSSRRPPPPGAP
27552	57920	A	27718	285	1266	RSQIQRGTDRAPKCTSGPP\HRV AQPQDDAPREEPPYLPNGMPPG RDAPHLPDWAASQRGSSHPRR WPPSQRRSLLPRRVADRPEAAI SALWEAKAGGWETLPEMEITIH NKTRQSKRITHQTNRPNTSSKTI RITKTDLTSWETQSPGSPDRHR KPSTATKHNRFSKIYSRFSIFQC DQGLNGRCGQGKGAGKEQRM QEQGENFQAPPFQSHPALRSLQ MQQVQTEEHFGTLECGKLAQC SFHPTREEDRNQDGKTDMLHF KLELPLQSTEHVLGVQLILTFSY RLHSCGIPSVLSRYPYFSMLAFG ILSRTLRRFVTVSSLLITGI
27553	57921	A	27719	1518	1779	ARSGPGPLGECFETHGPHGCPP GQSPRPPQ*APSAWWTEVQPR* PRPAPEGSSRRPPPPGAPCPAQP PTRRCPGRHQTPPAAGAAVP
27554	57922	A	27720	507	1114	
27555	57923	C	27721	80	223	

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27556	57924	A	27722	1	2373	
27557	57925	A	27723	2	272	RARTPPLWPRARGPGSRVSGAP WFLLDLAGGGFLPPAVLCDLSA ASSTVSGRSNPHC*AWGGLEFF GEVERAESGFPVPEPSLISEMPH
27558	57926	A	27724	195	489	
27559	57927	A	27725	210	1308	
27560	57928	A	27726	203	474	
27561	57929	A	27727	224	892	
27562	57930	A	27728	1	457	
27563	57931	A	27729	3	1325	
27564	57932	A	27730	322	512	
27565	57933	A	27731	621	737	
27566	57934	A	27732	441	588	
27567	57935	A	27733	1	792	
27568	57936	A	27734	8	488	SGCRNSARADADPSLHASPPAP TMATVQLLEGRWRLVDS\KGF DEYMKE\LGVGIALRKMG\AMP KP\DCIITCDGKNLT\IKTESTLK TTQFSCTLGEKFEETTADGRKT QTVCNFTDGALVQHQEWDGK ESTITRKLKDGKLVVECVMNN VTCTRIYEKVE
27569	57937	A	27735	861	2161	
27570	57938	A	27736	349	625	
27571	57939	A	27737	1	630	MAQETNHSQVPMLCSTGCGFY GNPRTNGMCSVCYKEHLQRQN SSNGRISPPATSVSSLSESLPVQC TDGSVPEAQSALDSTSSSMQPS PCIK\QSLLSESVASSQLDSTSVD KAVPETEDVQASVSDTAQQPSE EQSKSLEKPKQKKNRCFMCRK KVGLTGFECRCGNVSCES\HRY SDVHNCSYNYKADAAEEN/LE KENPVVVGEKIQKI
27572	57940	A	27738	1	1089	
27573	57941	A	27739	41	334	AGKMTKLEEHLEGIVNISPQ*S VRKGHFDTLSKG\ELKQLLTKE LANT\IKNIKDKAVIDEIF\QG\LD ANQDE\QVDFQEFIS\LVAIALK AAHYHTHKE
27574	57942	A	27740	1	519	
27575	57943	A	27741	28	314	
27576	57944	A	27742	208	421	
27577	57945	A	27743	619	890	
27578	57946	A	27744	113	328	LGSGAWGGGDLPWEINPLSSCS LLREKDLLTTSGPQT\TSPRNISP ILNRDPTVQLTWQPLPEPLELW PKAL
27579	57947	A	27745	501	680	

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27580	57948	A	27746	166	405	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQ\PRNISPISNRD PTGKWTVQLTRQPLPEPLELWP KALRLTPSQIFSA
27581	57949	A	27747	425	484	
27582	57950	A	27748	448	520	
27583	57951	A	27749	3	679	GGGFSDRDRTIALQPGQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGEKFYFIPKAMG AMEGSGQRRTLPDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLREKD PPTTSGPQT\TSPRNISPILNPELA TLAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP EPLELWPKAL
27584	57952	A	27750	3618	3848	NLCKEPSSRRSIHKESLLNFPLM GLDPRPQEGFPRDSPR*REESTS LHDPMASSSSTVFWGLKRQKY FLWPFRAST
27585	57953	A	27751	1	297	
27586	57954	A	27752	244	420	RKETKERSRTPP*SPRTGQMTP CKLQPGVLSFPRTAQSWEPPAV PQSPLKNELRRKYLT
27587	57955	A	27753	1993	2205	
27588	57956	A	27754	138	833	
27589	57957	A	27755	1	875	
27590	57958	A	27756	1	1041	
27591	57959	A	27757	3	1447	
27592	57960	A	27758	23	3257	
27593	57961	A	27759	2	168	GKAGCWPRSRARKCRTSSPSIW AAWRPPTR*LTVTSRPGTSGSE PWAMAAASRWQ
27594	57962	A	27760	85	1271	
27595	57963	A	27761	5871	6056	TSSAASTAPRWRRKPHGHQKSL PASLRFPGR*TPQPDLPGPPAQP PAQPGPPQAATVPGRW
27596	57964	A	27762	1	280	
27597	57965	A	27763	1	714	
27598	57966	A	27764	2	558	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFTCQSGDFTRHT/GIGGKS ICREKFDDKNFILKHTGPGILSM ANAGPSVNV

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27599	57967	A	27765	1	927	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAENFRALSTGEKGF GL*GVPCFHR\IIPGFM\CQG\GD FTPP*MAPGGKSIYGEK\FEDEN FI\LKHTGPGILS\MANAGPNTN GSQFFICTAKTEWLDGKP\VVF GK\VKKGLNIVEAMERFGSRNG KTSKKITIADCGQLLISFDLCFIL NHQDHSFCALLSGEHPSTPFAR RILRILWLSLQFLWGSMFSLFPP MPSWIAAVKFMIIEIKTK
27600	57968	A	27766	1	798	
27601	57969	A	27767	1	575	PTRPPTRPPTRPIMAQDQGEKE NPMRELRIRKLCLNICVGESGD RLTRAAKVLEQLTGQTPVFSKA \RYTVRSFGIRRNEKIAVHCTVR GAKAEEILEKGLKVREYELRKN NFSDTGNFGFGMQDHIDLGIIY DPSIGIYGLDFYVVLGRPGFSIA DKKRRTGCIGAKHRISKEEAMR WFQQKYDGIILPGK
27602	57970	A	27768	1	1695	
27603	57971	A	27769	1	228	
27604	57972	A	27770	1098	1938	IWPRPRDC/RVSYTTVFPPATVT APV/VSGGSHDHIQQYSDIEDFR QATAASSVMVARAAMWNPSIF LKEGLRPLEEVMQKYIRYGGM GAALLSDPDKIEKAPSMGTLM GVYLPCLQNIFGVILFLRLTWM VGTAGVLQALLIVLICCCCTLL TAISMSAIATNGVVPGYLHTLV QNLVNNGYVRDETVRAAPYD WRLEPGQQEEYYRKLAGLVEE MHAAYGKPVFLIGHSLGCLHLL YFLLRQPQAWKDRFIDGFISLG APWGGSIKPMLVLASGSGTRA
27605	57973	A	27771	1	1710	
27606	57974	A	27772	163	1659	
27607	57975	A	27773	3	297	
27608	57976	A	27774	3	447	SSPHSSRSLSAPPLPGLPLWRHL RSPSAHRCTVGAPFWAGEGRSP LPQLAGRCGGRRASGNRG\ARG ACGPAGVPGGRGLGGPALGAA GRPGP*LPSRGAGLGTA/GPPCL SLPPPPWVPVQPEPPRRAPPPAP RRPVPSTAQGLRSASA

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27609	57977	A	27775	3	197	RPDAVPARSLEMKRFPMPPPPP\G*FSPGASLDVNPGCYKQAPSCSLAQILSNLSNLWSSAVSNF
27610	57978	A	27776	77	379	GRLLDKAGIPH/PPFPSGGLGCQH*RRSPLHEHPSSGP\PAGLKPSLSCLPAGQGSGPAARY/GLSLPPTPWAPVQPEPPRRAPPPAPGRSVPSTTQGLRSASA
27611	57979	A	27777	177	444	RGGQGSGPAACYA*/RLPPTPWAPVRPEPPQRAPPPAPRRPVPSTTQGLRSASTRRVTGRQLHLQPWCGIHWVKPAGLLSLVGRWRVLMS
27612	57980	A	27778	165	591	QRAGSPHSPRSLSAPPLPGLPLWRHLRSPSAHRCTVRAPFWAGQGRSRLPQLAGRCGGRGASGNPG\SHGACGPAGVPGGRGLGGPRTGSSQLALPAPGNEGLSTPASGRRKKLRTHPSIRRNKLQTRYLKSCNTHREGPRLH
27613	57981	A	27779	1	1605	
27614	57982	A	27780	2	1970	
27615	57983	A	27781	1	3522	
27616	57984	C	27782	183	254	
27617	57985	A	27783	39	346	QYISELQFLASTVRQTPATSPAHKNFQTPEPQQPGIPPEPPPPGACYKCWKSGHQAKECLQPGIPRK/HASHLWQPLPEPPGTLAQGSLTDSFPDLLGLAAED
27618	57986	A	27784	1	354	
27619	57987	A	27785	72	299	
27620	57988	A	27786	273	530	LGSGDLPWGINPLSSCSLLREKDPLTISGPQTHQPKEHLTNFKSGPH*KSDCSTAPG\ATPRAPGTLAQGALTDSFPDLLSLAAED
27621	57989	A	27790	1	1068	
27622	57990	A	27791	148	527	
27623	57991	A	27792	2	1910	
27624	57992	A	27793	1	1047	
27625	57993	A	27794	96	488	WDRMAGGSSNTFGFPPPPLPYRSCER*QRDGGPRSPGSLSVPPWPR/PPILAALEEPFSPPLHRGRPSLGWPRPELAPSAQRSAAS/RPEASKDHEPTRKKE/PTPDTQP*EL*HSLPRSSASLALGPHYLYEL
27626	57994	A	27795	3	2086	
27627	57995	A	27796	3	412	
27628	57996	A	27797	2	390	

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27629	57997	A	27798	1	629	MKVGLDQIIEVVPSHSVTSGAA AGECGGVHCDSVCAEGRWGPN CSLPCYCKNGASCSPDDGICEC APGFRGTTCQRICSPGFYGHRC SQTCPQCVHSSGPCHHITGLCD CLPGFTGALCNE/RLFTVCPSGR FGKNCAGICTCTNNGTCNPIDR SCQCYPGWIGSDCSQPHCADKC VHGRCIAPNTCQCEPGWGGTN CSSVKKQSTVCES
27630	57998	A	27799	108	1071	YPLFLSSISACDGDHWGPHCTS RCQCKNGALCNPITGACHCAA GFRGWRCEDRCEQGTYGNDCH QRCQCQNGATCDHVTGECRCP PGYTGAFCEDLCPPGKHGPQCE QRCPCQNGGVCHHVTGECSCP SGWMLSFPGWRPI*FSKSL*MQ GTVCGQPCPEGRFGKNCSQECQ CHNGGTCDAATGQCHCSPGYT GERAAVPDVRK\CQDECPVGTY GVLCAETCQCVNGGKCYHVSG ACLCEAGFAGERCEARLCPEGL YGIKCDKRCPCHLENTHSISLIA AKKSNSLHAIALDFRAQCQSVK DRCHASDLPIDIVSTETLR
27631	57999	A	27800	243	1296	ETQEESSEFLPCGSHQPNG*LLF CSTYKRCLCNWGPC*AY*RACP CPALQQCPDI/CPQAQLAIPCAP QQQQLSRCLSFPSSLLQDPNTP G/EYRKDEGRAGSRGAGEKQC THNSPRWLQNTVSNQGSSMPG FQSHVPSLLGAFVQCTNCTRVC SSPANKIFTTFRLGDPLVSPCHQ GFGSNTHCCVESWQSSCSGMH KDLGALHTPAPGSPTNVAATQ ARREPRCRLAVLSTLDRSTRQK VNKDIQELNSALHQADLTDIYR TLHPKSTEYTFFSEPHRTYSKTD HLVGSKGLLSKCKRTEIITNCLS DHSAIKLELRIKKLTQNCSTTW KLNNLLLNDYWVHNEMKAEID
27632	58000	A	27801	552	827	
27633	58001	A	27802	70	200	
27634	58002	A	27803	18	1057	
27635	58003	A	27804	652	960	
27636	58004	A	27805	1	474	
27637	58005	A	27806	1	140	
27638	58006	A	27807	1	1260	

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27639	58007	A	27808	126	893	EDGSGGGKFPEGARQGGTGQR RRRKAMRRTGAPAQADSRGRG RARGGCPGGEATLSQPPPRGGT RGQEPQ\MKETIMNQEKTRHTC RHKVRIGGKGTARKKKKVVHI TATA\DDKK\LQFLLKGS*GVN NISGIE\EVNMFTNPRNKLIHF*Q PLKVQGISWAANTFHHLQGHA *DKSSWTEMLPSIFKPSLGAG*V *LVLRRLA\EALPQTNLWDGKS TTLLLGEDDGDDDESSQILWEY FGWRVPRNEANLNLSSTF
27640	58008	A	27809	180	589	KELPLLIFCRWQFESLHELNVPF FKVGSGDTNNFPYLEKTAKKG SPNGDLPVGCKSNGHP*SKFIRS VKPLNPQLLASLQCTSAYPLQP EDVNLRVISVSRREGVPFLGHL LWGRRSLFYNQNSNKHGILYN
27641	58009	A	27810	623	1082	
27642	58010	A	27811	548	645	
27643	58011	A	27812	329	510	
27644	58012	A	27813	3254	3628	
27645	58013	A	27814	1	960	
27646	58014	A	27815	349	681	PMASNRAITLTAWPKIPFLGICE AKNPRSENMRL/AHHFGSGLPP SWELWEQGPPGNSSRYIEFLNK HTYIKGTLRVYTKKFCMLVIKS FESKSCVWRYDFDSKSSVNVTV
27647	58015	A	27816	240	473	
27648	58016	A	27817	825	1043	
27649	58017	A	27818	2	418	GKVVCFEAFLQQILGKHQFYW CLEGLGHCHHHIGAKYPEDIVD EESAQQDAASADIVEVQELYSI KGEGGQAKKVVGNPVLPQQVPD ANDAAQAQAHQVLGVKFIIDD L*AERPGKSTP*GRATPPTFLVF PRTLCEGI
27650	58018	A	27819	2	427	
27651	58019	B	27820	51	672	
27652	58020	A	27821	43	667	
27653	58021	A	27822	516	1056	WSRAPAPQQCQHWLHPAGRTL HLRCLLGIWHQCDGDSGQVLR GTNENLVFPQDLLEKGLEANNF AMLGTWEMSSFPGIFIALLLRF DISLKKNTHTYFYTSFAAYIFGL GLTIFIMHIFKHAQL*GVKS*GS SGSDRIQRGNRGISIEGAGEERE MMQLVPEPLRARPDRWGLGPH RRA
27654	58022	A	27823	1	1019	
27655	58023	A	27824	1061	1258	

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27656	58024	A	27825	44	621	
27657	58025	A	27826	406	727	
27658	58026	A	27827	2	1337	
27659	58027	A	27828	1236	1391	
27660	58028	A	27829	228	502	
27661	58029	A	27830	1	1035	
27662	58030	A	27831	146	392	GHRSHQSPEETPNLIPRTPIPPLG TGTSIRSTRIPRTEASGPNGLN\ WYLTPTPPGGQRPSSAASPRGF PPTNNSSRLPAEPE
27663	58031	A	27832	15	300	
27664	58032	C	27833	289	414	
27665	58033	A	27834	3	576	AALAERWLGEVLVRVGVRVPG GSGGLRHWCPCGLLGRGLGQA PEHKVRLSMEFCSTCTADHISLS SFWRSSFQQPLVPAVSLQSPDR RLSHDPAASSWSGFCGISPAFSA FSECSPSSLRSHPPALLQAAES* FAASSSPSPTWSLSGSGTRKPW S/VACNWLLSDSSSHRRSFWES GIITMVLALTLEELV
27666	58034	A	27835	1	231	DELLVGGNPRGDAAEEGRCPP GGVGVRYQIQPIWPRRLCSRNP GAAD*GPGS*RWDRCPRDEIWR FLGALVGSVSSG
27667	58035	A	27836	18	398	KVRWERSWSESESESQEGRRR AQALVPSVAS*/SSRPWDRPPST K*GCLWSSAARAQQTIYHSVPS GGHPSSSHWLPAVSLQSPDRRL SHDPAASSWSGFCGISPAFSAFS ECSPSSLRSHPPALGSF
27668	58036	A	27837	1059	1446	AVWSLPAPPAPCLLAGLLCTCC RTP*TASLCARGPVPRPRA*EAT RGTSA*ALHSPPGTLTPTVTRTS PSHLSARAAAPSHPARPTASRSS RLPAWLAVRLSIPPRRGSLGGA GAQAAAASTRFTCCS
27669	58037	A	27838	1	211	ATALAERWLGEVLVRVGVRVP CGEWRAQALVPIVAS*ATRPSG RGPPTQQT*RTSRIGRS*QTTMR HART
27670	58038	A	27839	316	537	
27671	58039	A	27840	255	475	RPWVRAPYKLLPALLHAPLCAP PSSPWRPV/PASAPSFKLLKS*IF CKQLSLLPTWSLSGSGTRKPWS GPVTGS
27672	58040	A	27841	622	1127	
27673	58041	A	27842	364	666	

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27674	58042	A	27843	37	299	ILLCSVQTLPLLRREFYGHIPKC QQSLNIICSPSSLRIPGFLHRNRL STPFHVQQPQREHF*YCRSQIH GENSAWHIRSHHAEKAHF
27675	58043	A	27844	84	428	PAEIERSTAKTPGPPGSLEMGLL TFRDVAIEFSLEEWQCLDTAQR NLYKNVILENYRNLVFLGIAVS KQDLITCLEQEKEPLTVKRHEM VNEPTGPRQKRRVTSSR**MKR YVII
27676	58044	A	27845	1	719	
27677	58045	A	27846	669	830	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHWR
27678	58046	A	27847	223	382	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHWR
27679	58047	B	27848	1	491	
27680	58048	A	27849	1	1113	
27681	58049	A	27850	505	1105	ITCTLYPSLRIVYEAFPATGDNM FRRIIKDALFRTIQFCQIMNRSQ YMFTCRCRTEMQVPQHRRKKT FKPTVLLNHFVMEIIVLTAGRID AAFQDEVAASEGFLKQPVGKD YKFGGPSVKDEKLFGVGTGMG HHN*LSV*TSIQHLLSNTQG/CL RVCPALRL/HSRNLSAMVISFSF SCGARSAISPINARKRWASPVC
27682	58050	A	27851	1	2697	
27683	58051	A	27852	1	1998	
27684	58052	A	27853	864	1025	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHWR
27685	58053	A	27854	1605	1766	CLVQNQNIFC*ILS*WSSLV*QS ACRQLMPLLHLPNDQQAPVWT ENQPGGHWR
27686	58054	A	27855	677	735	
27687	58055	A	27856	1126	1568	SSSSTGRSRHKEVSPGCQQDGL RCQEWWSVRPG\YEATGGVWG KQLGIPASGLPGRRSSESPRKSC TPVTSRTGLPVCPWAALSPESR SFSLSVRPVCVC\CVGTKMSCA PECCFFLVSLSLLSLFLRLLLGL AAHCQFFPAVPLCIL
27688	58056	A	27857	1142	2450	
27689	58057	A	27858	1	1131	
27690	58058	A	27859	229	402	
27691	58059	A	27860	505	597	
27692	58060	A	27861	1	657	
27693	58061	A	27862	248	382	QPPKITLLYQQWIQTKKKSLKS FLP*QEFRKMQKKHSTKSSITL

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27694	58062	A	27863	1	1341	
27695	58063	A	27864	1	739	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKTSRRQEITKIRAELKEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKREKNQIDAIKN DKGDIITDPTEIQTTIREYYKHL YGNKLENL*H*MPTRESRKDLK LTP*HHN*KN*RSKSKHIQKLAE GKK*LRSEQN*RK*RHKKPFKK SMNAGAGFLKRSTKLIDR
27696	58064	A	27865	1	1920	
27697	58065	A	27866	444	763	
27698	58066	A	27867	1	651	
27699	58067	A	27868	94	964	VNADWVLQRELEQTSLWSSKQ RACCLSHVVGLRMISSCTTRKM AEEEQRKIPLVPENLLKKRKAY QALKATQAKQALFGKEGAEER KRAQ/WFKRLESFLHDSLAAET *QG/RISRQLEVQPHALELPDKC SLAFVVRIKRIDGGSLLVQRTIA RLCLKKIFSGVF\VKAPPRIQKW LRIVEPYVTWGFPNLKSVRELIL KRGQAKVKNKTIPLT\DITVME EHLGKFGVICLEDLIHEIAFPGK HFQEISWVLRPFHLSVAHHATK NRVGFLKEMGTLGYRGERINQ LIRQLN
27700	58068	A	27869	176	334	
27701	58069	A	27870	3	452	AASTGGGSHLLLSIMAALRPLV KPKIVKKRTKKFIRHQSDRYVK IKRNWRKPRGIDNRVRRRFKGQ ILMPNIGYGSNKKTKHMLPSGF RKFLVHNVKELEVLLMCNKSY CAEIAHNVSSKNRKAIVERA\A QLAIRVTNPNARLRSEENE
27702	58070	A	27871	2	423	
27703	58071	B	27872	193	1698	

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27704	58072	A	27873	263	714	KLNVPIIKATNTIMNMTMNLK MSLTAPPSDICRGPKLSFAGKIQ AIPEKLKTTATAQRPLDTIGLEV PVPAAWLLSAVRNCSKLRATS GPNLDTMNGSRRQTGSWTEGS RSSMKPHLLSDITGALR/SPKVS *AFCRLATWPFNFLQSGILS
27705	58073	A	27874	347	902	
27706	58074	A	27875	17	1178	
27707	58075	A	27876	1	1155	
27708	58076	A	27877	3	1109	EKETMQSLNDRLASYLDRVRS LETENRRLESKIREHLEKKGPQ VRDWSHYFKIIEDLRAQIFANT VDNARIVLQIDNARLAADDFRV KYETELAMRQSVENDIHGLRK VIDDTNITRLQLETEIEA\LKEEL LFMKKNHEE\EVKGLKTPNYA ALG*T\VEVDAP\KSQDLAKI\M ADIR\AQ\YDELGSERTERKLDK YWSQQIEESTTVFTTQSA\EVGA AETNLHRSLKRTV\QSLEDRPW TSMRNLKAQLGEQP*GEVEAPL RPTRWSQLNGILLHLES\ELAQT \RAEGQRQA\QEYEALLNIKVKL \EAEIATYRRLLEDGEDFNLGD ALDSSNSMQTIQKTTTRRIVDG KVVSETNDTKVLEALSQQKAG
27709	58077	A	27878	1	1305	
27710	58078	A	27879	209	560	
27711	58079	A	27880	219	512	
27712	58080	A	27881	528	803	
27713	58081	A	27882	3	432	SSPCVEFSTSMGACLRPATARSP SATCTAWTCTGWRRGRPWWR WTPENSGVAGGDGTSEEDSEE VEGAEWWGRRRRQRRGERCG GLRRAPCQGAPGKCLCPRPP\GP SPC*/CEALGAQRAS*PHRRELK VGGPGPGCELSPMV
27714	58082	A	27883	117	483	
27715	58083	A	27884	1	1497	
27716	58084	A	27885	228	776	
27717	58085	A	27886	1012	1677	
27718	58086	A	27887	194	562	
27719	58087	A	27888	1	423	
27720	58088	A	27889	232	308	
27721	58089	A	27890	1	1692	
27722	58090	A	27891	186	2191	
27723	58091	A	27892	2	141	
27724	58092	A	27893	1	1692	

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27725	58093	A	27894	186	2192	QRRPRPFPSQGISMTECFLPPTSS PSEHRRVEHGSGLTRTPSSEEIS PTKFPGL\YRTGEPSPPHDILHEP PDVVSDDEKDHGKKKGKFKKK EKRTEGYAAFQEDSSGDEAESP SKMKRSKGIHVFKKPSFSKKKE KDFKIKEKPKEEKHKEEKHKEE KHKEKKSKDLTAADVVKQWK EKKKKKKPIQEPEVPQIDVPNL KPIFGIPLADAVERTMMYDGIR LPAVFRECIDYVEKYGMKCEGI YRVSGIKSKVDELKAAYDREES TNLEDYEPNTVASLLKQYLRDL PENLLTKELMPRFEEACGRTTE TEKVQEFQRLLKELPECNYLLIS WLIVHMDHVIAKELETKMNIQ NISIVLSPTVQISNRVLYVFFTH VQELFGNVVLKQVMKPLRWSN MATMPTLPETQAGIKEEIRRQE FLLNCLHRDLQGGIKDLSKEER LWEVQRILTALKRKLREAKRQ ECETKIAQEIASLSKEDVSKEEM NENEEVINILLAQENEILTEQEE LLAMEQFLRRQIASEKEEIERLR AEIAEIQSRQQHGRSETEEYSSE SESESEDEEELQIILEDLQRQNE ELEIKNNHLNQAIHEEREAIIEL RVQLRLLQMQRAKAEQQAQE DEEPEWRGGAVQPPRDGVLEP KAAKEQPKAGKEPAKPSPSRDR
27726	58094	A	27895	12	413	PSRAPGLQKACTGHEGMAVHP PRIPVQSDHLISIEGLLCKLPCA GQVTKESGLVSFSLRPVLPQNT LSNSFYLFPFGYASPYVETFLPG AHSGPAPPGLPVRTPRTAKRL/G VAVAPSPTF*ISPRALRSTFVSN
27727	58095	A	27896	1	361	
27728	58096	A	27897	2	162	
27729	58097	A	27898	248	381	
27730	58098	A	27899	73	254	
27731	58099	A	27900	1	729	
27732	58100	A	27901	1	762	
27733	58101	A	27902	2	334	
27734	58102	A	27903	3	369	
27735	58103	A	27904	669	1006	
27736	58104	A	27905	3	250	
27737	58105	A	27906	721	876	
27738	58106	A	27907	3887	4013	
27739	58107	A	27908	3423	3627	

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27740	58108	A	27909	3	226	HETGCCGQAAERDSCWERPPIP LLLPSLSGDYETVRNGGLIFAG LAFIVGL\ILLSRRFRCGGTKKR RRINEDEP
27741	58109	A	27910	67	264	
27742	58110	A	27911	161	851	
27743	58111	A	27912	139	351	GGRRIETGGWERPPIPLLLPSLS GDYETVR\NGGL\IFAGLAFIVG\ LLILL\SRRFRCGGNKKRRQINE
27744	58112	A	27913	2	431	
27745	58113	A	27914	217	289	
27746	58114	A	27915	255	389	KPNIACSHS*VGTEQ*EHMDTG RGTSHTGACREALDRGPAWEK L
27747	58115	A	27916	14	460	NCLTRRRRRRRRTFLEEERLKP SRKKITKKHTKKRTASLILHAM ICCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT EQ*LNTTAITLCLLLREARKTL MTHQSTWTWMKLETIILSKLTQ EQKTKQRMFSLISGS
27748	58116	A	27917	503	1046	
27749	58117	A	27918	3	198	
27750	58118	A	27919	54	320	
27751	58119	A	27920	443	477	
27752	58120	A	27921	1	963	
27753	58121	A	27922	1	2292	
27754	58122	A	27923	3	736	SCCLHSRLVRARRLRRAVAVM AAQCVRLARRSLPALALSVRPI FPGLLCTATK\QRTSAKNLKGD MGQSEQRADPPATEKTLL\EEK VKL\EEQLKETV\EKYKRALA\D TEELTGRGSQNLLREAKLLRHF KPFCKDLLEVADV\LEKATQCV PK\EEIKDDNPHLKNPLWRGL\V MTEVQIQKVFTKHGLLKLNPV GAKFDPYEHEALFHTPVEGKEP GTVALVSKVG\YKLHG\RTLRP ALVGVVKEA
27755	58123	A	27924	253	363	
27756	58124	A	27925	235	318	
27757	58125	A	27926	1	426	
27758	58126	A	27927	146	254	
27759	58127	A	27928	1	1401	
27760	58128	A	27929	61	457	LESTLATAERFLIPSYPSSTGN*L VCFCTT*GQECYSVTRF\SLGYG SPGCLYA*SSLIPCWRWGTPRL CCEKPFTTHFCLRFVSPSKLAVS RWHIPLGSEEKRRSMSAGTISL HF1WMKSPTRTSFQHFCT
27761	58129	A	27930	1	567	

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27762	58130	A	27931	128	586	
27763	58131	A	27932	271	465	HLTRPGTLLRQNFQRNDQAAT LAVHQYPLLCSNRC/CIPRQT/W VWSGPPANSNRPAAEGPDC*KE N
27764	58132	A	27933	1	375	MQKSPIFCVAHAGSCRLELFLF GHLGGHHPDTKPGRDTTRKDN FRPISLMNIDAKILNKILANRIQ QHIKKLIHRDQVGFISGVQGWF NIRKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQGFMLKILNK LGIDGMYLKIIRAIYDKPTAKIIL NGQKLEVFPLKTGTRQRCPLSP LLFNIELEVLARAIRQEKEIKGI QLGKEEVKLSLFAHDMIVYLEN PIVSPQNLLKLISNFSKVSGYKI NVQNSQAFLYSNNRQT*AIAGA PPPASLPPCSLISDCCASNE*GSV GIGPSKPGAGYNLLLCHLISPSIS PTSSPKSDTCPIADFSNKSPDRSS AGDILLAMQSLGSMAIFTILILP THEHGMFFHLFVSSFISLSSGL
27765	58133	A	27934	1	1059	
27766	58134	A	27935	1	533	LSKQGHLNLQRF\LLPFG\C*CLP LRGGV\YRGRQ\ASLSCGGLHP V*AS\RQLCLPTQALA\MAGTPP PASLPPCSLISDCCASNERGSVG MGPSEPRCGNNNLVVC\RFLSL SEKRSSIRVGVTRFS\RCHLSQL CLATKGNSLTPCTSQVRRCLTL LQLTLGAMQPLSCGLPTLSDKP
27767	58135	A	27936	140	426	
27768	58136	A	27937	1	918	
27769	58137	A	27938	54	102	
27770	58138	C	27939	244	462	
27771	58139	A	27940	234	282	
27772	58140	A	27941	328	1212	
27773	58141	B	27942	245	338	
27774	58142	A	27943	483	635	
27775	58143	A	27944	9882	10134	
27776	58144	A	27945	2	370	
27777	58145	A	27946	1682	1945	
27778	58146	A	27947	1172	1732	ESTAAEADTRFGCSWAVWAVE AEGEDCCCCCCC\CCCCCCCCC CCCCCCCCCCCCLPPSAGGRGP SGSARYFALIDAAQREDGGDA YRVGLAAALEVNAAETVACGG LEGGEAPTDAGTRYVLEPEAPQ LSVLWKRVEVQRLVPVRVVVA AWHAARKARAWLRRAARPGP PASCALRRPSGYAAARN

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27779	58147	A	27948	272	393	
27780	58148	A	27949	333	622	
27781	58149	A	27950	11	1850	
27782	58150	A	27951	1	1107	
27783	58151	A	27952	1	1348	
27784	58152	A	27953	3	431	KLQNELLLLHVSHPGHADAKG GFPWP*AAPPLWLCRVQPSFWL LSWAGIEGLWLFHTHDTSCQWI YHSGVALADVLHESPALQQTS VWTSRSFHTSSEIQAEVPKPQLL TSVHAQAQYSMEAPKAWGLYP LKPWPELYLGPF
27785	58153	A	27954	364	1117	EGHRAEGQCTGSVVLLTSSIGR SGKQSSGCHFWLLQHQICTCPS RVMGPRKKHRPTARGSRPPQPL PSGFPSAGAMGQVHCLAAPHS LERVRNPRQTQ/PPGWEG/PPTR ANLALLPTPPAATATNSSIPDSP PGSDGSVPAGLTTWLAVLTLD CPKAFGKVASQACLLWKGEQP PKTPPVTPSRVSLLASEPNTIRL KNVFPRVFPACTWKSHRHSTPA HESSQKGLYPAKPQGWSCPRL WEPTSCISVTWM
27786	58154	A	27955	1	224	QWRHCNRSLLPVQGKSGALEG IGPPRVF\PPE*RAFGGQRAPPDI P\PPSPRHPTKDRRTAARSGPRR KRGQTNE
27787	58155	A	27956	681	879	LQISHPGHADASGGFPWPWAA PPLWLCRVQSPS*LLSQPGVECP QLFQAHSASRHLNSMRPQMNS S
27788	58156	A	27957	835	1482	
27789	58157	A	27959	1	522	
27790	58158	A	27960	2	396	
27791	58159	A	27961	1	1501	
27792	58160	A	27962	473	860	
27793	58161	A	27963	370	3675	
27794	58162	A	27964	52	117	
27795	58163	A	27965	3	290	PRKTVQFGGTVTEVLLKYKTG ETNDFELLKNQLLDPAIRDD\QII NWLLEFRSSVMYLTK\DFE\QLI SIILRLPWLNRSQ\TVVEEYLAF LGNLVSA
27796	58164	A	27966	1	2988	
27797	58165	A	27967	1	666	
27798	58166	A	27968	274	930	
27799	58167	C	27969	13	231	
27800	58168	A	27970	46	386	
27801	58169	A	27971	3	451	
27802	58170	A	27972	160	494	

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27803	58171	A	27973	1	2406	
27804	58172	A	27974	201	1069	
27805	58173	A	27975	450	647	
27806	58174	A	27976	329	697	
27807	58175	A	27977	141	1506	
27808	58176	A	27978	1	1773	
27809	58177	A	27979	3	460	PHRVMGVPISRGTL*SVFP*PS* CTTWPGSLGSCTTACQVRCQPQ APHQP*APPERTTSAPAAQSPSR SSLWVTAPLVSACPTCSPATHP TRSQMPSTHTPCCRGSSPRPRGS PSWTRTWTTCPKASKADPKAP WPCSLMPFYAQTQTLGET
27810	58178	A	27980	1	1803	MGKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRE PTKWEKIFTTYSSDKGLISRIYN VLKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKKHMKKCSP SLAIGEMQIKTTKKLMLYYDVI RICHDSHKELEQKLAAFLGMED AILYSSCFDANGGLFETLLGAE DAIISDALNHASIIDGVRLCKAK RYRYANNDMQELEAAYRRSTR PLSTRLFSFRSRVLTEFRVCPCL VHTTWGGNLMRLSARSLWQR AAVNIPKLEGIIEEY/ALLV/WR AML/TEVNLSPNPGLVDRINFG AHKDMALEDFHRSALAIQGWL PRFIEFGACSAEMAPEAVLHGL RPIGMACEGDMFRATAGVNTH KGSIFSLGLLCAAIGRLLQLNQP VTPTTVCSTAASFCRGLTDREL RTNNSQLTAGQRLYQQLGLTG ARGEAEAGYPLVINHALPHYLT LLDQGLDPELALLDTLLLLMAI NGDTNVASRGGEGGLRWLQRE AQTLLQKGGIRTPADLDYLRQF DRDTSQGSSRVDCSVWELCRA GRTAGVMAVAAKTKNAGKWH NHIIRRFDINPGDRLYDQGGRA HHPFAGTHHQKYYRHRSRR
27811	58179	A	27981	1	1974	
27812	58180	A	27982	344	508	
27813	58181	A	27983	3	492	
27814	58182	A	27984	65	261	

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27815	58183	A	27985	3	529	DAWAFHKMAPKAKNEAPAPP KA\EAKAKGF*RAKKGSF*KVS HSH\KKKKIPHVHPTFRAGRRPL R\LRRQP\KYPSGRALPWRNK\L DHLCLSIKFP\LTH*VLPMKKIE DN\NTLVFIVDVKANKHQIKQA VKKL\YDI\DVAKVNT/LWIRPD GEKNGICSDLAP\DYDA\LDVA NKIGII
27816	58184	A	27986	105	241	PFFFFEMESPSVAQAVFSLVFRS PHCGGIQAHLFNL*RDLFKIWT
27817	58185	C	27987	175	363	
27818	58186	A	27988	724	958	
27819	58187	A	27989	3	823	
27820	58188	A	27990	1	877	
27821	58189	A	27991	487	786	
27822	58190	A	27992	147	623	RSAVANGLTKRRMGLKLNGRY ISLILAVQIAYL\VQAVRAAGKC DA\VFKGFSGLFCSSLGDTMAQ LPAGPGDDKTNIKTV\CTYWGG ISHSCT\VTALTDCQEGAKNMW DKLRKESKNLNIQGSLFELCGN GNGAAGSLLPGFPVLLVSLSAA LTTWLSF
27823	58191	A	27993	213	579	ASLLLLAFLAELASLKAGLQKS REYSCSSFISSLSSTDAHCVLSE YARPLS/QRPAPNGSSPRCQASE AQSPGHRPPPPLFSSPLAALQLD SHRFPSDPNGKDESRPPRLCTKL GRGCAGCGK
27824	58192	A	27994	1	800	
27825	58193	B	27995	54	165	
27826	58194	A	27996	46	313	
27827	58195	C	27997	30	151	
27828	58196	A	27998	169	1173	
27829	58197	A	27999	456	651	
27830	58198	A	28000	487	833	RNKFCDDQTEGNKIKNRREEK HRCRGQSKLNIIIDNVVKAVNG GKSQREQAEFADCITFGIRHNTS PKMSRVRGGG/TTPWAVLGMA EASSSLQSSSQNPGQAGWQTGP WVVSLGC
27831	58199	B	28001	1	2268	
27832	58200	A	28002	1	639	

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27833	58201	A	28003	1913	2388	PIIHNTTAMKKAAKAEPPFTTIV CTE*AILSQRTCSL*FTVINDICP GPRAH/VVQDIHGKLFTGSAIA NRFQDAMAIPFLGTQGKRVPR NGMAIPFPGNRNVIAGAFIPHR QHLGQIQLNPVRQCSNLFAHLL AQRSEAIFHMRRHHRIRDTVKK TILF
27834	58202	A	28004	1	1566	
27835	58203	A	28005	951	1217	
27836	58204	A	28006	1294	3108	
27837	58205	A	28007	1	1896	LFDWLVSQNELKANPAKGVSA PKAPRHLPKNIDVDDMNRLLDI DINDPLAVRDRAMLEVMYGAG LRLSELVGLDIKHLDLESGEVW VMGKGSKERRLPIGRNAVAWI EHWLDLRDLFGSEDDALFLSKL GKRISARNVQKRFAEWGIKQG LNNHVHPHKLRHSFATHMLES SGDLRARGAYLCAKLLSGAAQ VPEWRSAFAWFARCAEQARQN QYLQVSSCVPALEGCDVNGAS FTLEQMLAWRDHPQVTGLAEM MDYPGVISGQNALLDKLDAFR HLTLDGHCPGLGGKELNAYITA GIENCHESYQLEEGRRKLQLGM SLMIREGSAARNLNALAPLINEF NSPQCMLCTDDRNPWEIGHEG HIDALIRRLIEQHNVPLHVAYR VASWSTARHFGLNHLGLLAPG KQADIVLLSDARKVTVQQVLV KG\EPIDAQTLPAEEIGRLAQFA PAYGNTIGRQPLSASDFALQFTP GKRYRVIDVIHNELITHSHSSVY SENGFDRDDVSFIAVLERYGQR LAPACGLLGGSGLNEGALAAT VSHDSHNIVVIGRSAEEMALAV NQVIQDGGGLCVVRNGQVTSE GAKERMMGKRYKETSGSIGLK VPAPLNLNLSLQPREQLGGQST
27838	58206	A	28008	1	3257	
27839	58207	A	28009	1	2145	
27840	58208	C	28010	193	363	
27841	58209	A	28011	1	397	
27842	58210	A	28012	2	405	FVSAQGPGGKRFGTAPATPGCL VHDLS*APCLRWYQHPTEEELR ILAGKQQKGKTKKDRKYNGHI ESKPLTIPKDIDLHLETKSVTEV DTLALHYFPEYQWLVDFTVAA TVVYLVTEVYYNFMKPTQEMN ISLV

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27843	58211	A	28013	3	353	GYIEKRISCIALLF/SF*IPVNFLR FHDTFI*FCYSS*SIIQLSLWQSQI LLCV*LLRSIDFLYLIW*PLTYN EHASILLSLRAPYQLFDL*NDRS HIRYSATLVNNPAVCFAVGHD
27844	58212	A	28014	106	1814	
27845	58213	A	28015	37	2847	
27846	58214	A	28016	1	2430	
27847	58215	A	28017	1	2660	
27848	58216	C	28018	80	328	
27849	58217	B	28019	1	1074	
27850	58218	A	28020	602	853	
27851	58219	A	28021	505	649	
27852	58220	A	28022	672	1903	
27853	58221	A	28023	3	319	
27854	58222	A	28024	1	219	
27855	58223	A	28025	2	508	
27856	58224	A	28026	1	1011	
27857	58225	A	28027	1	699	
27858	58226	A	28028	175	351	
27859	58227	A	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	C	28031	115	231	
27862	58230	A	28032	2	139	
27863	58231	A	28033	1	788	
27864	58232	A	28034	115	358	LIVVRSRRGTSRSGSPRATAMA FKDTGKTPVEPEVAIHRIRITLT SRNVKSLEKVCADLIRGAKEKN LKVKGPVRMPTKVK*IVVRSRR GTSRSGSPRATAMAFKDTGKTP VEPEVAIHRIRITLTSRNVKSLE KVCADLIRGAKEKNLKVKGPV RMPTKVK
27865	58233	C	28035	179	283	
27866	58234	A	28036	57	431	
27867	58235	A	28037	54	440	RVPELWVGTEVKERKNARSGV PSTQRLECGSAESAAGAPASVS VQVTAVPAPLFPGWTGGGRAV NLTEAERMRVVINSVCHWRLY E*TANRFS*KQDVGKLTNCVCH PEGMLKAVTTQAQVFLVIRHN
27868	58236	A	28038	1	2693	
27869	58237	B	28039	131	350	

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27870	58238	A	28040	1	594	MLDITNDQGNASQNHNAIPPYS CKNGHNQKIKAGGLWTTVHSL LLFQLEQRTQQGYGPITHPKTP LHPPALLAVDRGSRSSVPATDS LPSAHDRQQQFHTWVCSRLLA TVRADPADGQQPQARADVCGC RGTGFINLVMIHLMGFEVGRIQ QLEQVAPRPQGVSWEVDSSDH LQGSPRVEPPGTWDLRVLCSQG Q*EAVNCGPQTPGLD/SFDYGH SCRSKVVSHCGFDLHFPDH**C KNGHNQKIKAGGLWTTVHSLL LFQLEQRTQQGYGPITHPKTPL HPPALLAVDRGSRSSVPATDSL PSAHDRQQQFHTWVCSRLLAT VRADPADGQQPQARADVCGCR GTGFINLVMIHLMGFEVGRIQQ LEQVAPRPQGVSWEVDSSDHL QGSPRVEPPGTWDLRVLCSQG
27871	58239	A	28041	1	285	
27872	58240	A	28042	1	1059	HNLSSSNSFPKMSFPNSSPAANT FLVDSLISACRSDSFYSSSASMY MPPPSADMGTYGMQTCGLLPS LAKREVNHQNMGMNVHPYIPQ VDSWTDPNRSCRIEQPVTQQVP TCSFTTNIKEESNCCMYSDKRN KLISAEVPSYQRLVPESCPVENP EVPVPRYFRLSQTYATGKTQEY NNSPEGSSTVMLQLNPRGAAKP QLSAAQLQMEKKMNEPVSGQE PTKVSQVESPEAKGGLPEERSC LAEVSVSSPEVQEKESKEEIKSD TPTSNWLTAKSGRKKRCPYTK HQTLELEKEFLFNMYLTRER/R ALEISKSVNLTD\RQVKI\WFQN RRMKLKKMSRENRIRELTANL
27873	58241	A	28043	358	2292	
27874	58242	A	28044	2	300	HSLS/SFFFFFFFFFFFFFFFFFF FFFLFFFFFLLLLLFVSFSFSFSFS SFSFSFSSFSSFSFSFFFLLPSSSSS SSSFFFFFFLLLLPFFFFFFEMEH
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	
27878	58246	A	28048	3	212	

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27879	58247	A	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP NNNNNFFFFFFFFFFFFFFFF FLLLPLLLPLLLLLPLLPLLPLLP SSSFFFLLLSSSHSSPSSPSSPSPS SPSSPSSPSSSSSSSSSSSSSSSS SSSSSSSSSSSFSFSFSFSFSFSF SFFFFFFFFFLFED
27880	58248	A	28050	544	729	
27881	58249	A	28051	1667	1896	
27882	58250	A	28052	1	477	
27883	58251	A	28053	25	448	RSQFFFFFFFFFFFFFFFFFFFF/ ILLVLLLVLLVLLLLLLLLLLL LLLL/ASSSSSPSPPSPSPSSSSSSS FSSSSSSSSSLSLGAYVLYFMVT HSSPVLCCLCNLIINNI*EE*FFR FRHNCDLFLAASTLGVDWLLL
27884	58252	A	28054	47	376	
27885	58253	A	28055	1	1740	
27886	58254	A	28056	3	1464	
27887	58255	A	28057	1	394	
27888	58256	A	28058	143	429	STLQKKEARARHLVTPLDILQL FNGFPLLVDCYKLLRYSRVHSF PRFWIFFSIKDHIGFPKENTQRK MRLHPPPQS*TPPRE*VPSFSSG VGKSS
27889	58257	A	28059	165	408	
27890	58258	B	28060	21	253	
27891	58259	A	28061	1	150	
27892	58260	A	28062	1081	1303	
27893	58261	A	28063	147	437	

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27894	58262	A	28064	107	2499	PIEDPEGRRRMREFILRSIQGVL RMAPQIQPKPLLTKSSTSVSQA RL/TSKQKALLPRQCSGSAKAQ AEREKIEETCQVGMKPPVPGGY TLQGKWITTFCNQVQLDTIKIN GCLKGKLIYLLGDSTLRQWIYY FPKVVKTLKFFDLHETGIFKKH LLLDAERHTQIQWKKHSYPFVT FQLYSLIDHDYIPREIDRLSGDK NTAIVITFGQHFRPFPIDIFIRRAI GVQKAIERLFLRSPATKASVSK LKCFWEPTRGTQKYEASQVTG AFPLRPKKGAATPSQLVIVNSS DAHNKCDEESEVRIKSTLGLKL DCKKGTALTKGTKEDEEDGAM SGVDQLCLLSSVDSSGRPQLMT DWHGVKGQFSCFKCGEEKELQ QKRKLTGKGWNVFFMVLEVG KTKIKALEVLASGKGTASWFIQ DFLAVNSSHGRWGKKEEFLFQ KWKVDPWLPVRWELVQTGTL THLVPEGRSDSVTCAWMPLGS KQVYKEPAGFPDMLRLRGSRV RMAVVTVHSQLRNLSLGDQHF NYPLPLKKKKKKKKDTLIYPA DWLESCQSDNLSLAERDLVLV LRLALCALYGLLAPGNGNTESA ELHPGDKTEAQRPMALFKVTR PLNERPGDLASHVSRFAKSFLK PAMESLECPQSRLVGEARKGHS ELVEKIERGCESTVGEGTTRKG SKRDHLDSQCKLGQRSQPWGQ
27895	58263	A	28065	1	1770	
27896	58264	A	28066	85	204	SPCSTSPFRQLA**RRGPHRSPFP TVAHLIGEWRLMRNAG
27897	58265	A	28067	1280	1531	
27898	58266	A	28068	1	882	
27899	58267	B	28069	77	1188	
27900	58268	A	28070	1016	1400	
27901	58269	A	28071	1091	1770	CRGGSGCAVCAELAPGAVHTV AAERAGAQEAAAGAGPPQLGG LIAWATHLQHSAAVPLLSQRM CHTCCLSPRKLVIGCRAAKSLSS SPCGKWLCAALIRQPSVKGLPS CGVPLPLSLSRIQMCSSEATSSW ELNPDFGEAATSP**ESGF/LQS VVSTALLPDNTTGETFHHDGRA DIGSQFIHRFLVCCHLLVLRWLI TLDTKADVVDIGHRLRCFDCRC VDSTICD
27902	58270	A	28072	1568	1819	

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27903	58271	A	28073	778	879	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRCANY
27904	58272	A	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT LKVLIIGKLSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTFTSVSG
27905	58273	A	28075	355	614	CMRRPSCSCPASTRDNTAPHSR TLKVLIIGKRSSGRKLSRILPLLR SSSM*PTRAPN*SSASFTFTSVSP L*NFIRLHPVY
27906	58274	A	28076	1	2226	
27907	58275	A	28077	31	117	
27908	58276	A	28078	1	547	
27909	58277	A	28079	290	730	
27910	58278	A	28080	3	267	TLVKVKDAEDQLGARVGYIEL DLNSGKILESFRPEERFPMMSTF KVLLCGAVLSRIDAGQEQLGRR INTILRMTWLSTHQSQKSILRMA
27911	58279	A	28081	1	1785	
27912	58280	A	28082	551	685	
27913	58281	A	28083	2	211	
27914	58282	A	28084	1407	1874	PRAAAAPTNLSPELSASPRPRV ACASAWGAGTDVTGWEAAMP RVGRCLPRTGLGSARRLRRPEL GGGAGPAPEAMRGFGADAGST EQPRLPARS*PRLPQRPRRPRKS ERPAGLAPRLRPPQPAEPPGLGS QERGRGTDRAAADPGLPRTSPE SS
27915	58283	A	28085	1284	1786	
27916	58284	A	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR CL
27917	58285	A	28087	423	676	
27918	58286	A	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRCANY
27919	58287	B	28089	743	852	
27920	58288	A	28090	1	1100	
27921	58289	A	28091	548	652	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRCANY

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27922	58290	A	28092	1	2438	MRLFGYARVSTSQQSLDIQVRA LKDAGVKANRIFTDKASGSSSD RKGLDLLRMKVEEGDVILVKK LDRLGRDTADMIQLIKEFDAQG VSIRFIDDGISTDGEMGKMVVTI LSAVAQAERQRILERTNEGRQE AMAKGVVFAENDKKMLSNAFI ETADFRTLIETDDRTIVVGRRGT GSFNLARAATRLLWRYAMLME IASYISSHYKLSSQISSETLLNEH LKKWNSAQGDILRKCRLVAKE YLDENNPEESIGDLQFNLNISEI ENNIVSLLERSDRKVVILMDKL DEAYEPDNIGIG\IIAGLAYASIE LNQKAKCIRPIIFLRDNIFRSLSK EDPDYSRNIEGQVIRLHWDWA QLLMLSAKRMKVAFKLDIEKD QRVWDRCTADDP*KGGNGFKR CLQFTLYRPRDLLSLLNEAFFSA FRENRETIINTDLEYAAKSISMA RLEDLWKEYQKIFPSIQVITSAF RSIEPELTVYTCLKKIEASFELIE ENGDPKITSEIQLLKASGILQSL YSVGFVGIRDKNTSSYSFCHDG RTPDKGFESNEKLLIHPCYWLG LNLNRNALAPEEAEEINDEYDI NIISDNSAIRNKTIGQITTHLDQI PIGNEGATEFEQWCLDALRIVF ASHLTDIKSHPNGNAVQRRDII GTNGGKSDFWKRVLEDYKTRQ VVFDAKNFEELGPSEYRQLQSY LTGPYGKLGFIINRDESEVVRSK
27923	58291	A	28093	673	916	
27924	58292	B	28094	1	4725	
27925	58293	A	28095	959	1387	CMRRPSCSCPASIRDNTAPHSRT LKVLIIGKRSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTFTSVCIS RCMSAVMVMAVLTIACRFLKM TVSVGHICSLNFALQTSTTAMA VPAAATRASRAQPNGRHPWRI CWKTQKA
27926	58294	C	28096	997	1302	
27927	58295	A	28097	659	2534	
27928	58296	A	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	
27932	58300	A	28102	40	198	QAARTTGFYAHLLRHYKTPVG HS*Y*WKLHGENKSSAFAVC*P TCRNPFIDCW
27933	58301	A	28103	390	1186	

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27934	58302	A	28104	2	1287	GRVGFASTAQSPRILRSEPVRTP PIPAFSPLKTLRIMSLHQFLLEPI TCHAWNRDRTRPVCLDYYSLV VSFEIKK*IALSPNNHEVHIYKK NGSQWVKAHELKEHNGHITGI DWAPKSDRIVTCGADRNAYVW SQKDGVWKPTLVILRINRAATF VKWSPLENKFAVGSGARLISVC YFESENDWWVSKHIKKPIRSTV LSLDWHPNNVLLAAGSCDFKC RVFSAYIKEVDEKKASTPWGSK MPFGQLMSEFGG\SGTGG\WVH GVSFSASG\SRLGWGSATDSTV SVCWMPSKS\LQVSTLKTEFLPL LSVSFVSENSVVAAGHDCCPM LFNYYDRGCLTFVSKLDIPKQSI QRNMSAMERFRNMDKRATTE DRNTALETLHQNSITQVSIYEV DKQDCRKFCTTGIDGAMTIWD FKTLESSIQGLRIM
27935	58303	C	28105	198	362	
27936	58304	A	28106	1	915	
27937	58305	A	28107	403	519	
27938	58306	A	28108	88	237	
27939	58307	A	28109	527	1205	
27940	58308	A	28110	2	272	
27941	58309	A	28111	39	543	
27942	58310	A	28112	1	789	
27943	58311	A	28113	401	912	
27944	58312	B	28114	147	653	
27945	58313	A	28115	586	650	KIQCLCLWLLFLIIFLHAFQETIL ALRVLNVFNKRINSLGKNLAFN LFVYNKANSMP*RLLWKAPRS DK*IQ*SLRIQNQCTQISSTAVH STVTKLRIKSRTQPLLQQL
27946	58314	A	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL KSGSGKVYQGPAKGAADTTIIL SDEDFHGRWSGASLTLRRHSLV AG
27948	58316	C	28118	183	254	
27949	58317	A	28119	98	445	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSG ACYMCRKSGHWAEECPQPGIPP KPRPICVGPH*KSDCSTHLAATP RAPGTPAQGSLTDSFPDLLGLA AED
27950	58318	A	28120	32	143	

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27951	58319	A	28121	39	346	QYISELQFLASTVRQTPATSPAH KNFQTPEPQQPGIPPEPPPPGAC YKCWKSGHQAKECLQPGIPRK/ HASHLWQPLPEPPGTLAQGSLT DSFPDLLGLAAED
27952	58320	A	28122	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPKEHLTNFKSAA ED
27953	58321	C	28123	80	106	
27954	58322	A	28124	166	423	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQLKEHLTNFKS GPHWKMDCPTHPAATPRAPGT LAQGSLTDSFPDLLGSAAED
27955	58323	A	28125	1	354	
27956	58324	A	28126	1	702	
27957	58325	A	28127	317	427	
27958	58326	A	28128	467	640	SARKRFQLSP**NKITLLKPASS AISALAATPRAPGTLAQGSLTD SFPDFLSLAAED
27959	58327	B	28129	1	320	
27960	58328	A	28130	1	605	
27961	58329	A	28131	273	529	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQPKEHLTNFKSG PH*KSDCSTAPG\ATPRAPGTLA QGALTDSFPDLLSLAAED
27962	58330	A	28132	459	601	DVDRHVRGSNFHHNEIRSLAAT PRAPGTLAQ/GLTDSFPDLLGLA AED
27963	58331	A	28133	112	331	LGLGDLP\WEINPLSSCSLLHEK DPPTTSGPQTDQPKKRLTNFKS ATPRAPGTLAQGSLTDSFPDLL GLAAED
27964	58332	A	28134	1	579	
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	A	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	B	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	A	28146	1	573	

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27977	58345	A	28147	163	593	GFLEVQTPHPPNLDGPRRANRN TFLWTCHVGIPDLPALPAPASFL GTQLTLKKASDGPRTEKVTQD LAQPFWTTGRQLRFVLHLSLQQ KDLSKCWRGAEVVLGPTRLFL* GYSEGVKENGTGGVNK*AFSM CDSKWFNPCLTF
27978	58346	A	28148	159	405	PRLRVKYTQLCIL*S/CWRERKK FHLGKRVELRQGTTLGRVGWP KRRLSQGSAGCFPAGLAHSPPH LAEAPGSGFCTALFLWL
27[illegible]	58347	B	28149	123	1561	
27980	58348	A	28150	1	1771	
27981	58349	A	28151	68	698	
27982	58350	A	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	A	28154	1	245	
27985	58353	A	28155	5	422	
27986	58354	A	28156	3	1372	
27987	58355	A	28157	1	1653	
27988	58356	A	28158	586	867	
27989	58357	A	28159	1	1410	
27990	58358	A	28160	1	1441	MDIKKGITDISASLRVESGWEA RTRKEKTHINTVIIGHVDSGKST TTGHLIYKCGGVDKRTIEKFEK EAAEMGKCSFKYAWVLDKLK AEREHGITIDISLW\KFETSKYY VTIIGAPGHRDFIKN\MITG\TSQ A\D\CAVLIVAAGVGEFESWYSP RNGQTREHALL\AYTLGC*NKL IVGV\NKMDST\EPPYS\QKRYE EIVKEGSTYIKK\IGYNPSTVAF VP\ISGW\NG*QHCLEAKWLTCP WFQGDGKVTP*GLAIASWEPRL LWRALALQSYPPTRPTDQAPLR PASPRMSYQKLGGIVNVATEV KSVEMHHEALSEVLPGDN/VGA FNVKNVSVKDVRRGNVAGDSK NDPPMEAAGFTAQVIILNHPGQ ISAGYAPVLDCHTAHIACKFAE LKEKIDRRSGKKLEDGPKFLKS GDAAIVDMVPGKPMCVESFSD YPPLGRFAVRDMRQT\VAVGVI K\AVDKK\AAGAGKVTK\SAQK
27991	58359	A	28161	125	370	
27992	58360	A	28162	156	547	
27993	58361	A	28163	108	919	

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27994	58362	A	28164	1	712	LNSEGNSGSGDSISYDAPAGNS FLEDCELSRQIGAQLKLLPMND QIRELQTIIRDKTASRGDFMFSA DRLITLVVEEGLNQLPYKECMV TTPTGYKYEGVKFEKGNCGVSI MRSGEAMEQGLRDCCRSIRIGK ILIQSGGETHRAQVYYAQFPPDI YRRKVLLMYPILQTG\NTEFEA VKVL*DHGVHPSVIIQLSPFLIP HGGQ\SIIQRFPEFPI*PTEVHPV APTHFGQKYFGTD
27995	58363	A	28165	1	606	GIRSAMQNTQNLLQMPYGCGE QNMVLFAPNIYGLDE\LNETQQ LTPEIKSKAIGYLNTGYQRQLN YKHYDGSYSTFGERYGRNQGN TWLTAFVLKTFAQARAYIFIDE AHITQALIWLSQRQKDNGCFRS SGSLLNNAIKVNHSGASFDLSI MISARMRIGSDNVKNSKGKPQ RKIKPGWHQKRGDRTKVDCDT LSYRDGYG
27996	58364	A	28166	1	4626	
27997	58365	A	28167	15	4479	
27998	58366	A	28168	256	852	
27999	58367	A	28169	319	405	
28000	58368	A	28170	606	896	
28001	58369	A	28171	1	372	FRRVACVGSAGD\TAGAEP/RG ACATAWVCEMAADISESSGAD CKGDPRNSAKLDADYPLRVLY CGEYCEYMPDVAKCRQWLEK NFPNEFAKLTVENSPKQEAGISE GQGTAGEEEEKKKQKRGKT
28002	58370	A	28172	1	731	LSRGSAAGGRALGRPWGARRV ACVGSAGD\TAGAEP/RGACAT AWVCEMAADISESSGADCKGD PRNSAKLDADYPLRVLYCGVC SLPTEYCEYMPDVAKCRQWLE KNFPNEFAKLTVENSPKQEAGI SEGQGTAGEEEEKKKQKRGGR GQIKQKKKTVPQKVTIAKIPRA KKKYVTRVCGLATFEIDLKEAQ RFFAQKFSCGASVTGEDEIIIQG DFTDAII\DVIQEKWPEVG**QPL EDLGRK
28003	58371	A	28173	335	2297	
28004	58372	A	28174	23	416	
28005	58373	A	28175	1	681	
28006	58374	A	28176	1	1668	
28007	58375	A	28177	1	1587	

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28008	58376	A	28178	250	687	AATSLPFRASTIASANSILRVGV MTSIHHFVFSKRVCCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQQTQIKSVRPDYLLVE PPHHMGPSFFASSGLHYDQ*PH HRLHLYWVFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	C	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	C	28181	151	351	
28012	58380	A	28182	2	355	
28013	58381	A	28183	19	428	
28014	58382	B	28184	61	2118	
28015	58383	A	28185	1	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSVPDSSGP ERILSISADIETIGEILKKIIPTLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RFV\ECIKIILDLISESPIKGR\AQP YDPNFYGWKPMDYG\GFTMMF DDRRGRPVGFPMRGRGGFDRM PPGRGGRPMPPSRRDYDDMSPR RGPPPPPPGRGGRSGSRARNLPL PPPPPPRGGDLMAYDRRGRPGD RYDGMVGFSADETWDSAIDTW SPSEWQMAYEPQGGSGYDYSY AGGRGSYGDLGGPIITTQVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGSEDRIITITGTQDQI QNAQYLLQNSVKQYSGKFF

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28017	58385	A	28187	221	1634	KNMETEQPEETFPNTETNGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSVPDSSGP ERILSISADIETIGEILKKIIPTLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RVVECIKIILDLISESPIKGRAQP YDPNFYDETYDYGGFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMPPSRRDYDDMSPRR GPPPPPPGRGG\RGGSRARNLPL PPPPPPRGGDLMAYDRRGRPGD RYDGMVGFSADETWDSAIDTW SP\SEWQMAYEPQGG\SG\YDYS Y/AQGGRGSYGDLGGPIITTQVT IPKDLAG/SLFIGKGGQR\IKQIR HESGS/SSIKIDEPL\EGSEDRIITI TG\TQDQIQ\NAQYLLQ\NSVKQ
28018	58386	A	28188	218	497	
28019	58387	C	28189	183	254	
28020	58388	A	28190	1	1056	
28021	58389	A	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYAEIG NR*GRNLGLTEVTGAVCEALR QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	
28024	58392	A	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN FSSFPFLVENGDAFYLAATLRA PGTVAQGSLTPSQIFSA*WRHPS ISPFS
28025	58393	A	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ SPWNSGPRLSD*LLPRSSGLSG
28026	58394	A	28196	372	782	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQTDQPKEHLTNFKSE KKETRFIRGPKTPAPVMD*GRQ PSLGV*PLQGCLSDYSPRFQRC QTTQGHLPWSFTLSSKSHFSGG RGKSLLQVPEIWPPGQGMPAA QDSS
28027	58395	A	28197	189	380	SLCIFSSASALQQQWQHEGWC GQLLPRGHGPNRKLQQQRQWI LL*VPEILPLGQGMPAAQDSS
28028	58396	A	28198	33	302	FRICALSTKLFCLSTPWCQTHIL SYPQYLPLLPIYSVLDLRHAFFT IALHPSSQPLFAFT*TDPDTH*A QQITWAALPQGFTDSPHYVQ

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28029	58397	A	28199	1	532	MRVRNREEGNVGKWGERQVD QRDAVMRVRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTEGA GGAESISVRLPRRSGSVSLQLLS REDLGRSQSESLGPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA*QLKTD AARSPRKPDTYTFCSPGSFSCTH S/SVESHNYHCSRPGLQSGLPHY SRYHT*PS*LH\SLIHLTFTPFPHI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRVPLVENQILTG ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFSLSPCCLHCQGKRLCG HHEEARRRKNVSIPRKEAGIIHC KGHQK\ASDPIAQDNAYADKL AKKAASVPTSVPHGISQAPPPLP THQARYWQIDFTHMPRVRKLK YLLVWVDTFTGWVEAFPTGSK KATAVISSLLSDIIPQFSLPTSIHS DSRLAFISQITQAVSQALGIK
28032	58400	A	28202	3	518	KRPHPYLPLLTLFSDSAHLHPG EINNHVAHTRPVWWSLHTDVH EIWCRDSDRGTSLGRSIPCPPVL CSVRKIHLQPQVLRPTSPRNISPI LNQVSGLFLLSSPTSLTVPQPLS PFNLGATLQS/APFS*FQFLSFSG RDKGDTFYPWSQNSGACHRLG KAAFPWCLIIAGTPL

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28033	58401	A	28203	3	1626	SEGEAKGSITLTVCTALYLKLT LFHKTGVFGPLRFPVVNTLNPS PFHDGTRELGASEAIGQCQSSA AKLRRSGKESESLGPEFQGLWK WLPGSSQCFARESLEEKLSLCF RPSDPGAEPPRTAVRPITERSLL QGDEYCCALGQGVPNPWSTDR YWNWATLQEIGPSSCRKTSSGL PLILRYGHVRDLHGSSSHHRPG GPKRNKWFRELGLGSACCMRP RDLVPCVPAAPAVAERGESTA QAVASEGASPKPWQLPGGVGP VGAQKSRIEVWEPLPIFRRMYG KACMSRQKFAAGAGFSWYVPV AVVGAKVHDVNLHMLSFPSK WKLHTCMKFGAVTQIVTSLGR SSCSLLLEKDPPMVLRPTSPRNI SPISNLTKETRFIRGPKTPAPVT DWEGSLPLVFNHCRDASLIIHP GFRGVRPRRDACLSPSPLANLIN LTFKVYNNRKKLQFLAFTVRQ TSAMSPAHKNFQ\SLNLSGQAF LQNLLPQELATSARNPATRPRN ACSPGFLLSHVPSVRDPTGNWT VQLTWHPLPEPLELWPKAL
28034	58402	A	28204	921	1009	
28035	58403	A	28205	1	1005	
28036	58404	A	28206	1	2706	
28037	58405	A	28207	1336	1490	
28038	58406	A	28208	466	560	
28039	58407	A	28209	863	1672	
28040	58408	A	28210	1	876	
28041	58409	A	28211	133	746	SVKMVRYSLDPEN\PMKSCK/S QRGSNLRVPFKDHS*KLPQAHQ RVCHIRKSPTKY\LKDVHLTRN QCVPIPDRYNG*QLGQVCRRPK QMGPGTTKGR\WPQKGVLKFL PAHALKTAEM*C*TLRVLDVDS LVIEHI\QVNKAP\KM\RRRTYR AHGRINPYMSSPCH\IEM\ILTEK EQIVPKPEEEVAQKKKIS\QKKL KETPTLWHGE
28042	58410	A	28212	3	466	
28043	58411	A	28213	1	2772	
28044	58412	A	28214	1	1353	
28045	58413	A	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR S*DY*CWR

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28046	58414	A	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEKASSQATLPNQPVEKAI IMQLGTLLTFLHELVPTALPSGS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQKIWNSW*SC LVLI*PPCVILSFLYVQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
28047	58415	A	28217	2383	2651	
28048	58416	A	28218	125	1396	
28049	58417	A	28219	466	643	
28050	58418	A	28220	73	150	
28051	58419	C	28221	1	240	
28052	58420	A	28222	2	499	
28053	58421	A	28223	192	351	
28054	58422	B	28224	1	2103	
28055	58423	A	28225	247	400	
28056	58424	A	28226	288	589	WCSRRRGWYLLLGFHNYWRSS TFLVRCTPSCPGGCCPRYGIYPV RSCPRLPGGVSRYGSIHSG/RWC SWSPSWSPWLTSVTPRLYVAL M*AVVCPVVGKQP
28057	58425	A	28227	319	398	
28058	58426	A	28228	1299	1506	
28059	58427	A	28229	1250	1907	
28060	58428	A	28230	547	638	EKRKSNCPCLQMT*LYI*KTPSS QPKISLS

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28061	58429	A	28231	488	2358	RLSLGHWAAGKQGASDSCEKP TQPPSGVLESTTP/CAAPSPPNR DSGPCPASSPGLSRPLLSGTAW APPPAPPWARVRPPREVWRAD LLTPQGGGPATGVSGGEECDSP VGGNPGIWKAWGHRRTRVAGI GRRGGPGEADKQPLLVILRQTG SGVDLQQTPTDLQLRVLTVRR NTNKRKGHPHQNPICTSPSSKT EGRSMRQKVNKDIQELNSALH QVDLIDIYRTLHPKSTEYTFFSA PHHTYSNIDHIVGSKALLNKCK RTEIVANCLSDHSAIKPELRIKK LTQNCSTTWKLNNLLLNDYWR SKRKTHSKASRRQEITKIRAELK EIETQNTLQKINESRSWFFENIN KIDRLLERLIKKEREKNQIDAIK NDKGDITTDPTKIQTTIREYYKH LYKNKLLNLEEMDKFLDTYTL PRLNQEEIESLNRPITGYEIEAII NSLPTKKSPGSDGFTAEFYQRY KQELVTFLLKLFQSTEKEGILPN SFHEASIILIPKPGRDTTKKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHDQLGFIPGMQGLFSTC KSINVIHHINKTKDKNHMIISID AEMASDKIQQPFMLKTLNKLGI DGMYLKIIRAIYDKPTANIILNG
28062	58430	B	28232	1	2664	
28063	58431	A	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPP\ACPKRAPE GSTKHGKEQPVPATAKTGQIV
28064	58432	A	28234	804	920	RDIYSNKCPQEKPEKI*NGHPNI TIKRIREARAKTFKS
28065	58433	A	28235	786	935	
28066	58434	B	28236	3	1555	
28067	58435	A	28237	895	1389	GELLEVVMTLAWSWGLFLARII QTQVFKAFNLFVLILRSSWAFC WTHGDELWALVSRKPK*HPGF CDHAPSTFPPPGLCP/EPTPPPGA VSQYPCPPPSCPWPRWLVLPLP VLAGTSSPWKGFSYPPCCFSPF HLPARFLHRGNCLSTFDLVVLP PLEMPVLALS
28068	58436	A	28238	704	799	EKRKSNCLCLQMT*LCI*KTPSS QPKISLGW
28069	58437	C	28239	178	1287	
28070	58438	B	28240	1	1028	
28071	58439	A	28241	476	678	
28072	58440	B	28242	1	1059	
28073	58441	B	28243	1	924	

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28074	58442	A	28244	39	200	LPLFLIECPLFPSPA*LPWPGLPT LC*IGVVREGIPVLCPFSKGMLP VFAHSV
28075	58443	A	28245	225	314	
28076	58444	A	28246	243	311	
28077	58445	A	28247	21	1593	RKRTAPAGPRRHPKHCECPNCG SGKGRPS/CSQTHPPPGKLKSSP *SRKAENSKNQSAFSPPKDHSSS PVMEQSWMENDFDELTEVGFR SLAETQQQQKEKFRPISLMNID VKILNKILANRIQQHIKKLIHHD QVGFISGMQGWFNICKSINVIH HINRTNDKNHMIISIDAEKAFD KIQQPFMLKTLKKLGIDGTYLK IIRAIYDKSTASIILNGQKLEAFP LKDRTRQGCPLSPLLFNIALEVL ARAIRQEKDIKCIQLGKEKVRL SLFAEDMIVYLENPIVSAPNLFK LISNFSKVSGYKINVQKSQVFL YINNRQRESQIMNEFPFTIARRR IKYLGIQLTRDVKDLFKENYKP LLKEIKEDTNKWKNMPCSWIG RINIMKMAILAKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQK
28078	58446	A	28248	129	239	FFLTMSMECSSICLCPPLFR*AV VCRSP*RGPSHPL
28079	58447	A	28249	3	254	GTAWAPPPAPPWARVRPP\EKC GAPTCSHPREEAPRLASPAGKN VTVPWGETQGSGRLGVTGEPE LLGLGGAGALARLISSLCW
28080	58448	A	28250	80	517	GHFLGQQPRPQLHSPAPD\PPAP TPTDAEGLPQQQQLPQLEPQPE CQGPVEAEARQLKSCMKPVRR RPAEEELKTKNMDDNTFAMAE HPDVQESVGPLVAPTPLRPWPQ MTLQVCWSLLEFHSRPCLPGY HQQRLQNSKDCCLFLP
28081	58449	A	28251	1	670	
28082	58450	A	28252	1450	1650	QWISRQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKSS
28083	58451	A	28253	1010	1294	QRFSWQKLYKPEESGGQYSTFL KKRIFNPEFHIQPN*AS*VKEK* NPLQTSKC*EILSPPGLPYKS\PE GSAKHGKEQPIPTTAKTCQIVK TIQA
28084	58452	A	28254	41	812	
28085	58453	B	28255	1	2957	
28086	58454	B	28256	650	3212	
28087	58455	A	28257	1	556	

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28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA SRDSS*AVSHLCGTPLEIGWSNL PGSHSQSPWNSGPRLSD
28089	58457	A	28259	1	253	
28090	58458	A	28260	409	884	
28091	58459	A	28261	1	2256	
28092	58460	A	28262	118	302	
28093	58461	A	28263	558	659	
28094	58462	A	28264	1	400	
28095	58463	A	28265	308	433	
28096	58464	A	28266	1	711	
28097	58465	A	28267	559	657	
28098	58466	A	28268	1	400	
28099	58467	B	28269	232	498	
28100	58468	A	28270	1	2978	
28101	58469	B	28271	128	290	
28102	58470	A	28272	3	193	DVNIFIRYGLWCFLSPFGLL*QF WRLEVQYQDAADSMSGGDPLS HS
28103	58471	B	28273	125	197	
28104	58472	A	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGNKNGGEASM VRGCLERAET*GCPNGMPQGE RLSRFGLRTETTGTVTFRLHCL QQSR
28106	58474	A	28276	3	334	
28107	58475	A	28277	2	1698	
28108	58476	B	28278	1	1281	
28109	58477	A	28279	198	532	NSLFLLCLCQALVSG*CWPHK MS*GGFPLFLLTGIVS/GRNGTS SSLYLW*NSAVNPSGPGLFLVS RLLTIASISEPVIGLFRDSTSSWF SLGRVYVSRNLSISSRFSSLFA
28110	58478	A	28280	3	610	TDFCFCFWLPGLSVLFLSFFLSF FLSFFLSFFLSLSFSFSLSLFLFLS VSLSFLPSFLFLSLSLSLFLSLFS LL/YCLSFLSLFSFFLFLLSFSLSS SLLFSSLLFSSLLFSSLLFLLLLL LSLSLLFFLSFLFSESVLWEGSV AGLQTPALSSALNRAVLPVSCS MIDQLCDPGKYFISLCLFLHLR VRTCGVWFSVLVIVC
28111	58479	A	28281	203	470	QAKSVWKKILSFRI*LHRMSDG IFWLCFYISMHLCWLVLYWAV WFKLQTTRLSRWLTDSLPVSY GYCQGMNEGCSSQFKTVFPTLF SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK EISKG/LTKTPRLLVMSPSSCSR RGIWPNPDTCPLLLL
28113	58481	C	28283	1	603	

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28114	58482	A	28284	179	445	QLSGLASGMRESRDVLGLRFTP LLLWIVHSRAWALVESAVMST WECWVGDERGTGVKLAGAHT ELPTGPGV*YSPPCVHVFSLFNS HL
28115	58483	A	28285	128	381	
28116	58484	A	28286	1	1392	
28117	58485	C	28287	1	3169	
28118	58486	A	28288	1905	2449	AQLPTPAPLPFLGRRWGTWGFP GHAFHSWFWYST\GEGAMGSF LALLSFPPLGMKLAILEDFFGIS GTAAPLGSSFGSSLRSSLSVTEA LLARSL/HFLLILLPLLFLLLFLIA FQRTLLVGQCPAKSPLGNALEC NLGAAGSRAHGGEHATGGLQL LALFEAGQSLQPLTACVPGPRP LTCL
28119	58487	A	28289	693	905	EESIS*KWPYCPSFHNLHPQAY KAIPHPASLGKT*YNQDNNNAG KLFKANRNPALGCQQPVCSKT DGFRF
28120	58488	A	28290	3	427	
28121	58489	A	28291	1	1195	
28122	58490	A	28292	158	779	
28123	58491	A	28293	227	378	
28124	58492	A	28294	1	621	
28125	58493	A	28295	1	351	
28126	58494	A	28296	1	507	
28127	58495	A	28297	1	543	
28128	58496	A	28298	343	428	
28129	58497	A	28299	785	1178	

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28130	58498	A	28300	842	2592	IREEVESLKRPITSSDIEAVINSL SIKKKVQYQTDSQPNSTRGENL GNTIQDTGMGKDFITKTPKAM ATKAKIDKWDLIKLKSFCTAKE TIIRVNRQPTEWEKIFEIYPSNK GLISRIYKELKQIYKKKTNDPIK KWAKDMNRHFSKEDIYAAKK H/DEKMLIITGTWMKLETIILSK LTQEQKTKHRMFSLLIPDDGNS LTRRMLLIGISVKTPVGTGAIPG PVGGTTAAGAYGRKEKALSNC DSILALALAKMSENQMSMESFF EKGKDPMRRQQKTLTLTKKKN AFKRKYQESYLNYGFIATVRAS FLVANCIVKAKKPFTIGEELILP AAKDICYELLGEAAVQKVPHV PLPVSTITRPIDEIAEDIEAQFLE RINESLWYTIQIDKSTIADNKAT MLVFVQYIFQEDVHEDVFFQES LRATSQPLKTPQTGKEWVHDPF VDKPSESTLSMLEEDQLLEIAN DGSLKSMFEKTSNLHIVCIKVK AEYPEIATKALRRLLAFPWVAA VDRECQWGSRDVEMRRLLDPK AGFSLLGVGNCHCLRTLEFVGL SMSSLCGAMLLCGLRAAPYISL RDHKGQGTLL
28131	58499	A	28301	1	1662	
28132	58500	A	28302	2	406	CWWDCKLVQPLWKSVWRFLR DLELEIPFDPAILLLGIYPKDYKS CCYKDICT/RVCVPAALFTIANT WNQPKCTSMIDWVKKMWHIY TMEYY\AAIKKDEFMSFAGT*M KLETIILSKLTQEQKTKHRMFSL YWKS
28133	58501	A	28303	1	1404	
28134	58502	A	28304	68	2269	

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28135	58503	A	28305	189	1890	MKMASSLAFLLLNFHVSLLLV QLLTPCSAQFSVLGPSGPILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDRQSAPYRGRTSILRDGITAG KAALRIHNVTASDSGKYLCYFQ DGDFYEKALVELKVAALGSNL HVEVKGYEDGGIHLECRSTGW YPQPQIQWSNAKGENIPAVEAP VVADGVGLYEVAASVIMRGGS GEGVSCIIRNSLLGLEKTASISIA DPFFRSAQPWIAALAGTLPILLL LLAGASYFLWRQQKEITALSSEI ESEQEMKEMGYAATEREISLRE RKKIQYLTPDVILYPDMANAIL LVSEDQRSVQRAEEPHDLPDNP ERFEWRYCVLGCESFMSERHY WEVEVGDRKEWHIGVCSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTEPRTNLKLPEPPR KVGVILDYETGHISFYNATDGS HIYTFLHASSSEPLYPVFRILTLE PTALTVCPIPK/GREFPRFPTLVP DHSLEIPLTPGLANESGEPQAEV TSLLLPAQPGAKGLTLHNSQSE PYSYRHTLKHFTDIHSIIP

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28136	58504	A	28306	172	1905	MKMASSLAFLLLNFHVSLFLVQ LLTPCSAQFSVLGPSGPILAMV GEDADLPCHLFPTMSAETMELR WVSSSLRQVVNVYADGKEVED RQSAPYRGRTSILRDGITAGKA ALRIHNVTASDSGKYLCYFQDG DFYEKALVELKVAALGSDLHIE VKGYEDGGIHLECRSTGWYPQ PQIKWSDTKGENIPAVEAPVVA DGVGLYAVAASVIMRGSSGGG VSCIIRNSLLGLEKTASISIADPF FRSAQPWIAALAGTLPISLLLLA GASYFLWRQQKEKIALSRETER EREMKEMGYAATEQEISLREKL QEELKWRKIQYMARGEKSLAY HEWKMALFKPADVILDPDTAN AILLVSEDQRSVQRAEEPRDLP DNPERFEWRYCVLGCENFTSGR HYWEVEVGDRKEWHIGVCSK NVERKKGWVKMTPENGYWTM GLTDGNKYRALTEPRTNLKLPE PPRKVGIFLDYETGEISFYNATD GSHIYTFPHASFSEPLYPVFRILT LEPTALTICPIPKEVRRVPPI/AD LVPDHSLETPLDPGA*LMKVGE PQAGK*HLCFSLPTLGAEGLPF
28137	58505	A	28307	1	2220	
28138	58506	A	28308	134	509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAQRSP AEKMGETPGAAVSRIRLGGRV ALRRHVRGEPLRAPDCPLGPDA WVPTRGSHFPGFFPREQSLS/W GATPPSYRSSEVRSGAESGRPAP DSVGSGVQAH
28140	58508	A	28310	1	1066	
28141	58509	A	28311	77	273	
28142	58510	A	28312	1	415	
28143	58511	A	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	A	28315	2	671	PGEFTRAPRVRRRAMGISRDN WHKRRKTGGIRKPYHKKRKYE LGRPAANTKIGPRRIHTVRVRG GNKK\YRALRLDVGNFSWGSQ CCTRKTRIIDVVYNASNNELVR TKTLVKNCIVLIDSTPYRQWYE SHYALPLGRKKGAKLTPEEEEI LNKKRSKKIQKKYDERKKNAK ISSLLEEQFQQGKLLACIASRPG QCGRADGYVLEGKELEFYLRKI
28146	58514	A	28316	3	1259	
28147	58515	A	28317	1745	2681	

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28148	58516	A	28318	1	2502	
28149	58517	A	28319	1097	1417	
28150	58518	A	28320	1	398	MTAEERDKFPTDQQAIPSMDPH WDPDSDHGDWSHKHLLTCVLE GLRRIRKKPMNYSMMSTITQG KEENPSAFLKWLREALRKYTPL SPNSLRGQLILKDTFITQSAADI RRKLQKQALGPEQNLEALLNQ ATSVFYNRDQEEQAQKEKRLSS RSVTIRGILGQSVTRPEAHKGL QDIVKHLKAQGLVRKCSSDCN TPILGVQKLNGQWRLVQDLGLI NKAIIPLYPVVPNPYTLLSQISEE AEWFTVLDLKDAFFCIPLHSDS QFLFACEDPTDHTSQLTQTILPH GFRDSPYLFGQALAQDLGHFSS SGTLALQYVDDLPLATSLEASC QQATLDLLNFLANQGYKASRS KAQLCLQQRDGQTTLYSNQGA PEGKYSSSRMRPRVRNSLQNLK AGPSTTPALSLPTGQNLSLYVT ETAGIALGVLTQAHGMNPQPV AYLSKKIDVVAKGWPHCLRVV VAVAILVSEAIKIIQGKDLTVWT THDVNGILGAKGSLWLSDNCL LRYQALLLEGPVLQIPMCAALN PATFLPEDGEPIS**PLTLRWPLP QLPLNSEASLLLLHQFSYLGMP LVGGSSHEPA
28151	58519	A	28321	318	363	
28152	58520	A	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP PLPARWPIH
28153	58521	A	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD TSEHLKEQTADTSSLRTVTLTA RVCGFILEVSETKNSPEGTNSG HILTSQMGLSPIAKRRETSASAA ALVSATIPICRVQGPLRVLGQE VFLLLLRLPTAPLPINDKPP/PN/ TPLPRRKQAKKSPKDHKNPWAI GYVPFKQ*GEGNLA*PGYMSPS

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28154	58522	A	28324	350	1563	FLYIQLYPTPITCSLKYQRKQNG SLFWTSRMPSSVFPCTLTPSFSL PLRIP/PDHTSQLTWTVLPPGFR DSPPLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSEASCQQA TLDLLNFLANQGYKVSRSKAQ LCLQQVKYLGLILAKGTRALIK ERIQPILAYPCPKTLKQLRGFLG ITGFCQLWIPGYSEIARPLYTLIK DTQRANTHLVEWESEAETAFK TLKQALVQAPGLSLPTGQNFSL YVTERAGIALGVLTQTRGTTPQ PVAHLSKETDVVAKGWPHCLR VVAAVAVLVSEAIKIIQGKDLIV WTTHEVNGILGEKEVYGYQTN AYLDTRRSALRDWCFKYARPV AAILLLLAFGPCIFNLPVKFVSS RIEAIKLQMVLQMDPQISSTNN FYRGPLD
28155	58523	A	28325	830	1143	
28156	58524	A	28326	234	510	PWQSLP*VAQKVPKDHRSLPLE P*TRSLNNS*QHWWLCPPARAP STCSTSCPARDGPPPPSPAPHGP RNTSVPG\HSRPGSPPP\PPRTPP VS
28157	58525	A	28327	2	816	
28158	58526	A	28328	1	1311	
28159	58527	A	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	1	484	
28162	58530	A	28332	72	299	
28163	58531	A	28333	737	847	
28164	58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	A	28339	65	244	
28170	58538	A	28340	2	584	GKSRRMFPAQEEADRTVFVGN LEARVREEILYELFLQFLI\AGPL TKVTICKDREGKPKSFGFVCFK HPESVSYAIALLNGIRLYGRPIN VQYRFGSSRSSEPANQSFESCV KINSHNYRNEEMVVGRSSFPM QYFPINNTSLPQEYFLFQKMQR HVYNPVLQLPYYEMTAPLPNS ASVSSSLNHVPDLEAGPSS

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28171	58539	A	28341	2	367	MTMHYEIPVRTRRSKGTT*LPQ NA/SVNNMPH*TGAI*ADISMTN YARIERNHLGRGNSNSKDPKLR ESSEHLRKLKTRVVNEQTRLGL IMETFVGRGGEAPFYFQCDKHL SRSFQGLGLICL
28172	58540	A	28342	98	387	RKQPPKVLQWLLLAF*SHRSW LSSPWPSDLWRPWAGGACARL LLQQPRDSASLKERQQPQSGAY R*NSHLPGTEHLGEGVAVCAAS ADLNVTACWL
28173	58541	A	28344	1	269	
28174	58542	A	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	A	28347	59	310	
28177	58545	A	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLFSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQLCGQFW NRCGVVLKKMYILLIWGGEFC RCLLGLLGAELSSIPGYSC
28178	58546	A	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSISDLSCFPLWAFSAINFPLHT ALSASQRFWYVVSLFSLVSKNI FISAFISLCTQ*SFRSRLFSFHVV ERL*VRF/CNPEF*FDCTVV\WR *FVIISVLLHLLRRALLPTMWSI LE*VWCGAEKNVYSVDLGWR VL*MSIRSAWCRAEFNSWVSLL TFCLVDLSFSLAALNIFSFISTLV NLTIMCLGVALLEEYLCGVLCI
28179	58547	B	28350	1	3135	
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLFSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFQVCGQFW NRCGVVLKKMYILLIWGGEFC RCLLGLLGAELSSIPGYPC

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28181	58549	A	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLL*AFSAINFPLHTA LNASQRFWYVVSLFSLVSKNIFI SAFISLCTQ*SFRSRLFSFHVVER L*VRF/CNPEF*FDCTVV/WRDS LL*FLFFYIC*GELYFPVCGQFW NRCGVVLKKMYILLIWGGEFC RCLLGLLGAELSSIPGYPC
28182	58550	A	28353	1	3531	
28183	58551	A	28354	1	3126	
28184	58552	A	28355	2357	3083	FFSLFFFIILASGLSILLIPSKNQL LDSLIF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLLWAFSAINFPLHT ALNASQIFWYVVSLFSLVSKNIF ISAFISLCTQ*SFRSRLFSFHVVE RF*VRF/CNPEF*FDCTVV/WRD SLL*FLFFYIC*GELYFQVCGQF WNRCGVVLKKMYILLIWSGEF CRCLLGLLGAELSSIPGYPC*FF VLLICLMLTVGC
28185	58553	A	28356	6412	7092	FFSLFFFISLASGLSILLILSKNQL LDSLSF*RVFCVSISFSSALILVIS CLLLAFECVCSCFSSSFNCDVR VSILDLSCFLLWAFSAINFPLHT ALNVSQRFWYVVSLFSLVSKNI FISAFISLCTQ*TFRSRLFSFHVV ERL*VRF/CNPEF*FDCTVV/WR DSLL*FVFFYIC*GELYFQLCGQ FWNRCGVVLKKMYILLIWGGE FCRCLLGLLGAELSSIPGYPC
28186	58554	A	28357	1	2019	
28187	58555	A	28358	1	1263	
28188	58556	A	28359	77	304	
28189	58557	A	28360	1	756	
28190	58558	A	28361	1	369	QQRTLLASNEAFKSQAKSASQP ASKYMKENDQLKKG\AAVDGG KLDVGNAEVKLEEENRSLKAD LQKLKDELASTKQKLEKAENQ VLAMRKQ/SPEGLTKEYDRLLE EHAKLQAAVDGPMDKKEE
28191	58559	A	28362	879	1156	
28192	58560	A	28363	54	407	

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28193	58561	A	28364	620	1246	GSTWHGWDGSRCRSQNRWSC MTKRSSQPSSLS*SRSRRWMS SSPNW*KTGPESSMSRMSSAG* SAASSRSCATRWTRRRPAAWR G*GVTPVAWWPPWTCSWSRPR EPGSGWPKPSVCWNSSEMRTT MSSSGSSTPWPPVSRRRPWTER RLGSVRGDRLRERSRPAVNRTP RMSRVPSGAPRGTPSRRWWM MKCWDHQMRGLVEEEVG
28194	58562	A	28365	86	402	KGWWCRKKGWNWKRSWFLT FLQGLLEGPHPPSPTPAPRRTT* SLYSAPSRMVQVLLDDLHKWF LYSCLVSAISIGIKFPLKIHISPGS GVLEARETMSHFKEAAL
28195	58563	A	28366	54	353	
28196	58564	A	28367	66	352	
28197	58565	A	28368	442	700	HWNKVPAENPHLPWVRCSPPT PLGKPKPCSSWNRRSGTDVSGT GLSESGSSWPSGSCNGVTGTDA YGP\GYVKSGSFPGPRVRGTV
28198	58566	A	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR SKDATPDPPRGLGKFPPRLPQA PRLLGSQRLLSTLCSTLSGRGG KNTSRLSFSPSGSVKGRVRDVK EPGPIRAHRTAFFPNASS\GSEG R*SPSVVAWRGFR/CVGVWRFP TVGVWHAPPRCTR*SPITGSAP LSVWSPPACTGSPTCTAGA
28199	58567	B	28370	163	387	
28200	58568	B	28371	112	419	
28201	58569	A	28372	1	1902	MSRIAWKLLWKLIQGYLGQPA GTARRHPGIGIFKSPPGDFTCNG LIAVIKNQSDNQRGMSPGSWSP GRENNPTLVEVLEGVVRLPETV HTAVRYTSIELVGEMSEVVDRN PQFLDPVLGYLMKGLCEKPLAS AAAKAIHNICSVCRDHMAQHF NGLLEIARSLDSFLLSPEAAVGL LKGTALVLARLPLDKITECLSEL CSVQVMALKKVFVGATSRRVA KLFREGLKAHGNSFETSGEAER CCTWRPKEMTCVE
28202	58570	A	28373	1	2019	

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28203	58571	A	28374	2	1455	SAAVAARSPQPQRPSATLGPGP QRRPPSAAPTPAWAAAAAPGS RRRRPLPARPLWAPARGAAAA GPAEAPMLARRKPVRAALTINP \TIAEGPSP\TSEGASEANLG\DL QKKLEELE\LDEQ\QKKRLEAFL TQKA/RRVGELKDDDFERISE\L GAGNG\GVVTKSPAQDPSGLIM \ARKLIH\LEIQAGASGNQIIPR/D LQVLHDGTWPTMGG\FYGAFY SDGE\ISICIEHMDGGSL\DQVLK E\AKRIPEEI\LGKVSHRSFSGGL AYLREKHQIMH\RDVKPS\NILV \NSRGEIKLCDFGVSGQLIDSM\ ANSFVG\TRCYM\APERLQG\TH YSVQSDI\WSMGLSLVELAVGR V\PIPPRDAEELEAIFGRPVVDG EEGEPHSISPRPRPPGRPVSGHG MDSRPAMAIFELLDYIVNEPP\P KLPNGVFTPDFQE\FVNKCLIKN P\AERADLKMLTNHTFIKRSEG\ EEVDFAGWLCKTPAG*TKPGTP \TRTAV
28204	58572	A	28375	229	257	VSLSASPLVSLAGRSPSRPLGRG CQSLDGYGVGWQAQSPGADE GNRSFT*PELADKNVPNLHVM KAMQSLKSRGYVKERLPSSAP GDCACHPTP
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP KQQK*PGGTEDS/YDASGPPPKF LIKEIKLGVPRFFPIRGV*NPGPG KNFGGPFKKT*FCWARVPKM* FFKGGPSSSSPAVSLFNAKESSPI LLRWMTTSTTKSAYKLEFGC
28206	58574	A	28377	1	367	
28207	58575	A	28378	1	1001	MSWEMEQDEVYKEMSINHKN EGTRVEKPNRYRIIHIQPDAINH VSRKKDVPSASGAGHSRSSTGS RPGVRRLWPLLLRSAPSGPLNN AVPAPGKGPGRWGGSPSLSRSG GKASTRVAPGLSAHSQAASGV PEPAEPQHQRTKASGSRRRSLR VVPEAPKPRTRTAREGKGAGA GHTGGAQEQRRRRRWACRGLR GRPGAVSPGGAEAINQLASEHC GNPAAALHRCIASLPRNLLVW AGRMLMPKKNRIAIYELLFKEE VTVVKKDVHMPKHLELADKNS RGYYVKEQFAWRHVYWYLTN ED/MPVSP*LPSSAPGDCACHPT PQPSRDWQASV

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28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG ADEGNHGDTGYPHW*GTSRNV SRQTVQTRSLGT
28210	58578	A	28381	168	378	
28211	58579	A	28382	1	900	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAENFRALST\GEKG FGL*GVPCFHRIIPGFMCQGGDF TRHNGT\GGKSI\YGEKFEDENFI LKHTG\PG\ILSMAKCWDPTQN GSQFFNLALAKTEWLGWASHV GVLAK*KKGMNIVEAMERFGS RNGKTSKMITTADCGQLRIKFD LVFYLNHQDHSFWKPQGEHPS NPFARRILRILWLSLAVPFWVPC FPCSLPCLAGLQS
28212	58580	A	28383	393	683	HAKDGMEQRGNNECPKVGKQ VTLQHSDPEDRKTSTRCGENLY MSSDPTSWSSAIQSWYDEILDF VYGVGPKSPNIVLLVII*IIERIPR TNKEHLVPV
28213	58581	A	28384	119	193	
28214	58582	A	28385	1	567	
28215	58583	A	28386	957	1145	EQNLLIYLVSIVQDCMDKGCII* LRHTSGNCMYVSDKFDFKEQCI FSPRSSQKSLSGNDLQK
28216	58584	A	28387	153	2257	
28217	58585	A	28388	369	539	KKPARRRHLFTLLCCVFSPKLC TAGGPMRRTFKSYDEAGTGLL SVADFRTVLRQYSINLSEEEFFH ILEYYDKTLSSKISYNDFLRAFL Q*TPKL
28218	58586	A	28389	3	1364	
28219	58587	A	28390	1	996	
28220	58588	A	28391	296	549	ETSSSVTVSDP\EMENKGGQTL\ NNSSLMAEAPGTMCRFTLAPH V\LAVQGTITDLPDHLLSYDGSE NLSRFWYDFTLENSVLCDS
28221	58589	A	28392	1	1065	
28222	58590	A	28393	412	428	WILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPPLPARWPDSL MQLARQVSRLESGQ
28223	58591	A	28394	3	505	
28224	58592	A	28395	1	1201	
28225	58593	B	28396	518	1606	
28226	58594	A	28397	1	798	
28227	58595	A	28398	737	3067	

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28228	58596	B	28399	133	239	
28229	58597	A	28400	3	376	
28230	58598	A	28401	1	1194	
28231	58599	A	28402	405	611	
28232	58600	A	28403	204	4198	
28233	58601	A	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMFTFITQLLLVVEV KDSLERLAVEVVFILQKAMYE KQAHIYMKSLCPQMVLMLRFI QWVQIMPMLKLENLQHLMAR WNETVKEKK*DTLLFSMHERN
28235	58603	A	28406	359	517	
28236	58604	A	28407	68	487	
28237	58605	A	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQTQEPSWLHPVDP APGLQVELPASHAPCARTPQPL GGRWDWAPWSRGWCSLGRLG PHRSPWSGWEAQA*QWIPHQG CRWSCLPVTRRVLALLSPWVV DGTGRRGAGGGARWGGSGRT GAHGVGGRLRHSRLQVPSPAL LFKYYYCDIFK
28239	58607	A	28410	1	609	MVFSNLKGHWLQPIRLDSGSR NTAIGCDNQYKPTGVKLQTFA VSVTALKAARLGLFVPPGGLV VSLGSGVKLQIFASQVVCFDRA LIGAFTIPELDTKVLHVPIRLVR YRVWTQRFSKAPPDSGAQLASP SESHTRAAGGAACQSQCRAPA LLSPWVVDGTGRRGAGGGAHR GGSGCTGTHGVGGRLRHSGLQ VPSSA*VSHPLRGFL/LQPEPPR* APPPAPRRPVPSTTQGLRSAGA RHWDWQAAPPAALVWDSLGE ASWAPESGGALENLCVHTLYL TNLMGTWRTFVSSSGIVNAPIS ALSKQTTWLAKICSFTPEPRETT SPPGGTNNPRRAALRAVTLTAK VCSFTPVGLYWLSQPMAVLRE PESNLIGWSQWPFRLLKT
28240	58608	A	28411	548	753	TLLWE*SRLRKKSHLMMTLNH STHSITFGLDKHCASYLMGFLYI VELLIAQCGSPGATLIQWRMAS MD

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28241	58609	A	28412	1	903	MAKKIQLTYKCVQNWWVLGL TDFKNEAADPRRVKLQTFVVS VTALKAARLELFIPPGGFVVSL ASGVKLQTFAVSVTAHKGSVD PKTRHKGSPSPHQTQEPSWLHP VDPAPGLQVELPASPAPCARTP QPLGGQWDWVPWSRGRCSSG RLGPRSSPRWGAGSGMAGCRS RALPHGEAAKAQRKVTAAAGP GAKHLTAWGWQGQLATPSVG PAEPTHTQNSHWPASAVCSPSS RLRLSLHTYPQAEGAGSGLGQP RKGLPQCSSRLKGSSSAAKVGA QAEEVPRASEACEG*RAPQVLP KWEPRQRRCRERARPARAAST LSPLISI
28242	58610	A	28413	1178	1480	CRHLIQSHSICLHQWDCHTQHL YHPQ**WNQQQQLHHRCLLQG SIHLVFGPQWDPRRRRPLRGTR SAMARMDILRISREYITQEITEA ATKRKVLSVPKE
28243	58611	A	28414	126	407	WIPHRGCRWSCLPVPCRALALL SPWVVDGTGRRGAGGGARQG GWGSTGAHGVGRRLRHGGLQ VPSPAPRESS*GPARNRSQRRRS DSSLRERK
28244	58612	A	28415	27	363	
28245	58613	A	28416	1	576	
28246	58614	A	28417	813	923	YSLIHAAPQQRS*SLSGPHQTY DISSYTCQCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVP TRLRSPASFTQWIPHWGCRWSC LPVPRRVPALLSPWVVDGTGG CGAGGGAHRGGWGCTGAHGG GGRLRHGGLQVASPAPREGS*G PARN*AQSRWAGTAGGPSTPSA AAGPGAKPLIAPGRQGNEPCH WCGARQAHAHPELQLATSASW TRAFRECVSPAWPSCLGAACFH CLLIGPFPFSFSSQHLSTSLGHLV LLSWHLTSLSVSFRILTRLLRVF TGSWGGGAA
28248	58616	A	28419	1	616	
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28253	58621	A	28424	1300	1648	
28254	58622	A	28425	1	599	

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28255	58623	A	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK YVGLWDFKSRTDEELSFRAGD VFHVARKEEQWWWATLLDEA GGAVAQGYVPHNYLAERETVE SEP\RDTQAVRHYKIWRRAGGR LHLNEAVSFLSLPELVNYHRAQ SLSHGLR
28256	58624	A	28427	3	438	
28257	58625	A	28428	37	403	
28258	58626	B	28429	1	1176	
28259	58627	A	28430	2	2150	
28260	58628	A	28431	1593	3025	
28261	58629	A	28432	322	2168	
28262	58630	A	28433	183	591	
28263	58631	A	28434	2	258	
28264	58632	C	28435	52	363	
28265	58633	A	28436	1	3363	
28266	58634	A	28437	1	918	
28267	58635	A	28438	1	1422	
28268	58636	A	28439	3	10899	
28269	58637	A	28440	277	586	
28270	58638	A	28441	3	3364	
28271	58639	A	28442	1	1851	
28272	58640	A	28444	3	253	CGIEDNNFSLALNPDTDILLS/HS GGRGAEAPTMCLKLTVSKRAC FEGLE\WQFNLWRNKK**C*DK KHKTAGCSIS*VMRSVYR
28273	58641	A	28445	1	950	MGSSAVQSQLAALAPRVLTGG LADVTALLRAPATPGRLVAGA RGGWGYVQSCRGAGAAAVKP LGSAETAVPIARLGCRRFSRSRC CRRRGRGSLLSFSAAKPIVFKEK LTMKTDSLMEEKLECSLWCCL SDPSTPGRCCVLERRIVPWMQQ LLANIKQAEKHEKNHPEVTVA MALTDIDLQLQFSMSQPE/GPPS PGSRPS*PPPAAALLWTPAGQA CPGPGGAEAADPSRNSTEWLRP PHHSSDCLRGLAHIVSQWVSEC LLCSPGSPPRSPLWALCWEHWE TWPALPEGNQPSPEGLPPCSRS QWPQTPPASDPQ
28274	58642	A	28446	3	213	LTQHCWTHLVRSSHSRTGSSRL HNHQLHQPCA*S*LCQKEHASR GWSEQFNLWRNKK**C*DKKH KTAG

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28275	58643	A	28447	142	772	LVNVDVDADLVGLCVSHRHTV EEQYSTLALLNHGPQVALKYV HMDEVPMPACCLEGQGCLPAL CGECKLQGSFILSAPGRQGSQR VGPREAQGHIVIGRKLFSTALM LIGGQRLEESAAIESGCMEATP QGMAGSPQVGQAKSPSVPNKE PIGDF*GGSQDYRGGIQKPID*Q CGPVL/SRQSELWCGGRSHSVE FLLGSAASAPPGPGQA
28276	58644	A	28448	1	1935	
28277	58645	A	28449	2	1571	
28278	58646	A	28450	2	301	PRPFYSKNFYKILSLYSSEFNNS FVDA\LGSD\QDSGNEDVFDME YTEAEAEELKRNAEVIVFIPEYS WSNSVSLFPLCPGAKGPTFSVH CRVHFGPFSSH
28279	58647	A	28451	1	1329	
28280	58648	A	28452	240	503	
28281	58649	A	28453	1039	1896	
28282	58650	A	28454	1	2397	
28283	58651	A	28455	1	4011	
28284	58652	A	28456	3	1088	
28285	58653	A	28457	1	4878	
28286	58654	A	28458	1	174	
28287	58655	A	28459	3	161	
28288	58656	A	28460	992	1102	
28289	58657	A	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV GFPQGCQLVHIW*M/PLDAGPE HNSLKGFLVPLFPLAATPRAPG TPAQGSLTDSFPDLLGLAAED
28290	58658	A	28462	3	278	HEAAMSMLRLQKRLASSVLRC GKKKVWVRPL*TNEIANANSR QQIRKLIKDGLI\IRTPVTAHSWP SCRTNTLSRRMGHS*SLRTLLD PVNM*GLLNASWITKC*LLDPV NM
28291	58659	A	28463	1	1043	
28292	58660	A	28464	185	804	VTSGCGKKKVWLDPNET\NEI\ ANANS\RQQIPEASSKMGLIIRK P\VTV\HSRA\RCPVKTPLARRG RGRATWGIR*GGKGYKPNARN AQRKFTW\MRENGGL*TRGCL RKIPVNPKKDRIANMY\HSLLPE G*RGNVFKNKADFSWEHIHKL EGRQRPRKKAPWLTQA*GPAG S*DPRKPRKRR*RAPPRPKKEEI HQRLFSKE\EETKK
28293	58661	A	28465	221	350	GPSSFRLPTLSSLHVSHGREET* HSLET*RDAVSLRIFKSLSV

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28294	58662	A	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQGNKRGYKQME EHSMLMGRKNQYRENGHTAQ GNLQI\HAIPIKLPMTFFTELEKT TSKFIWNQKRARITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKLK SFCTAKETTIRVNRQPKKWEKI FATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAIIQKSG NNRCWRGCGEIGTLLHCWWD CKLVPHILTHRWELNNEITWTQ EGEYHTLGTVVGWGEGGGIAL GDIPNAR
28295	58663	A	28467	1	1863	
28296	58664	A	28468	2	1308	

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28297	58665	A	28469	1	1901	MPESPTPLLGRDILAKAGAIIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQQGLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCLPLRNQQECHQATQV LLNVLATCGYKVSKQKAQLCS QQVKYLGVKLSKGTRALNNEE QIEHNCQQVIAQTYATRGDLLE VPLTDPNLSLYTDGSSFVEKGL QKGGYAVVSDNGILERNPLTPG TSAQLVELIALPRALELGEGKR GSSESICFLSFLVPPMTIYTEQDL YNHVVPKPRNKRVPILTFVVGA GGLGGLGTGIGGITTSTQFYYK LSQELNGDMEWVADSLVTLQD QLNSLVAVVLQNRRALDLLTA KRGGTCLFLGEECCYYVNQSGI VTEKVKEIRDQIQRRAEELQNT GPWGLVSQWMPWILPFLGPLA AIILLFLFGPCIFNLLVKFVSSKI EAVKLQIILQMEPQMQSMT/KI YHGPLDQPASPCSDVNDIKGTP PEEISTAQHLLCPNSAGSS
28298	58666	A	28470	1	432	
28299	58667	A	28471	1	4314	
28300	58668	A	28472	1	330	
28301	58669	A	28473	1	1425	
28302	58670	A	28474	3	1110	NEEQIEHNCQQVIAQTYATRGD LLEVPLTDPNLSLYTDGSSFVE KGLQKGGYAVVSDNGILERNP LTPGTSAQLVELIALPRALELGE GKRGSSESICFLSFLVPPMTIYT EQDLYNHVVPKPRNKRVPILTF VVGAGGLGGLGTGIGGITTSTQ FYYKLSQELNGDMEWVADSLV TLQDQLNSLVAVVLQNRRALD LLTAKRGGTCLFLGEECCYYV NQSGIVTEKVKEIRDQIQRRAEE LQNTGPWGLVSQWMPWILPFL GPLAAIILLFLFGPCIFNLLVKFV SSKIEAVKLQIILQMEPQMQSM TKIYRGSLDQPASPCSDVNDIEG TPPEEISNAQPLLCPN*AGSSWS SRRPTSPTALGFSC
28303	58671	B	28475	1	1989	

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28304	58672	A	28476	1	1280	MGNITADNSSMSCTIDHTIHQT LAPVVYVTVLVVGFPANCLSL YFGYLQIKARNELGVYLCNLTV ADLFYICSLPFWLQYVLQHDN WSHGDLSCQVCGILLYENIYIS VGFLCCISVDRYLAVAHPFRFH QFRTLKAAVGVSVVIWAKELL TSIYFLMHEEVIEDENQHRVCF EHYPIQAWQRAINYYRFLVGFL FPICLLLASYQGILRAVRRSHGT QKSRKDQIQRLVLSTVVIFLACF LPYHVLLLVRRYWEASCDFAK GVFNAYHFSLLLTSFNCVADPV LYCFVSETTHRDLARLRGACLA FLTCSRTGRAREAYPLGAPEAS GKSGAQEEEVTKFEGGRNGHT AKKSPCNSVQDFTGIKAVKLQI VLQMEPQMQS\KLKIYSRPLDR PASPCSDVNDIEGTPPEEISTAQ
28305	58673	A	28477	1	717	
28306	58674	A	28478	2	409	
28307	58675	A	28479	1	675	
28308	58676	A	28480	227	399	
28309	58677	A	28481	332	436	
28310	58678	A	28482	980	1399	
28311	58679	A	28483	132	218	RINLMHFRN*TSQQALSLSYNL FLMQRH
28312	58680	A	28484	1	34	
28313	58681	A	28485	985	1170	
28314	58682	A	28486	1	1203	
28315	58683	A	28487	505	716	REPCPVSQREVWRPGCLD/HCP RQSGSLGETLRGTAE\QPWPHS QVLSNLRVLQLPLISLPSLRRRA LFPAA
28316	58684	A	28488	1	998	
28317	58685	A	28489	477	955	TPIHNGFKENKIPRNPTYKGCE GPLQGELQTTAEGNKRGYKQM EEHSMLMGRKNQYRENGHTA QGNLQVQCHPHQATNDFLHRI GKNYFKVHMEPKKSPHRQVNP KPKEQSWRHHTT*LQ/YYTTRL Q*PK*HGTGTKTEI*INGTEQSP QK*CRISTTI
28318	58686	A	28490	37	430	
28319	58687	A	28491	507	829	
28320	58688	A	28492	643	945	CALLHSLPQHCVQHPYRSYTHR MASCRWKWGHCHSGIKMYSIP WYSTPMEGKALGDAHPQIAHS H*GAAFL*ALY*EKS*SMANRL WYSRL*PLAGDGRRE
28321	58689	A	28493	1092	1346	

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28322	58690	A	28494	173	527	
28323	58691	A	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSVPSPALPCSLKYPFYD HRTKFTLTTQPFSHTLAQKENQ SPLKHMGKKRLQNIFLPIRP*DQ TPWLERS
28325	58693	A	28498	921	1008	
28326	58694	B	28499	1	2169	
28327	58695	A	28500	455	523	YPLYHFLLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVYSEIQLLPGLVL GGCMCRGIYPFLLDFLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLLRVFSMKSC *ILSKAFSASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFASILLRIFTS MFIRDIGLKFSFFVVSLPGFGIK MMLAS
28330	58698	A	28503	1	957	
28331	58699	A	28504	41	412	IALIILRYIPSIPSLLRVFSMKGC* ILSEAISASIEIIMWFLSLVLFI*W ITFIDLHVLNKPCIPGMKPS*SW WISFLMCCWIWFASILLRIFASM FIRDIGLKFSFFVVSLPGFGIRM MLAS

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28332	58700	A	28505	1	1699	MDEFLDTYTLPRLNQEEIESLN RPITSSEIEAVINSLPTKKCPGPD GFTAEFYQRYKEELVPILLKLIQ TIEKEGLLPNSFYEATNILIPKPG RDTTKKENFRPISLMNINAKILN EILATESSIKKLIHHDQDSFIPGM QGWFNICKSINVIHHINRINNKN HMIISVNAEKAFDKIRHLFMLK TLIKLGIDETSLKTVRAIYDKPT ANIILNGQKLEAFPLKTGIRQGC LLSSLLFNIVLEVLARAIRQEKEI KDIQIGREEVKLSLFADDMIVY FKNPIVSAQNLLKLIGNFSKVSG YKINVQKLQAFLYTNNRQTESQ IVSELPFTIAAKRIKYLGIQLTRD VKYLFKENYKPLHKEIIEDTNK WKNIPCSWIGRINIMKMAILPK VIYRFNASPIKLLLNFFTELEKN CLNFIWNQKRAHIAKTILSKKN KAGGITLPDFKLYYKSTVTKTT WYWYQNRYIDQWNRTEASEIT PHIYNHLIFDESDKNNQWGKDS LHNKWYWENWLAICRKLKLD SFLTHYTKINSRWIKDLNAGSKI QY\HADRTKSRERRAIASSYVSS
28333	58701	A	28506	2	1689	WRAWGRGATRRSSCHRQSAPS LSRVGRSSQIRSALSAASGLWR RKPASAKFGRPRTGSLHLPVK* KAFVSLQESSA*MNLRQ*PE*D WISWIN*QNFGN/CQGSTLKIPV VERKILDLYALSKEHSFSPATEQ SWTENDFDELREEGFRRSDFSE LKEEVRTHRKEAKNLVKRLDK WLNRITSVEKSLNDLMELKTM AREQLRDECTSFSSQFDHLEER KYKLPSENKHLYANKLENLEE MDKFLETYTLPRLNQEEVESLN RPITGSEIEAIINSLPTKNSPGPD RFTAKFYQMYKEELVPFFLKLF QSIEQEGILPNSFYEASIILIPKPG RDPTKKENFRPISLMNIDAKIFN KILANQIQQHIKKLIHHDQMGFI PGMQDWFNIRKSINVIQHINRT KDKNHTIISIDAEKAFDKIQQCF MLKTLNKLGIDGTYVKIIRAIY DKPTANIILDGQKLEAFPLKTST IQGCPLSPLLFNIVLEVLARAVR QEKEIKGIQSGKEEVKLSLFAD DMTVYLENPIISAQNLLKLKSN FSKVSGYKINVQKSQAFLYTNN
28334	58702	A	28507	1	1428	

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28335	58703	A	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC WIMFIDLRMLNQPCTPGMKPT* SWWISFLMCCWIRFASILLRIFA SMFIRDIGLKFSFFVVSLPGFGIR MMLTS
28336	58704	A	28509	765	950	LLPQFQNLLLVYSEIQLLPGLVL GGCMCPGIYPFLLDFLVYLHRG VYSIL*W*FVFLWDQW
28337	58705	A	28510	778	981	SQKEWYQLLFVPLVEFGCESIW SWAFFGWQAINYCLNFRTCHW SIQRFNFFLV*SWEGVCVQEFIH FF
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI* TLK
28339	58707	A	28512	1	1641	
28340	58708	A	28513	1	2307	
28341	58709	A	28514	1	3793	
28342	58710	A	28515	178	674	ERPRIMDLAGLLKSQFLCHLVF CYVFIASGLIINTIQLFTLLLWPI NKQLFRKINCRLSYCISSQLVM LLEWWSGTECTIFTDPRAY\SS MGKENAIVVLNHKFGN/IDFLC GWSLSERFGLLGVSQKCIPPCL THFFGSAPPLVFLLLVIQNLQKN QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCGLFFGSI* TLKYFFPIL
28344	58712	A	28517	1	2167	
28345	58713	B	28518	65	2652	
28346	58714	A	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	A	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	1	669	
28351	58719	A	28524	1	1089	
28352	58720	A	28525	91	507	AGTASASPAPNRSLSGSEPTSSS VTQENGADVQGHERVPWKAR SRRFCPMEGTFRKVPSHGSHVP EVSMLWKACSGSFRPVEGHSV RCALTPASGCSP*AGTASASPAP NRSLSGSEPTSSSVTQENGADV QGHERVPWKARSRRFCPMEGT FRKVPSHGSHVPEVSMLWKAC SGSFRPVEGHSVRCALTPASGC SPSKSKATVGCRCSDFCTVEEF LQKIFLQVESLDRRPRCLPLT
28353	58721	A	28526	1	1213	
28354	58722	A	28527	130	211	KPHYAAHGQPFTAE*RPGTDNR ADNRQ

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28355	58723	A	28528	793	1382	NTTAAGRVIRLTSENGSHTTFR YDVLDRLIQETGFDGRTQRYH HDLTGKLIRSEDEGLVTHWHY DEADRLTHRTVKGETAERWQY DERGWLTDISHISEGHRVAVHY RYDEKGRLTGERQTVHHPQTE ALLWQHETRHAYNAQGLANR CIPDSLPAVEWLTYGSGYLAG MKLGDTPLV**ERPADR*ASDG ASPADGSTALAA*DQTCVQRA GAGEPLYTGQPARRGMADLRQ RLPGRHETRRHTAGGVHPRPPA PGNAAQLRPL
28356	58724	A	28529	1039	1689	
28357	58725	A	28530	1	2406	
28358	58726	A	28531	1	2928	
28359	58727	A	28532	2	1271	
28360	58728	A	28533	250	929	
28361	58729	A	28534	3	273	GKLIAVIGDEDTVTGF\LLGGIG ELNKNRHPNFLVVEKDTTINEIE DTFRQFLNRDDIGAFRLLGLCW LRNRKPDHLPPLPLPCAVTQCH
28362	58730	A	28535	2	415	
28363	58731	A	28536	1	690	
28364	58732	A	28537	2551	2651	
28365	58733	A	28538	2	295	
28366	58734	A	28539	1	316	CGHGGRQSWVSRLR*CQEAAG MADSCPRSGGAILAFKSAPEVI RRALSAQSLRATSSSSASGAGA FCLSPSKYFPETSASSSATARYV LGWAASSGLLTSSQKMG
28367	58735	A	28540	1	400	
28368	58736	A	28541	257	516	
28369	58737	A	28542	1	590	EQIASDTCHLQRVVFKNISPAD AHRNLCLALRGHKTVTYLTLQ GNDQDDMFPALCEVLRHPECN LRYLGLVSCSATTQQWADLSL ALEVNQSLTCVNLSDNELLG*G C*VAVHN/S*DTPSAFLQRVVV GKTGHLTEANLQGTLLLCWVF SRELTHLCLAKNPIVNTGVKYL CEGLRYPECKLQTLVLWNCDIT
28370	58738	A	28543	1	2633	
28371	58739	A	28545	127	2030	
28372	58740	A	28546	1	3066	
28373	58741	A	28547	259	3222	
28374	58742	B	28548	1	2640	

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28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADQRLIF AKSWPRASRYQQGHQDLFILRS DLPSQVVQTQNISSCRNSC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QK\SDGTLQEHDGICEIHVAKY AEIFGLTSAEPNRFTQFRLSETK EITNPYAMRLYESLCQYRKPDG SGIVSLKIDWIIERYQLPQSYQR TSPCCCHMKKDVFASPSTMISS SRVSNNTSKTTIIKNQCQKDDS RRSLLVKNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGGVR RCLQQQCEQTVRILHAKVAQK SYGNEKRLIIRPTIRVGPWSQTN NQTDDTSGTVVQSDYQTDDTS GTVVRTNNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	B	28551	1	1954	

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28378	58746	A	28552	1424	3807	HPLWKWLEGDMNMNIKKIVK QATVLTFTTA/LLAGGATQAFA KENNQKAYKETYGVSHITRHD MLQIPKQQQNEKYQVPQFDQS TIKNIESAKGLDVWDSWPLQN ADGTVAEYNGYHVVFALAGSP KDADDTSIYMFYQKVGDNSIDS WKNAGRVFKDSDKFDANDPIL KDQTQEWSGSATFTSDGKIRLF YTDYSGKHYGKQSLTTAQVNV SKSDDTLKINGVEDHKTIFDGD GKTYQNVQQFIDEGNYTGDPL EAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRT PDFRRRFLQVCVNEINGAVIGIP CVSIRKPDGSGIVSIKIAWIIERY QPPQSYQRMPDFRRRFLQSRPA CMHDWLCAEALAWSIQTASYL VTMQVNLTSLSSDTDRDLSVVS NSGWVSSGSLVRFNTIKTSSGEI KRTVPRILPDPDDPRSAIAEAPS EMPGHEVPVEEHFPEAGTNSGS PQGARKGDESMTKASDSSSPSC SSGPRVPKGAAPGSQTGKKQQS TALQASTLAPANLLPKAVHLA
28379	58747	A	28553	2372	3570	EALLPGDQDSQSGKGVAAREV WFLPSSFAPVLLRLVGNHHVG DNSIDSWKNAGR/VFKDSDKFD ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTT AQVNVSKSDDTLKINGVEDHK TIFDGDGKTYQNVQQFIDEGNY TSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQSA KKRDAELANGALGIIELNNDYT LKKVMKPLITSNTVTDEI
28380	58748	B	28554	1	2232	
28381	58749	B	28555	200	2602	
28382	58750	B	28556	1	3198	
28383	58751	A	28557	1	2169	
28384	58752	A	28558	1	2259	
28385	58753	A	28559	1	2418	
28386	58754	B	28560	1	1974	

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28387	58755	A	28561	3	2077	
28388	58756	A	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG AIQAFAKENNHKAYKETYGVS HITRHDMLQIPKQQQNEKYQVP QFDQSTIKNIESAKGLDVWDSW PLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVGD NSIDSWKNAGRVFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGKHYGKQSLTTA QVNVSKSDDTLKINGVEDHKTI FDGDGKTYQNVQQFIDEGNEGI LPISEPPIKQDFRLLG
28389	58757	A	28563	610	2303	SLPNLDNAAICSSSSSPTRTR*SL SEGATQ\AFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNSIDSWKNAGRVFKDS DKFDANDPILKDQTQEWSGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSLGTLQGFPAPAWLALAHP VHPLKHKSGGSNRLSAAIWGIK RKPARVCPGTGIHASSQIQGEW RTECAVGPKAKAKATAGWRR GNNQHISSTYDINRADTQVRRA VNNYDIIVMSNSFNGQSEHQTY ESIVIDSAPNLGIGTINVVCAAD VLIVPTPAELFDYTSALQFFDM LRDLLKNVDLKGFEPDVRILLT KYSNSNGSQSPWMEEQIRDAW GSMVLKNVVRETDEVGKGQIR MRTVFEQAIDQRSSTGAWRNA LSIWEPVCNEIFDRLIKPRWEIR
28390	58758	A	28564	1	2079	
28391	58759	A	28565	1	774	

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28392	58760	A	28566	1	2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFFKR GAIFRVHKHAVNPMSPKCRRPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKET/YPKQQQNEKYQVPQF DQSTIKNIESAKG\LDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYTSGDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGINSNDI YMLGYVSNSLTGPYKPLNTTG LVLQMGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ MNNASTMSKRTSAGCHCWQG
28393	58761	A	28567	1	3987	

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28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL/VFEANTGTEEHPQPQ\ERP RTQSFTSAFAERRECIPNVPADT KLSKIKTLRLATSYIAYLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKELASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHRSRAYKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHLPDLCSPSQDAQTTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTV
28395	58763	A	28569	2	1778	
28396	58764	A	28570	1099	2224	DGQQLIALHRLALRELQQAVH AGLPQQAKILFDGGSE/TRQNPL QQLVHMGLPRPLDKKNFQEP
28397	58765	B	28571	1	1938	
28398	58766	A	28572	1	2367	
28399	58767	A	28573	4659	13369	TVFRPFHVGVHVLLIVDSCSKL EQHSTLSRAILLIYKGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTGKRAVSATQLMDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQGGEDSPNRFFDGG RKKQIRTVRQFIDEGNNTPADT QTLRDPHYVEDKGHKY
28400	58768	A	28574	6803	8521	
28401	58769	B	28575	2010	17745	
28402	58770	A	28576	1	1060	

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28403	58771	A	28577	1	3585	
28404	58772	A	28578	44	317	LKALLLTQSLFGGLLTQTRMKF GAVTRIG\DLPWEINPLSSCSLL HEKDPPTTSGPQTHQPKEHLTN FKSGCSSPCRAKSQFFLSLCSST
28405	58773	A	28579	98	617	KALLLTQSLFGGLFTRTRMKFG AVTQIG\DLPWEINPLSSCSLLR EKDPPTTSGPQTHQPKEHLTNF KSARFKKIKACYHSPATAWPFK AYKLSLQFPHFTCPKTRQALQV SSGSVPYQPNCFAYPPHGAKPI YSPILNTSLHNPLFCSGSQTCFL YYSFAPFIPASLRFHLD
28406	58774	A	28580	1	1500	
28407	58775	A	28581	42	257	
28408	58776	A	28582	3	425	KTGKYD/AVIALGTVIRGGTAH FEYVAGGAS/NTLAHVA/QDSEI PGAFGVLTLKA*TNDERAGTKL HGGWGGKCLTACRSALWADL QIRPYDHKNRGSNVHNRVPAS GAAAMAIHCLECGWAPLAAGD NVGKVCVPDAGLLPA
28409	58777	A	28583	327	1512	SYWTIHIQVSLEINHSYLPGG\IS SLKKMAGRNSERKTVLVKSSF QEVNRGTEALALWENGDFEAP VLTFTTALLPEGATQAFGKENT QKASKERYGSLNITRNNMLQIL NKQQTEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNSIDSWKNA GRVFKDSDKFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGGVNADVGDVVVRLPVW HRRGGEAVFMQVSRLQILRHLP HGVVAVDRDHHIAHDRRRHVA GDRSGSVRL
28410	58778	A	28584	845	966	
28411	58779	A	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKAVDTQ RH
28412	58780	A	28586	464	847	

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28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ GIKRPDALPGPLLHA*PDNLRCS CPRSGTAAGSIHQDARLRYSVW RWGLLDRLAAVICRQSTHSRCR RKQRRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	A	28589	404	733	
28416	58784	A	28590	2	246	
28417	58785	A	28591	466	861	
28418	58786	A	28592	122	926	
28419	58787	A	28593	171	733	
28420	58788	A	28594	1	774	
28421	58789	A	28595	1	1575	
28422	58790	A	28596	1	105	SVKLGWNGVSTYVPFCLTICSV SFFQENLHLTTCRA*PSIPPPAA RRSPKKCSP*KLRLP*LSGKSSS YNL
28423	58791	A	28597	237	461	
28424	58792	A	28598	1	1341	
28425	58793	A	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGFLPRKRSSRHRGKVKSFP KDDPSKPVHLTAFLGYKAGMT HIVREVDRPGSKVNKKEVVEA VTIVETPPMVVVGIVGYVETPR GLRTFKTVFAEHISDE/CRLLPL RQKKAHLMEIHVNGGTVAEKL DWARERLEQQVPVNPVFGQDE
28427	58795	A	28601	1	1251	
28428	58796	A	28602	37	1307	EFGFDGVMSHRKFSAPRHGSLG F\LPRKRSSRHRGKVKSFPKDDP SKPVHLTAFLGYKAGMTHIVRE VDR\PGIHRCNKKERWWRAVT HCIRPPPMVVGGHLVG\YVET\P RG\LRTFKT\VFAEHISDECKRRF YKNWHKA\KKKAFTKYCKKRQ DEDGKKQLEKDFSSMKK\YCQ VI\RVI\AHTQ\MRLLPL\RQK\KA HLMEIQV\NGGTVA\EKL\DWA REKLE\QQ\VPVN\QVFGQDEMI\ DVIGGDQRAKGFKGVTRS\WPT N*LPFKA\HLG\LSRVACFGAW HPARVAFSVARAGQKGYHHRT EINKKIYKIGQGYLIKDGKLIKN NASTDYDLSDKSINPLGGFVHY GEVTNDFVMLKGCVVGTKKR VLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	A	28603	1	2133	
28430	58798	A	28604	3	245	

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28431	58799	A	28605	1	1824	
28432	58800	A	28606	1	1035	
28433	58801	A	28607	1	496	
28434	58802	A	28608	1568	1793	
28435	58803	A	28609	1	1392	
28436	58804	A	28610	1	1389	
28437	58805	C	28611	104	253	
28438	58806	A	28612	114	469	VSRPTYAKVFTTSKTAPQKVFP TAWCSA/TGHETALSATQVPIQ WIATAPNSPAPPSDPRRQSWVS QIPSSATSPNFTM*EPRTQEVTE PHDSRPAIPSPAVPRRESCTGRP HLPATTP
28439	58807	A	28613	3	2196	
28440	58808	A	28614	237	348	NPVN*SQTT*TSE
28441	58809	A	28615	950	1094	
28442	58810	A	28616	146	822	LGFLLRLSEMPRKQGVYRTRIW KFEDGLSNVLVI/PIEQINHMRD VFGSGSERATCLARGRGYINSL ARCQNLVNRDLDHLSLPQDSTL VHYIDDIVLHGFSEEEKGQVAQ SADLDEGLLKIPGDTFGPEADK DFLHKDLSTEIVGQSYNTHHM AQDSIPWNPSGQEPQVREHEAC HHLGSGSPPSWELCEQGPPVTE SFQVLVTSGLDKENMAYMHCG IICSNKKG
28443	58811	A	28617	1	1791	
28444	58812	A	28618	244	416	
28445	58813	A	28619	2	1520	
28446	58814	A	28620	95	421	PVTSTSTKRTPTQKPHPKVISLK DQIHHVDKSMMMRKNQCKNV EKSKNQNSSSPHDHNSSP\SARA ENWTEYESDKLTEVGFRGWVI NSSELKEHVLTHCKEAQNLHN
28447	58815	C	28621	46	174	
28448	58816	A	28622	425	1291	
28449	58817	A	28623	1	1410	
28450	58818	A	28624	14	348	GLFPNKIPFSVLEIRTWAHLSGR HHSAHCTSCAWPQVACLPLAT HPSCTCTFCSLQAPGRPGQSPLS PRRACGPEDLPPPPYV*DLAPSL GPSLGPLMSQSQPRRTPPLRG
28451	58819	A	28625	96	295	PWKPHPAWRQRWELCHPPFP/I RPLTAALREQPGLLGRSTTVFT LMAREPPQPAAADSCLCIVQME A

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28452	58820	A	28626	105	389	CQFAHGTASSPRVCLRHRCRS WQKAWAVVCCTFCSLQAPGRP GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQPRRT PPLAWGS
28453	58821	A	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	A	28629	301	987	
28456	58824	A	28630	239	384	VLPAGAQAAARSSDTRP*PEPH FS\ESVFPRWIFSAFQSLNNFFQA RF
28457	58825	A	28631	1	1054	
28458	58826	C	28632	243	392	
28459	58827	A	28633	1	1104	
28460	58828	A	28634	194	863	YLLFVKNMSSLEISSSCFSLETK LPLSPPLVEDSAFEPSRKDMDE VEEKSKDVINFTAEKLSVDEVS QLVISPLCGAIS/LNWKGLTENT FEGKKVISL\EYEAYLPMAENE VRKICSDIRQKWPVKHIAVFHR LGLVPVSEAKP*SFAVSS\AHRA AISLKLLSYC/AFDTFKRPRVPI WKK\EIYEESSTWKGNKECFW ASNTLITYVFRACNLNFVKLLL
28461	58829	A	28635	3	338	SSPPTAPAKLRIVPLVGGLPAR WCLSVCASQCPDTRVHVFLHW WCSSLCPAPVCLSLCRGL*GHF PPDSEDQSSPNCSGYTLEEYKL LRSQTIPSCNGKFPCPPRRAYDG
28462	58830	A	28636	405	800	
28463	58831	A	28637	265	539	
28464	58832	A	28638	3	1116	
28465	58833	A	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	A	28641	563	594	
28467	58835	A	28642	245	580	
28468	58836	B	28643	1	435	
28469	58837	A	28644	673	1012	QPQVSFSSEYAIHIMRCPHSKIS SLYYFNCFRY*DCYCH\TFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLNTGA WVRAWKATSTSVVHLTKWVL
28470	58838	A	28645	1171	1328	MVIGGTKNERKHIDSDEPLFPSP NSSARGRAISSTS*ALVPGVRGF LSSIPLSLTTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGSAVDLSHGLHLGLHL KNDL*FYSFNSGIDKPEIAKLSG CSFGGTFLIWG
28472	58840	C	28647	199	309	

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28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLSLPKLK L*SYKSFFKWSPRCSP
28474	58842	B	28649	107	264	
28475	58843	A	28650	301	470	EIQLVLSLSGGGYSHAVLMIVS SHKI**FYKGLFPTFALHFSLLLP CEEGCICFPF
28476	58844	A	28651	2	263	WEKKDTEWRKKVILSSV*LRL VIF*PFSLM\LFSHPVWR*ARSH ESHLAITHLWALYF*PPCQICFL *DRGHQATDGLTNGTPSELN
28477	58845	A	28652	63	191	DLPWTPGPAC*PMLQC**GGAN IYARRQGADAAGDQGSSCRL
28478	58846	A	28653	1	554	MPTYCPGASLLILTYKTPKELLS IYVSTIRKSRCRERRNRRLGAR NFRSEEQIYDQWRLDQVGKFFP FPRPRENYHFGSEHVGSFSLDK CCNEKLYEVIDLHLKKKFLNTE TLSLVKCEVSRCWVTLNLLLPY H/VLFQI*LSWRERQNQSCKTTN GSSNGAPDAVHN*NLLWSLGP AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWLPALPEN GYMKQFCVSGLGVLFHGCVFL CWHHCCFVL*VWSLGSPRSRG LHLVKAFFLCYPRSNCFLLNWG IVGVVQLRFPQEGCLWCH
28480	58848	B	28655	1	400	
28481	58849	B	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTLALPVSSQPFSLHTA EVQGCAVGILTQGPGPCPVAFL SKQLDLTVLGSPSCLHAVASAA LILLEALKITNYAQLTLYSSHNF QNLFSFSHLTHILSAPRLLQLYS LFVESPTITILPGPDFNLASHIILD TTPDPDDCMSLIYLTFTPFPHISF FSVPHVDHIWFTDGSSTRPDRH SPAKAGYAIESSTSIIEATALPPS TTSQQAELIALTRAFTLAKGLH VNIYTDSKYAFHILHHHAVIWA ERGFLT/IARVLHH*CLFNKNSS QGCFTSKGSWSHTLQGPPKGV RSHYSRKCLC
28483	58851	A	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	A	28661	1	704	
28487	58855	A	28662	41	275	
28488	58856	A	28663	159	1504	
28489	58857	A	28664	275	552	
28490	58858	A	28665	178	619	
28491	58859	A	28666	3	369	

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28492	58860	A	28667	1	340	
28493	58861	A	28668	516	734	WTGDWRRTCDRENQHVSGAA RTAFIPTNGAISPGINYSPGH*Y* DCHLPQA*P*LCRAAGQNRCH VARTCLG
28494	58862	A	28669	1	1163	MHTHARETCLALGKPADDATL TAAIEAVGLENAARVLKLYPFE MSGGMLQRMMIAMAVLCESPF IIADEPTTDLDVVAQARILDLLE SIMQKQAPGMLLVTHDMDKW GRIIADVESQYRYQTTNPKIFAG GDAVRGADLVVTAMAEGRHA AQGIIDWLGLDVDKLGALEERR KVLQVKTENLQAERNSRSKSIG QAKARGEDIEPLRLEVNKLGEE LDAAKAELDALQAEIRDIALTIP NLPADEVPVGKDENDNVEVSR WGTPREFDFEVRDHVTLGEMH SGLDFAAAVKLTGSRFVVMKG QIARMHRALSQFMLDLHTEQH GYSENYVPYLVNQDTLYGVGL YPLGALASGW/WALASGWLPK RRERKD/GDTGAHGVPRGSRKP RIARKVRGT
28495	58863	B	28670	1	4770	
28496	58864	A	28671	1069	1398	VIGAQPVLRIRRKQARRQINRL TLILLHYCLTTKLKNGVKPGIV AAFYFLPGAG*IHPAGCHGTQL *SFGKMRVQYTRVTLSQQASG KISAYLIDLGKPLLKLIIHCGVH
28497	58865	A	28672	4246	4453	
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	A	28675	1085	1246	
28501	58869	A	28676	1	1254	
28502	58870	A	28677	1	2175	
28503	58871	A	28678	340	994	
28504	58872	A	28679	37	261	TITPAGRRMHCKGACMKPLLD VLMILDAVRELE*TITPAGRRM HCKGACMKPLLDVLMILDAVR ELEKQAIKLHEGWENELVIGVD DTFPFSLLAPLIEAFYQHHSVTR
28505	58873	A	28680	410	896	WAWAASAVQPRSIWQ/GAGVG NLTLLDFDTVSLSNLQRQTLHS DATVGQPKVESARDAPHIAITP VNALLDDAELAALIAEHDLVL D/WYG*RCGT*STERQQR*RG* RSAPAMTAHDRDAIASSSETCA RSRWSVEYASPVCAPPDSRSKR RSASNSAASHVF
28506	58874	B	28681	1	2298	

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28507	58875	A	28682	1915	5313	
28508	58876	A	28683	1	4221	
28509	58877	A	28684	1	1007	MAALQMVNGQKWVSSNQKY WLVYKTTDPPRLRPIFSGYQPM CPFNGRPFWIHKNPMGVHWAV ATGLALIPIVGIAEFGWFWFGG ETYMAAWNVSGLGTFGAIQST FNVTLWSFIGVESASVAAGVVK NPKRNVPIATIGGVLIAAVCYV LSTTAIMGMIPNAALRVSASPF GDAARMALGDTAGAIVSFCAA AGCLGSLGGWTLLAGQTAKAA ADDGL\FPPIFARVNKAGTPVA GLIIVGILMTIFQLSSISPNATKE FGLVSSVSVIFTLVPYLYTCAAL LLLGHGHFGKARPAYLAVTTIA FLYCIWAVYITHIDACVVVYIA GYRAAKLTCA
28510	58878	A	28685	867	1681	
28511	58879	A	28686	865	1290	RWWENRLFRKNPARAQKMVL PERFG*SAYPNGFAGTWRLDKL PIAQIHAHMIGYLAAVDMEKQ QISPAQVVVRHNRCPAIVVHLI GRARELSLKDLVVGIKNQPATV KAFIRPRTAPDVRLAKLLLQAV NRHFGNVMQMVAA
28512	58880	A	28687	1	709	
28513	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPQT AFIQVGPRVHAHLQPRAAPL*A GEVWKPRLVGRSHWASRPSPA LQKGEPGSPSWENACVPQAPH RLLHQQKAF
28514	58882	A	28689	3	227	NSQDFPACGGLCHAELDRTAA GLVHQH\RHPGHTSVAAEKLCH GDVEGDGCNGPASD/PGYI*GQ AAAPAPLPDLL
28515	58883	A	28690	1227	1719	
28516	58884	A	28691	1	1701	
28517	58885	A	28692	15	3298	
28518	58886	A	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR AVWRYQTDIAANLE*RRLPSGA GKSDWSSGDSEKAKTAAHTIY RDAGRRVRGYRQL
28519	58887	A	28694	1	370	

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28520	58888	A	28695	1	910	MDKERIIQEFVPGKQVTLAHLI AHPGEELAKKIGVPDAGAIGIM TLTPGETAMIAGDLALKAADV HIGFLDRFSGALVIYGSGNYTL ARKTQAVEFNDKGDIDTPGEYF NHPRWYHALITTLQDVDMLSP LIWGFRNYKDVQVIKATPHKIV ILMGILLSPSVFATDINVEFTAT VKATTCNITLTGNNVTNDGNN NYTLRIPKMGLDKIANKTTESQ ADFKLVA\MGAAVASVGLIPL* PEMHHQAHLSLLYRSLVIHLRR QVISVWVSKNGLLMMPLSLNL TVRKRYAGAQTRCSPIRVLK
28521	58889	A	28696	605	2021	
28522	58890	A	28697	2256	2336	CIKCCARRIAREPGYLFS**RCK YPG
28523	58891	A	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN V*SWIKSS/MQMGQKMGVKISD EQLDQAIANIAKQNNMTLDQM RSRLAYDGLNYNTYRNQIRKE MIISEVRNNEVRRRITILPQEVES LAQQVGNQNDASTELNLSHILI PLPENPTSDQVNEAESQARAIV DQARNGADFGKLAIAHSADQQ ALNGGQMGWGRIHASLPGIFA QALSTAKKGDIVGPISSGGRFD GTVEVKDGHLIVNGKKIRVTAE RDPANLKWDEVGVDVVAEAT GLFLTDETARKHITADTPAALR WLEENQLEDGHECLLRRVISSD GRSRGFINGTAVPLSQLRETSTT TGARRVIRAIRRINSSDASTIPTL MAITISNNTVSDMHSSMTMMS TRIRTLITTIYNGDLRMIRQRKL CKTAIARTYGNDDTFHPGMRH QRMHRVFKNAPHLDQPVVTLN IYPKADESSSLKASRGTRGAAY RPARQNLYSASSGKKDENPVIE FKNVSKHFGPTQVLHNIDLNIA QGEVVVIIGPSGSGKSTLLRCIN KLEEITSGDLIVDGLKVNDPKV DERLIRQEAGMVFQQFYLFPHL TALENVMFGPLRVRGANKEEA EKLARELLAKVGLAERAHHYP SELSGGQQQRVAIARTLAVKH KMMLFDETTFDFDPELVHEVL KVIHEFAEKGITNDSLTENPAKT QGEGGCLQSQERGPQREPTPRH
28524	58892	A	28699	1	2307	
28525	58893	A	28700	3	976	

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28526	58894	A	28701	2	136	YLSAV*FCSPGQPPSALLVCGR RGYWCLWPLSSCHLTLRLCVS
28527	58895	A	28702	1	608	
28528	58896	A	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	A	28705	1	1184	
28531	58899	A	28706	478	627	
28532	58900	A	28707	33	1072	
28533	58901	A	28708	35	516	RVVEFADEGQGPAALSLWSGS SPETLKLHWPHVQN*IRFSSWK TFRIRSRDFWADRLMRTLLRNF LSKWDHL*GQTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRRDGGLAGLRGN SGAQGGDA
28534	58902	A	28709	1	777	
28535	58903	A	28710	531	704	
28536	58904	A	28711	294	617	
28537	58905	A	28712	804	1020	HFLSGGRRQRPPRWTIVA*SPR* PRCRCWGSG*RPGTRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRRQRPPRWTIVA*SP R*PRCRCWGSG*RPGTRGALPV VRKQPGDPKTPLASCPELNQPV PEPAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSGLRRLLGR PSHEGPWLKGTSCRSGTTCRDR PWV
28539	58907	A	28714	2	1580	
28540	58908	A	28715	286	352	
28541	58909	A	28716	1	531	
28542	58910	A	28717	1	1440	
28543	58911	A	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLLQLVEVLPE ANRQLRQSGAGDGGQQAVF*F HRFLASVHQHKAASASPPYLFR IKCPVPRLRAKPALLLIDNRLYG
28544	58912	A	28719	1	3534	
28545	58913	A	28720	1846	2121	
28546	58914	A	28721	176	462	TSRHSVYISDTELKPRKSSKPTF CGCDSLFSPICHFP/HGLSDVALI VQQLRQRG*PLQPARLPVHWR HQNAVVDGVLSGENGGAGWG RAWLRIRRS
28547	58915	A	28722	225	3465	
28548	58916	A	28723	937	1770	
28549	58917	A	28724	142	484	

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28550	58918	A	28725	1	1521	MIPITWPKFAELHPFCPPEQAEG YQQMIAQLADWLVKLTGYDA VCMQPNSGAQGEYAGLLAIRH YHESRNEGHRDICLIPASAHGT NPASAHMAGMQVVVVACDKN GNIDLTDLRAKAEQAGDNLSCI MVTYPSTHGVYEETIREVCEVV HQFGGQVYLDGANMNAQRRD\ MAGKPGPLTVRKMRGSRVTVR AL*/ASVWIGFDDHRRNLGHTT ASGAIKDQISGYEGGAKSAQPA WDAYMKAVLEGVPEQPLTPPP GIVTVNIDRSTGQLANGGNSRE EYFIEVNEIVVNPNATLDWQLA LRQAAGKTDLARDMLQMLLDF LPEVRNKVEEQLVGENPEGLV DLIHKLHGSCGYSGVPRMKNL CQLIEQQLRSGTKEEDLEPELLE LLDEMDNVAREASKILGGHDN GGNALLHKALPPGNVGKWAM APIPPPFPQPGKSVTICWKPASS ENRSNLLEIFLRELISNASDAAD KLRFRALSNPDLYEGDGELRVR VDEVLSPASVPYS
28551	58919	A	28726	1	1279	
28552	58920	A	28727	3	762	
28553	58921	A	28728	1	1472	MTQDELKKAVGWAALQYVQP GTIVGVGTGSTAAHFIDALGTM KGQIEGAVSSSDASTEKLKSLGI HVFDLNEVDSLGIYVDGADEIW QTCKAQRCQSPCSKTLGAQPEN PDLSQISRFPQDERRISNCSSGK AANPVLYWSKIEEKIASEPASIY SPMTLKDFSKFVKDEIGFSYTG YSRSGGGTASHGSPKSWAIGSL GRFGNEYSGWFDLQLKQRVYN ENGKRVDAVVMMDGNVGQQ YSTGWFGDNAGGENYMQFSD MYVTTKGFLPFAPEADFWVGK HGAPKIEIQMLDWKTQRTDAA AGVGLENWKVGPGKIDIALVR EDVDDYDRSLQNKQQINTNTID LRYKDIPLWDKATLMPRIPTQR YGLAKA/SLEAD/VRY/MANAM GPEGVRVNAISAGQTRTLAAPG IK\DSRK\MLAHCEPVTPIRRTVT IEDVGNSAAFLCSDLSAGISGEV VHVDGGFSIAAMNERDPFTDL HRYRMNLNMMNYGAQRNM

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28554	58922	A	28729	2	419	RPRPRPRHMLQGTHRQRHLHA GPGVARRRWGGMARRAARGR PRLRLCIFSRSRQLGLRLRFLSST VNEGDQVKTVA\RSGHFCGGLS SFSFSSSFSSGKKRPSNSPGSMR LGSPPSGAGRAGGIVTVAC*AR LSTCNTKQ
28555	58923	A	28730	725	2804	
28556	58924	A	28731	661	1218	DVREGDRDPFMIKVHSCVFVDF AKTMHDGA/SVSLRGNLISHKG EDRY/VFRDKSGEINVVIPAA/V FDGREVQPDQMINISGIADKLP VIAPTNATSKLKLASQPEDDSEI YDGCNGAQPGDYWFAAFVSG MFSRWLAKTILSRHILSVTIRSC KNGEWLAVGGAENGAYSDSR VAVMLLLSAWGLFDF
28557	58925	A	28732	1	624	
28558	58926	A	28733	1	1281	
28559	58927	A	28734	114	266	
28560	58928	A	28735	1487	1570	
28561	58929	A	28736	1	3402	
28562	58930	A	28737	1	2466	
28563	58931	A	28738	372	647	SGWSWNTKFPTGGFRWPAQPG TELESSQPR*LVMPATTSPFRAL DVCEYLPACVAVISGCHPSRFA RSYVSAPD*QNVQLTYPHIVLN RHL
28564	58932	A	28739	1	2235	
28565	58933	A	28740	3	293	
28566	58934	A	28741	737	963	
28567	58935	A	28742	3	282	RRLRASGCIDKLPSG**YARPAR *DPAPGFR*STPVRKCDQTRSPA MKVIAAADRKLWCGAICPLSA KPPAGRAPNAPAAPASPNRPMT PSL
28568	58936	A	28743	2	289	
28569	58937	A	28744	1	1662	
28570	58938	A	28745	421	2634	
28571	58939	A	28746	134	954	
28572	58940	A	28747	1036	1383	
28573	58941	A	28748	2	589	
28574	58942	A	28749	1	801	
28575	58943	B	28750	14	499	
28576	58944	A	28751	3	916	
28577	58945	A	28752	3	589	
28578	58946	A	28753	1	1675	
28579	58947	A	28754	1	522	

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28580	58948	A	28755	1229	1660	LMVSGFLTSPKDHERIIVAKPEQ FWKLRQVMFMAIVISLPTIGER FSPFLLKSPLIRPSRCGTTDFISG LTARPEFSQSRMVLIAASTITSL MCAGSFLPIRPLASICSLNATTS **LPFSSGRDSSRKRRTQAITCSP RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF NSIWSCASAILGNLGILTGSPPL ALCRTLCLTYPI*CPRDAKALR RPRECVIRHD
28582	58950	A	28757	1	850	MPVMFLASLSGKHQGHHFPKG ERGKFKIKERGTVATEDRRSGD STFYAIQPTRRQKRVYGLALLL QLHRRRQNLNIDSVSSVGLAAL VTAFIGVDFFANGEQTYSQPLW TWMSVGDFNIGFNLVLDGLSLT MLSVVTEGYSR*EHRPTPSQPR YISSRLSASTRTTM/PGDEQVGV SEEARVALSDHREHGQRQAVQ HQVKTDVKVAYRHPRPQRLAV CLLAVSEEINADKGGYQRRQA HRAY
28583	58951	A	28758	20	282	
28584	58952	A	28759	38	966	RDGLESRGRVCSLRTAFQRSSS EAFTSDLQAAELQNRASNRPAR IGHAHLVIFPVQSSWM*RKLAS PRNNLVIPQEKALKEYIKIGNLV MSLAAAPLNR*GLL/IEWNDND GGCKGACDRVPHQNVTALNLR DQCINGECYDEVLFHGLEEYIN NLQGDGVIVLHTIGSHGPTYYN RYPPQFRKFTPTCDTNEIQTCTK EQLVNTYDNTLVYVDYIVDKAI NLLKEHQDKFTTSLVYLSDHGE SLGENGIYLHGLPYAIAPDSQK QVPMLLWLSEDYQKRYQVDQ NCLQKQAQTQKDCVLLIFAKQ
28585	58953	A	28760	1120	1335	
28586	58954	A	28761	846	1245	TVRKRGTRHPHGSRRTLSLPLR HSSDRCNRTRSADRSTGPRL/A QPRYISSRLSASTRTTMPVTTES MVSDRPSSTRLKPMLKSPTDIH VHSGWLYVCSPVAKKSTPMKA GTTAGRPTEPTPTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	A	28763	188	322	

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28589	58957	A	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE TTNRPRKVKIRHPVASFFHLFFR VSAIIVCLLCELLSSSFITCMSKK WLAVVIVGVVLQGANLYGYLR CKGQEVRETFAEPSLQATQMK LKRARLADDLNEKIAQRPGPM ELVEKNILPVDSSVKEAIIGKTL KIYYLGAPAEAATKEDERTTSG PGHHATNYHFLLKFDFYLSWL HFVHKDAILSGHPLVRLLSTRV LRGPNDVFHGVSSVDSVLAIFV LAEPMGSLSASLEN
28590	58958	A	28765	1	3219	
28591	58959	A	28766	3	245	
28592	58960	A	28767	2	1193	CANQLRDCLVIPTITGLVRLVV AGANGDRLGQPVTGADVRLSR CRKVMPSRSVEMGLVPSSSVIV TVLPLIGFVLLAFSRGRWSENV SAIVGVGSVGLAALVTAFIGVD FFANGEQTYSQPLWTWMSVGD FNIGFNLVLDGLSLTMLSVVTG VGFLIHMYASWYMRGEEGYSR FFAYTNLFIASMVVLVLADNLL LMYLGWEGVGLCSYLLIGFYY TDPKNGAAAMKAFVVTRVGD VFLAFALFILYNELGTLNFREM VELAPAHFADGNNMLMWATL MLLGGAVGKSAQLPLQTWLAD AMAGPTPVSALIHAATMVTAG VYLIARTHGLFLMTPEVLHLVG IVGAVTLLLAGFAAL*Q*K*HP RHPKHRNAG**TRVLQRGAGC AGAIRVTDHFRG
28593	58961	A	28768	3	2191	
28594	58962	B	28769	1	2263	
28595	58963	A	28770	1089	4965	
28596	58964	A	28771	41	249	
28597	58965	A	28772	533	709	VSFLIVSSSLIALWSERQFVIISV LLHLLRSALLPTMWSILE*VWC GAEKNVYSVDLG
28598	58966	A	28773	2714	3599	LGSQWH*IYKLPWAVWSFSQY
28599	58967	A	28774	45	188	GKVQCHRGLIHVNWLPPVKKF *LRQKGKPTSSSQETPKTEPGRL LKP
28600	58968	A	28775	722	856	GNDLCPKTIRTGDAWCVPGTT RKSAWK*GKISGSLSFLPVRDG

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28601	58969	A	28776	474	1338	PANQKKPRTRWIHSRILPEVRR GAGTIPSETIPNNRKGGNPP*LIL *GQHHPDTKTWQRHNKK*KFQ ANIPDEH*CENPQ*NNGKPNP\E HSKKLIHHNQVGFISGMQGWF NICKSINIIHHINRTNDKNHMIISI DAEKAFDKIQHPFMLKALNKL GIDGTHLKIIRAIFDKPTANIILN GQKLEAFLLKTDTRQGCPLSPL LFNVVLEVLARAIRQEKEITGIQ IGKEEAPQKQQRLFCRYYHGK RAPQLLITHLEEDDEWDIIRYY NVMSEEEIKRMKEIVKPKII
28602	58970	A	28777	2289	3225	LTNQNKSRTRWIHSRILPEVQR GAGTVSSETIPNNRKRWTPP*LI L*GQHHPDTKTWHRHNKKRKF QANIPDERQCKNPQ*NTSKPNP AAHQKAYP**PSQLHPWDARL VQHMQTNKHNPSHKQN\HDKN HMIISRDAEKSFNKIQQPFMLKT LNKLGISGTYLKIVKMHTMSSS HLFYLALCLLTFTSSATAGPETL CGAELVDALQFVCGDRGFYFM EQCTMAVSIRGRELLGPSEQEM LHKESGKQRQKANTIPVTSKIV HLALYATLLLFVMEQFLGESHK SREIFSFEQQISELGKESMKFSEE KEKE
28603	58971	A	28778	1177	1272	
28604	58972	A	28779	480	766	SSEIQHWFQGQPRWSRCRVSGR RHEASTVLPLCFLLPQNSSSMQ LG*NRSMP/HVSESSRTLVL*EV TKHQVSSNFKMRDKDRSGRAS SLRKHRRE
28605	58973	A	28780	1	1344	

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28606	58974	A	28781	971	2314	PTNQKKSRTRWIHSRILPEVQG GAGTIPSETIPINRKRRNPL*LIL* GQHHPDTKAWQRHNKKEEL*T NSPDEH*CKNPQ*NTGKPNP\EH IKKLIHHDQVGFIPGMQGWFNI HKSINVIQHINRTKDKNHMIISI DAEKAFDKIQQPFMLKTLNKL GIDGTYLKIIRAIYDKPTASIILN GQKLEAFPLKTGTRQGCSLSLF LFNVVLEVLARAVRQEKEIEGI QLGKDEVKLSLFADNMIVYVE NPIISAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTKSQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKTILSQKNKT GGIMLPDFKLYYKPTVTKTKW YWYQNRDIDQWNRIEPPEIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHHP* GSIPSRSLLVATTPTRGVTAALE
28608	58976	A	28783	1	1938	
28609	58977	A	28784	1389	1499	
28610	58978	A	28785	1	351	
28611	58979	A	28786	1	329	KNLDEKLLPASSSSCRIWATSP VHHLWQVLKKILF/GLEPYEIST LFEQRQAM/LQSIKEGVVAVDD RGEVTLINDAAQELLNYHNFIR SRSLPVFVLASACGSGTRRRRA
28612	58980	A	28787	1	419	VRPGHLLDIDDTDMPSLRYSDP EAQRIGQPFKGDDILKALNGEE NVAINRGFLAQALRVFTPIYDE NHKQIGVVAIGLELSRVTQQIN DSRWSIIWSVLFGMLVGLIGTCI LVKVLLG/IIFG*TYKSQLFEQR QAMGRL

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28613	58981	A	28788	1	1795	MWIISCVMKRTAMNCVLWRK RRRKVCASIFTGKNRANQKRD NVELFDARCRPLNDAADTVRY LPVLTVQLLDKQPRLTVLKKIL FGLEPYEISTLFEQRQAMLQSIK EGVVAVDDRGEVTLINDAAQE LLNYRKSQDDEKLSTLSHSWSQ VVDVSEVLRDGTPRRDEEITIK\ DRLLLITTVPVRSNGVIIGAISTF RDKTEVRKLMQRLDGLVNYA DALRERSHEFMNKLHVILGLLH LKSYKQLEDYILKTANNYQEEI GSLLGKIKSPVI\AGFLISKINRA TDLGHTLILNSESQLPDSGTAA CGQSLNVLYQRIVGERKLHTGS LMSAAGKSNPLAISGLVVLTLI WSYSWIFMKQVTSYIGAFDFTA LRCIFGALVLFIVLLLRGRGMRP TPFKYTLAIALLQTCGMVGLAQ WALVSGGAGKVAILSYTMPFW VVIFAALFLGERLRRGQYFAILI AAFGICTATQRNRLLPCKNQPC KANQYQGTGDVLNQLHIDFRA FSGVMVAGSRQIFANEISSGAS NVGVVIFSTQDSANTFNVLNAS GGSRSVYPVMSDDMNGSSWKF STRMQKIDPALSVTSGQLMSHV
28614	58982	A	28789	190	2058	
28615	58983	A	28790	199	293	RYPPAETELS*RLCRLLR*STTV RL*LCRPL
28616	58984	A	28791	685	1557	
28617	58985	A	28792	1	2850	
28618	58986	A	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR TATTQRHCRRMHMMTIGYQFQ PGALVR*SRANHFPGRGDVNLS SRYSNAPGRRHQHQMRRGFVA RSQ
28619	58987	A	28794	409	1305	

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28620	58988	A	28795	379	1703	LKTVLVDGVVKAEKLVEGAKA VLRQAINGDLDWKAKRQPKLE PLKLSKIEATMSFTIAKGMVAQ TAGKHYPAPITAVKTIEAAARF GREEALNLENKSFVPLAHTNEA RALVGIFLNDQYVKGKAKKLT KDVETPKQAAVLGAGIMGGGI AYQSAWKGVPVVMKDINDKSL TLGMTEAAKLLNKQLERGKID GLKLAGVISTIHPTLDYAGFDR VDIVVEAVVENPKVKKYPSAG VFHQLYCRDVVIPMFAIYTFGP QIVGLLGLGVGKNAALGNVVIS LFFMLGCIPPMLWLNTAGRRPL LIGSFAMMTLALALLGLIPDMG IWLVVMAFAVYAFFSGGPGNG FNRVKEEFDHERFLVALTNYGT AMCAFEDAARYAN/LARAVWR GYWSFPVDSGKIRPHGDQIKLH EKHAV*SSVESRQRHHHLWRC SDVQILLRQCGI
28621	58989	A	28796	713	902	CRLARPSPLKRCFQFCSTTHSCI PPPLAATRWPVRRRWRPSMCC WSRTYR\PG*AKRRYTSPA
28622	58990	B	28797	1	1521	
28623	58991	A	28798	348	599	RHFQRSLSRSSDSNP*LDPTLFA SALASRQRVTESWSERHPDPLQ VRRKTEDVKTTPPFLQQSAHRS VNIVLWIRGFSPTLLV
28624	58992	A	28799	582	732	
28625	58993	A	28800	1	1443	
28626	58994	A	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA SGG*TGETDAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	A	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP GLAITPGQQLFITIKLWNDDH\K RPREALLDSLKKLQLDYIDLYL MHWPVPAIDHYVEAWKGMIEL QKEGLIKSIGVCNFQIHHLQRLI DETGVTPVINQIELHPLMQQRQ LHAWNATHKIQTESWSPLAQG GKGVFDQKVIRDLADKYGKTP AQIVIRWHLDSGLVVIPKSVTPS RIAENFDVWDFRLDKDELGEIA KLDQGKRLGPDPDQFGG
28629	58997	A	28804	1040	1079	
28630	58998	A	28805	300	567	SAGFKKSGTRHCDVRPGACGT TLYQRR*VH*\WSTVH\KPETSS SKMHGQRGSGLLAKSLVANVI CSLIRNPLPIMPMPLCAFVSLKM IKKRPRRH

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28631	58999	A	28806	167	327	KNNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTDRRTN SPAYLSEL
28632	59000	A	28807	1	1197	
28633	59001	A	28808	1	4104	
28634	59002	A	28809	1	1368	
28635	59003	A	28810	82	1143	
28636	59004	A	28811	72	212	
28637	59005	A	28812	1	1078	MKDVTLVRPQDAGANTCAHIL SQLPHLQLPTLETLGLINALGY APGDMQPSDSATWGVAELQHE GGDTFMGHQEILGTRPLPPLRM PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQAVAIGDNL EADLGQVYNITANLSVISFDDAI KIGRIVREQVQVGRVITFGGLLT DSQRILDAAESKEGRFIGINAPR SGAYDNGFQVVHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ RVFAIFAVAIDITQVINIQYCRC QQAACGRRKDQCRNQSKENQY GNITQTDITIRTIAHGV\VIAAMI DNPPRIRKPTKSAS*LWWPLFY LLAVSLFTLWNRYRVFHGLSAS SSPLRPTPY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVDHNG YSGNACTRLHHAGGIRQ**PNF GYSPPASSCGQVSQNSS
28639	59007	B	28814	1	2703	
28640	59008	A	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWTITTAVCV SSCRRWKKPAALVRPLPPASAP GFITTSAKPCCASRNG*KSSFQR TLHVSRHQSRTS*SPQVDTSDN SSEIVNNQAPTARTGSGLRVAV LEQRVQEPLAANAPPQLRVSAI NAAS
28641	59009	B	28816	430	823	
28642	59010	A	28817	1	2667	
28643	59011	B	28818	204	2659	
28644	59012	A	28819	1	2817	
28645	59013	A	28820	1	1089	
28646	59014	A	28821	1	1891	
28647	59015	A	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRDALPTEE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPYYELPERRDPV SSAGALFVSRWIVERSCADKFR VFCGASGFR

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28648	59016	A	28823	1	1030	MMCIMYRTASSLANQYHIDSE QARRGSQNAFDVNFEAWQLEI NHVLEAASAQSQRNYQISALVF ISMIIVAAIYISSALWWTRKMIV QPLAIIGSHFDSIAAGNLARPIA VYGRNEITAIFASLKTMQQALR GTVSDVRKGSQEMHIGIAEIVA GNNDLSSRTEQQAASLAQTAA SMEQLTATVGQNADNARQALG TGKNAATTAQAAAVQFIDRCQ ADFTRGAYRYRSGTYFICQYLT VTVSGIDAHQRGQTDTQRILLQ LFLVQFDTHRQTLNDFDPVTGR ILRWKQLDRAAGDITGHRTDN TSTLQRQPGVTYFGGSLLHGW\ *SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	
28650	59018	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLALWLKKHRFRLDQVQN FYPSPLANSTTMYYTGKNPLAK IGYKSEDVFVPKGDKQRRLHK ALLRYHDPANWPLIRQALEAM GKKHLIGSRRDCLVPAPTIEEM REARRQNRNTRPALTKHTPMA TQRQTPATAKKASSTQSRPVNA GAKKRPKAAELQCPLVMTSGN LSGKPPAISNEQALADLQGIAD GFLIHNRDIVQRMDDSVVRESG EMLRRSRGFLPTGRGLRIDYKQ KMRGTRRAGCNFNQSGQGRPS LKRGIEQTDIKKAKKQATGLAG ESMLQDDAFYAVITHAAGPQG ALPLTPQMLMESPS\ATCSA*RR TPGWAGTPTSSPAKRC*LSALRI TSSGSTPSCSRRHWRKRARRSD ACHHSRFSPTVWPVTQPKKGR
28652	59020	A	28827	1	1392	
28653	59021	A	28828	1050	1154	
28654	59022	A	28829	1	2649	
28655	59023	A	28830	59	511	
28656	59024	A	28831	1	2421	
28657	59025	A	28832	4594	4770	PSTSTIHAYVSGKSRISPHTREA MI\NDHSKRAWLYALRRRAGR TRHRCPGRTGRQRLL
28658	59026	A	28833	1	727	
28659	59027	A	28834	1	3069	
28660	59028	A	28835	1521	1841	FLPKSLGDSSGESRKHRRRRRA FSPDQHPAGNYRTRLSARPFV* RCLYYSR*ARRGNYRQH*TTSP ALYQAASPFQ*SIAG*RAGKTR YRSSVYLCVDHFDHSGSW

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28661	59029	A	28836	1	1644	
28662	59030	A	28837	1	1245	
28663	59031	A	28838	1	1518	
28664	59032	A	28839	3	491	
28665	59033	A	28840	1092	2827	
28666	59034	A	28841	162	1760	
28667	59035	B	28842	1	3378	
28668	59036	A	28843	434	763	
28669	59037	A	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAKC ETRMYPEEPVYLPPRYRGSIVIH SIAF
28671	59039	A	28846	855	1134	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAKR ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCVACNLCAVAWP VGCISLVS
28672	59040	A	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARHNAQQ EDALVEKAKQ/VTWRLLAAGV CLLTVSS/VARADSLDEQRSRY AQI/KQAWDNRQMDV/VFIHAM PTNTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCR ELSRRLLRLHAQYQNTKRVHT QFSGYKTPEMANTAVPTISSQR RALFNPH
28674	59042	A	28849	1	1247	
28675	59043	A	28850	533	1029	SKSIMLLCRSVVSMIRRSTVAA FTLAAISVARSVALNLIIRDIGM QAMPLCRSTTGRNRWTSSAKR TILR*RQRILPLTPC*HRMFRSFL KKILSDGKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIQPAQ KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	A	28851	749	1050	SPHMPGITAGTPFSVPLAISAPSI SAKSLPGKTA*AWPNIMALTPG ISLR**TEFSAITLYGSADSPECA RTT/INIGTFLAHFRHVFAHGFG NIIHRHFPG
28677	59045	A	28852	260	717	RQLRTELSAGIAAFRTGNAPAIL RFMKLAPPP*WRRKPLTGV*RV *RGRDSVR*VAFVPTVSAIQQL DPRSLLQQDAFKKAGLDPEQPP KT/WQDLA/VLCRETESLRHEV RLRQRLAGLDPTGKL*AWNGM MPYDADAKDAPQKPLSAEPAC
28678	59046	A	28853	776	2730	

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28679	59047	A	28854	383	1367	RPTCWTSIEWVRRVRTAALRSS GKTWVFCCRRRIAGELMLTNR HTGGVMVTTFRASEAFAGALE LTGKATLVALINRCIGAVIRYM LIAVIPDIFQRLQVVLNVWILAV ANETTVRQRRVRRFKVDLVVR VHLLLHIEVETVGVVTFIGHAR HHAKLSSIETAEAIAQVFTRRA VETETITRFFFPLIHCLTQTFNN GDTFRAKLLVVVNMLAAEQRV NGFVDADVTQRNRRTTVFEDF RNIIVSIETHATSTRYG*CVGPP AMRACSGAVQPVQWLHPGKL RQGEPSRDLVRQRPAALCLPRR HRILRGYNGNIQRRLYSTGNGL
28680	59048	A	28855	1	1477	
28681	59049	A	28856	1	793	
28682	59050	A	28857	1	1020	
28683	59051	A	28858	1	613	SAGDGARIEQFDRKGMVNNKF NYFIMSKLAEAGIPTQMERLL\S DTECLVKKLDMVPVECVVRNR AAGSLVKRLGIEEGI\ELNPPLF DLFLKNDAMHDPMVNE\SYCE TFGWVSKENLARMKELTYKAN DVLKKLFDDAGLILVDFKLEFG PVQGEVVLGDEF/SPDGSRLWA QETLEKMDKDGFRQSL\GGLIG AYEAVARRLGYT
28684	59052	A	28859	1	1002	
28685	59053	A	28860	1	422	
28686	59054	A	28861	625	750	RNVQALQGAHGTGGALTDPA* QHLGTLCADLL*NGLSPSPRD
28687	59055	A	28862	1	1449	
28688	59056	A	28863	105	297	
28689	59057	A	28864	55	423	DRPQRNRATLMQLYSRGSPGIR RLEHRFEKVQGKPGFEVFIPGF KQGKLGRPLGVKALVFGIDTGL FQLQAVKNLDGF*FDEASASQP GSDNILRELRVRATGRADGSGT GFTEDANSFTSYR
28690	59058	A	28865	1	2340	
28691	59059	A	28866	314	696	

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28692	59060	A	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK CHGINPLRSWVGTG*VE*EEKY NMQT*E/LENWKPISNLHDMSS SHSKTLGYKRLTKSNPISCQILL YKSRSKGRKNQRSTRTHCHHPS PKIYSASAKEPWILATNLPVEIR TPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDI MLLIALMLQLTCWLAGVHAQK QGWDKHFQANTVRNRNVLST VRLGMEVLRHSGYTITREDSLV AATLLTQNLFTHEEAPANSVPA AAVIRRVQALIGITGRKAHAGG SWNGTASSDNFPNIFILPQNDF MALAAAVAPPELEALLAAGKV SVKIQEPCDEILFSRAKVWNGE KWACVTIVGGHTNIVHIETHDG VVFTQQACVAEGEQESPLTVLS RTTLAEILKFVNEVPFAAIRFIL DSAKLNCALSQEGLSGKWGLH IGATLEKQCERGLLAKDLSSSIV IRTSAASDARMGGATLPAMSNS GSGNQGIGTELNVSCRFPATNL FVHDPTQQAMQRNQRRFAVQT FPVWRVAQHCAVRPFRQRIGQ LRDIFHLKGDQFTNRPAKIVAF
28693	59061	A	28868	2095	2722	
28694	59062	A	28869	789	2509	
28695	59063	A	28870	57	440	CSWDPQDPHGILQGAGKEDSQ AQKTTARQKRKTRKTATRQKK HEKQSEESTNEDT*ARKVEETQ HKHDAESTSGSVIQGCVQLFTQ SFTATPAASATTATRPTILCSSR ARAGYPSTTGVSRRESPL
28696	59064	A	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK KGHFVVAHPAF/P/DQFLHAAM DIKQPVISIDNLLAIHKQAEVTR FIGGDMQRADRDHPRIAVALID KRIRFGISRRFRAQSIIHRIFAQR MHIFRPVIGQHQATGNSRLSAS TQRLHHNPAFFGPFH
28697	59065	A	28872	1609	2112	HQPVLTVVMVPVSPLIIRADNP FRDEVGFLCQPAVTVIPVKIVR VTGDTVIRPHAEGAVRVQLRV GQAVTCRVCGIRDADIQIRCGG VNAGQPAGGAVAVTPGLARAA DADEFAVVVPGVIAVRQQAVQ VLAL*LPGRGISGGEFITAEVRS VSRCRRSRVYSTRGIL
28698	59066	A	28873	2	712	
28699	59067	A	28874	337	383	

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28700	59068	A	28875	65	436	REVWEHAKRMLGDSSLDMGM DDELTYMVAYEYIGRLGKTATI HWKVKSSPSMVWSASVWKKM ALR*LSRTLRPNQEHSLS*ASVP ELKCAASWTKRKKNSTFIASSA IRLTLTWKPKPFLSRL
28701	59069	A	28876	206	403	
28702	59070	B	28877	1	2046	
28703	59071	A	28878	1	1335	
28704	59072	A	28879	1	974	MEAPPIEDVSSRDLNRRRNYGH PADLFWFYSVLRALPEVYASSD AHEKFVKDFVAAWSLNVLYQR IVGERKLHTGSLMSAAGKSNPL AISGLVVLTLIWSYSWIFMKQV TSYIGAFDFTALRCIFGALVLFI VLLLRGRGMRPTPFKYTLAIAL LQTCGMVGLAQWALVSGGAG KVAILSYTMPFWVVIFAALFLG ERLRRGQYFAILIAAFGLFLVLQ PWQLDFSSMKSAMLAILSGVS WGASAIVAKRLYARHPRVDLL\ SLTS\WQMHVCRQLASQLPLSH GAMPRCRRPGHSSNPDRLANVI ARRVLRGMSNRQPVSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDLNTQ LWISTNAFRFGN
28706	59074	A	28881	568	717	
28707	59075	A	28882	1760	3092	
28708	59076	A	28883	1	1206	
28709	59077	A	28884	1	575	MSGSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKQPLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPPSRWDDGIS GIIADYSITAQTQHAKLNTEDD/ SNESTGSVWQGLWRLQDD
28710	59078	A	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YYAWRA\LPSLKAKLALGEDY LNSDIFDGFNYVGGSVSTDDQ MLPPNLRGYAPDISGVAHTTAK VTVSQMGRVIYETQVPAGPFRI QDLGDSVSGTLHIRIEEQNGQV QEYDISTASMPYLTRPGQVRYK IMMGRPQEWGHHVEGGFFSGA EASWGIANGWSLYGGALGDEN YQSAALGVGRDLSTFEA

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28712	59080	A	28887	491	681	PTGHRAQKKWNT*TRHSNSY* KNFAKKLI*GDIREKLQKLEGF AGMNATQLIEVATEVYINCDQE AKKETEQRLRKKANLLAAALT KRKINIVKGRECSHGCGHGRGQ VEQRAKRWLRLRGGWVKAFP VRTEKAREVTKVLLRDIIPGFGL PLTLASDNGPAFIAKIVQELTQL LKIKWKLHIAYWPQSSEKVEH MNQTLKQLLKKFCQETHLRWD QVLPMVLLRVRYTPTKQTGYS PMRSCSANLK
28713	59081	A	28888	1	963	
28714	59082	A	28889	123	593	KRQVLAGFLITPRRLPKNWTHC WCWWSM/PAQVKQVLFGETG VAQHLKPGTAVMVSSTIASAD AQEIATALAGFDLEMLDAPVSG GAVKAANGEMTVMASGSDIAF ERLAPVLEAVAGKVYRIGAEPG \QVRP*KLFTSC*RAYILLPEPKR WHLQPVR
28715	59083	A	28890	263	467	
28716	59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPLYT GLPRGPHGRAAGNPVDQQFAA GDLGLSPHADAHPGGTDDVRW CLIST*KRWDSGV*AGAGQYSG WRRRSLRWR
28717	59085	B	28892	1	2118	
28718	59086	A	28893	1084	8334	
28719	59087	A	28894	2029	3313	
28720	59088	A	28895	1168	1236	
28721	59089	A	28896	1	284	
28722	59090	A	28897	1	1188	
28723	59091	C	28898	20	878	
28724	59092	A	28899	1904	2281	CSAYAGLHPFWLKSTRFCTHIL APATAISPNTTIDAPPITAAGMV *ISAPNFGEKPNSMAMTAAATN TSVE*TLVTAITPIFSA*VVTPLP PTEPESIVARPSPTNARPIYGSIL RPVIPATALR

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28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV RLCWNLISLGLWSCFSKGWVT TPTTLSCPSPPRRGRMAPWAW GRSRARMCWSWSWSTRPSRPC AVRWSWSSGATGSCWRRPVST APPRPPPWRPAAPTPAPLWART RMPSHWPSTTAPAATAY*/DPD AGYQPTPLAAPAEPGSKYSLAS LDRGQGRGGGGGGALEYVPKA VSQPRRHSRPVPSGKYVVDNSR PPTDLEYDPLSNYSARHLSRAS SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSKPSCLMWAASCRN PASLLASE*TVSNA*IPAERAAC KMEQRANSSSVPSGERSVRRLR T*SSAPRAIPIKRSEA*AISTARVI PSGDSIAASRPVLPGSRPQAFSIR RISFSISRTS
28727	59095	A	28902	1	2916	
28728	59096	A	28903	1	2001	
28729	59097	A	28904	179	324	
28730	59098	A	28905	1591	1806	
28731	59099	A	28906	531	949	
28732	59100	A	28907	44	477	
28733	59101	A	28908	161	333	
28734	59102	A	28909	1	394	MEGVAFLTFLAARAAVGNRPA SPQIVRKQREGHGGILTRDPVA FDDVAVNFTQEEWALLDISQR KLYKEVMLETFKNLTSVGKSW KDQNIEYEYQNPRRNFRSLIEK KVNEIKDDSHCGETFTQVPDDR LNFQEKKASPEVKSCDSFVCAE VGIGNSSFNMSIRGDTGHKAYE YQEYGPKPYKCQQPKNKKAFR YRPSIRTQERDHTGEKPYACKV CGKTFIFHSSIRRHMNSHWEKP YECSKCDKAFHSSSSYH
28735	59103	B	28910	1	534	
28736	59104	A	28911	238	434	LPCKIHTPNHGPLKNIPSTKN*Q RRRNTSQR*LRHQPFFSSASRPG SRLRFAIGPLQPAEAGMVT
28737	59105	A	28912	358	878	KLCHIACIHSVSFQCESFHVFTG FLSSVCPFMKSKIFDRSEGFPKL LTLIGVLSSVSPFMISKGSEGNK GFPTLLTLIGFLSSVRFFMYLK* LGRIKAPPTYLTFIRSLYRVHYV CLCPFMNSKVLGRSEGFPTFLT CIGLLSIVCRFPTLLTLIGFLSSV SPYMISKGTGMR
28738	59106	A	28913	1382	1416	

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28739	59107	A	28914	1	333	MFQDPVAFDDVAVNFTQEEWA LLDISQRKLYKEVMLETFRNLT SVGKSWKDQNIEYEYQNPRRN FRSLIEKKVNEIKDDSHCGETFT QVPDDRLNFQEKKASPEIKSCD SFVCGEVGLGNSSFNMNIRGDI GHKAYEYQEYGPKPCKCQQPK KAFRYHPSFRTPQRDHTGEKPY ACKECGKTFISHSSIQRHVVMH SGDGPYKCKFCGKAFHCLSLYL IHERIHTGEKPYECKQCGKSFSY SATLRIHERTHTGEKPYECQQC GKAFHSPRCYRRHERIHTGEKA YQCKECGKAFTCPQYVRIHERT HSRKKPYECTQCGKAL*YSLKS GSLMP*ALFFWLRIVLAMWAL LWFHMNFKVVFSNSVKKVIGS LMGMAWNLQITLGSMAIFMILI LPIHEHGMFFHLFVSSLISLSSGL
28740	59108	A	28915	1619	2353	
28741	59109	A	28916	1	1252	MSYSVMFALLLLTPLLFSLLCF ACRKRRLSATRTVTVLHSLGIT LLLILALWVVQTAADAGEIFAA GLWLHIDGLGGLFLAILGVIGFL TGIYSIGYMRHEVAHGELSPVT LCDYYGFFHLFLFTMLLVVTSN NLIVMWAAIEATTLSSAFLVGI YGQRSSLEAAWKYIIICTVGVA FGLFGTVLVYANAASVCGTDH GGRMMRSWNGGQLISKLLAIT P\DKLVLDFGSQAEDNIAVLKA QHISIS\AETQGAKVEFTVDQLQ QSEYLQLPAFITVPPPTLWFVQR RRYFRISAPLHPPYFCQTKLAD NSTLRFRLYDLSLGGMGALLET AKPAELQEGMRFAQIEVNMGQ WGVFHFDAQLISISERKVIDGK NETIPTPRLSFRFLNVSPTVERQ LQRIIFSLEREAREKADKVRD
28742	59110	A	28917	2	2282	
28743	59111	A	28918	518	1046	
28744	59112	A	28919	8	893	
28745	59113	B	28920	1	3129	
28746	59114	A	28921	1	1284	

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28747	59115	A	28922	3612	5412	PGLKHQNNGHRGPDAETKGVT RDFGPNAKPLAG/VRLN/LERLR DTHHIDVAPLVARLDQMMESV SQLLQLARAGQSFSSGNYQHV KLLEDVILPSYDELSTMLDQRQ QTLLLPESAADITVQGDATLLR MLLRNLVENAHRYSPQGSNIMI KLQEDDGAVMAVEDEGPGIDE SKCGELSKAFVRMDSRYGGIGL GLSIVSRITQLHHGQFFLQNRQE TSGTRAWVRLKKDQGAYPMSE KVVFSQLSRKFIDENDATPAEA QQVVYYSLAIGHHLGVIDCLEA ALTCPWDEYLAWIATLEAGSE ARRKMEGVPKYGEIVIDINHVP MLANAFDKARAAQTSQQQEW STMLLSMLHDIHQENAIYLMG VFIMLIFFPAPVASEKPLSPDCW TTTHTLRMIGENSGLVSYMREK AVSPNCWNVIHYSGFLHLELLS SYDVDVNQIINTICEWISLIKTR GVRRPEFQTLLTGSGSEHGERFI MNRPTLFFTDLAFHVDRFTQYV HDTAQSRFTYRDFNRVFEVFYI QTATQTVGGTHCDAPGWWFP GAVQSVPAAALIAVAAAPGLA SFLPFARRVPRTVVALLAQAAA YADGMPARADGSFNSP
28748	59116	A	28923	1	2910	
28749	59117	A	28924	470	723	PGFGDARKLISLNFFIWV*TA*I M*P/LAGSDFVYRNS*RNVFIAQ TLQLRSRQPVTMHHATRAFQT EHNLILRFECCEYSRYLFT
28750	59118	A	28925	599	1117	
28751	59119	A	28926	279	455	SLSHSSGRCSRGGISFWVVWEF GPVACLAASVV*L*VSVVWLW LSPSGQGCLGCRVWL
28752	59120	A	28927	1	2913	
28753	59121	A	28928	1	2328	
28754	59122	B	28929	55	327	
28755	59123	A	28930	9	107	
28756	59124	A	28931	1	2106	
28757	59125	A	28932	1	1123	
28758	59126	A	28933	260	709	
28759	59127	A	28934	467	631	LEVIEAPQPNWS*SVQQSACST WPGCWVDLEDPQVWVWYEW TTKRASLLPIFQD*LKALRKAQ VWAFAS*STWPGCWVDLEDPQ VWVWYEWTTKRASLLPIFQD
28760	59128	A	28935	989	3010	

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28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	A	28937	1	1006	
28763	59131	A	28938	185	384	
28764	59132	A	28939	2	615	WAFRVIRFIVTANWSLKAVWM RRLIVVAALLTLRTVPMRQLNR LLLITPSLSRHMVSTGPATSCVN RGFLSPTVVSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGEE QISLGVRNTSPDVPYLIQSWVM TPDNKKSADFIITPPVFVLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRAVPSTTKRKEGNTLKIAHK RMITN
28765	59133	A	28940	1	1686	
28766	59134	A	28941	76	981	
28767	59135	A	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPAHRQWSASYWRSA *SSSFRLNKKCHTQNHSNCIKM ARE

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28769	59137	A	28944	1	2539	MPIEEPALRSWQRPFLKWAGG KYSLLPELDRLIPAGKRLIEPFV GGGSVFLNSDKHERFLLADVSA DLINLYQMLAVVPDSVIYEAM KAFRHLNDAENYTLIREAFNAQ RLDAVERAAAFLYLNRHCFNG LIRYNLDVFFNVGFGKHKQMT NNESKGPFEGLLVIDMTHVLNG PFGTQLLCNMGARVIKVEPPGH GDDTRTFGPYVDGQSLYYSFIN HGKESVVLDLKNDHDKSFGHT GPLKDAPAYDTIIQAMSGIMME TGYPDAPPVRVGTSLADLCGG VYLFSGIVSALYGREKSQRGAH VDIAMFDATLSFLEHGLMAYIA TGKSPQRLGNRHPYMAPFDVF NTQDKPITICCGNDKLFSALCQ ALELTELVNDPRFSSNILRVQN QAILKQYIERTLKTQAAEVWFT PFSNKYNGHRIARTDKASMPTV YSESLFVEGIIRASTSMTTKQGP SLRTGRTLRKFCPLSETAATTDS SIFPSKFTPTASRLPGFSFIRSPK MTQSVLLPPGPFTRRQAQAFTT TYSNITLEDDQGSHFRLVVRDT EGRMASVQTRPPADREAFTRIH LPEHTLYPHTPAIAAGVFIDGDI PMTTQTQHDLAPANQPEFELTV TPVPDEQRIDFWPQYFGAIPQW LLLEPHIFAWMDRFCEGYSGGI WSFYTLSNGGAFMSPEPDNDET WRLFNCLNATMPPYRMTCGTV
28770	59138	A	28945	907	1917	
28771	59139	A	28946	1	3033	MVWGFTCSTTATLEGQSTAAS SRTSNQDISASSQNHQTKSTETT SKAQTDTLTQMMTSTLFSSPSV HNVMETVTQETAPPDEMTTSFP SSVTNTLMMTSKTITMTTSTDS TLGNTEETSTAGTESSTPVTSAV SITAGQEGQSRTTSWRTSIQDTS ASSQNHWTRSTQTTRESQTSTL THRTTSTPSFSPSVHNVTGTVSQ KTSPSGETATSSLCSVTNTSMM TSEKITVTTSTGSTLGNPGETSS VPVTGSLMP
28772	59140	A	28947	636	725	
28773	59141	A	28948	1	1123	
28774	59142	A	28949	2345	3644	

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28775	59143	A	28950	34	437	CGRLLQKSGFVVSVGIDGIERL NTRRARGLPNGTACGQQFSSFR GAFCTQVAHIVFCTEGDTDQ/D ARKRERFPLRG*SPAEIQSPPAG RCCRVHDHRLFRYAGSFFQYPE HPERYRFSADAQRPHHRERRLP
28776	59144	A	28951	1	457	
28777	59145	A	28952	176	757	KPMKSTAAAADAALLSA\ERQ VIDDAAAHLSEVAQGDDVDAI EQAIKNVDKQTQDFAARRMDQ SVRRADRSDLIETFDHVCTVIFI RDGITSAEVETADTARGNVDVI RTGEVGAVCGTEETKSILQYLQ YAITKDIFATLCVLLQDGKNNV LLTHTSQVFQPHIFAESDQLRN RRIFGDRFDSPVSIRMMFGI
28778	59146	A	28953	1	1503	
28779	59147	A	28954	425	619	AGWSFLPSPAEQNRWRFPLSRF CQIPAPLQVRS*LACRFFAAYSP PLLRKSPAASMAYTTSRLH
28780	59148	A	28955	55	476	SYHALANVFYQRRMAITQVAG RQAQVFKAHLRDDVHHHIDGQ VTATESVMEGNRHAVL*TRAT NRFFQVGAQFAIARFFSLVGLL WRVLESGKIAFSATIPGRYPFLS LRLFNFLRHFDCLILRGCRKVL HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	B	28957	12	271	
28783	59151	A	28958	309	1238	GSGSCYSALVKRKWSARSLRA DRNGARRGAYVGRKFGHFGPG LAGFFSAHASNLCRRSDRAPAH YHQLLNFADPVDMMQ*KRGM VFLLLMDQRQQRVDDWRRLPS LLSVWQSCGDSGRRAPGGR*FH WRFQATVFQALAEDLRRNLQI VVATVAF/GMGINKPNVRFVVH FD/IPRNIESYYQETGRAGR/DGL PAEAMLFYDPADMA/WLRRCL EEKPQGQLQD/IERHKLNAMGA FAEAQT/CRRLVLLNYFGEGRQ EP/CGNCDICLDPPKQYDG/STD AQIALSTIGRVNQR/FGMGYVV EVIRVAAFLEPDYSHRP
28784	59152	B	28959	1	2123	
28785	59153	A	28960	1	2834	
28786	59154	A	28961	1	2505	
28787	59155	B	28962	145	494	

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28788	59156	A	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHA F*PLLGDFGCRNGVIQGRENAH LMNGGGRRVTALHFQQYRFHH LFNILTARHHLIDNANHAQIDR* RFAFMRLAGGTATHQ
28789	59157	A	28964	1	1423	
28790	59158	A	28965	1	863	
28791	59159	A	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	A	28968	1	1215	
28794	59162	A	28969	1	1678	
28795	59163	A	28970	1	4674	
28796	59164	A	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFGHQLIAGDHFF HHFQAHLVQFGGDFFQLFNLG EGQLVVSIFTPVRLAVHGVKIE TVFVGFSSLIHGSQTVLVSSASG ASVASTRGKCTIVTSGISG/VIA KND/GLPRVHGATAPSCASQFL VFAAPTPRPDRHG*RTDDSTPQ RLSSPAVEKAPTASSASGNSRN DKPLREITLITSDRPVPDAAVSP TGFWPLTIPFHRCRRMSSLPGIPI RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSGRRAPGGR*FHW RFHGHGFPGAGGGSPAKPVNR RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	
28800	59168	A	28975	904	1473	
28801	59169	A	28976	738	893	
28802	59170	A	28977	1	1108	MADTRYFGMHMSQETPASTTE AQIKNERRISPFWLLPFIALMIA SWLIWDSYQDRGNTVTIDFMS ADGIVPGRTPVRYQGVEVGTV QDISLSDDLRKIEVKVSIKSDMK DALREETQFWLVTPKASLAGV SGLDALVGGNYIGMMPGKGKE QDHFVALDTQPKYRLDNGDLM IHLQAPDLGSLNSGSLVYFRKIP VGKVYDYAINPNKQGVVIDVLI ERRFTDLVKKGSRFWNVSGVD ANVSISGAKVKLESLAA
28803	59171	A	28978	1	861	
28804	59172	A	28979	5	337	
28805	59173	A	28980	1	612	
28806	59174	A	28981	128	1742	
28807	59175	A	28982	1	2688	

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28808	59176	A	28983	361	738	FLQPFPFKREINKFIRDIANNMK TDFFSAVTLFTDCVTVMLWII*F FQRKFFLKGFI*PPLGSFYRE*IIT SLFLYLLCNIFLATHRISCDDFSF NIQHVKKFWDSCNLIRFLIRLDL SDDQTVHC
28809	59177	B	28984	1	1263	
28810	59178	A	28985	363	569	KGYSRRSGKHRQGCCNVLRLR FPDHQTAPRPMPLKRQTRAPGQ SPPGLPADPHPGQF*LPLLRGRF AR
28811	59179	A	28986	1	1035	
28812	59180	A	28987	275	721	LMVSGFLTSPKDHERIMSGEAR AILIASNSSVLVCAFRNFNKSFT DLLPSELAQSASERISFNNTLKD SGMPGSI*WLPSTMFLYILVRPF TSSDLTVSISCRVYAAPYASSA HTSISPKR*PPNTQRLLTGPVGT FWGRKPPLFPTP
28813	59181	B	28988	1	2082	
28814	59182	A	28989	1	1567	
28815	59183	A	28990	1	453	
28816	59184	A	28991	1	777	
28817	59185	A	28992	1	1431	
28818	59186	A	28993	1	561	VDSRGYPYGSRGAGKCRESERL GSESRNPGSIGLENELTAEDVAS ADMVILTKDIGIKFEERFAGKTI VRVNISDAEFLMTNRISRLKTA LFANTREISLERALLYTASHRQT EGEPVILRRAKATAYILEHVEISI RDEELIAGNRTV/ITARRDYVA GNGPLLAAERAGSIPDASAGPL CYQRRRL
28819	59187	B	28994	1	3414	
28820	59188	A	28995	1082	1297	MIMWLAAVAIREINHDSGSATF RTPRDPRTVAGKYNLGASLYK SELLA*LHSAGAGCLSCQRAKL GLGRRR
28821	59189	A	28996	1	2115	
28822	59190	A	28997	168	317	
28823	59191	A	28998	1331	1471	RWSNGTLENGTL*LLTLPSASLI STNKSPLDDVE*RSLISKAPGDT
28824	59192	A	28999	147	1456	
28825	59193	A	29000	1	439	

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28826	59194	A	29001	722	2805	TPRAERTASSVALPTSRLLRAR AETTTAPSTPMKTHRVISMVFF TCSQTGTPSASPVKSSLKVSSLN IIIASTTNRPS/VQQF/WPVSPPG DGTRRYP\SISLTVLTGNDNVNL LRAGIDLAIYFDDAPSAQLTHH FLMDEEILPVCSPEYAQRHALT DTVINLCHCTLLHDRQAWSND SGTDEWHSWAQHYAVNLPTSS GIGFDRSDLAVIAAMNHIGVAM GRKRLVQKRLASGVYPPRCAY PRTHLLETSTTSGVNGVGTYSA PFWRMLLNSFVMAFSITLGKIT VSMLSAFAIVWFRFPLRNLFFW MIFITLMLPVEVRIFPTVEVIAN LQMLDSYAGLTLPLMASATAT FLFRQFFMTLPDELVEAARIDG ASPMRFFCDIVFPLSKTNLAALF VITFIYGWNQYLWPLLIITDVDL GTTVAGIKGMIATGEGTTEWNS VMVAMLLTLIPPVVIVLVMQR AFVRGLVDNPAANYIHYGVRE SGMTAIANGIAHHGGFVPYTAT FLMFVEYARNAARMAALMKA RQIMVYTHDSIGLGEDGPTHQA VEQLASLRLTPNFSTWRPCDQV EAAVGWKLAVERHNGPTALIL SRQNLAQVERTPDQVKEIARGG YVLKDSGGKPDIILIATGSEMEI TLQAAEKLAGEGRNVRVVSLP STDIFDAQDEEYRESVLPSNVA ARVAVEAGIADYWYKYVG
28827	59195	A	29002	2253	2546	
28828	59196	A	29003	279	629	NGAGHL*RPPVDGATAAPAGG RYAHLRVCPESLPWLHLPAWRI YRSGS*SAPCHCRNHRSGSAWQ KHYGNRFRFRTVRPYRGRALH LRGRNTAITQAADWRLATAQL LEIAGVGDE
28829	59197	A	29004	313	638	RWRQRWFWCLHCLVLFRITPR TFALSQCRPWDDSRSQDTSMSH SIQWNRMYCNCSMQDEQEADE ANGKGPAQVGDRQAWAGR/CR SHRREGTIPGNPHPRAS*RAGW QR
28830	59198	A	29005	1	1182	

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28831	59199	A	29006	1	535	RPYVLP\VAGSNALGA\LGYVES ALEI\AQQCEGAVNISSVVVASG SAGTHAGLAVGLEHLMPESELI GVTVSRSVADQLPKVVNLQQA IAKELELTASAEILLWDDYFAP GYGVPNDEGMEAVKLLARLEG ILLDPVYTGKAMAGLIDGISQK RFKDEGPILFIHTGGAPALFAYH PHV
28832	59200	A	29007	1	1953	
28833	59201	A	29008	1	656	MKLMAIQEQARGEQCFRDSEW DLQFHIQVALATQNSALAAIVE KMWTQRSHNPYWKKLHEHIDS RTVDNWCDDHDQILKALIRKD PHAAKLAMWQHLENTKIMLFN ETSDDFEFNADRYLFAENPVAI AKELELTASAEILLWDDYFAPG YGVPNDEGMEAVKLLPRLEGIL LDPVYTGKAMRGLIDGISQKRF KDEGPILFIHT\GGAPALFAYHP HV
28834	59202	A	29009	1172	1371	
28835	59203	A	29010	338	528	RHPRCDPYGFCPFTADADDA** LGACHHYWRGQRKIYAGSGDS RCQPDGRRSAPARRPLRRQR
28836	59204	A	29011	413	2798	
28837	59205	A	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P SSFKEGIDHSATFFFAARFALVA AAIFCVFADGFFAFLASFFAAFG FVFFSPRKALSGSKFTFLPT

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28838	59206	A	29013	767	1428	FTPLSLRAVVIQLANRQYLDEK SDRAVHQGHIPRQFY*SLRRNL TNRHIQLIAIGGAIGTGLFMGSG KTISLAGPSIIFVYMIIGFMLFFV MRAMGELLLSNLEYKSFSDFAS DLLGPWAGYFTGWTYWFCWV VTGMADVVAITAYAQFWFPDL SDWVASLAVIVLLLTLNLATVK NVGEMEFWFAMIKIVRPLSGSR TKKMSKSDDNRNNVIGLLEDP KSVVKKIKRAVTDSDEPPVVRY DVQRPKRSALLERAPERFQEVF ILKGREDKRLLPLIHALESQGG GYPVGKPPISRREKRPCRASGA YSPPVLLILIMDPLGNLPIFMSV LKHTEPKRRRAIMVRELLIALL VMLVFLFAGEKILAFLSLRAET VSISGGIILFLIAIKMIFPSASGNS SGLPAGEEPFIVPLAIPLVAGPTI LATLMLLSHQYPNQMGHLVIA LLLAWGGTFVILLQSSLFLRLL GEKRVNALERLMGLILVMMAP
28839	59207	A	29014	1	632	
28840	59208	A	29015	1	1215	
28841	59209	A	29016	38	457	LNRLLKLVHASQSSRAMVFSSI RSFMFFSTLFILVRRQFSR*TIML SANSDSLTSSLPIWLLFISFSCLT ALARTSSTVLKRSGESGHPCLV PVFRGNTFNFSPFSIMLAVGGV LHCEINCRICSTGRSANPPLDSCI
28842	59210	A	29017	899	991	
28843	59211	A	29018	1740	1868	
28844	59212	A	29019	1	1084	MSAEITAPWYRLQLDLFTKLVA TCMEQFRPKTIPPLAIPERLNAH CEELYELIASLNNILNLYMPAG QEAEHRFAMGELPDEVLEICQR LAKLTEMLRGLAELFLNDLSEK TGSHDIVRLHRLILQMNRALGM FEAQSKLWRLASLAQSSGAPVT KWATREEREGQLHLWFHCVGI RVSDQLERLLWRSIPHIIVTSAT LRSLNSFSRLQEMSGLKEKAGD RFVALDSPFNHCEQGKIVIPRM RVEPSIDNEEQHIAEMAAFFRK QVESKKHLGMLVLFASGRAMQ RFLDYVTDLRLMLLVQGDQPR YRLVEL\PANASPTVSAACWW AYSHLPKGLI*KVICSARCISTK SLFRPSTARW
28845	59213	A	29020	1	2022	

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28846	59214	A	29021	878	1267	LNSWLPSVPTV*SSVFNAL*TG* ISPAFNPFADM*SASGLP*IKSPL STSTLFFTSLRASLIRLAVRTSPN FSVAVSL**SKSIMLLCRSVVSM IRRSTVAAFTLAAISVARSVALN RFLIKSTGNACK
28847	59215	A	29022	294	2305	
28848	59216	A	29023	5	337	GAPQHQMMSTYRINGRESPML TYPSTPNFFWLAWQARDFMSK KYG\RRFPIARFLWRSTPAPGVR KTIFIFISLVFVLMCANSWITIW RTSAAAGCHCQVVCAGMNTW RVG
28849	59217	A	29024	1	1753	MPSTRYQKINAHHYRHIWVVG DIHGEYQLLQSRLHQLSFFPKID LLISVGDNIDRGPESLDVLRLLN QPWFTSVKGNHEAMALEAFET GDGNMWLASGVYRIPLAVIWII GSLTSKAYKAEVQQRREAFNR AKMDYDHLVRQIQQVGGLEGF IAKRTMLEKMKDEILGLPEEEK RALAALHDTARERQKQKFLEG FFIDVASIPGVGPARKAALRSFG IETAADVTRRGVKQVKGFGDH LTQAVIDWKASCERRFVFRPNE AITPADRQAVMAKMTAKRHRL ESALTVGATELQRFRLHAPART MPLMEPLQPTVSVVDKVVEKK GTKEVAEAYLKYLYSPEGQEIA AKNYYRPRDAEVAKKYENAFP KLKLFTIDEEFGGWTKAQKEHF ANGVIAVVAAGIGYWKLTGEE SDTLRKIVLEECLTNQQQNQNP SPCAEVKPNAGYVVLKDLSGPL PYLLMPTYRINGTESPLLTDPST PNFFWLAWQARDFMSKKYG\R RFPIARFLWRSTPAPGVRKTIFIF ISLVFVLMCANSWITIWRTSAA AGCHCQPTGIAQALLSTRQHGG AQCPLLPLSPLLSSSSF
28850	59218	A	29025	865	974	IMPRISGSQSGEHQQPLVATAR WFARA*ILIIPL
28851	59219	A	29026	1936	2490	
28852	59220	A	29027	1105	1518	
28853	59221	A	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	A	29030	3338	3553	
28856	59224	A	29031	95	1289	
28857	59225	A	29032	1	732	
28858	59226	A	29033	1	672	

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28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTTRL AEGLLEAAEEAGIPLVVNHVGG MFGIFFTDAESVTCYQDVMAC D/GGTL*AFLPYDAGRRCLQHG RYQ
28860	59228	A	29035	852	933	PAPYALLLLPMHPHGLRRRDR QGRIHNLNDRRRHWHRVRVCH LLRRERSRKDAPADGHPPL\RA VGGRNQN*FGELRTTTCFTQTD FLTFNLTSVTSNEASFTQFRTQG LVVFHQSAGDTVTDRTSLTRDT TTFNGDVQVQFLNHVDQFQRL TNYHAGSFTTEVLFQRTLVDYD FTVARFDENASCGTFAATSAVV LIFSHCLRLLCRVVVLVTRVNF QFTEHSTTQRAFWQHAFNRDF NHTLRTASNHLFKGRLFDTTDV AGVVIVHFVSTLVAGYSNFVSV QNDDVITGIYVRSVFRFVLTAQ ATSQFSSQTAQSFTGRVNNIPV AFYGFWFSCAKYYRHGARWCS NGRKIDQRHTHCFFCPCIRTDFA VEIGKEEFIT
28861	59229	A	29036	1	797	MIVFIENFKTSSPKYADILLPDL MTVEQEDIIPNDYAGNMGYLIF LQPVTSEKFERKPIYWILSEVAK RLGPDVYQKFTEGRTQEQWLQ HLYAKMLAKDPALPSYDELKK MGIYKRKDPNGHFVAYKAFRD DPEANPLKTPSGKIEIYSSRLAEI ARTWELEKDEVISPLPVYASTF EGWNSPERRTFPLQLFGFHYKS RTHSTYGNIDLLKAACRQEVWI NPIDAQKRGIANGDMVRVFNH RGEVR\LPAKVTPHPVGTWTAE
28862	59230	A	29037	1	1019	
28863	59231	B	29038	1	2727	
28864	59232	A	29039	1	2250	
28865	59233	A	29040	1	2850	

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28866	59234	A	29041	1	1339	MTGKCGKFGNFLESWRAQKTG ICGKVWNFLENLLNGFGQNAY SDTDNEVQAEVVSDKDKELVG NWSKGHSCYAKRLAAFCPCLR DLWNFELERDDLGYLVEEISKQ QTIQEEADHKNLESLQTEDAIE KKTPFSGEKFKLAAEICISNKDP NINSQDDGENVPRVAVHPNGC FAWKLPVLSRKFERKPIYWILS EVAKRLGPDVYQKFTEGRTQE QWLQHLYAKMLAKDPALPSY DELKKMGIYKRKDPNGHFVAY KAFRDDPEANPLKTPSGKIEIYS SRLAEIARTWELEKDEVISPLPV YASTFEGWNSPERRTFPLQLFG FHDKSRTHSTYGNIDLLKAACR QEVWINPIDAQKRGIANGDMP YVFSSQMAKFTPRT\GLSSLIWK AHKCGEALETLQKQ*C*QSGAT LPAGPRARAWPPYPRLFPTGLA CVDLHGNARKAT
28867	59235	A	29042	378	530	AFLPYDAGRRCLPGTVSV*SGL YVRGAQHGRYQ*HHRCCTSDK IWRADKG
28868	59236	B	29043	1	1617	
28869	59237	A	29044	417	607	
28870	59238	A	29045	954	1163	
28871	59239	A	29046	444	3793	
28872	59240	A	29047	475	732	
28873	59241	A	29048	1	219	
28874	59242	A	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	A	29051	1	411	
28877	59245	A	29052	172	378	LSLLRELGPVVAALLFAGRAGS ALT/VRNRPDARYRATLQYGD DGGGSAASGYFSPFLGWGYFIT TVDG
28878	59246	B	29053	1	1641	
28879	59247	A	29054	1	3036	
28880	59248	A	29055	1	1419	
28881	59249	A	29056	1	1500	

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28882	59250	A	29057	2	1760	KSQLHDPCCAPIQQEAVRAVV GQPPQQHLGFPVERGVCQREC DFEKELEARIASLSDSVSNAREE RMALRQEQEQLQSRIQSLMQR APVWLAAQNSLNQLSEQCGEE FTSSQRTHGHSEGNITKRGLLG ELRFENGDPSNDQSYGRHKDG MAEIGTFHGGDLRGLTNKLDY LQQLGVNALWISAPFEQIHGW VGGGTKGDFPHYAYHGYYTQ DWTNLDANMGNEADLRTLVD SAHQRGIRILFDVVMNHTGYAT LADMQEYQFGALYLSGDEVKK SLGERWSDWKPAAGQTWHSFN DYINFSDKTGWDKWWGKNWI RTDIGDYDNPGFDDLTMSLAFL PDIKTESTTASGLPVFYKNKMD THAKAIDGYTPRDYLTHWLNQ WVRDYGID/GFRVDTPKCLRCN PSITIGTNYSAS*PQWSSIPGAL* G*/PAWAG/GLPWAPSVLLLDH LRQGFTMLEENLGNTIQDIGMG KDFMSKTPKATVTKAKIEKWN LIKLKSFCTAKETTIRVNRQPTE WEKIFAIYSSDKGLISRIYKELK QIYKEKNKQPHQQVGEGHEQT LLKRRHGCSQQTHEKMLNHQ
28883	59251	A	29058	1	1119	
28884	59252	A	29059	3	2599	
28885	59253	A	29060	225	1245	RGSTGAHPRSAGKHYAKTSAG NAAGDP*YGQMGPHHRGCGKP VPLPDHQSENLRWW*RRAWCG SGGYR\MAEGRHAAQGIIDWLG LDVDKLGALEERRKVLQVKTE NLQAERNSRSKSIGQAKARGED IEPLRLEVNKLGEELDAAKAEL DALQAEIRDIALTIPNLPADEVP VGKDENDNVEVSRWGTPREFD FEVRDHVTLGEMHSGLDFAAA VKLTGSRFVVMKGQIARMHRA LSQFMLDLHTEQHGYSENYVP YLVNQDTLYGVGLYPLGALAS GWLPKRRERKDATPGPTGYPG AHGNLELPERSEGPRAGGEPRR RTGHTQKGSPDRGQTPPKGP
28886	59254	C	29061	201	1244	
28887	59255	A	29062	1	2530	
28888	59256	A	29063	675	920	RTYRLAGRQKQRRGGGTDSRS QNPWRSHRRHLP*RSSGAGKR GGKRFAGGAERRNPRLCRKPEP PAGGDGRRRRLAAAGAD

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28889	59257	A	29064	498	707	
28890	59258	A	29065	510	554	
28891	59259	A	29066	600	734	PECLSAPDH*YKHCCSTGTQAR QPDADCPLLPPRLAAHNERQTR
28892	59260	A	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD LWPGEVLGIVGESGSGKTTLLK SISARLTPQQGEIHYENRSLYA MSEADRRRLLRTEWGVVHQHP LDGLRRQVSAGGNIGERLMAT GARHYGDIRATAQKWLEEVEIP ANRIDDLPTTFSGGMQQRLQIA RNLVTHPKLVFMDEPTGGLDV SVQARLLDLLRGLVVELNLAV VIVTSSPDQDWGFTPEPRLAAR FPGSTHSSRSRRNRGRRHPRPRS LPTPSAPHSRAPGDGVKLVPPP ARVTRNEPAPSDSVTLGVPHEP GACIGTPILTFVRPSTSAINAAA EESTGTILFGAGGFKRTDLNDT ESDSTTLVASRYWDLSSGWQR AINLRWSLDHFTQGEITNTTML FYPGVMISRTRSRGGLMPTWG DSQRYSIDYSNTAWGSDVDFSV FQAQNVWIRTLYDRHRFVTRG TLGWIETGDFDKVPPDL*LKSR VGQRSELGSQYTPRARVEPPKL LSRKVRAHFGSRAPGAGRA*RH LRAPDCGVRWVWAGSGAGDG GGRGCGGSGTSEWILGSGRRGE
28893	59261	A	29068	84	128	
28894	59262	A	29069	1547	1822	CSRCSIPAFRVKPAPLKPRVFSP AWNVPERLWHLAPSTFSGGEQ QRVNIAR/ELYRRLPHSAA*RN YRLP*RQNSAALSRLYAAFLPR PQYHH
28895	59263	A	29070	1520	1656	
28896	59264	A	29071	563	976	
28897	59265	A	29072	1	1011	
28898	59266	A	29073	1	1097	
28899	59267	A	29074	1	2490	
28900	59268	A	29075	1	879	
28901	59269	A	29076	1	1317	
28902	59270	A	29077	1428	1619	YAARRRALCGSPCPFPGGCNGE NCRLPPQLHADLTARIFYETRG WWWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG* HQLWARWQNNGLAHTPRADS THQQSALDGRISSLT

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28904	59272	A	29079	1886	2329	PLLVWINTRPSLTTGRESASPAT LVCHATVPSLVIASHVLSFL*W SFTVLVISRIGVAFAHAIFWSIT ASLAIRMAPAGKRAQALSLIAT GTALAMVLGLPLGRIVGQYFG WRMTFFAIGIGALITLLCLIKLL PLLRRTVKYTSGC
28905	59273	A	29080	1	2319	
28906	59274	A	29081	3	194	STSSLAAQSLRFGYETSQTGLA TYCGEKIQ*FFADLQQPVCADS YPLLVQMKKLGPIVFFFDI
28907	59275	A	29082	3109	3384	
28908	59276	A	29083	703	1000	DCFLRRLIKRPFGTSMKDQAVR FEEGFMAMGALGLAMVGMTA LAPVLAHVLGPVIIPVYEMLGA NPSMFAGTLLA\WIWAAVFLAK ELAGGVRLLVLIF
28909	59277	A	29084	2040	4603	
28910	59278	A	29085	3	94	
28911	59279	A	29086	3	148	YAEHMLEVMSSIGDYT/NPRPA SRPVTKFDQRGHRLGHGVWNL MFERVK
28912	59280	A	29087	27	227	
28913	59281	A	29088	344	1067	
28914	59282	A	29089	798	1049	
28915	59283	A	29090	1	1473	
28916	59284	A	29091	1	720	
28917	59285	A	29092	45	208	
28918	59286	A	29093	1	2499	

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28919	59287	A	29094	1	725	MHPRFQTAFAQLADNLQSALE PILADKYFPALLTGEQVSSLKSA TGLDEDALAFALLPLAAACART PLSNFNVGAIARGASRRSAKNIP RAVRQVFWRILLFYVFAILIISLI IPYTDPSLLRNDVKDISVSPFTL VFQHAGLLSAAAVMNAVILTA VLSAGNSGMYASTRMLYTLAC DGKAPRIFAKLSRGGVPRNALY ATTVIAGLCFLTSMFGNQTVYL WLLNTSGMTGFIAWLGIAISHY RFRRGYVLQGHDINDLPYRSGF FPLGPIFAFILCLIITLGQNYEAF LKDTIDWGGVAGTYIASGGEPA VNSHAFGVLRNVVSIAVFFHQF GDAIKRLFPTDLLPFIRTWRTVF RKLQTAFGVDEIHQASAFRTKC TAVDRVIRIAFDMDRLDFFSWR SGYISRIPLIGLYFACALERHQN ERQPIILLSDQNAIATINQLAIER DVLNCRVIIARSLSELVAIREEIE PLLIINNSHYLLDDAVNNYITVK NIITAAGIEQIKHFLATAFIRQQP ERFFSAPGSFHYSNVRGESWQH ITRQICAQLVAQHHITADEAQRI IAREGEGENLIVNRLAIPHCWSE QERRFR*TVAWWRAA*CAVCD DGDCRSVLPDLHVWQPDGIPV AAEHLRDDGFYRLAGDCH
28920	59288	A	29095	3	453	
28921	59289	B	29096	1	3684	
28922	59290	A	29097	1	231	LLVFINQEEADFHTQRGGPVFQ QATFTL*QLALFAIEPGLMTDP DIQVRGTTLPYGRGAAHGVYT SNWKLTFRRILY
28923	59291	A	29098	1	2862	

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28924	59292	A	29099	1	1567	MKLNKAGFNVPESYSLLKMPP VGCLISALKKAEDRQEVILRLF NPAESATCDATVAFSREVISCSE TMMDEHITTEENQGSNLSGPFL RVRAGESIKFFNVLLADTPGLDI DTMDKDVAHDSRSIQLAMLRD DEILTHPVFNRYHSETEMMRY MHSLERKDLALNQAMIPLGSCT MKLNAAAEMIPITWPEFAELHP FCPPEQAEGYQQMIAQLADWL VKLTGYDAVCMQPNSGAQGE YAGLLAIRHYHESRNEGHRDIC LIPASAHGTNPASAHMAGMQS RKTAGICCVHLWAGFGKVAIIG AGPAGLQASVTLTTQGYDVTIY EKEAHPGGWLRNGIPQFRLPQS VLDAEIARIEKMGVP\IKCTTEV G\NTLTLEQVKAENRAVLVTVG LSSGSGLPLFEHSDVEIAVDFLQ RARQAQGDISIPQSALIIGGGDV AMDVASTLKVLGCQAVTCVAR EELDEFPASEKEFTSARELGVSII DGFTPVAVEGNKVTFKHGDLR TAPFLGVADKRNKSAGNHP
28925	59293	A	29100	107	892	LAICTGTYSGRQVLPRFVDRGA SLIAEERNGAGRRRAGIRTTSA GGGLCAYAIVEF*CWRNCARFE LN/AGISVPI/SEFIGATMQQTVH AEQSAISHAWLSGEKALAAITV NYTPCGHCRQFMNELNSGLDL RIHLPGREAHALRDYLPDAFGP KDLEIKTLLMDEQDHGYALTG DALSQAAIAAANRSHMPYSKSP SGVALECKDGRIFSSEYAENAA FNPTPDIQRAVLAEKADAPLIQ WDATSATLKALGCHSIDRVLL
28926	59294	A	29101	1	3100	
28927	59295	A	29102	1878	2699	GTARNLTVSLSLSYSSSGTPSNA PNARMEELGPHPGEASSLFHPE SPLLDELFLPEYKAGRTPNPDI\ GHYVRRADV\DGKSRLLRGLDS NKDQSYFLYTLSHEQIAQSLFP VGELEKPQVRKIAEDLGLVTAK KKDSTGICFIGERKFREFLGRYL PAQPGKIITVDGDEIGEHQGLM YHTLGQRKGLGIGGTKEGTEEP WYVVDKDVENNILVVAQGHE HPRLMSVGLIAQQLHWVDREP FTGTMRCTVKTRYRQTISLGPL RKPPHNRCLEI
28928	59296	A	29103	358	1160	

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28929	59297	A	29104	234	930	KRAFLCSFCANRRNAANSALAL PGNCPVAHAQKRHSAPGTLSPD ARNEKQPLYG\GAAPETPNPRL PPLDSGILGGYIAPDNLTITLSV GHSLFDERFGLAPQMPKKLQK MTRFPNDSLDAALCHGDVLLQI CANTQDTVIHALRDIIKHTPDLL SVRWKREGFISDHAARSKGKET PINLLGFKDGTANPDSQNDKLM QKVVWVTADQQEPAWTIGGSY QAVRLNQFRSVMN
28930	59298	B	29105	1	837	
28931	59299	A	29106	1	1701	
28932	59300	A	29107	733	1323	
28933	59301	A	29108	1	736	MKPSVILYKALPDDLLQRLQEH FTVHQVANLSPQTVEQNAAIFA EAEGLLGSNENVNAALLEKMP KLRATSTISVGYDNFDVDALTA RKILLMHTPTVLTETVADTLMA LVLSTARRVVEVAERVKAGEW TASIGPDWYGTDVHHKTLGIVG MGRIGMALAQRAHFGFNMPI/R L*RAPPP*RSRRTLQRPLLRFGY SVTRVRFRLPDPAVN**DASSV WRRTIRGPSLGLSPGWNTRVSL CAFFG
28934	59302	B	29109	1	1359	
28935	59303	A	29110	874	1926	
28936	59304	A	29111	1	777	
28937	59305	A	29112	137	376	
28938	59306	A	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGN FC*RHGS*KITAGYIVPLPEESA TATGASWTHPWGRQDASW
28939	59307	A	29114	1846	2126	LMELIEKHVSFGGWQNMYRHY SQSLKCEMNVGVYLPPKAANE KLPVLYWLSGLTCNEQNFITKS GMQRYAAEHNIIVVAPDTSPRG SHVADADRYDLGQGAGFYLNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMGG LGALVLALRNPDEYVSVSAFSP IVSPSQVPWGQQAFAAYLAEN KDAWLDYDPVSLISQGQ/LRCG NHG*SGVE**FLRRQLRLQI*KD WPQ*EAAHVH

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28940	59308	A	29115	184	985	LGKRLVTYHTDANGQPVNQIL VEAATDIAKELYLGAVVDRSSR RVVFMASTEGGVEIEKVAEETP HLIHKVALDPLTGPMPYQGREL AFKLGLEGKLVQQFTKIFMGLA TIFLERDLALIEINPLVITKQGDL ICLDGKLGADGNELFRSLILRE MRDQSQE\DPREAQAAQWELN YVALDGNIGCMVNGAGLAMG TMDIVKLHGGEPANFLDVGGG ATKERVTEAFNPPGYIGPYQGV PPAGPGVTRMGKSVRRIVQVG CQVAAGSH
28941	59309	A	29116	1825	3186	
28942	59310	A	29117	366	1903	
28943	59311	A	29118	1	2139	
28944	59312	A	29119	345	431	AASGSADDNLHHQYN*GDIAF CLHALLP
28945	59313	B	29120	1	2616	
28946	59314	A	29121	1	1521	
28947	59315	A	29122	1	783	
28948	59316	A	29123	96	215	
28949	59317	A	29124	1	292	MWWGGLLYWLAALVTLLWA ASQIQALKKLTCAISQTLEEQPV LNSKSWLTSLQNDYSLPDSLTE RIWLTLISQRISRGELREF*TGRR KLVTEQCLV
28950	59318	A	29125	3	529	
28951	59319	A	29126	1	884	MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI GDGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLLRMKVEEG DVILVKKLDRLGRDTADMIQLI KEFDAQGVSIRFIDDGISTDGEM VLDKLARGYADLSKAESQWDE MMRTAGSLKLGTIHASELIRSL LKSSRPSGLAQAIMEVGRVNKT LYLLNYIDDEDYRRRILTQLNR GEGRHAVARAICYGQRGEIRKR YREGQEDQLGALGLVTNAVVL WNTLYMEEALSWMRRNGEEII DEDIARLSPLMHGHINMLGHYT FTLPEDILKGELR*RHLPPPSSSA SPALPIGIHVHKHLLGDNRYPI WIMQPSAHHPARQPEHDNHFR

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28952	59320	A	29127	143	523	NQTLMIKGAAHGIFNPLCIKAT AG\AGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPRLILPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	B	29128	1	4107	
28954	59322	A	29129	1892	2720	PTAWSPPRPTSMTSISWVICCM ERSNLSQPMPATKGR\QARGAG \EVDVDWLIAERPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRQFGFVKARFKGLLK NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFRALISTA SALAGLILLCLFGPALLAGYITE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRNGRVFLLVFILPFS LRRVGHAHH
28955	59323	A	29130	1332	1635	
28956	59324	C	29131	1	1677	

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28957	59325	A	29132	1	1114	MAEACNIGLEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFVTPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGTLRDSNFVLEGLLEQQTG LNPVEIMTDTCGCLEKQEEPPS LLRLNNRIKQLLPPVDLTELLLE IDAQTGFTHEFAHVSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFVTPVK TINSGSNRKYFGSGRGITWYNF VSDQYSGFHGIVVPGTLRDSNF VLEGLLEQQTGLNP/D*NHDRH LRLSGETGRATIIASSK*SDQTA TPTGRFNGTVT\EIDAQTGFTHE FAHVSESGARAQDLHISL\LRY* WLKPVIS/ALEPLIKHNIPALTRH RLSWVKQNYLRAETLVSANAR LVDFQSTLELAGRWGGGEVAS ADGMRFVTPVKTINSGSNRKYF GSGRGITWYNFVSDQYSGFHGI VVPGTLRDSNFVLEGLLEQQTG LNPVEIMTDTCGCLEKQEEPPS LLRLNNRIKQLLPPVDLTELLLE IDAQTGFTHEFAHVSESGARAQ DLHISLCAVLMAEACNIGLEPLI KHNIPALTRHRLSWVKQNYLR AETLVSANARLVDFQSTLELAG RWGGGEVASADGMRFVTPVK
28958	59326	A	29133	1	2908	
28959	59327	A	29134	735	932	
28960	59328	B	29135	1	1413	
28961	59329	A	29136	1	1469	
28962	59330	A	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	A	29139	1	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNL\LL RRFHEATAQNAPDVVVWGSGT PMREFLHVDDMAAASIHVMEL AHEVWLENTQPMLSHINVGTG VDCTIRELAQTIAKVVGYKGRV VFDASKPDGTPRKLLDVTRLHQ LGWYHEISLEAGLASTYQWFLE NQDRFRG
28967	59335	A	29142	538	1116	
28968	59336	C	29143	1	2967	
28969	59337	C	29144	1	2214	

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28970	59338	A	29145	1	469	
28971	59339	A	29146	780	1052	
28972	59340	A	29147	617	2408	
28973	59341	A	29148	2	488	
28974	59342	A	29149	1	1083	
28975	59343	A	29150	527	3213	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNILKEHGCGVTPIMS MRRWLAKNRPQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGYAVVALIKPGAQIGR SPVNCDVASCHVISFNLRVELAI MRRLLCRIAVLMSYRIEQRLMF LERLRHVGLIAHPAKKAIKKTR KPGMKVTFEQLKAAFNRVLISR GVDSETADACAEMFARTTESG VYSHGVNRFPRFIQQLENGDIIP DAQPKRITSLGAIEQWDAQRSI GNLTAKKMMDRAIELAADHGI GLLRLAGGGKRLYWHLLDQLH RRNDNISLDLGNNAEAVILRED MLPRENFRPGDRVRGVLYSVRP EARGAQLFVTRSKPEMLIELFRI EVPEIGEEVIEIKAAARDPGSRA KIAVKTNDKRIDPPTQHEDEED EGLYDDPFPLNECSVGPGHRHR FAPPEAQFRRPETLKGAPTSRIP ETSVGVSAGSDFEPHLMRELTC RLTALTWCYPGSAYAVHQPDE
28976	59344	A	29151	1	812	
28977	59345	A	29152	1	1830	

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28978	59346	A	29153	1	1308	MMPLIDLEDPRLLVRREIGMLL HVDYLDLVHEKVTCRGRNGGQ DREKTTMEKVRSSGTICPQAPE VVNHYFTTDDGYRIISARFGVP RTQVRTWVALYEKHGEKGLIP KPKGVSADPELRIKVVKAVIEQ HMSLNQAAAHFMLAGSGSVAR WLKVYEERGEAGLRALKIGTK RNIAISVDPEKAASALELSKDRR IEDLERQVRFLETRLMYLKELK ALAHPTKKVTLSLHREGKQINH KAVQRLMGTLSLKAAIKVKRY RSYRGEVGQTAPNVLQRDFKA TRPNEKWVTDVTEFAVNGRKL YLSPVIDLFNNEVISYSLSERPV MNMVENMLDQAFKKLNPHEH PVLHSDQGWQYRMRRYQNILK EHGIKQSMSRKGNCLDNAVVE CFFGTLKSECFYLDEFSNISELK DAVTEYIEYYNSRRISLKLKG\L
28979	59347	A	29154	1	836	
28980	59348	A	29155	1	1566	
28981	59349	A	29156	297	936	RTSSSLMRSSSSLLRICSGVSPRS IPRWFTSVSLPSSFIR\RITTFRYT PGHVAPASRRSCYKYRR*PMRL YTMIQSLS/VGSRPSGLRAFSSD CSPLPRTCSLSRRRVLMITTSRS *SLTYGVDPSVRPVLAAASEYF SRR\YAGFQNPHNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSSICTSTGGNTTL PPSSPPDC
28982	59350	A	29157	5	861	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNILKEHGCGVTPIMS MRRWLAKNRPQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGY
28983	59351	A	29158	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW
28984	59352	A	29159	3	601	
28985	59353	A	29160	415	549	

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28986	59354	A	29161	2	501	
28987	59355	A	29162	1	1347	
28988	59356	A	29163	3	2461	
28989	59357	A	29164	1419	1640	IFCASLSLGLYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPQGC DPHMESLI
28990	59358	A	29165	1135	2067	
28991	59359	A	29166	1	1364	MAGNRRFMCTPKTHGLSISQH GTFPEHAGCKIRCAGRSGRVRP AELLAPYTGDIAAEGISKAMRG GAKFLHHGIKRQQRYVAEAITE EWRMAPGPLEVAWFAGVIYHL YYYRARFFCAAQPLVSGFHEAE LSLDDAKWVLHPGPDAGFHVF DVDGRFVLAWMLFQGSYLAG ALGDQPVHIHLGQLLALWRPL QITQLIEVMLVGRGGDQAVGQ ATLGIDTNGGLYAKGPLIAFLG LMHLRIALLLFVLGRTGCAYDG GRPQLAEKLYSELRAQGIEVLL DDRKERPGVMFADMELIGIPHT IVLGDRNLDNDDIEYKYRRNGE KQLIKTGDIVEYLNAALLIAVT VLTSMEASDLVDLGMTLSPAD YAERLAALTQKCGLDGVVCSA QEAVRFKQVFGQEFKLVTPGIR PQGSEAGDQRRIMTPEQALSAG VDYMVIGRPVTQSVDPAQTLK AINASLQRSA*CRDAGTLRLRA WLC*FLQRRYHRYKGPAVPQV ELCQICQRNEFCTQRVPGMCHV
28992	59360	A	29167	627	854	NAGDRRNRNPSCTAARQYG*S RFYNCRR*RHGRKNLSAERNGL PEYRNCNPDHRPSVFLAAGRCF APTMCHDASE
28993	59361	A	29168	1	1593	
28994	59362	B	29169	1	3789	
28995	59363	A	29170	940	1326	
28996	59364	A	29171	1	1377	
28997	59365	A	29172	1	2547	
28998	59366	A	29173	561	845	AKIVQLRPRILRPSRSARRCPSA PRSRRQRRRSGPLPEPAPRVS*Q IFPSQYWRYRQSTENQKQRLDP RGQIVNVPARRIIRQKRKCCKV AGSA
28999	59367	A	29174	1	1284	
29000	59368	A	29175	624	866	
29001	59369	A	29176	1	1384	

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29002	59370	A	29177	2268	2684	RCRRCKRRLLRRFRRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCHCG*RQC SSDGRKITSVHRGRNADGRELT HQAVRLLAYLSDRFARHHRHL RNAHRRGPDRIPKERHFPATKL RHTPAV
29003	59371	A	29178	1	2142	
29004	59372	A	29179	1	2463	
29005	59373	A	29180	3	126	
29006	59374	A	29181	1	2013	
29007	59375	A	29182	891	1000	FDSFHWHSHPMLCCDRGQHKE NPQSRGPISCQ*IQQ
29008	59376	A	29183	1	846	
29009	59377	A	29184	90	411	
29010	59378	A	29185	1	1580	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK AAEIPRSTFYYHLKALSKPDKY ADVKKRISEIYHENRGRYGYRR VTLSLHREGKQINHKAVQRLM GTLSLKAAIKVKRYRSYRGEVG QTAPNVLQRDFKATRPNEKWV TDVTEFAVNGRKLYLSPVIDLF NNEVISYSLSERPVMNMVENM LDQAFKKLNPHEHPVLHSDQG WQYRMRRYQNILKEHGIKQSM SRKGNCLDN\AVVECLFGTLKS ECFYLDEFSNISELKDAVTEYIE YYNSRRISLKLKDLYASCLTVQ LFGVSTVMGLLIRILGSIFQKAL NISKIESFVAVTTIFLGQNEIPAI VKRFMIAESHEVLPHLYGMGH CGSRRWYAEWRPLHRVHEPSG
29011	59379	A	29186	1375	3174	
29012	59380	A	29187	604	1268	
29013	59381	A	29188	1	288	
29014	59382	A	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	A	29192	1	3156	
29018	59386	A	29193	1	1824	
29019	59387	A	29194	1	1922	
29020	59388	A	29195	1369	1743	

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29021	59389	A	29196	21	432	GPGCNGVHRLCTE\QRDVRGTV RIVLKTFNNCRDTVFVAFEVNN TVSLLVATTDMTSGDTAIVVTT TGFVSAANEVQILAFFQGDVSF FPVATTTDTLSVTFNFPFNYQG VNDFDFDFKQFLHSSFDFCFGR VFSNFE
29022	59390	C	29197	1	1743	
29023	59391	A	29198	2005	2571	
29024	59392	A	29199	170	486	LQTQKDGIPAVVERLEYDPNLP RTSRWFRNDFSVPVLQLLGSP*
29025	59393	A	29200	1	1713	
29026	59394	A	29201	1	6729	
29027	59395	A	29202	1	753	
29028	59396	A	29203	1	1470	
29029	59397	A	29204	665	1773	ASSQVKSGWLSAKIPVISSIYGP LLSVRLLSHAWPNSLCPQLHCF LPGAIWSASSLLKSGNRPLIRLA SIVLPVPGGPISKRLCPPAAV/HF QSSLSLFLTDNITEIML*RPDTW THVMYVLHHADKPNLYHGLPE NPEISETVKFWKGIWKPLAAVG FAATFAASIFHYVGVGPNRADE EENNLHEEKDEERKCSQDIQLV KERVIFLTGQVEDHMANLIVAQ MLFLEAENPEKDIYLYINSPGG VITAGMSIYDTMQFIKPDVSTIC MGQAASMGAFLLTAGAKGKR FCLPNSRVMIHQPLGGYQGQAT DIEIHAREILKVKGRMNELMAL HTGQSLEQIERDTERDRFLSAPE AVEYGLVDSILTHRN
29030	59398	A	29205	948	1620	

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29031	59399	A	29206	1782	3667	HRRRCRHGYPVPAYRCRIWKC GQFHPTGIAGCGRTGHRRLPW* RRLSAEQTWRTFYGALCAERQ RPGGP*RG\SRSIMIEIREGRGCD GPWGPHAKLKLDHLGKEVLES RLPGILELSRTFAHVDPSRFRLS HLSLHDGRYSDQSYRYNDTRD MVPINGSIHRIGREPHYHYQRG QQYIGLCRNCNVIDTHICIYLVD QPIMDDIRRLLLYSEISSAIIWLL PVVQGEHYMLVDPDTNEREER GRSETRGFPRVPLGRTVSTVWY PLSNAATLAATRCSRSPHAFAE PSSNNGFITATPLGRTHFLGMA FPPSACWRLLRAEPERVEAVLS ASGMNKAMRCGVSLICNFRLD YAPIEKQWDLHFADYFAEDLK LLAPLAKDGLVDVDEKGIQVT AKGRIRRLRRIRHLSMMPDAAL VASYQAYDFLRIRHKQRASAK QPNHCGTQHGSNGSLRTLWNSI DSGSVLTWCASLIFSSRKSLSPI QLVRSVDRGDVKKRYSMREFS LGETHSEAEFRELLEQNPSFVFF KPQSFAPVKGASAVPLVGRASV ASDRSIIPPGTTLLAEVPLLDNN GKFNGQYELRLMVALDVGGAI KGQHFDIYQGIGPEAGHRAGW YNHYGRVWVLKTAPGA
29032	59400	A	29207	1351	1806	VIVGITSNSVTVAAVSSWCRTW VPVSVLCLNCYPASMALVRGVI RGV*TCLSLCPNCAAIFIFAFGA VIFCITSVGFLFPPMVYKSGLRF FVFT*MRDTGVPQRLRAPRRSL SAKLGPACPFAYIVPHIWCRWI GWGTCVCLAICVCVCVAD
29033	59401	A	29208	1308	1647	RSWEVSIVEFYVVRPTGHV*HA SGNLSHHRKRHPLADQAARKG ETVPPRGRRS\WRTQAHP*HLR QHRGQHPASLPTRTGTPQPGRR AIYRIPVRTAGQFQRIEVGDFQR VGHQ
29034	59402	A	29209	1	2184	
29035	59403	B	29210	81	1356	
29036	59404	A	29211	1	2349	

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29037	59405	A	29212	514	1136	ILRIMQRGMKQFAGLLRLSGIK MLPSA**LGELLHAAGSFFQRG CLLFSTGGKIGVARRNFTGTGI DGI*TFADMSDGVSQRALHM* NALRQVAHFTAPVNGQGIRQV TTGDFANVSNNFCQRSKQHTA NAVPRHQQNQYHHQRDNRQLP LGKSVIICVVSDDIAIQFFTAEG VLSKRFAHCLMPSLGGLSKIGP SMPLFRIISQFS
29038	59406	A	29213	1	2992	
29039	59407	A	29214	1	168	
29040	59408	A	29215	1	537	
29041	59409	A	29216	1	1881	
29042	59410	A	29217	1532	2160	KHWSDSIPGTEADWSASTTSGC AGFAAFACSSS*VICLLSGAVA AYAPQLRHQAIRKVIIRRTSAFP LMD*TWSFLSSTNGLASCSASIS SAGSGAGSASGVTKVSVDTAS GWPIFVTDRLSSCSTRFTLPGAN RLITVEPSLKRPISWPFSSATEPS FSPAGQVQRLMIPSRGGVMVP AQTVSMLPTIVAPTGPYSSHLL GSFTLSPP
29043	59411	A	29218	1	1713	
29044	59412	A	29219	2159	2715	TIPAKPVPSMVASGTVRFGFLTI PVLTAADSTPTKAHRQSRILLMI A*PSVVSAVFQLAA*VAASNQC QPTIAVITTGIRTSTRPIVA/CITG FVTGAVEIVLVANSVIDISVGSP FSIPQMFSARLGIATMAICPIMV SFSVAAINSASHNRQGFALQFFF NDAACGSGEFRILMQEEHPDSV VFC
29045	59413	A	29220	2	102	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM SVDLCHRDFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG\I IGGAGSLAFPLPALIWCAVRYT PQVTCLLTFVTGILPISEPPSNRI FACWGKPAWTACCNSLRARR
29046	59414	A	29221	1	1464	

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29047	59415	A	29222	3	29	MQTEQQR/AVTRLCIQCGLFLL QHGAESALVDELSSRLGRALG MDSVESSISSNAIVLTTIKD/GQC LTSTRKNHDRGINMHVVTEVQ HIVI/LAEHHLPDPEP*EQQRR
29048	59416	A	29223	5	307	
29049	59417	A	29224	5	948	
29050	59418	B	29225	1	696	
29051	59419	A	29226	1	1083	
29052	59420	A	29227	817	978	LAGCYTMLPGNGPAGMHACIS KLDK*AAVKKRISEIIHENRGRY GYRRVPLSLH
29053	59421	A	29228	198	362	
29054	59422	A	29229	1	2907	
29055	59423	A	29230	1	2541	
29056	59424	A	29231	1	1566	
29057	59425	A	29232	3	601	
29058	59426	A	29233	1	1347	
29059	59427	A	29234	940	1326	
29060	59428	A	29235	1	2547	
29061	59429	A	29236	527	1383	SWRSVQLLPATSIPSWQTETNQ FMGRDRPTPTAESPYAVLLRQP LAKLNIIQ/RPVMNMVENMLDQ AFKKLNPHEHPVLHSDQGWQY RMRRYQNILKEHGCGVTPIMS MRRWLAKNRPQADVRVIYNVR TPQDVIFADEWRNYPVTLVAE NNVTEGFIAGRLTRELLAGVPD LASRTVMTCGPAPYMDWVEQE VKALGVTRFFKEKFFTPVAEAA TSGLKFTKLQPAREFYAPVGTT LLEALESNNVPVVAACRAGVC GCCKTKVVSGEYTVSSTMTLT DAEIAEGY
29062	59430	A	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	A	29239	1135	2067	
29065	59433	A	29240	1	1566	

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29066	59434	A	29241	1	1605	MKVPRGDVMFQLNLRKDDGQ FEDQLLLLVLLPKHRGHLLLQV ADDVWFKNRRAKCRQQRQQQ KQQQQPPGGQAKARPAKRKAG TSPRPSTDFRSRDGIPEKATRTS CPSDSSVFSLQRPPLSSTGRGSS LSWDSSQVLVILSTLTPSGTIVT AEPKYPFEKRLEVVNHYFTTDD GYRIISARFGVPRTQVRTWVAL YEKHGEKGLIPKPKGVSADPEL RIKVVKAVIEQHMSLNQAAAH FMLAGSGSVARWLKVYEERGE AGLRALKIGTKRNIAISVDPEKA ASALELSKDRRIEDLERQVRFL ETRLMYLKKLKALAHPTKKVT LSLHREGKQINHKAVQRLMGT LSLKAAIKVKRYRSYRGEVGQT APNVLQRDFKATRPNEKWVTD VTEFAVNGRKLYLSPVIDLFNN EVISYSLSERPVMNMVENMLD QAFKKLNPHEHPVLHSDQGWQ YRMRRYQNILKEHGIKQSMSR KGNCLDNAVVECFFGTLKSECF YLDEFSNISELKDAVTEYIEYYN SRRISLKLKG\LTPI
29067	59435	A	29242	3	1119	
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRREIE SIIEAGRVSDDGEIAKLGDNVE AWYRARLAGAFTLQECVMAA STFFIPSVNVIGADSLTDAMNM MADYGFTRTLSVTDNMLTKLG MAGDVQKALEERNIFSVIYDGT QPNPTTENVAAGLKLLKENNC DSVISLGGGSPHDCAKGIALVA ANGGDIRDYEGVDRSAKPQLP MIAINTTAGTASEMTRFCIITDE ARHIKMAIVDKHVTPLLSVNDS SLMIGMPKSLTAATGMD
29070	59438	A	29245	104	1381	
29071	59439	A	29246	1	375	
29072	59440	B	29247	1	5082	
29073	59441	A	29248	119	343	RMPKRRRWGKLSTIRCSTTCKK RLT*IVLPVRTPGRLCSSLKSVP ASHCLASCKAYSNKPWKRQPS KRHYVTMR

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29074	59442	A	29249	468	935	VPLAVPYGRLWRTIFSPLPSSFR STRVR*EVSGRSSPSISSLASLVR PIT/SLLIVNAHPVELLQVVFPTL DKHIAAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPTE AVDLFFHFNAVTKGFHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	A	29250	407	2145	
29076	59444	A	29251	1	177	
29077	59445	A	29252	1	1767	
29078	59446	A	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	A	29255	2	314	
29081	59449	A	29256	2977	3913	
29082	59450	A	29257	1	2091	
29083	59451	A	29258	1	751	
29084	59452	A	29259	1	927	
29085	59453	A	29260	1	1113	
29086	59454	A	29261	1	875	
29087	59455	A	29262	1	450	
29088	59456	A	29263	1	522	
29089	59457	A	29264	1	912	

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29090	59458	A	29265	1	2416	MLAQSLQALEQDGFLNRIAYPV VPPHVEYSLTPLGEQVSEKVAA LADWIELNLPEVLAVRDERTRY DIAVPRKRYGHAVSRNTFALRS QERYGHSVLETVGNSGSSKQFS MDILDPCARGPGQISLITVNHKL HVRCESIAYSVQTMVVKGGSA FAAFFIAVVLWMIGYVPNVEQS TQALLGMQFIMIALPTLFFMVT LILYFRFYRLNGDTLRRIQIHLL DKYRKVPPEPVHADIPVGARLS FAERVMEGLSDGGQSLQSPSAL FSKQTLKNMSIYKIPLPLNILEA ARERITWTLNTLPRVCVSFSGG KDSGLMLHLTAELARQMGKKI CVLFIDWEAQFSCTINYVQSLR ELYTDVIEEFYWDALPLTTQNS LSQYQPEWQCWEPDVEWVRQP PQDAITDPDFFCFYQPGMTFEQ FVREFAEWFSQKRPAAMMIGIR ADESYNRFVAIASLNKQRFADD KPWTTAAPGGHSWYIYPIYDW KVADIWTWYANHQSLCNPLYN LMYQAGVPLRHMRICEPFGPEQ RQGLWLYHVIEPDRWAAIGSP ADREEDAEEYLEAIMEARVTV AGMGLVMEVQDYFDGEA\DRL AKAWLP\EYTPQIKSLKDERKE AYRQIVEMSTEPQDVDLVRPA NKFEMTRVREGEKEADLPVWK HHLLCDESGNYPALLNHWETK VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	
29092	59460	B	29267	1	10161	
29093	59461	A	29268	1	882	
29094	59462	A	29269	1	2484	
29095	59463	A	29270	548	945	
29096	59464	A	29271	17	352	DLQDTGCFMLMNTGEKAV/KS ENGLLTTIAC/GPTGE/VNYALE GAVFMAGASI/QWLRDEMKLIN DAYDSE/YFATKVQNTNGVYV VPALPGWSLLWTRTCHRIFPRH RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIIELN TDFLCLINHMVVGQHIAFTGVD DDTGA*TFEGLCRLIR
29098	59466	A	29273	1	975	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29099	59467	A	29274	65	562	DFRWHGDSRKVHRKNRLIKPL MILLTRLSNRTNWPLTAAVIWP GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSSSTSS SIIIIIINSSSSLQCQPCASKYLAH YFTVSSIAAYSTPVVSTQEPWA TRHHPHHQQTDRRRPATRKSPR QYHNETNRQ
29100	59468	A	29275	1409	1641	PENGRPVYAGGRDAAWRDVY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSALGLCL* RLAGGDWCRDYSL
29101	59469	A	29276	1	3252	
29102	59470	C	29277	1	2760	
29103	59471	A	29278	1	723	
29104	59472	A	29279	14	338	
29105	59473	B	29280	1	1201	
29106	59474	B	29281	1	1866	
29107	59475	A	29282	1067	2753	
29108	59476	B	29283	1	1144	
29109	59477	A	29284	3	724	LAQLYGDPPAWPTPTRGVSEIR LALRFKSNDSLLRHFKDTSTLY LEIVDYPGEWLLDLPMLAQDY LSWSRQMTGLLNGQRGEWSA KWRMMSEGLDPLAPADENRLA DIAAAWTDYLHHCKEQGLHFI QPGRFVLPGDMAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL Q/PLNSGHSIYDMRWPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	A	29285	1	1863	
29111	59479	B	29286	1	813	
29112	59480	A	29287	1	546	
29113	59481	B	29288	1	2691	
29114	59482	A	29289	1	1212	
29115	59483	A	29290	1	2328	
29116	59484	A	29291	1	531	
29117	59485	A	29292	188	358	
29118	59486	A	29293	2545	2713	LLVVQFFFQHL*VPSGTSP*L*H LSGILWHFLLQALLYPRVFLVL LCRSLGAVCLY
29119	59487	A	29294	1	2046	
29120	59488	A	29295	3	654	
29121	59489	A	29296	2	182	
29122	59490	A	29297	1	1215	
29123	59491	A	29298	141	266	

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29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN ASGHAKRQSDGDLRSRAATGG DHSAGDWCGRRVQTSAG*LWR KARPWPNR
29125	59493	A	29300	2353	2758	SQAYHQVLPVCEAAPIPDDNHT LAALR*HGVYEKHMDQDCWA SFLPEERLFWRPIPAPRSDRVEC VDSLPLTAVGKVDKKQLRQWL ASRASARAQRRSPLAEARKPQY VHQGMDNARTALQKPEQARA HTEVHWT
29126	59494	A	29301	5	793	FLQRFVADLPCGAQVVKFSTFR TQCRQTEATLKVLFLHGTFNVV TSIGATTQVTNDARTDLRKQLV IDILFGIRRQTLLHFLDRHNRHF CRCRSRNTFLFQLLRMIRDFND FELV/NPLSLDSVLGMQPLREEI QQADRDDDKHHQGAGLLELET ANRFPQGDADPACADHADDGR RADVGFEAIEGVGDQQWHHL WQHAVEDLFELVGTGGANAGP GSIASTASESSLESTPVVWINSA STPARQRTGRGRRRPRTAWRRP
29127	59495	A	29302	1	2457	
29128	59496	A	29303	1	292	
29129	59497	A	29304	1	440	
29130	59498	A	29305	593	864	RTSAEPINPAPPVIRIFLISARLC* WTLSPLITLN*L*STSITSTSAVA SASSSCARVQSPVSFFGNWWM LGSTTRVSPLCHWAISSADF
29131	59499	A	29306	2	696	VPAGRYTGRDLHLHI/ILPFRES LPARHRVRRYRPLEAC*TPCTD GYHRIFYRLKGESAKDGSVMT LRSFLDKDGHPIDVEDINDQAR HLVRLMPVLRLRDARFMRRIR NGTVPNVPNVEVTARQLDFLA RELSSHPQNLSDGQIRQGLSAM VQLLEHYFSEQGAGQARYRLM RRRASNEQRSWRYLDIINRMID RPGGRSYRVILLGLFATLLQAK GTLRLDKDARPLLLIE
29132	59500	A	29307	3	1405	
29133	59501	A	29308	1204	1411	LRPALYQPARLSDAAVRKTG*F AVVSGSEHAESDAG*SGELLEQ LSEVLR*PDEIFLWRCRAEREQL GL
29134	59502	A	29309	236	645	

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29135	59503	A	29310	1	776	MELAALRSENPQPDEKPLGETL KDLFSRPVLPEMTDVHLPLNLN IEEFMGEQLHVTGDTDIYREHH AAEMSNIDGNTKLDALDIDSSQ GIVDASGTAHLSDNWPVDITLN STLIVEPLKGDKVKLKMGGAL REQLEIGVNLSGPVDMDLRAHT RLAEAGLSLNVEVNSKQLYC/L AHCMSSMPKESGADEKNSDNR WCRVYWLGAGALYHQRNERR GGSGR*ADLRRKPDVAGTGRA KRALCL*ES*YLRSGRTGTRIH
29136	59504	A	29311	955	1095	HRRHPIPFLIHHRDQPFRHQLRK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	A	29312	1029	1490	RLPPAVDPTARLRRPASGRRYP CIPAFVGTPAVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWSGL\DRQANPAQVEIIEIRQ L/VRKSPQTAHSPARIWRRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSGKYQRSRRARRPASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQTL SLSDKCRQGTVSGRLSLRKSDC TPISHASCSSSSLHGH*VSVAVR LRMTDFSRTVGKDVQRFDAGL GWTLERLLSAHAAFRVALKAG DMAILASRPPTVTPNSMRLLGR LYRSGVYGR

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29139	59507	A	29314	2	2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWGYDYTGNADN NANFGKAVPADFNGGSFGRGD SDEWTFGAQMEIWCSYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRCGAKSPFCAIT FRVRWTIRKSTKCCANRAYKR NITVGRIRRLRRIRQPLPDATLC VLSGLQTEHNRRWPNSVCHFSP DSTFYNDLSGRMKNVRLMFNG IHRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVEIVGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLLLSPESDLYHFERDD FWFPPGDINGREHHLHIILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFYRLEGESAEDGSVMT LRSFLDKDGHPIECRGI*PIKAR HLV\RLMP\VL\RLRECPVLMRR IR\NGTVPNVPNVEVTARQLDF LARGGQARYRLMRRRASNEQR SWRYLDIINRMIERPETRYTREI GFTSTNIDLIYGLPKQTPESFAF TLKRVAELNPDRLSVFNYAHLP TIFAAQRKIKDADLPSPQQKLDI LQETIAFLTQSGYQFIGMDHFA RPDDELAVAQREGVLHRNFQG YTTQGDTDLLGMGVSAISMIGD CYAQNQKELKQYYQQVDEQG NALWRGIALTRDDCIRRDVIKS LICNFRLDYAPIKKQGDLHFAD YFAEDLKLLAPLAKDGLGDVD

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29140	59508	A	29315	1	2237	MLTGYRAVSRHKSQRYTADDA EEMIGKLTGMPIPLNSLRQWIL GLPGDATDYKLDDQYRLSEITY SQNGKNWKVVYGGYDTKTQP AMPANMELTDGGQRIKLKMD NWIRADGYHTLQTLFQFLDYG DTISIELRDDGDIRLLTPVEGVE HEDNLIVRAARLLMKTAADSG/ LSSDGKR/RSSSCARVQSPVSFF GNWWMLGQTTRVSPLCHWAIS SAISHRRAFAQVINIRFKRQTKA GDFQFTGAFIGSRQAISHRRFHL IDNPERFVIVHFARGTDKPRLLG VLCHDKPRINSNAVTAHARAR LKNINARVTIRQANQFPDVNPLI GTNQRHFISKSDIHIAEAVFEPSI IAADRLNPLVNELIIMPDIEKRL DAFVRIAHEELLYLLGILMNPA NKDHVLPLILTGPKESADYFRV LDEFVVHTLGENARRHYRIIIDD AAEVARQMKKSMPLVKENRR DTGDAYSFNWSMRIAPDLQMP FEPSHENMANLKLYPDQPVEVL AADLRRAFSGIVAGNVKEVGIR AIEEFGPYKINGDKEIMRRMDD LLQGFVAQHPGSYNDLLLMEL LPHLLVEGMLISAVSAESLPWL HLSCVANISKRQLICAVPLPKPP KAGLLGKNIMGTGFDFELFVHT GAGRYICGEETALINSLEGRRA NPRSKPPFPATSGAWGKPTCVN NVETLCNVPAILANGVEWYQNI
29141	59509	A	29316	1	2892	
29142	59510	A	29317	19	649	
29143	59511	A	29318	2471	3036	KVTWVTCSILPMTLSPSAAFSSL FRMKILSLK**KRILR/SSGKPAA RQGDMTQYGGSIVQGSAGVRI GAPTGVACSVCPGGVTSGHPV NPLLGAKVLPGETDIALPGPLPF ILSRTYSSYRTKTPAPVGSLGPG WKMPADIRLQLRDNTLILSDNG GRSLYFEHLFPGEDGYSPQRVT VACAPRRGKTG
29144	59512	A	29319	1	1476	
29145	59513	A	29320	688	1578	
29146	59514	A	29321	1	1653	
29147	59515	A	29322	1	218	MLIVFSLPSDTLVLSPL*PNFRT RPFRPSSVPR**PKKDLKIATSA MMEAAYSSVIANVVLVPVMDA KWLAR
29148	59516	A	29323	3	260	

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29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR WLGHDKRATLLLWKLEAAGSP LRPLSVQVTTPQEVAETDNHAD NSYNAGLFIVNSLYTAEGVMD KHSLWQRYVPLVRHEALRLQV RLPASVELDDLLQAGGIGLLNA VERYDALQGTAFTTYAVQRIR GAMLDEL\AAVTGCRAACDAT RVKWHRQ*GNWSRNLAAKPR KLR*RNV
29151	59519	A	29326	1	2349	
29152	59520	B	29327	1	747	
29153	59521	A	29328	275	729	
29154	59522	B	29329	1	2469	
29155	59523	A	29330	1	969	
29156	59524	A	29331	148	1180	
29157	59525	A	29332	56	170	VHA*GSLFFPELSMHQDLSQGH EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	A	29334	482	765	
29160	59528	B	29335	1	1713	
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNTT**A SAPGN/ARWNSYVG*KHH\SCQ WGDYRRQCFRGE
29162	59530	A	29337	1	3189	
29163	59531	A	29338	1	1344	
29164	59532	B	29339	1	1233	
29165	59533	A	29340	1	1572	
29166	59534	A	29341	1	3591	
29167	59535	A	29342	1	843	MNYSHDNWSAILAHIGKPEELD TSARNAGALTRRREIRDAATLL RLGLAYGPGGMSLREVTAWAQ LHDVATLSDVALLKRLRNAAD WFGILAAQTLAVRAAVTGCTS GKRLRLVDGTAISAP/GGGSAE WRLHMGYDPHTF\TDFELTDSR DAERLDRFAQTADEIRIADRGF GSRPECIRSLAFGEADYIVRVH WRGLRWLTAEGMRFDMMGFL RGLDCEVPDPKRRTNSLWRITK MVIWSLQVAIRGTVSLTAYKTQ LKNARHRLNEAPRRRILQMVQ PLS
29168	59536	A	29343	2	3203	
29169	59537	A	29344	227	634	IKTLPLSPDKLTRISKSIYRKQR AALFTHSFTTWVLAILEHRRFF AK*TRSISKAHVISCVAGHTLA AAPQPHYFTRETYSPERVSTLM TSPICTNSGTLTTAPVDRVAGLP PVPAVSPFRPGSVSTISSSTKFG

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29170	59538	A	29345	1	1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29172	59540	A	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTGSPGHRGKPGT REDEHGV/ELRDRRLNFEWWK PEYGINLYQDYYKQDGFVEIPD QNNPSLGDMVIMQIGQNVPVW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGVFHR FAVDSYPEAIRALSSQVDGFKE YMQSEIGSRSKFAIFVDGVNVG HHEEEKFKCAKEIRIVPIPTGSK TGGLFQVVLGAAIMVAAFYTG GASLALMGTMSSSLFMMGGA MVLGGVMQMISPQPGWRNFEV QSSKNKPSYAFGGAVNTTGGGI PSPGPVWISRRRWRNFLSRFLC RGYELKLTRLARVFFRLYNEST
29175	59543	A	29350	1	8043	
29176	59544	A	29351	1	876	
29177	59545	A	29352	2020	2224	CVESRCCHATRCGSK*YSGP\PE DTDLKTEAAGAGVACDAAEAP DEAPPAKLHVLPPIIPEIVLKITI
29178	59546	A	29353	1	2346	
29179	59547	B	29354	50	340	
29180	59548	A	29355	284	520	
29181	59549	A	29356	2	304	
29182	59550	A	29357	79	177	
29183	59551	A	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHDRHHWH\GNRE NKVNCQLICVDIIINTAQPITSES /DQRQH/TLLRRQTRRDRRHWS HEP
29185	59553	A	29360	2	388	YTVSFLLVITQLGFCSVYFMFM ADNLQQMVEKA/TRDLQHLPA QGDSDADPHPGHSFLHADNPA LPDPVGVYPEPQGAVRLLDIGQ HHHPWEHGSDL*VYHGGDSIS QQPTLDGKLEDLLAVLWYSHL
29186	59554	A	29361	467	3014	
29187	59555	A	29362	1	1174	

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29188	59556	A	29363	1	986	MKVTFEQLKAAFNRVLISRGV DSETADACAEMFARTTESGVY SHGVNRFPRFIQQLENGDIIPDA QPKRITSLGAIEQWDAQRSIGN LTAKKMMDRAIELAADHGIGL VALRNANHWMRGGSNGWQA AEKGYIGICWTNSIAVMPPWVP KECRIGTNPLIVAIRSTPITMVD MSMIKHTLPQRAAGTDRKLAM SREAQLLERHGYAFNELDLGK REPVTEEEKLFVAVCRGEREPV TEAERVWSKYMTRIKRPKRFH TLSGGKPQPGKKIVIRPLPGLPV IRDLVVDMGQFYAQYEKIKP/V PVE*WTKSASSRAFTDARAARK
29189	59557	A	29364	99	375	THQPARRFPAYHYAHPAAAAA PGDPLGADLQLCARHYHRQRH CVPRHAGYPRSDGLHPQPRGR WRIRCSDCLRVP\SDRGDAGDY FHL*LADR
29190	59558	A	29365	871	1206	
29191	59559	A	29366	1784	1966	RPLDVSFMSSFTSNSPLTDLVG YLTFSAIFLSWRLSLLSDAA*TP YPPWGSVHCRRFCSL
29192	59560	A	29367	1	1276	FHIKLVLTGATWTALPYCHSHV GLRASLKPTPPFWGRAPLGTRP SQQKTECRLINFPETPIFGNSFK YDIEVSNKSPDEEVKLRRHHLA RCMKNFKTDIYFVSTFEPSTKS VDLLTVETFAGTVCEYADMPK EWTTTRGLYDPTHLISASCHKV EGLFSFEDRTVATLIRLFIHPVK SMRGIGLTHALADVSGLAFDRI FMITEPDGADIAVKTFTGIRLKV PCPPDHPAFSITNHQTEVTALV VFECDIAVRGSDRLRLSPGPGG SNTDWVIFGLLIKENPGSLLAV GVNLLGKILLSVVAAVSESGQN FLSVLPVRSEGPCFVVIDVDVEL PGLRDIADEVKTGVIAVTPAVIP ALWEAEVDVNIAAFRSQKAYIS GQVNKSGQQAITN/DATDYSRG HQKLPCLQSECFHGIYHRIDVA

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29193	59561	A	29368	1	1815	STLEDPHYYHIAEVSPVVIIISIY GATGEKYGFITYRCSEHAALSL TKGAALRKRNEPSFQLSYGGLR HFCWPRYTDYGYFELQINRLAL FSTNVTAETPYMHLAPPVGTQL PLPHLSHDNSSKNSGGCLPGAS VSCNYREPAVRLALASTLPLLR AQSPFFMHKDKDPLFWFLTVPP KWFRKGEVILSSRPRKKTEGSW FPKTFFGFGKSHVLVKEFYNRK HHIAKQQHAVERT\RELFCPKG LG\YSKPQTQGDYAIAQHF/L*T NLPTGCWAKYAVISFMRTD/TV DDKH\WPEEHLAKN*LGLLADS G\IR\IKLPWGAPHEEERAKRLA EGFAYVEVLPKMSLEGVARVL AGAKFVVSVDTGLSHLTAALD RPNITVYGPTDPGLIGGAPENG DSDSALYRLRKEMEEFHLVVG SDIFGKHQHGTETDSTTCPSTLE EFETQWFITGGINRILLATDGDF NVGIDDPKSIESMVKKQRESGV TLSTFGVGNSNYNEAMMVRIA DVGNGNYSYIDTLSEAQKVLNS EMRQMLITVAKDVKAQIEFNP AWVTEYRQIGYEKRQLRVEHF NNDNVDAGDIGAGKHITLLFEL TLNGQKASIDKLRYAPG
29194	59562	A	29369	3	1993	
29195	59563	A	29370	1	1782	
29196	59564	A	29371	1	3858	
29197	59565	A	29372	1	705	
29198	59566	A	29373	104	471	LWWAGA/SYLCWMGYQMLRG ALKKEAVSAPAPQVELPKSGRS FLEAIIYFGSVFSLFVGDNVGTT ARWGIFALIIVETLAWFTVVAS LFALPQMRRGYQRLAKWIDGF AGALFAGFGIHLIISR
29199	59567	A	29374	50	620	
29200	59568	A	29375	194	767	LWW/AGGLYLCWMGYQMLRG ALKKEAVSAPAPQVELAKSGRS FLKGLLTNLANPKAIIYFGSVFS LFVGDNVGTTARWGIFALIIVE TLAWFTVVASLFALPQMRRGY QRLAKWIDGFAGALFAGFGIHL IISRLALIVPGLLQKNGGWRRM AIISAVIALVCHAIALEARILPDG DSGQNLSLLNVGSLVS
29201	59569	A	29376	1	1038	
29202	59570	A	29377	1	513	
29203	59571	A	29378	485	1166	

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29204	59572	B	29379	54	275	
29205	59573	A	29380	2	215	IFLLLLPPHHLLLLLLLLLLLLL LLLLLLLQ/MIPLEFCRLYRKQG CICFWGSLGEILLMAEGEAGAS PSH
29206	59574	A	29381	100	393	FLLLLLLLLLLLLLLLLLPLLL LFSSSFLLLSSSFFFFL\SSFSFSSF SFSSSPSSPSPSPSFFLLSSSFFGV ISLDVVTLAWQSARITGVSHRT
29207	59575	A	29382	264	911	ILGFLRDGNFWRKSQSFFPVHH LLICLLRKSSETMQLTDEHLIHD HPKRPPITELVVPGLHEHLRSN VGDYRCEPPHLTKRNIFCILSEA TDITY*LTSISFPGFCFRLT*LLPL TEITGEAVVQIPIKFCPMCFFQS CAKIWTRGMQWHLEAWRCQK PQSPKGGVTALAQEAPKSGLLE GQFMPMPPQYLAVQKKVVWF DVSVDESKLVNRVYG
29208	59576	A	29383	1	261	
29209	59577	A	29384	3	195	
29210	59578	A	29385	1	399	LERLSAPCISLLLSRSLSSLSLSS LLFFFFFFLLLLLLLLLLLLLLL LL/SPPPLLLLLLLLLLLLLLL LLLLLLLLLLLLDPPGDTIQGA PSRGYHPRDTIQGAPSRGHHPG DTIQGVPSRGYHPGGTIQGAP
29211	59579	A	29386	15	159	SPLHLSLV*VKQLLLLLLLLLL LLLLLLLLLLLLLLLLLLLLL LLLLLLSSSSFLPS
29212	59580	A	29387	17	429	SFFFFFFFFFFFFFFFFFFFF/C LLLLLLPLLLLLHRKHLICVTLG CLRWLGQLCVRLQGSCAWLQT LGWVHTYACVCTFFLDQQVAG RILLVEDPRSSLLQCCLLLDA\P LCCRFQKNMHFIRT*R*VHCSGI TSIQFNLEP
29213	59581	A	29388	3	282	RELLRGGNVYIGP*SILSFFLLLL LLLLLLLLLLLLLLLLLLLLL LLLLVN*GVCCTLLSGPEISCRS DFAQGPTPLQGAPQTALGNLAS
29214	59582	A	29389	3	264	
29215	59583	A	29390	296	421	
29216	59584	A	29391	3	210	
29217	59585	A	29392	1	252	
29218	59586	A	29393	1	1731	
29219	59587	A	29394	1102	1362	NLGTAATLFFLFFFFFFFFFFF FFFFFFFFFFFFFFFFFFLFLFLF L/VPLLLLLLLLLLSSSSCSSP PPSSSSLEKLYLSI
29220	59588	A	29395	3	2368	

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29221	59589	A	29396	1	318	MEKKSPAYFCCRDMQVIHSDA ALQRLLTRFNDPEGWSNLAKN QYLSTSMKQKIWQRALSHRKN NPKADSDAYETSADMILSELIS HGEVDDQMLLNATALIRSDDW DFLESALISWDNLPAVVLKELQ QNTPRNDIWAKFFLRQENSSRA QVDEALRVYYALDPDALAQLD VLAKRPYKTAAFRGEKTHRVP RRSVRQNIIDQADRLHGAQRLV INTNRTRVVDQLIEFLHHQHVN AHLAEIVRHHQPNRAGTSDRHL NAMVNSRLDVRNNEQTEYKTV RGLTRGLMLLNMLNKLDSTSP CRMLVCCVPRAPPNPGGLNPR AHSLNRSP*NPLKLLSPTGPFEG MRPLGTHFWGGIGHGQGPEWG PQFGLGMNLLVKSLGHWATW VLARAKILRFELGASMMVAST
29222	59590	A	29397	2	4002	WQE*VHYIWGVMHGDLGISMK SRIPVWEEFVPRFQATLELGVC AMIFATAVGIPVGVLAAVKRGS IFDHTAVGLALTGYSMPIFWW GMMLIMLVSVHWNLTPVSGRV SDMVFLDDSNPVTGFMLIDTAI WGE/DHGTFMGAAPIRILPAYG LGTIPVAGFGRMTRSSMLEVLG EDYIRTARAKGLTRMRVIIVHA LRNAMLPVVTVIGLQVGTLLA GAILTETIFSWPGLGRWLIDALQ RRDYPVVQGGVLLVAT
29223	59591	A	29398	187	1710	
29224	59592	A	29399	1	791	
29225	59593	A	29400	353	646	FYWNWVPFTNWQNPRLMGQK *HARWLHLRSLLPAM*ATLL*R ENNR*LLLLTLTSIFKTFRIRRLS VSKP*VKAKKKTRLIIWSTSKFL SCMMLKFT
29226	59594	A	29401	406	1023	
29227	59595	A	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLLIEKMRES GDIHSHHGWLHLPDHKAGFSE EQQAIWQKAEPLFGDEPWWVR DSPGYFALMVRAKFNNCVIVFR R*AQQRHRYTDVVVEIACRIKR VAALA
29229	59597	A	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	A	29406	1973	2582	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29232	59600	A	29407	1	1483	MFVLADFGHTRRTNRSLGHNIL PARIAPDAINKWLSGFFSREVQ LRWVGPQMTRRVKRHNTVPLS FADGYPYLLANEASLRDLQQR CPASVKMEQFRPNLVVSGASA WEEDRWKVIRIGDVVFDVVKP CSRCIFTTVSPEKGQKHPAGEPL KTLQSFRTAQDNGGGEGEARA ANTGATHRGRHRSPSAVRYRD RLNMYVLRRMDLLYRVKTLW AALRGNHYTWPAIDITLPGNRH FHLIGSIHMGSHDMAPLPTRLL KKLKNADALIVEADVSTSDTPF ANLPACEALEERISEEQLQNLQ HISQEMGISPSLFSTQPLWQIAM VLQATQAQKLGLRAEYGIDYQ LLQAAKQQHKPVIELEGAENQI AMLLQLPDKGLALLDDTLTHW HTNARLLQQM\RAGGWSVKEG REKEYFQSPRGWGRSLMPSLGI IIRPP*RKPKNTENRRCISASVTS EKEAPETINQYKAAVRRPFLFL ATALAQSEVRVCIAWTN
29233	59601	A	29408	2	1406	
29234	59602	A	29409	1	1818	
29235	59603	A	29410	441	583	GVYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGLSS VSSR
29236	59604	A	29411	835	1143	RQLPVSLYVRAVAFENGCFGSC SVGG*GPPAARLGEEQVRGGSS SPCIIRAPRRLHSFLLLLLLLLLL LLLLLLLLLLLLFHLSSSSSFSST SSSSSCSRSFM
29237	59605	A	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	A	29414	1002	1145	GVYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGLSS VSSR
29240	59608	A	29415	2	289	
29241	59609	A	29416	1	919	
29242	59610	A	29417	329	405	
29243	59611	A	29418	48	268	
29244	59612	A	29419	2	4625	
29245	59613	A	29420	1	867	
29246	59614	A	29421	1	684	
29247	59615	A	29422	409	543	
29248	59616	A	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	A	29425	3	202	
29251	59619	A	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH S

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29252	59620	A	29427	1	1774	
29253	59621	A	29428	3	184	MSENMRCLVFCPCDTLLRMMV SSFIHVPPKDMMSIFSICLSAASI SSL*ASVCSYPSLNF
29254	59622	A	29429	667	834	
29255	59623	A	29430	1	738	
29256	59624	A	29431	39	230	QMAQHLPHLVFGSHSGSLWEL LSH*VYLLILSLPPPHTPQQAPV WDVPLPVSKCSHCSIPTYK
29257	59625	A	29432	985	1205	IPGSRGKNWVVTGTGQGCHRG PAESDGPAG\GARHWEQPPA*Y LVLFLCSQRRWPGRQQRGQSG RSWPSVRAAP
29258	59626	A	29433	339	592	PLQAWGPSLCS*AIGTPSRKPSP STAHVKHRRLCIPTRRGFSSDN WDPVSSPTCNDARQLHAQVDL EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFQLHPCPFFQGS*LLCI GLAHAPLAQRSLLLSTF*CLLLS IHQTHSPSSFCPLLARSCDPLEE KRHSGFRNFQPFCSGFSS
29260	59628	A	29435	517	603	
29261	59629	C	29436	1	1188	
29262	59630	A	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIISEGSVLFHWSISLFWYQ YHAVLVTVVL*YSLKSGSVMPP ALFFWLRIDSAMRALFWFHMN FKVVFSNSVKKVIGSLMGMAL
29264	59632	A	29439	1	1308	
29265	59633	A	29440	162	377	YSHCSIYTRKIQFLCCPSIKTHL GTNLTS*TFFT*VNIISIYLEASLF FSFLDLGRADKGSSLTGVRSIIT
29266	59634	A	29441	1	480	
29267	59635	A	29442	731	850	
29268	59636	A	29443	531	845	
29269	59637	A	29444	11	649	
29270	59638	A	29445	1	2433	
29271	59639	A	29446	1247	2420	
29272	59640	A	29447	29	94	
29273	59641	A	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGGRRSSTSGKGTAGCPQSPCF CRCSTLRRTAASPGISPPCPKICS CSPLESIWMSNGLCRSCPPSEDS TCGC*GCCCCCCCCCCCCCCR RRCPSLGSDAGTELETQRPGAG TGPGPTVAPATFLQSRRLMVGA GTPTLGVRTPGFGLQLGFFYWL EDVERDTS
29275	59643	A	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

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29278	59646	A	29453	1	599	
29279	59647	A	29454	1	504	MWNCLTNKLLFQESLQKTATR LSAFSWEEAKVQLSWVVLNLA TSAMLPKFYPNEIKVTYLRCTG DEVGATSVLAPKISPLGLSS/VK ALKEPPRARKKQKTIKHSG\NIT FDEIVNVAQHMWHRSLARELS GIIKEILGTPQSVGCNVDGCHPH DIIDDINGGAVECPAN
29280	59648	A	29455	1	1269	
29281	59649	A	29456	434	655	PFSSPASSSGR*KTTSFPAKLFN ACRISLLASAEVNPNISAYLAT WISQIPSCSCRVPSDFLIWSTNR YSIRF
29282	59650	A	29457	1	801	
29283	59651	A	29458	2	722	GRVGGGGQGANYLRVVPESGV YSTPSRLPPLPPKVRPPTRFKSV YLEVAPKGE\VGA\TSALGPQRI GP\LGPVSKKKLG\DDISKA\TG\ DWKGP*GITVKLT\IQNRQAQD *GGCLSASALIIKALK\EPPRDR KKQKNIKHSGNITFDEIVNI\AR QM\RHRSL\ARETLWNHLKRSL GTAQSVGCNVDGRHPHDIIDDI NSGAVECPAVSDIFIVTVGVKG GPPSVFTEISWEVLEMVTGGVG
29284	59652	A	29459	1	330	
29285	59653	A	29460	140	214	
29286	59654	C	29461	181	381	
29287	59655	A	29462	427	957	
29288	59656	A	29463	3	241	WLRAERAPEGSPETKGS\PPPPP RSVLHLSA\SSPGLRPPEGL*TC RGSPSADSPRRGKHGGKTTHLV SWLSQQKIPMAR
29289	59657	A	29464	122	473	
29290	59658	A	29465	1	771	
29291	59659	B	29466	1	1017	
29292	59660	B	29467	1	2568	
29293	59661	A	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I SQ*PQQRYECRDNQQPLDQL/V/ EQFIQTLEKAITQHRQQLNQWT QKVDIARRR
29294	59662	A	29469	1343	1714	
29295	59663	A	29470	321	2645	

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29296	59664	A	29471	611	1215	RWCVWSLFLQML/EMCPEFLPS GGFVVSLTSGVKLQTFTVNVTA HKGSVDPKRVKLKTLAVSVTA LKAACLELFLLPGGFVVFAGFR SEAADLCAEGASSGLGQPREGL PRCSGGLKGSSSAARMGAEAK GAPRASQGCEGRHHAVTSHRS DMGEEEGESQRYLSCPQPSCPI NLLQEDASKVIVFAESGINPDSV LDLIMLH
29297	59665	A	29472	335	453	KYIWNVNLQHSVSMLL*FITS*L SGMDSLFPAAHCV
29298	59666	A	29473	1	1041	
29299	59667	A	29474	3	874	TEGQKNLIVEVTSNDAVRFYP WTIDNKYYSADINLCVVPNKFL VTAEIAESVQAFVVYFDSTQKS GLDSVSSWLPLAKAWLPEVMI LVCDRVSEDGINRQKAQEWCI KHGFELVELSPEELPEEDDDFPE STGVKRIVQALNANVWSNVVM KNDRNQGFSLLNSLTGTNHSIG SADPCHPEQPHLPAADSTESLS DHRGGASNTTDAQVDSIVDPM LDLDIQELASLTTGGGDVENFE RLF\SKLKEMRDKAATLPHEQR KVHAEKVAKAFWMAIGGDRD EIEGLSSDEEH
29300	59668	A	29475	1	1773	
29301	59669	A	29476	1	1023	
29302	59670	A	29477	2	616	
29303	59671	A	29478	1	972	
29304	59672	A	29479	1	339	
29305	59673	A	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG EGTYGTVFKAKNRETHEIVALK RVRLDDDDEGVPSSALREICLL KELKHKNIVRCAGGGCSLPVW PLGGGGG*HWTSVRRTCLAEPF FCPRLHDVLHSDKKLTLVFEFC DQVKGGVWRTVALGR
29306	59674	A	29481	1	843	
29307	59675	A	29482	1	873	

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29308	59676	A	29483	13	945	NRGPAGVPAAAAMQKYEKLE KIGEGTYGTVFKAKNRETHEIV ALKRVRLDDDDEGVP\SSALREI CLLKELKHKNIVRLHDVLHSDK KLTLVFEFCDQDLKKYFDSCNG DLDPEI\VKSFLFQLLKGLG\FCH SRNVLHRDLEAPATWLINREW GSWKLG\DFGPGVRAFWGFPV\ RCYSAEV/VSHLW\YRSPDV\LF GAKLYSTSIDMWSAGCIFAELA NAGRPLFPGNDVDDQLKRIFRL LGTPTEEQRPSMTKLPDYKPYP MYPATTSLVNVVPKLNATGRD LLQNLLKCNPVQRISAEEALQH PYFSDFCPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE
29310	59678	A	29485	3	1225	
29311	59679	A	29486	1	864	
29312	59680	A	29487	1	1413	MVNPVFFDITVDGEPLGRISFEL FADKVPKTTENFRALSTGQKGF GCKSSCFHRIIPGFMY/QGGDFT RHNGTGGKSI\HGEKFDDENFIL KHTGPGTLSMAIAGPNTKGSQL FIYTAKSEWLDGKHVVFGKLSR GDSLKEPTSIAESSRHPSYRSEP SLEPESFRSPTFGKSFHFDPLSSG SRSSSLKSAQGTGFELGQLQSIR SEGTTSTSYKSLANQTRNGSLS YDSLLTPSDSPDFESVQAGPEPD PPLGYTSPFLSARLAQQREAER HPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLPG REEEPGLGDSGIQSTPGSGHAPR TSSSSDDSKRSPLGKTPLGRPAV PRFGKPDGLRGRGVGSPEPGPT APYLGRSMSYSSQKAQPGVSET EEVALQPLLTPKDEVQLKTTYS KSNGQPKSLGSASPGPGQPPLSS PTRGGVKKVSGVGGTTYEISV
29313	59681	A	29488	1	3126	
29314	59682	B	29489	46	114	

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29315	59683	A	29490	1	704	AALLALGPRNPWTLWTPLTPN YPDRQPWTDKHPDLLTCGRCL QTFPLEAITAFMDHKKLGCQLF RGPSRGQGSEREELKALSCLRC GKQFTVAWKLLRHAQWDHGL SIYQTE\QRPRRPRSWAWPRWL QPCRQWWGQQLRPRAPV/HSG SGLTRRSPTCPVCKKTLSSFSNL KVHMRSHTGERPYACDQCPYA CAQSSKLNRHKKTHRQVPPQSP LMADTSQEQASAAPPEPAVHA
29316	59684	A	29491	3	1605	
29317	59685	A	29492	1	453	
29318	59686	A	29493	2	128	
29319	59687	A	29494	1	543	
29320	59688	A	29495	39	1092	
29321	59689	A	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/ TLRPKAL*LTPSQIFSA*RLKTD TARSPRKPPSFQGPVSLASITVV GIDGQASKPLKTPQLWCQLRQ YSFK
29322	59690	A	29497	1	281	VSDHAGTPALVLHP*RQVPLF* GRGKYPSTPSPSPLAELATSAR NLTTRPRNACSPGFLPSRVPSVR DPTGNRTVQLTWQPLPEPLEL WPKAL
29323	59691	A	29498	1	542	MRAPPKSGQLQHCRPSRGALRS GDLPWEINPLSSCSLLHEKDPP MTSGPQTNQPKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAPIPYFRTPTSY LCAPIPYVRTPTSYLCALTPFPL FWRHIRTSKRLN/LQQPGIPPEPP PPG/CLLQVPEI*PPGQGMPAAQ
29324	59692	A	29499	1	1044	
29325	59693	A	29500	596	833	LLLDLPAED*CCLIASEAP*TITD AEL*VTLTVEGKSVPFLINTEAT HSTLPSFQGPVSLASITVVGIDG QASKPLKNE

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29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCTPTPYFHDPTPFPLFW KELATCAGNLATGTRNAGSPG FLLSRVPSVWDPTENRTVQLT WQPLPEPLELWPKA/HLTDSFP DLLGLAA\ED*HCTIASEAP*TI\ TDAELWVTL\TVEGKPFPFLINT EATHSTLPFFQ\GPVSLASIT\VV GIDG\QA\SKPLKTPQ\LWCQH* TIRRFKHSFLVIP\TCQVPLLG\E DTLTKLSASLTIPGLQLYLIAAL LPNPKPPLRPPLVSPDLNPQV*D IGVEWGKGD
29327	59695	A	29502	6958	7935	
29328	59696	A	29503	1	486	
29329	59697	A	29504	1	492	
29330	59698	A	29505	2	502	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFMCQGGDFTRHNGTGGK TSKKITIADCGQLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKV\PKPAENFR/A L*SIEEKGFGL*GVPCFHR\IIPGF YVSRGGDFTPP*MAPGGQVHL MGKKFER*RTSSLKHTG\PGHL VPWANAWTQTQMGSQFFICTA \KT\EWLDGK\HVVVLAKVKER HEILWEAM\ERFWVPGNGKT\S KKIISIADCGQLLISFDLCFYLNH QDHSLLCSPLRESTPLPHLLAGS
29332	59700	A	29507	1	380	LCCSPCRRRLLGREEAGEEPTSP VTQYLQPRSPEECKMFACAKL ACTPSLIRAGSRVAYRPISASVL SRPEASRTG/EGAATVGVAGSG AGIGTVFGSLIIGYARNPSLKQQ LFSYAILGFALSEAMG
29333	59701	A	29508	76	385	EEPTSPVTQYLQPRSPEECKML ACAKLACTPSLIRAGSRVAYTP TSASVLSRPEASRTGEGSTAFN GAQNGALHL\IQRELHTSAIRRD IDTWCKFIGCSAATE
29334	59702	A	29509	2	230	
29335	59703	A	29510	242	427	SAPDLTCNSKTWKNGRIICFHP ASLVSLY*QPQLASWTMKKQD ENTQEGKSWDSFSRDVIHI

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29336	59704	A	29511	1	1497	
29337	59705	A	29512	199	766	EEPTSSCHPNISSRAVPEECKMF ACAKLAMRPPSLIRAGSRV\AY RPIS\ASVVISTQRLSRTG\EGST GI*MGPQNGVS\QLIPKGSFQTS CNQAGGHLITGCQIYLGAGCLQ Q*GVGWFLVAGIGNSLLGKPYP LGYGQKTLSPESQQLVPP*CYP GDFALALKLKAMGL\FC\LMVA FLILFADVTEITA
29338	59706	A	29513	427	840	
29339	59707	A	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ*DGTLLC\RR CGS*GLPTFKKSTCGKCGYPAK RKRKYNWSAKAKRR\NTFGTG RMRHLKIVYRRFRHGFREGTTP KPKRAAVAASSSS
29341	59709	A	29516	1	668	
29342	59710	A	29517	649	992	
29343	59711	A	29518	1	2994	
29344	59712	A	29519	3	486	
29345	59713	A	29520	2	898	NSRVDDFVCPRSRRSKRDLIEFS CRIILFPLPSLPPRISFHPSPTLAR VRIGGAVRRPHQSHSISSSSFGA EPSAPGGGG\SPGSLPRPWGPKS CSSSLCGARS*FFWRDVKN\TGL VFG\TTLIMLLSLGSFSVSSVVV S\YLILGFSSSVHHQLSGI*QSSVI PSCNRKFRKKGHPFQKPNWNV DITLSSKSFSINNMNAAMVHIN RALKLIIRLFLVEDLVDSLKLAV FMWLMTYVGAVFNGITLLILAE LLIFSVPIVYEKYKTQIDHYVGI ARDQTKSIVEKIQAKLPGIAKK KAE
29346	59714	A	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGFFFTQVANIIS VAWNLVFCIRFLENTVGIVTI*R RCPIPFSWAF
29348	59716	A	29523	1	4368	MLFSYLEKYFYVADELSHCVEP EPSQVPGGSSRDRQQGKPPPLP ALKAKTSSRSGPYATEIKKSTD DSIFKVLDWFNRSSYSDDNK/LI PPTSPRNRVQRKNR\PKSQVAV DLVTDDTTLRENGSKTLSPSKIE LKPVRSDSPFQAEGDMLVSESC QDNNVNIKSKFMNLSQKGTPK EGPGILQPFESYGTPSQGSKNM DYSQDSKSPGKGNGASPSNSNY SYSVLKESDAENQVPCNTNNIG NLGEEEPKFHAH

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29349	59717	A	29524	33	3339	TDQAKVDNQPEKLVRSAEDVS TVPTQPDNPFSHPDKLKRMSKS VPAFLQDESDDRETDTASESSY QLSRHKKSPSSLTNLSSSSGMTS LSSVSGSVMSVYSGDFGNLEVK GNIQFAIEYVESLKELHVFGAP VEGLNSSGWKKTGVIPY*KG\Y LLPNKGQMGKKKTLVVKKTLN PVYNEILRYKIEKQIL*TQKLNL SIWHRDTFKRNSFLGEVELDLE TWDWDNKQNKQLRWYPLKRK AKALQRFQLKAMGNS
29350	59718	A	29525	946	1183	
29351	59719	A	29526	2048	3359	
29352	59720	B	29527	1	300	
29353	59721	A	29528	1	1495	
29354	59722	A	29529	1	2769	
29355	59723	A	29530	450	3061	
29356	59724	A	29531	421	1464	
29357	59725	A	29532	238	930	RLSLVSSHCGTILSSEVVCAPPT AYIDFARQKLDPKIAVAAQNCY KVTNVAFTGEISPGMIKDCG/AT WVVLGHSERRHVFGESDELIGQ KVAHALAEGLRE*FACIG\EKL DER\EAGIH*GRLFFEQTKVIAD NVKD\WSKVVL\AYEPLLAIGT CKTSTPQQAQEVHEKL\RGWLK SNVSDAVAQSTRIIYGG\SVTGA TCKELASQP\DVDGF\LVGGASL KPEFV\DI\INAKQ
29358	59726	A	29533	1	929	
29359	59727	A	29534	3	623	
29360	59728	A	29535	3	202	
29361	59729	A	29536	1	1046	
29362	59730	A	29537	1	1320	
29363	59731	A	29538	1	1052	
29364	59732	A	29539	922	1245	NRCLGNSFKCFLCILQVGRAHA FLLCSDFMPCEAVCSSIIYSFIPV TKTQGAAPHTR\AHSLTPDPKPS CCCCCCPRPGEDPGHMCVVWP WQPSVIYAKYWTYEHAQW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS GHYALQEAQETSQSGRESQA
29366	59734	A	29541	1364	1916	
29367	59735	A	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ PWAMIIDVFS\RYSGS\EGSTSDP *PKGE\LKVLMDKELPRLSLQS GKDKDAVDKL\LKDPGRPMGD AQGGTFSEVHPCSVAAIT\SA\C HKYF\EKAGLKLMPWEMFTDF LGQSIGSQGFPKMFCLGIYFP

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29368	59736	A	29544	175	355	FSQQLLGQAD**SFLL\GCSRLL TAVSRPKRPGEAGITPRVRCLLS NMKDILVASKFWQL
29369	59737	A	29545	482	1196	
29370	59738	A	29546	196	818	
29371	59739	A	29547	170	370	
29372	59740	B	29548	147	257	
29373	59741	A	29549	1	1278	
29374	59742	A	29550	2	152	
29375	59743	A	29551	2	187	
29376	59744	A	29553	1	915	
29377	59745	A	29554	62	430	RQQDELALIAETLKCVDH*LSL DVLPRGCA*HRELCIHDLLKGN PLRRNILAG*TQERMQLQVESQ SIPEEILGLQPQLGPMGGLWNV RFLLIPTVLWGFHCSQERAFPR KLQVKSFPVAQG
29378	59746	A	29555	149	381	
29379	59747	A	29556	1	656	
29380	59748	B	29557	146	1320	
29381	59749	A	29558	629	1417	WCASHWGSGHAARHA*ASHPL HGLLCSPSLPEEHHPLLHGAQS HRPPKG*GM*AHGTGLAGSSTC SPAQGL*IHQSAPCV*LKVCECT NRHSVSSCSDEDVCICSLCLGQ* GP/ECI*CRIFLGPFNRLIEGAPH L/CRSAMLNPLQEGAREQASAR SGWLLRLLTQEQLLCRACIQTR RDREGKTRHRKGTPEIGKGRAF WKKSLKIILILFNCLRYWNAYM EIWVPALTGIPPNVTVNYATSSS KDSRTDGRVDLLMAVTDGM
29382	59750	A	29559	318	608	ISQARRAAPWGPVQPEPSR*APP PASGHPVPSTTQRLRSAGARRG TGGQLHLQPRCGDPLGETSWA PESRRSAASLLKPARPRAHWEE QTTPDALL
29383	59751	A	29560	88	564	SCLPVLRRALAFLSPWVVDGTG RRGAAGGGRWGGSGRTGAHG VGGRLRHGGLQVPSPALQEGS* GSVRNRAQ\PGGLALLGDPVHP LQPLARVLSPSLPG/DQQGWPA APSVGPTKPTPTRNSSWPPSAA HSPGSCSCLSLHTSLESCRCPSIN TSLHKHA
29384	59752	A	29561	3	339	RYKDSPRPHQTQEPSWLHLVDP APRLQVELPASPALCARIPQPLG G\HGTGRRGQGAALVGEARAG LPSLPSFFFSFLLSFLSFFLPSFPL FFSLFFPFCPVNCGEQCPIGKM

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29385	59753	A	29562	327	890	VMRIQVLLYYLRFADQGTGFH LVLCLRHTAGVQ*SWDS*SGLT PELV/HLDGSHV/LAASPRGSPG/ SPK*MGADQRSSESSPGPQPGG PRAEGPHHIQEAPRSA*AQGAG AEAARLGAGQASGCQSTRRPA GSRREPGVSLDGGHRAVVGIQF QAPSRRAAWGHPLHDAPGRRL MSRQLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGQWLRKVYWVPQQCRPTG AVLDFSPGCSCLPAGQGSGPAA RHA*ASHPLHGLLCGPSLPDEH HPLLHGAQSQRPPKG*GMRAH SAGLAGSSTCSPGAGSTR*SQL GS*VW*GRGESLCL
29387	59755	A	29564	1	2715	
29388	59756	A	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ KLLHFLYSLQKGISPNAIPPHSP HPTTAPVYSSQCERRRRQVISAF PT/GD*SLHSN*E*QGGVEGEAP AGTWAVRGA*GPAGVPGGRGL GGLRTRSSWPALLAPGRQGSGP AARH/GLSLPQPPWAPVQPEPP* GAPPPAPRRPVPSATQGLRSAS ARRRTGRQLHLQPPCGIHLVKP AGLLSLVGTWRVFMS
29389	59757	A	29566	1	470	MGQPLLLVRDSGGLQLWQKV KGEPVQQHERRIIPPAREEKVK RSPAGPPPSGGLDSSRHKIPSHE QA/SGVQPACRTNHQPRGIWCS PSLPDEKCPLLHSAQSHRSPKG* GVRAHGVGLAGSSTCSPSAGSN G*SQLGS*V*NKGR*IYPRTGRC
29390	59758	A	29567	777	1063	QLPPPSVFPTTPKTELVLGTPGH GQPHRGGHESSDSAGGHLP/LR ALRSGWDPSPPSSVCATPTSSGL SSTPQLPLHQRTSSSTASWSPG WGMGSC

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29391	59759	A	29568	195	1899	GSASGVVRSSRWARGLAGFRS EAADLHSECYSS*KQCGPKD*A EARFIAKSEGTKLPQCGRGPH*I QRFSTSPPDSGAQLASPSGSRTR AAGGAACQSWCRAP/STPQPLG GRWDWAPWSRGWRSSGTSGR TGAHGAGGR/PQAWRAAGPQP CPAGRQLRPETLKQNIILSLIQCI GASLVPTGTAELEPSPSLQLRGT TDAAQAIKNEFARVQKRNLCR RGPICFEGDALSWFFEKINKIDR RLARRIKKKREKNQIEAIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDPYTLPRIS QEEVESLNRPITGSEIEAIINSLP TKKSPAPDGFTAEFYQRYKEKL IVLEVLARAIRQEKEIKGIQLGK EELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSGYKINVQK SQAFLYSNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKE NYKPLLNEVKEDTNKWKNIPC SWIGRINIVKMAILPKIEKQTWN NSQTLQCQPFCESDVCTSTLQIQ ERFEVAPLHKKALSSEEITIDKT DPSPAIEELTV
29392	59760	A	29569	77	640	
29393	59761	A	29570	384	746	APWSRGWCSSGRLGLHRSPWS GWEAQAWRAAGPEPRPAGRQL GAMSCKVETGT*DSEQRHRFG ESWGHPWAGAQPTGPVLSGIL NVLSSFSVLALPRPTGWPRPCS AASPSRCPAQSHQH
29394	59762	A	29571	189	545	GLSCLPAGQGSGPAARHV*ASH PLHGLPCGPSLPNEHHPLLHGA QSHRPPKG*GMQAHDAGLAGS STCSPGAGSTR*SQLGS*VCCTG RLVGTQQLRPESG*VSQPSPRL WAAAEGSC
29395	59763	A	29572	87	374	AYSSQLGESRRYSLDQCLAK*I CEGRTCIFEEPCNCSSLYVRSNG GNHSHSTTTFKYNGSNWIPRW QGPSGSTQPSKARRPVAFSQGN CAMEKGN
29396	59764	A	29573	1	2453	
29397	59765	B	29574	182	1356	
29398	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS LGLSCLPVEQGSGPAARHA*AS HPLHGLLCGRSLPDEHRPLLHG AQSHRPPKG*GMRAHGAGLAG SSTCSPGAGSTRNREN

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29399	59767	A	29576	142	442	PKGVGRALAAFPQDRAPGPAA RHA*ASHPLHELLCGQSLPDKR HPLLQGAQSHRPPKG*GVQAQ GTGTGRQLHLQPWCGIHWVKP AGLLSSLGPRCFYKL
29400	59768	B	29577	1	2464	
29401	59769	A	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL SPWVVDGTGCRGAGGGAHRG GSGRTGAHGVGGR/PQAWQAA GPEPCPMGRQVRPGEKSSAVPV GQPGWGTQYTLRSHWLGC
29402	59770	B	29579	1	2598	
29403	59771	A	29580	1	2028	
29404	59772	A	29581	5917	6355	QEAQPEESANDAQGDGPPGGK PQPQPEERSSCAQGVGPPGGQQ ESQDEERSSDAPEDGPPGGQQK PQPEERSSDAPEHDPPGGQQQP QPEERSSDAPEHDPPGGQQQPQ SEERSNDAPGDGPPGGQQQP*P EERSSGAPGHSSPDV
29405	59773	A	29586	875	2090	
29406	59774	A	29587	228	505	MLGRKPNHTSASRNTRLRHCSR ARAQVKRMRQQRREEREAK\R QPGTASGTSGIAERDSGKCSRK RGVQKVPG**NTRQSKLRPREQ CTTADP
29407	59775	A	29588	188	592	AAPPRSPSYRMIRKTR*MLGR/E AEPHVCQQEHQVEALQHGQGP GETDATAAERR/RGRQRRQPGT ASGTSGIAERDSGKCSRKRGVQ KVPG**NTRQSKLRPREQCTTA DP*TLSTFPEGRGTELEPGFDSG ASVLMRGCRAALSASSSP\QGP GPQEM*ATRNSWGRRQ*GRHC KLPVLITGLQGDVVEGVHVGC ASQEPLIQNDQEDEVDAWQKA EPHVCQQEHQVEALQHGQGPG ETDATAAERRAGGKDASLVQH LVPAVLLSVTQGSVPEKEEFKK SLVNEILGKVNYDQGNNVPQQ TLEHCPPFPKGEARSWSLASTP

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29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRRQPGTASG TSGIAERDSGKWSRKKREFKKS LVNEILGKVNYDQGNNVPQQT PSHHPNLEHCPPFPKGEAGAGA WLRLRGLGSYEGLPGCALCFFF PSRVLGLRRCEQQEIAGQQQGR DTQHGQQ/RSAEGRGRPG*GPG RTGPPAAQLPQSLRTTRRSRPW GRRQ*GRGR*PPQGLMRC*RRP HHTGWSPQNEKRQPGRSFQQH KSH*RE/RR/RARPVGQQVKAK RSQQFDDECGEDVRQEHSSRRD RVAVKS
29409	59777	A	29590	2	394	
29410	59778	A	29591	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESPSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
29411	59779	A	29592	1	561	
29412	59780	A	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W TALWEMLYAEEANPFSTIRILF QLEQPALGTSQYKILCLSST
29413	59781	A	29594	2	704	WRGGSGSGGWESGRRGFFVAL PERSGVCQVVSIMFSFNMFDHP IPRVFQNRFSTQYRCFSVSMLA GPND\RIMPPSALDQLSRLNITY PMLFKLTNKNSDRMTHCGVLE FVADEGICYLPHWMMQNLLLE EGGLVQVESVNLQVATYSKFQ PQSPDFLDITNPKAVYLFQISGV LLDKGECAGECVCRLENALRN FACLTTGDVIAINYNEKIYELRV METKPDKAVSIIECDMN
29414	59782	A	29595	1	1680	
29415	59783	A	29596	1	2220	

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29416	59784	A	29597	2	1114	SGRRGFFVALPERSGVCQVVSI MFSFNMFDHPIPRVFQNRFSTQ YRCFSVSMLAWPNDRSDVEKG GKIIMPPSALDQLSRLNITYPML FKLTNKNSDRMTHCGVLEFVA DEGICYLPHWMMQNLLL\EEG GLVQVESVNLQVATYFQELSSC YLPHW\LMQNLLL\EEGGL\VQ VESVQPFKWATY\SNFQPQSPD FLDITNPKAVLENALRNFACLT TGDVIAINYNEKIYELR\VMETK PAKPVSIH\ECDMNVDFDA\PLG YKEPERQVQ\HEESTEGEADHS GYAGELGFRAFSGSGNRLDGK KKGVEPSPSPIKPGDIKRGIPNY EFKLGKITFIRNSRPLVKKVEED EAGGRFVAFSGEGQSLRKKGR
29417	59785	A	29598	15	569	
29418	59786	A	29599	30	525	YCLHHFFFQVSLLVFAWCSEM HGNRQLWE\RTGEMGRRTPGL SWTAKSPIGR/RSLRSARVPRTV AHSQRAKGSHSLWVLRPQKRR CAGKSPPPSRLARSPRCPEPLVA LARQPLCVRRAGPEERARAQR RPPRVPPLLSQPGRALLLLLLRS SFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	
29420	59788	A	29601	758	1076	LPMNRPPRWTGTILAPIIELLLE LQQKENMALGSRTHHGSSPNS GSAFCQMACCSSLKPAL*SGRC SQP*WLWMSPLSRIFSISNSTSA SSSIGNAIRRRRSRPGP
29421	59789	A	29602	632	835	
29422	59790	A	29603	428	1214	FIAITVLPHWRSPQWYYPYWRG PVTA/LVRKVPAVAGERSSLWS VVGLIWKPGLGLALQGVGFAVI GTFVSLYFASKGWAMAGFTLT AFGGAFVVMRVMFGWMPDRF GGVKVAIVSLLVETVGLLLLW QAPGAWVALAGAALTGAGCSL IFPALGVEVVKRVPSQVRGTAL GGYAAFQDIALGVSGPLAGML ATTFGYSSVFLAGAISAVLGIIV TILSFRRGQETAHQPDQQRAAY DLQRSNRRVLPASPASACRCSD AHSR
29423	59791	A	29604	1	825	

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29424	59792	A	29605	242	945	NGCIVRGKTSGSTFICVAMSVA ASTVRR*CWLPGRKAAAWRTC WAPMT*AVMC/WSRLMYGAR LSLLVGCLVVVLSLIMGVILGLI AGYFGGLVDNIIMRVVDIMLAL PSLLLALVLVAIFGPSIGNAALA LTFAGLPHYVRLTRAAVLNCL APLIVQASLGFSNAILDMAALG FLGMGAQPPTPEWGTMLSDVL QFAQSAWWVVTFPGLAILLTV LAFNLMGDGLRDALDPKLKQ
29425	59793	A	29606	1	2433	
29426	59794	A	29607	1	1383	
29427	59795	A	29608	1	218	
29428	59796	A	29609	1055	1873	
29429	59797	A	29610	3	823	
29430	59798	A	29611	183	1163	
29431	59799	A	29612	4375	5125	
29432	59800	A	29613	1800	2031	
29433	59801	A	29614	2	848	
29434	59802	A	29615	886	949	
29435	59803	A	29616	123	315	
29436	59804	A	29617	34	343	HLCSYGRVYAADPYHHALAPA PTYGVGAMNAFAPLTDAKTRS HADDVGLVLSSLQASIYRGGY NRFAPY*MTKP*KPSNVGRKEA FRGLSIAIHAVVHHFSNS
29437	59805	A	29618	1	305	AAAYRGAHLRGRGRTVYNTFR AAAPPPPIPAYGGVVYQDGFYG ADIYG\VMLHTATPSLPLPLPLP TVTVTDEFMTFSPLSPLTCSSPH LRRWCHECFCTFD
29438	59806	A	29619	1	2115	
29439	59807	A	29620	1	273	FFSRVVPP\DSYQAQA/MVDIVT ALGWNYVLTLASEGNYGESGV EAFTQISREIGYPSLFGIQGCLHE CFAILCQVVYQFLLLMQLSDAQ TVY
29440	59808	A	29621	1	405	
29441	59809	A	29622	1	582	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29442	59810	A	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS ICYSHGRDLAPARPAQPPQPRD QPQVRPLCSPHAAAAAAAAAL TWSCGPPAGFLTAPSAGSRVRL AARQQKAAPRKASAEPRDKKP LAPKLPQNALLVGKGESPRFIPL SVFFSKTFQRTARILKRSASDRL PWVTSRTCPGGIRTCPAEMTRY LRFANLTGGISEVSGFRDESGIN FGSWIAIPPVEKMVCEGKRSAS CPCFFLLTAKFYWILTMMQRTH SQEYAHSIRVDGD
29443	59811	A	29624	1	2740	
29444	59812	A	29625	1	1614	
29445	59813	A	29626	88	540	
29446	59814	A	29627	2	577	
29447	59815	A	29628	1	2169	
29448	59816	A	29629	1	1619	
29449	59817	A	29630	674	867	LDGDGIESINSLGQYGHFHDIDS SYP*AWNENVLPFVCILFYFVE QWFVALLEDVLHVPCKLDS
29450	59818	A	29631	746	1985	
29451	59819	A	29632	1	2211	
29452	59820	A	29633	139	247	KTSAAHEKPKWRKE\RNARG* KRKRRKMLQRSQVNR
29453	59821	A	29634	335	556	
29454	59822	A	29635	1	586	
29455	59823	A	29636	908	1260	
29456	59824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA LSPDEFISPVCWLARLVRWRCF FAQKAR*SPAKYGILGELTTGS KLVKANGLMEASTIAAILLGSV AGGVLAYWHVLVAWPHAHWP TVSRQQQQLMASTLPFTSPLAQ IFPWRAITQRTMRMPFVIDARD ALLQGVFAAVNPSAHLNDSRH RRINKNVIEPGISCQRPQHLDRI AHPFGIHIHQLNAFTGRQFHRQ QLLYLRQTFVVDIDHHHPRRLY AAVNGVIDSANAHRTCTRQQC NIAARFDAHAMLINILRGVIIGM ISTNNAAHRLCQRRRSKIRSRDT GNTQPKLMQI

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29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH CWTTAVACHQCEDAPCANVCP VDAISREHGHIFVEQTRCIGCKS CMLACPFGAMEVVSSRKKARA IKCDLCWHRETGPACVEACPTK ALQCMDVEKVQRHRPRLNFLR LWYVVHAHTLMRMRPRFIQPW EEVVPRHHQHAACFQALIELLG RNGQILKP
29458	59826	A	29639	391	812	HSALCSCRMRRERLIRPTKTCK FNRLQRLCRPDKRSASGNFAVV IRLERVSLLAPFFYGVLLLKCL MPKRQCNEADHHQTHTCAGQ KKMATHPLPGENKFIIGEDREY RWALMFPNENAPVCWVGHVR *KSPLHQHIDRA
29459	59827	A	29640	589	1075	
29460	59828	A	29641	1	435	
29461	59829	A	29642	9	661	
29462	59830	A	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	A	29646	114	851	CDHRNIVIRSAENISANFSHTGS V*GWMFTVP*SPSGRVVF*FCH L*ATCGN*LN*THSLSQGQRAF CILGFLPWHSRRIRSHVGLENEC KVLLSGRSSQQMGEP*GR*FSP* VGPLGGRALLQLPQPNSV/YVL PVSGLLVPAGE/CPLNV*PLVCS SANVLLSTSSCFCLCLARVSGF YRHRMGA/SGGFL/M*V*RKGS SFNFLHMA\ASSWDSYSGHHFF *AGADYFFASSVSSLPLVLLHSL HSFF
29465	59833	A	29647	1	1422	
29466	59834	A	29648	1	768	
29467	59835	A	29649	1	885	

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29468	59836	A	29650	1	1253	MVSVTALKAAFLELFIPPSGLV VSLASGVKLQTFAVSVTAHKG SVDPKSDQHGLVVSLASGVKL QTFARRAEFPASQQQREVPRHD GGNHADRFTHDHRQLMATGG RHFAIHFVDRFGVPANGARRAG NIITQTVTNRFAGVESFQQCQLF GIYAVCERQGAEIPGPYARLFL ATFFIYTSSFKPPLPWLRSLPRN TTPAVVRTAKGQVTAKYVIVA GNAYLGDKVEPELAKRSMPCG TQVITTERLSEDLARSLIPKNYC VEDCNYLLDYYRLTADNRLLY GGGVVYGARDPDDVERLVVPK LLKTFPQLKGVKIDYRWTGNL QLTLSRMPQFGRQDTNIYYMQ GYSGHGVTGGSSRVGLMAGSQ ISRVSV/CINP*YHRFNLHWRYV ADAISADGAFRTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRTDISLYQHTAEQKHPYCW YPYPADSADI\SVNKHRRNATQ LHVSCSFFLLSDQRFHHEAVPR RVVLFTFNTCVDKYIADIRSRT NGLGFLYAFKQRNSHFVFNAQ RHRHSACLR
29470	59838	A	29652	1164	1273	
29471	59839	A	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT EEALDQSNADLITLLADWFKDL GFNVEVQPVPGTRNKFNMLAT RRHEGRYITCMQPLPIIAEQEQE PEMTVRYYISSADLTAEKFATA IRNHWHVENKLHWRLDVVMN EDDCKIRRGNAAELFSGIRHIAI NILTNDKVFKAGLRQGWEDIED FGETHLDFLKQYGDFENGIPVH DTIARVVSCISPAKFHECFINW MRDCHSSDDKDVIAIDGKTLRH SYDKST/RRRGAIH\VNNAFSTM HSLVIGQIKTDEKSNEITAIPELL NMLDIKGKIITTDAMGCQKDIA EKIQKQGGDYLFAVKGTQGRL NKAFEEKFPLKELNNPEHDSYA ISEKSHGREEIRLHIVCDVPDELI DFTFEWKGLM
29472	59840	A	29654	2	1587	
29473	59841	A	29655	236	666	
29474	59842	A	29656	1	1953	
29475	59843	A	29657	2202	2333	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29476	59844	A	29658	1	1126	MHEVTLEDPSSAQILITVITGHG EIITLKRSSRRQNDIRMYCRRRP EAFRDHHQLRFLPGTDQAIGIL MMSKVGTARPPDKTNIREMSV HTVVLICATRVFQCFNNAGNR DFIHRIAATRQAALHGREHRRT PRGVTTIGKMVRKTKTAAGWE HESGFYLDGVVKLNRFKSNVA GKMSSGGAANGSYHSNGLGGH IETGMRFTDGNWNLTPYASLTG FTADNPEYHLSNGMKSKSVDT RSIYRELGATLSYNMRLGNGM EVEPWLKAAVRKEFVDDNRVK VNSDGNFVNYLSGRRGIYQAG KDLDRFKNLVLVHAARYAADL SYLPLMQELEKRYEGKLRIQTV VSRETAAGSLTG\GYRH*LKVG NWKARLACR
29477	59845	A	29659	1	1989	
29478	59846	A	29660	3	159	YKELNLADSSLSEEALIQAMVD IPKLMKRPKVVANGKARIGRPP EQVL\EIVG
29479	59847	A	29661	360	744	
29480	59848	A	29662	1	996	
29481	59849	A	29663	441	446	ICRQYPSPDDRTASGAGGGDHQ QYGAGLRQTFCLCQRLSARTC* RLSASVCAT
29482	59850	B	29664	1	1608	
29483	59851	A	29665	1	2568	
29484	59852	A	29666	116	283	
29485	59853	A	29667	207	1270	
29486	59854	A	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

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29488	59856	A	29670	1	1167	MPWLSTGAAALITALAVVELN DDDDHHHRNNSPLPPTPPDDES DDTPVPPTPGGDEIIPDDPDDTP TPPKPVSFNNDVILDKTEKTLTI RDSVFTYTENADGTISLQDSNG RKATINLWQIDEANNTVALEG GNTSACRQALKIPKGSSDYTVT WKGGHFTFYRRWRCKVHKVV FEGSPPVTICRYVLNRKNSWHV AHIFRRHAKPEEQ/CSHLFPYPF H\HDLDEVLNDPDVKLVVVCT HADSHFEYAKRALEAGKNVLV EKPFTPTLAQAKELFALAKSKG LTVTPYQNRRFDSCFLTAKKAI ESGKLGEIVEVESHFDYYRPVA ETKPGLPQDGAFYGLGALFTNQ QGFFKSSLLSIFADSSSSVAGRS PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	A	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	A	29674	282	660	GPSSSEPSWAVAPGKAGDPHHS AEWARNSTPSKDQA*RRPHT\IC VTAYQGKVLLVGQSPNAELSA RAKQIAMGVDGANEVYNEIRQ GQPIGLGEASNDTWITTKVRSQ LLTSDLVKSSNVKVTTEN
29493	59861	A	29675	720	4525	
29494	59862	A	29676	218	990	
29495	59863	A	29677	54	723	
29496	59864	A	29678	1	2229	
29497	59865	A	29679	2	235	
29498	59866	A	29680	279	1275	
29499	59867	A	29681	692	1052	
29500	59868	A	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD CWVDDARLVLANAQMVVRKG GEVLTRTRATSARRENG\GKKY SWQARGLESLSQPVERLSP
29502	59870	A	29684	1	1941	
29503	59871	B	29685	1	4107	
29504	59872	A	29686	840	1006	CHESHRQTDGGAVFRVYPGGG PRRECWFGSSLDEATPGWLLQ/ LYERDRH*PASTG

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29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRKRLLLLSRK TRMP/GFTNPRYGAGAATNPDP EVFSWAATQVVTAMEATHKLG GENYVLWGGREGYETLLNTDL RQEREQLGRFMQMVVEHKHKI GFQGTLLIEPKPQEPTKHQYDY DAATVYGFLKQFGLEKEIKLNI EANHATLAGHSFHHEIATAIAL GLFGSVDANRGDAQLGWDTD QFPNSVEENALVMYEILKAGGF TTGGLNFDAKVRRQSTDKYDL FYGHIGAMDTMALALNIAARM IEDWQLDKRIVQR
29506	59874	C	29688	1	2130	
29507	59875	A	29689	238	1879	
29508	59876	A	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR KSVRTQV\LSAADVRAKLFTLK VQDPKIDRANPTMVNMRWMM SA
29509	59877	A	29691	596	723	MCASAP*WCELPAGVVRPPAST TADYFPLFTLVHGGCAHGRF
29510	59878	B	29692	1	441	
29511	59879	A	29693	1	1422	
29512	59880	A	29694	1	2856	
29513	59881	A	29695	2	367	QKAGAVQVLLSLWSSLSAAAA GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS GSLDRPSALHSGTILSGKITSDIC CPHF*SPGRPCSKQHWAEMLV HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLGEITSPAIIFSPTLHSPAAH HQYRKALHGRFPARSRDPPALA PGWRSARRER*SSPARAAARW CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE SYSFTDSV
29516	59884	A	29698	279	732	PPGATLPTVARGTPQMGKEGSS PAKSLAPPLCEQMGQEDGHWG AGWGLAQVLLIALDGLLDAQQ HGGEPLGPAGRWSRIPSPTRCS CPHSAPRGPLAIFSSTCIPGNQR KLGTAPHTFGQPAWR*ACRCRS GRGPP*RSSLWRCTEEGAVH
29517	59885	A	29699	353	2776	
29518	59886	A	29700	158	605	PERSGLQEAGGGSRGWGKRSL PPAETAGLSGYMCFRAWLSLSR WDSEDGHWGAGWGLAQVLLI ALGWSS*CASNGWLSHWFQPG R*SRIPFTDSV*LVHILLPVGPL AIFFINLAFPGIRESWEQLLILLE KPVGLEACPCKSGKGRP

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29519	59887	A	29701	1	753	MLALDQREAMRMIFPA\AGAP APALSPYAS/ARILVDQQFCYRQ VVEQNAIAKSCAMIVAADEFIP GNGIPVDSVVIDRKINPLQIKQD GGKALKLLVLWRSDEDAQQRL DMVKEFNELCHSHGLVSIIEPV VRPPRRGDKFDREQAIIDAAKE LGDSGADLYKVEMPLYGKGPQ QELLCASQRLNDHINMPWVILS SGVDEKLFPRAVRVAMTAGAS GFLAGRAVWASVVGLPDNELM LRDVCAPKSGEPIL
29520	59888	A	29702	294	479	KIHFGFFCHCAESGSLDGRHFA PGV*RSEQHESGSGAVSGTGY WCSRDYRSREIDGLYRNW
29521	59889	A	29703	1446	2103	IHTDHRPGEIAATTLANRAALS GAALRRRRRQNQTIAVGWRLA GTAHACNIISIRGYGSDEDA/Q/ QRLDMVKEFNELCHSHGLVSII EPVVRPPRRGDKFDREQAIIDA AKELGDSGADLYKVEMPLYGK GPQQELLCASQRLNDHINMPW VILSSGVDEKLFPRAVRVAMTA GASGFLAGRAVWASVVGLPDN ELMLRDVCAPKLQQLGDIVDE MMAKRR
29522	59890	A	29704	370	1080	
29523	59891	A	29705	547	928	RLTKVEMPFYGKGPQQ\ELLCA SQGLNDHINMPWVILSSGVDEK LFPRAVRVAMTAGASGFLAGR AVWASVVGLPDNELMLRDVC APKLQQLGDIVDEMMAKRRFIP LLRRWVDLALTRWLITVSKP

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29524	59892	A	29706	1	550	MESGVATRPIADFDVYIDKLTE FVYKTNLFMKPIFSQARKAPKR VVLPEGEEARVLHATQELVTLG LAKPILIGRPNVIEMRIQKLGLQI KAGVDFEIVNNESDPRFKEYWT EYFQIMKRRGVTQEQAQRALIS NPTVIGAIMVQRGEADAMICGT VGDYHEHFSVVKNVFGYRDGV HTAGAMNALLLPSGNTFIADTY VNDEPDAEELAEITLMAAETVR RFGIEPRVALLSHSNFGSSDCPS SSKMRQALELVRERAPELMIDG EMHGDAALVEAIRNDRMPDSS LKGSANILVMPNMEAARISYNL LRVSSSEGVTVGPVLMGVAKP VHVLTPIASVRRIVNMVALAVL FVNADETTVVNFHACFACVEV FTVRHTTNRYQHGVVTLRFSG CFFAFHRHINAVFFRFNIQAVFV ALRPEVIAIMHKLREQGHRVVV LSNTNRLHTTFWPEEYPEIRDA ADHIYLSQDLGMRKPEARIYQH VLQAEGFSPSDTVFFDDNADNI EGANQLGITSILVKDKTTIPDYF AKDKARHRTRPLWAWLKLLW QRIDEDNMTTLAGNLAYVSLLS LVPLVAVVFALFAAFPMFSDVS IQLRHFIFANFLPATGDVIQRYIE QFVANSNKMTAVGAGQSGDQF LFALFNCQCFDADELKRIKNEL EPKMGMELNLVQLIAYTDWNE TQQKQPDGSWVNYNYDWMFK
29525	59893	A	29707	898	1163	
29526	59894	A	29708	81	454	NRLLAGRISSGTGDHFSGAAGI DSSLRPVW*T*TLRDQMSGGQS AKQPGRFAQWFYP*RLPETG*V PE*CL**CELIRAN/DHFLVSILPL RSPCVPLHLSTTPLRLAMDLTG LSGFPIPLSQSA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	1	2218	
29529	59897	A	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	C	29713	1	3126	
29532	59900	A	29714	642	825	

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29533	59901	A	29715	107	1315	KCADLPVRGLRHCWRRREDPS GADRSFSALIHSGRAAFWPCR* QGALMSEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSPSQRSYS VLRSKFDAWLMEQAEEAGAQL ITGIRVDNLVQRDGKVVGVEA DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVAVGVKELI ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNENT LSLGLVCGLHHLHDAKKSVPQ MLEDFKQHPAVAPLIAGGKLV EYSAHVVPEAGINMLPELVQIP CIERNAINAVKAVNAARMAMR RTSAPRVSLDKVIETMYETGKD MNDKYRETSRGGLAIKV
29534	59902	A	29716	3	264	
29535	59903	B	29717	85	737	
29536	59904	A	29718	171	820	LGVCAMTNSQCG/CDEYRSKN GYEGARKALTGLSPDEIVNQVK DAGLKGRGGAGFSTGLKWSLM PKDESMNIRYLLCNADEMEPGT YKDRLLMEQLPHLLVEGMLISA FALKAYRGYIFLRGEYIEAAVN LRRAIAEATEAGLLGKNIMGTG FDFELFVHTGAGRYICGEETALI NSLEGRRANPRSKPPFPATSGA WGKPTCVNNVETLCNVPAIL
29537	59905	B	29719	1	486	
29538	59906	A	29720	1	605	
29539	59907	A	29721	285	449	TPAARDAQLSGGRGWY*CSAG NGLMQHRSQSGDWRAGRPFTE GW*PTPDWQIEA
29540	59908	A	29722	411	557	

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29541	59909	A	29723	1244	3261	KTINRTSLWYWTLHDHWSVTG RCAFTDVTKVEDHHEPQTQTR GLVMTTS*ATT*KLTVSLTTAC VMNWV*MQVIPSPTAKIRL*LR TSNWLTSTTTLTT/NNDVNGDSI DNGTEGSAVRVGLGTQFSFTK NFSAYTDANYLGGGDVDQDW SANDLTGITAKDAQMLSVVKP LQEFELFVLAALESRGTLADILK AAGATTANITQAIEQMRGGESV NDQGAEDQRQALKKYTIDLTE RAEQGKLDPVIGRDEEIRRTIQV LQRRTKNNPVLIGEPGVGKTAI VEGLAQRIINGEVPEGLKGRRV LALDMGALVAGAKYRGEFEER LKGVLNDLAKQEGNVILFIDEL HTMVGAGKADGAIDAGNMLK PALARGEWHCVGATTLDDIAS TVKRCWTSHQHQTKNRTRRTT TRNIRFPNQMIEQINIALEQKGS GNFSAWVIEACRRRLTTGGPHV MYVLHHADKPNLYHGLPENPE ISETVKFWKGIWKPLAAVGFAA TFAASIFHYERVIFLTGQVEDH MANLIVAQMLFLEAENPEKDIY LYINSPGGVITAGMSIYDTMQFI KPDVSTICMGQAASMGAFLLT AGAKGKRFCLPNSRVMIHQPL GGYQGQATDIEIHAREILKVKG RMNELMALHTGQSLEQIERDTE RDRFLSAPEAVEYGLVDSILTH
29542	59910	A	29724	1487	1821	QYRPESVLEDPRRSDHHRRTDS FRETSFIVQSIVCRVSLSRAILQS KRL*EPGEFPPPDPSSPEQRWPV CYPPK*SDR*PEYPHSPPGRQES QSRYLPAFRHRYSYQTTAY
29543	59911	A	29725	4063	6544	
29544	59912	A	29726	174	556	
29545	59913	A	29727	1	1926	
29546	59914	A	29728	1	1443	

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29547	59915	A	29729	1	817	MAFNEPLMLEPAYARVFFCAL AGQLGITRLTDTVSGITLDAGQI AEPLALFGEDDDMDPRPSRSYQ VANGIAVLPVSGTLVSKTRALQ PYSGMTGYNGIIARLQQAISDP GVDGILLDMDTPGGMVSGAFD CADIIARMRDIKPIWALANDMN CSAGQLIASSASRRLVTQTART GSIGVMMAHSNYGAALKTNGV EVTLIYSGDRKV\DGNPYEKLP\ KDVRADFQTRIDATR\SAYTGM SVQDV/LDTEAAVFSGQESWDN GLAE*LVHTDWL
29548	59916	A	29730	68	98	
29549	59917	A	29731	215	871	
29550	59918	A	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP EQRDGAGRFCSLAKETVTPQW *GVLTSLIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLLGYSLVCSRVLLAC FWPGSDFWPRSRRKTSHLTVEA FPV/VVIFVSWRNPQVAPTSAH QNRPSRNPVSRPPNTQRVARRK HYALADGY
29553	59921	A	29735	403	588	
29554	59922	A	29736	1	743	
29555	59923	A	29737	5	97	
29556	59924	A	29738	756	935	
29557	59925	A	29739	1	1056	
29558	59926	A	29740	1193	1405	
29559	59927	A	29741	1	2718	
29560	59928	A	29742	3	357	

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29561	59929	A	29743	3	1307	KYGFVHYTLHTLGGTARALVA TDYRPLTKLSLDNGFQTVDHLQ ISQCPYIPPYNFPTDTSPGTPGLL QPPEGHAYDAYWRCVRAVRG QRVSALHGPPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YGSGVRSWVQPGGFARYKYDQ TGNASTVKCDYYRMAAFGHH AYRMQALTCSMTACPCTTRQE TSSAWGSVSSMGDSRPPQEILG QPLLGRRIKYNCTGIGPWDGKG DESGASRPRKQQASGWLWACP RIFLVIPHSSHPAARRTNGSVGG SNRNRFVIITGPGPQLAPKGLW QWPIGQDPVTEIATLIGTHDLIM FDCIGSVSAPTIQPLEKLLSIVRY PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVFTSAF APVAVTAPPRQSRRQFPRLSPL DAHQRMGDVSIQAVKEARTC

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29562	59930	A	29744	1	2352	MLPDSSVRLNKYISESGICSRRE ADRYIEQGNVFLNGKRATIGDQ VKPGDVVKVNGQLIEPREAEDL VLIALNKPVGIVSTTEDGERDNI VDFVNHSKRVFPIGRLDKDSQG LIFLTNHGDLVNKILRAGNDHE KEYLVTVDKPITEEFIRGMSAG VPILGTVTKKCKVKKEAPFVFR ITLVQGLNRQIRRMCEHFGYEV KKLERTRIMNVSLSGIPLGEWR DLTDDELIDLFKLIENSSSEVKP KRRPNRKQRASNVQSLRWKKR RKKAVARRPTQSSDDAIRGQQP DGVDCRDCRAGERQRQQTDSA MMELMVVHPHIFWLSLGGLLL AAEMLGGNGYLLWSGVAAVIT GLVVWLVPLGWEWQGVMFAI LTLLAAWLWWKWLSRRVREQ KHSDSHLNQRGQQLIGRRFVLE SPLVNGRGHMRVGDSSWPVSA SEDLGAGIRQCQQLVAHGLQLL NVSFDLRHLFQRGRLEFGCALR LLTDSQSRLSRKPRGWRGLYG YSPPCGDIVRYHHHDLSVATLH VHINHDDCLEIAVLKGDMGDV QHFADDVIAQRGFFFAFSYEDT VIKIIEKDFTMSGKPAARQGDM TQYGGSIVQGSAGVRIGAPTGV ACSVCPGGVTSGHPVNPLLGA KVLPGETDIALPGPLPFILSRTYS SYRTKTPAPVGSLGPGWKMPA DIRLQLRDNTLILSDNGGRSLYF
29563	59931	A	29745	1	3075	
29564	59932	A	29746	755	1321	
29565	59933	A	29747	397	576	
29566	59934	A	29748	1014	1266	
29567	59935	A	29749	416	724	TPGLTKTPCPWEKVTLFSLQWS AYRQANTSGLRHSASSLLPLAC RY*R*WRWQKLAAVLTASARQ SVKSLAYCWQRFVTWRWGRFS LRRVQLPFPLKWGLRR
29568	59936	A	29750	230	1829	
29569	59937	A	29751	1	474	
29570	59938	A	29752	137	586	KTKTNIKL*AAPITRMVMVRHA \PHSGSVKK*SDITMSFATISVIG LGYIGLPTAAAFASRQKQVIGV DINQHAVDTINRGEIHIVEPDLA SVVKTAVEGGFLRASTTPVEAD AWLIAVPTPFKGDHEPDMTYV ESAARSIAPVLKKGAL
29571	59939	A	29753	2	557	

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29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPVYT**PTA QGLSARQGCTKGHQVRRYGFR HD
29573	59941	A	29755	66	372	
29574	59942	A	29756	1	992	
29575	59943	A	29757	1	393	
29576	59944	A	29758	1	3753	
29577	59945	A	29759	1	1098	
29578	59946	A	29760	320	703	
29579	59947	A	29761	2	673	AAFLRECKDPQTMVPKAINSVI WRIGLFYVGSVVLLVMLLP\WS AYQAGQSPFVTFFSKLGVPYIG SIMNIVVLTAALSSLNSGLYCT GRILRSMAMGGSAPSFMAKMS RQHVPYAGILATLVVYVVGVF LNYLVPSRVFEIVLNFASLGIIAS WAFIIVCQMRLRKAIKEGKAAD AHFTPYHATPLRNVMLHIYVLN GVSRFSVIDTNQIAQRCNRFAL LCGA
29580	59948	B	29762	51	623	
29581	59949	A	29763	1184	2406	
29582	59950	A	29764	103	473	
29583	59951	A	29765	444	699	CWPGKMSWGGFPLFLLIGIVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVYSGIQ LLPGLVLGGCMCRGIYA
29584	59952	A	29766	3073	3621	GVDNWRIIPIISARLQR*AGSFFS FLGETGSLSCGLSLSFKSCCEAK NCSGSRGSSP/G*IPGVQEWNQI FSRF/HGVGLASLRKQRAPGDQ SPTGLLGE*AHGEIPVGNGRSG KTRA/RGGPRGLEVSWSGSLTH SRG*ASLTSSHNSCHIRRGHGPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29585	59953	A	29767	362	1850	
29586	59954	A	29768	1	1401	
29587	59955	A	29770	1366	1515	YDQAELDQLIHGSSSN/EQDPR/ RLPKGLTPQTLR/TLCQWIDAH QDYEFSTDG
29588	59956	A	29771	1	1827	
29589	59957	A	29772	419	1295	
29590	59958	A	29773	167	451	
29591	59959	A	29774	94	304	SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
29592	59960	A	29775	345	652	
29593	59961	A	29776	596	2297	
29594	59962	A	29777	184	283	

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29595	59963	B	29778	16	1058	
29596	59964	A	29779	715	1234	FTWIGFYANRHFHCPVTTNDFP HFMKWRAAAHGGENIAFKLAN LPFFGDIRESHYQVVINRADRG FNPDFFTGARQQQKFVLIAGGF P*QLL*TNAVIGREFRNVQECIG LHTAGFANAVTKHF/W*M/PRL HCTIWRSGSRTITGRSRWSTAII NCRVCSFCAISTLASRTSAR
29597	59965	A	29780	938	1250	PGRVSGKADGSV/LAGNGLLPG FFCPLRLRGKYQPEV/IASTIRRR YQLLFLAVASHQATAAGCGVN ALSDLRLCSVCRPDKTHSVASG NGCRMRALPSSPFSVIL
29598	59966	A	29781	1	1389	
29599	59967	A	29782	3059	3537	SEGKTANLFNKAITCSGAGECT RPWASDIKAQCAGGISRFATGN GFKRLCDTLRYLQAIENGLKN WRLIHIATVRRCPFPT/LSPATID AINVIGQWLAQDDFSGEVPYQ ADCVILAGNAVMPTIDAACKIA RDQQILAEGDFGLRCEIRDWCA NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVLVHHFH AITHIRQQSQITRYIKLLRHRRH TQRRFTACRLRVDAPFPGNHQC CALHCLRKIDRIQHNFNARFNIR IEKYRRRNTHTARSAA/DPPSGR H*FQFAVVKHGRNFAAPVQVL RPSPALPLFAGQTPPPRRVPLPA GYQRHMLLQYDQATVN
29601	59969	A	29784	269	753	YRTPTLQLDQGRADARRGVW/ HVPFSHESV/WENIVMTRQAQG ANFT*TLFCFGIGFAVIA*NCAI DPDISIRFFSKEETAT/GDRPDQI AAHLWRFPTPGGRFVHHRGAY\ AAIIFRP*YLNGRSMAEQSMILV TGELLVELNLEPSQVGNEFAEK YYGPASQVV
29602	59970	A	29785	762	1182	
29603	59971	A	29786	3703	5889	
29604	59972	A	29787	925	1130	
29605	59973	A	29788	658	1212	
29606	59974	A	29789	904	1473	
29607	59975	A	29790	1205	2222	
29608	59976	A	29791	1	194	
29609	59977	B	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	

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29613	59981	A	29796	1	738	MQPWALPTVGELWVCGRPGA ALRAGTEPSSRALGVSETALPA EIKLRVIRVGHSSPLAQLASFQK PVLFVLRLNSRRFLFLSLARSED GILFAKSKHSSPLSLTPLRCIVL MRMYEQLMSGDLCQRVMMPS RNNPGYWNPQ**SEIFKGSPAQ TMATLTCSFKKPPPKIPYKAIAL ATVLFLIGAFLIIIRLPSCCQGYI KQRGGRPGPFQLLIIGHSWCSY PGFYPPAHRFTMHPKGLPWVN PNE
29614	59982	A	29797	1	186	DCRLRAGDPRRSHCAVSPTGGS RALSGYRY*SVDQPRNDGVDQ *ATLRASAHLQTAVVEFSA
29615	59983	A	29798	724	1015	RSHPQCGYLQNHTSSASFSAPA RKG*NRHYAFARNDRLVPAPCS HHHQ*PAFPAPVHLH*PVDLST AIDAPAVNGDGKARPSKRRYQ RLSVPEVVQY
29616	59984	B	29799	1	4182	
29617	59985	B	29800	1	1191	
29618	59986	A	29801	167	504	
29619	59987	A	29802	1541	1852	FALFANRVSLAANVSGRGSPC WWRRIAVVCCSTNR/RSALDIA HQVDVLSLVHRLSQERGLTVIA VLHDINMAARYCDYL\APCAA VK*LLRERLRKLCAAKPSK
29620	59988	A	29803	407	3584	
29621	59989	A	29804	3	150	
29622	59990	A	29805	1	921	
29623	59991	A	29806	300	560	IRDKNRVFLRESWRRLFTTAND QPHRPARRIISIAGIKWRYSDFLI NYCAGRAVF*RETGSVVERWH HHAGWKTPFRKRAGRTAGH
29624	59992	A	29807	100	315	PIKITSALASASRYVRATLSCSR NSTLRWKK*RKMALTKPSTTN GSRSNS**MNFFL*QAPPG*PSA LPFVH
29625	59993	A	29808	3	116	
29626	59994	A	29809	1	1469	
29627	59995	A	29810	1	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYQRA CSGR*VPNLRLPEVQSTDRLLS QRRRVSPDRQWWLACH
29629	59997	A	29812	438	1942	
29630	59998	A	29813	1	1464	
29631	59999	A	29814	3	602	

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29632	60000	A	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA SVVSRDGFVIAGGGGMVVVEE LEHALARGAHIYAEIVGYGATS DGADMVAPSGEGAVRCMKMA MHGVDTPIDYLNSHGTSTPVGD VKELAAIREVFGDKSPAISATK AMTGHSLGAAGVQEAIYSLLM LEHGFIAPSINIEELDEQAAGLNI VTETTDRE\LTTVMSNSFGFGG TNATLVMRKLMIISASTTSILR
29633	60001	A	29816	1	2472	
29634	60002	A	29817	1	469	LFNREVCCLGQGQS*QMAL*LL GIESYIT*L*SGGDN\ASIGVIPDP AAIAR*RPWRSACG**PKCPLA DVFAGHSGRKRPPSMAFTATLI SPGTGRRAINSVLAQFKAGESNI WLSALPTPLTPTIRITNGALPSTF SGSSTFARISPISSFSRP
29635	60003	A	29818	884	1084	
29636	60004	A	29819	1	1040	
29637	60005	A	29820	2711	3854	
29638	60006	A	29821	1	957	MKIGTQNQAFFPENILEKFRYIK EMGFDGFEIDGKLLVNNIEEVK AAIKETGLPVTTACGGYDGWIG DFIEERRLNGLKQIERILEALAE VGGKGIVVPAAWGMFTFRLPP MTSPRSLDGDRKMVSDSLRVL EQVAARTGTVVYLEPLNRYQD HMINTLADARRYIVENDLKHV QIIGDFYHMNIEEDNLAQALHD NRDLLGHVHIADNHRYQPGSG TLDFHALFEQLRADNYQGYVV YEGRIRAEDPAQAYRDSLAWL RAGQVADKVHASYYCTRNDLE LVAVCDSRLSQAQALAEKYGN ASVWDDPQAMLLAVKP*FVGL V\GAGQVADKVHASYYCTRND LELVAVCDSRLSQAQALAEKY GNASVWDDPQAMLLAVKPDV
29639	60007	B	29822	96	821	
29640	60008	A	29823	3	775	
29641	60009	A	29824	961	2073	
29642	60010	A	29825	1	849	
29643	60011	A	29826	319	541	
29644	60012	A	29827	1142	1756	
29645	60013	A	29828	44	283	
29646	60014	B	29829	1	1812	
29647	60015	A	29830	685	1146	

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29648	60016	A	29831	202	918	AVDTGLADHRDRTEHGGAFAA IVHRIVKHFITAWAICQQRNHA ALVVIRRLEANHRRHRTGRG\S VDRVSAARSLSSGTMPGNGVW RIGVFTQLSVA/WHQ*VDLLIVF QFVRDTTDDHDVGIFALAAND RAAFDNILDPTGSVDVLLPLPG RHNIANALAAAALSMSVGATL DAIKAGLANLKAVPGRLFPIQL AENQLLLDDSFLVNAAQQNILS VHILNQQTGKPAADVTVTLQE
29649	60017	A	29832	1184	2409	TLKACCLVRSMCRAVP*RC/GR QLVSSDNISNDPMNVIDWINMY ALAVSEENAAGGRVVTAPTNG ACGHPAVLAYYDKFRRPVNER SIARYFLAAGAIGALYKMNASI SGAEVGCQGEIGVACSMAAAG LTELLGGSPAQNMEGKIDRPEE YADIATKCVTNFREKNRDRCL VILSRNDEALNSQRTSEELHHY YEIVWDEEQTHKFKNISPHLQRI KAFKTLGGPHGNITVDMVISAQ ELLQEDMATFDGHIVEALMKM PEVNAMYPELKLHAIGWVKHK CIPGAKWPEIQAEMRIWKKRRE GERKETGKYTSVVDLARARAN QQYTENSTGKISPVIAAIHREYK QTWKTLDDELAYGRCFADRQN LMVCLRSMPNVFTGSCARMRC CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA MIPNFNWAFLGVTTWIFMAAG GAESVA\CTLTTSKAVRNRSFK* SSSPGILSGYVSRSSGSPISSLISP ASLCAGHMRFFCSSSKPTCSNP RTFAAALSSAWSSPSPNEGFSSN PAFLGTSLMMFHLELRRCIAPIV TTDLLPLTSGDVGLVLLCVGLD GSLWSDCRMTESVSTTNTPPIIT SRNS
29652	60020	B	29835	46	893	

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29653	60021	A	29836	3	2037	CTSSPDPPSGLPPGFAKLTSLIVT LVEVGVSPEPDEGWLYLAVVID LWSRAVIGWSMSPRMTAQLAC DALQMALWRRKKPRNVIVHTD RGGQFGDRWKGWLTRSIFRWI SFQPALAPTRKAALCYLAREVN PDMADYIKKLKLPGIHVREESR RYYPSGEVTAHLIGFTNVDSQG IEGVEKSFDKWLTGQPGERIVR KDRYGRVIEDISSTDSQAAHNL ALSIDERLQALVYRELNNAVAF NKAESGSAVLVDVNTGEVLAM ANSPSYNPNNLSGTPKEAMRN RTITDVFEPGSTVKPMVVMTAL QRGVVRENSVLNTIPYRINGHEI KDVARITTEEDFNHASAARFVC AAAERRCKTTINLVPENEVLNV LEGEDAETNALRAKRRCPKCG TAMDSYLIDPKRRKLHVCGNNP TCDGYEIEEGEFRIKGYDGPIVE CEKCGSEMHLKMGRFGKYMA CTNEECKNTRKILRNGEVAPPK EDPVPLPELPCEKSDAYFVLRD GAAVAARFNDDRHRRGLAVLY ADQADLYGVADSVSAGDSLSA LYKHERRLVVPLLVSSSLLFLY RHGIRLPCGPSGGIWAPWQIRR GRQAVNCLAPM/HHPGKNRAW KTYCSQ*AIVPQLPVCGI*PRSD SYHDYQRDPRCQPLRALWRRS DSPIGGYSSAIGI*TERHCRSGNP
29654	60022	A	29837	993	1832	
29655	60023	A	29838	124	276	QEGRCQVTITRKMPLSSDLGSL HGLAGNHSPPICARTPHVATVL RQLLELEDKHWNGSG*FARLG WKPQSPHLCQNPPCGHCPQTAP GA
29656	60024	C	29839	64	267	
29657	60025	A	29840	3	86	
29658	60026	A	29841	1	1481	
29659	60027	A	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK*VGGSSRVNVPQVFI SLVSQMFSENDLPLVRKRKTEP
29661	60029	A	29844	115	903	
29662	60030	A	29845	1194	2311	
29663	60031	A	29846	368	502	
29664	60032	A	29847	1156	1359	SEPVYPLCYLRQLAVQANPRR MRCIARHFNINGNRHLTTTINFI *SMVSLIANRLLIIDLIHTVDFY
29665	60033	A	29848	1	228	

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29666	60034	A	29849	102	296	YRNSHNLLQGWQIHRGDLLYH SSPHSR*KHRNRHNARARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	A	29850	1	4185	
29668	60036	A	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVVIDQCVFLIRV TNPAGSFFELRIHH
29670	60038	A	29853	2	834	
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNNLVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	A	29855	1591	3150	
29673	60041	A	29856	2	222	
29674	60042	A	29857	16	359	TTHKTRWQAPVPLRGSPVVAL RIPSDQSEAV/HSLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLSFFNRHYICFTRI RRFRWHRSSLFHGMNVKYRRS KINN
29675	60043	A	29858	207	470	ATIL*GDFYP/GSRNWLGVSSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTS\GHVLAGSCCW NGKTLRKSDSRWQQLLRRSLIR R
29676	60044	A	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCIMAIRSPIRMASSR SWEIKTMVR
29678	60046	A	29861	593	1881	
29679	60047	A	29862	3	198	
29680	60048	A	29863	1	1590	
29681	60049	C	29864	1	5421	
29682	60050	A	29865	63	185	LCQSHAPRKFPARPFRFFR*RQD CQTSVFLLRPVANRAPA
29683	60051	A	29866	1	715	
29684	60052	A	29867	1	1212	
29685	60053	A	29868	886	1185	
29686	60054	A	29869	190	433	AFAKLFIMAAALTSGVAHLSSS GTPFRPFCLPSC*LSSSRAAAIST CSLYAAWFPLTLIRCRGIRKSPII CGISRCRCWRQ
29687	60055	A	29870	1	439	
29688	60056	A	29871	14	106	
29689	60057	A	29872	2518	3024	
29690	60058	A	29873	448	537	

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29691	60059	A	29874	463	889	FFGLVTSSPSADSPAMLDTRNV SHTGLGPIIPLTFEAGIHTRPTPN SPPRSCLAPAIKA*FFSPAARITT CCASLYRSPLKTLRSVRFWRSS ASVLMRRSSSAAPMPEATLRVL SGLRGSRSDKAFTPHPTI*CLEA FPGSRAFVASAP*CLTLRANQR KGCW
29692	60060	A	29875	524	1006	SLLAWLSGINIFASSRIAIASPLA ASVPLSMDNISLCTPSGVPEKV TSTVLTSVPQSCKLMMKDFSGP *FP*EKRVSETSPNCTLICLLSCA STHVLRRNDPLMLTVPSWANS SQPHVNPNKNRIQIIPFNITPSLV NQIKIETRRAFTPLLPLCGLITK
29693	60061	A	29876	2005	2517	
29694	60062	A	29877	1	470	MQRRDGDIALIYRSKIGPRTSIT FTARRANPVQRIAARILLRDHLI CRMSCTAARHANTFDLIQGSG ADNFAAIYGGANDRITRADA/V SRGCWKLAPVRDIKRQTVAAF YHQDIQPGSCHDQNAL*STGFW REQSGGQ*P*AG*TNSRTRCCIT GR
29695	60063	A	29878	734	1306	
29696	60064	A	29879	743	901	
29697	60065	A	29880	771	1013	RLGTVGTDSLWCYQYQLCYQ* ALPFSTLPAKLAGNGCQRRRCA GTHSLWHADLGSVWPDADSLF QRDGRAGGGATRLLRR
29698	60066	A	29881	1094	1345	
29699	60067	A	29882	2	751	
29700	60068	A	29883	239	483	PTPQHLTYHALTGSTIMSQRGV DIPCHWHDITCGHAHSLPHRRG RKA*SMGNR*YSCTWCYCEGG TEKAIWPGDGCPGLSV
29701	60069	B	29884	228	803	
29702	60070	A	29885	488	636	
29703	60071	A	29886	1	2117	
29704	60072	A	29887	665	795	

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29705	60073	A	29888	1743	2013	LQCTQYAVGENPAVNFAGRPK GSPCFGPGGGLIN*AAADIPVAS DNPAHYADAIRYNARTPLQAG VYFVRDGPGPLASVRNKERYF ANNYIYDMGRNKDGRQSTWY MGLGTDIDTGLPMSLSMNVYA KYQWQNYGAANENEWDGYRF KIKYFVPITDLWGGQLSYIGFTN FDWGSDLGDDSGNAINGIKTRT NNSIASSHILALNYDHWHYSVV ARYWHDGGQWNDDAELNFGN GNFNVRSTARGWLPGTICRPDK MRQHRIRHCAPIAGCGTGCRPD KTRQASHQAQMSNAYDYSEIQ PPSEGEILLDAQPLESWSSKAFA RKVAYLPQQLPPAEGMTVREL VAIGRYPWHGALALLGAADRE KVEEAISLVGLKPLAHRLVDSL SGGEPGVDRMLVAQDSRCLLL DEPTSALDIAHQVDVLSLVHRL SQERGLTVIAVLHDINMAARYC DYLVALRGGEMIAQGTPAEIM RGETLEMIYGIPMGILPHPAGA APMNTAHAAAIDPNRIVALEW LPVELLLALGIVPYGVADTINY RLWVSEPPLPDSVIDVGLRTEP NLELLTEMKPSFMVWSAGYGP SPEMLARIAPGRGFNFSVRNTP LARTLQLILREGPRGHPALVQV VDLLIEPPQLPLLVPSVQTRIPRI QPQSHPAHGVNEAVRNPTVWV APFIDEIISSIHKYSI
29706	60074	A	29889	1	1584	
29707	60075	A	29890	1	1188	
29708	60076	A	29891	728	970	
29709	60077	A	29892	2447	2665	
29710	60078	A	29893	255	1360	

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29711	60079	A	29894	1	1890	MYSRFDIVVAEPICTLTTFGKET VVSDSQTRTTTTDDPLQVLQQV LDRADIRPTHNEDLPFQGGALG LFGYDLGRRFESLPDIAEQDIVL PDMAVGIYDWALIVDHQRHTV SLLSHNDVNARRAWLESQQFSP QEDFTLTSDWQSNMTREQYGE KFRQVQEYLHSGDCYQVNLAQ RFHATYSGDECQAFLQLNHGN RAPFSAFLRLEQGAILKLSPERFI LCDNSEIQTRPIKGTLPRLPDPQ EDSKQAVKLANSAKDRAENLM IVDLMRNDIGRVAVAGSVKVP ELFVVEPFPAVHHL\TITAQLPE QLHASDLLRAAFPGGSITGAPK VRAMEIIDELEPQRRNAWCG/SI GYLSFCGNMDTSITIRTLTAING QIFCSAGGGIVADSQEEAEYQE TFDKVNRILKQLENYRRALRDL KEEVAIRLSPFELSAFCSPSIASM ATRYPNGRHIPPDLRLPKERGIII VFTGNGKGKTTAAFGTATRAV GHGKKVGVVQFIKGTWPNGER NLLEPHGVEFQVMATGFTWDT QNRESDTAACREVWQHAKRM LADSSLDMVLLDELTYMVAYD YLPLEEVVQALNERPHQQTVIIT GRGCHRDILELADTVSELRPVK HAFDAGVKAQIGIDY
29712	60080	A	29895	159	475	VKVNLPWAMLLHSGYADHPYS RFDIVVAEPICTLTTD/GRCSHIS LYAAGIINSDSKGAVIMPPIIGA AIRLITSEPAPVPHRIGSRPAIITA TVIAFGRTRRTAP
29713	60081	B	29896	158	810	
29714	60082	A	29897	1	2070	
29715	60083	A	29898	1081	1218	
29716	60084	A	29899	289	1014	
29717	60085	A	29900	145	297	
29718	60086	A	29901	452	568	
29719	60087	A	29902	21	185	VHDQPSQEIQQRTEAPGAPRSS RRVAQCHPQPGES*SRAQIPPAS TPKPGGGDL
29720	60088	A	29903	1	711	
29721	60089	A	29904	2	825	
29722	60090	A	29905	812	961	
29723	60091	C	29906	1	1587	

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29724	60092	A	29907	3	403	LVFDDGDVQMGFWCGCPFCLL VFLLTVRSLSCRSVGVCWRSTR DLVCLGISSGGCRTVNIAEQQM LLPDCSSGIFVSEGYLAV*GVSL PLLGGASQLGLGSMAIFMILILP IHEHGMFFNLFVSSFILLSSCL
29725	60093	B	29908	168	863	
29726	60094	A	29909	340	612	
29727	60095	A	29910	1	834	
29728	60096	A	29911	92	548	
29729	60097	A	29912	1251	1682	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGGQSSWAPFEWEGAPR GEEWTLVSVGALK
29730	60098	A	29913	1	1278	
29731	60099	B	29914	1	2007	
29732	60100	A	29915	406	615	
29733	60101	A	29916	52	391	SNRLLKLMHSSRSSCVMFFSSIR SFKDFSLVFDDGDVQMGFWCG CPFCLLSFPF*QSGPSAARSVGV CWRSTPDPVCLGVSSRGCQTV NIAEQQMLLPDRSSGSFVSEGY PAV
29734	60102	A	29917	759	1190	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGRRSALGQLSEWQSGQ SPAGAAIAAFDNR
29735	60103	A	29918	84	3661	

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29736	60104	A	29919	1	1230	MDAGWSDVGSWSSLWEISAHT AEGNVCHGDVINHKTENSYVY AESGLVTTVGVKDLVVVQTKD AVLIADRNAVQDVKKVVEQIK ADGRHEHRVHREVYRPWGKY DSIDAGDRYQVKRITVKPGEGL SVQMHHHRAEHWVVVAGTAK VTIDGDIKLLGENESIYIPLGAT HCLENPGKIPLDLIEVRSGSYLE EDDVVRFADRYGRGNDMKKL TCFKAYDIRGKLGEELNEDIAW RIGRAYGEFLKPKTIVLGGDVR LTSETLKLALAKGLQDAGVDV LDIGMSGTEEIYFATFHLGVDG GIEVTASHNPMDYNGMKLVRE GARPISGDTGLRDVQRLAEAND FPPVDETKRGRYQQINLRDAYV DHLFGYINVKNLTPLKLVINSG NGAAGPV/VDAIEARFKALGAP
29737	60105	A	29920	1	1398	
29738	60106	A	29921	426	1861	
29739	60107	A	29922	863	1388	EPERTSIKSSGIFPGFSRQCVAPS GI*MDVVFTKQFDITINGDFCRS RDNHPVFRAVMVHLYRQALAR FHGDAFHLVAVARVDRVIFAPR TIHFAMHPMLMATIGFDLLDHF FHILYRVTVGNQHRIFGLHHYQ IFHPDGGDQARFSIHIAVFSFVIN HIAVANVALGGVGADLP
29740	60108	A	29923	1	2055	
29741	60109	A	29924	1	2047	
29742	60110	A	29925	1	1294	
29743	60111	A	29926	1	1020	
29744	60112	A	29927	1	1422	
29745	60113	A	29928	1	1698	
29746	60114	A	29929	210	340	YGDVEHESWLSCVRHAH\PRIP FA*PTLISLQKRLGKWSGVTGA
29747	60115	A	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK GYGHHHYRNLP/VPNGPPLSLL P*YCKAKFKPSTSQVP
29748	60116	A	29931	63	281	
29749	60117	A	29932	345	467	LPTRCTYTNLTRRRSPPAWYY* *YWHRDICRSTPARRQTE
29750	60118	A	29933	29	281	MFGKELGRRDVSQLGAAEITYI LKD*T*ES*EILCGGRFLLPLRG RTLGQGEWPSLYFHSDCSSHAE QCLLYGFADWAPLAFFR
29751	60119	A	29934	520	714	

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29752	60120	A	29935	222	527	LPSKLASGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAELGHLI SFHLALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGSLSPDIEG DLIQGQRHRDHIGP
29753	60121	A	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRRVLLIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSYLNDALNGGD AESAGLTPPELWPRHHGHGPA GVKLVEQLCQRLRVPNEIRDLA RLVAEFHDLIHTFPMLNPKTIV KLFDSIDAWRKPQRVEQLALTS EADVRGRTGFESADYPQGRWL REAWEVAQSVPTKAVVEAGFK GVEIREELTRRRIAAVASWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVFSLREQIRSHEIRRSAAVS NHQHFRRACGHIDRRTVQTLA HLTFRFGDKGVTRPEDFVHFW HRFRTKGDPLLTFWPSAPVTAT ILRIPLANGFFRHDHKSSCMTR VPQVPEDPVKSHAPQQFWIHH GKWFAWYDVAIGIPGPFAGRS\ CVILLGDAVREVTRVSNAVPAK RYIGGSPRRGFINSCNMPGIISPG
29756	60124	A	29939	1	114	
29757	60125	B	29940	1	4191	
29758	60126	A	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSSLLSLRAFW ASAPVTATNPPDTLGNGFFRHD HKSSCMTRVPQVRSPTELNRSQ GASRPRGVIQQLGHRDPNGDDS HRVRIGLIKHMP
29761	60129	A	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	A	29946	1	936	
29764	60132	A	29947	1	966	
29765	60133	A	29948	1	675	
29766	60134	A	29949	1	792	
29767	60135	A	29950	2	929	
29768	60136	A	29951	1	969	
29769	60137	A	29952	1	420	
29770	60138	A	29953	1	549	
29771	60139	A	29954	1	450	
29772	60140	A	29955	1	606	

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29773	60141	A	29956	1	726	MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLLTGQQTP AFGRRVSGVIECDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFP\WFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRL
29774	60142	A	29957	1	771	
29775	60143	A	29958	1	1491	
29776	60144	A	29959	145	1929	VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIG\LQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCLALHRIETEL MGKFDEGKLPTDPHLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIVPTPAELFDYTSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK
29777	60145	A	29960	1	1731	
29778	60146	B	29961	1	3345	
29779	60147	A	29962	1	1959	

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29780	60148	A	29963	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPV NVSKSDDTLKINGVEDHKTIFD GDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSAKK RDAELANGALGIIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPLYESLCQYS
29781	60149	A	29964	1	1557	
29782	60150	A	29965	1	2259	
29783	60151	A	29966	1	1959	
29784	60152	A	29967	1	2277	
29785	60153	A	29968	1	2418	
29786	60154	A	29969	1	2028	
29787	60155	A	29970	1	1650	
29788	60156	A	29971	1	1170	
29789	60157	A	29972	1	1446	
29790	60158	A	29973	1	1191	
29791	60159	A	29974	22	1893	

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29792	60160	A	29975	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KIRRKNGPVSATFTSDGKIRLFY TDYSGKHYGKQSLTTAQCDNL KTCHTSHGSVMAETAVINHKK RKNSPRIVQSNDLTEAAYSLSR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSL/KIDW/IIE/ RYQLPKVPSPEARKITRRWRI\V KQRI*LGFLLRLSEMPRKQGDY RTRIWKFEDGLSNVLVIQLNKLI ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNQRSGRSQNDF*RR GI
29794	60162	B	29977	1	1317	
29795	60163	B	29978	78	215	
29796	60164	C	29979	225	422	
29797	60165	A	29980	1	368	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGD/EKGY ESFPWFIKRIYSR
29798	60166	A	29981	1	409	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEKDAGDEKGY ESFP\WFIKHSTNITSLSLWFFSS CTH
29799	60167	A	29982	1	814	

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29800	60168	A	29983	3	678	GSVMAETAVIN\HKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQNRFTQFRL SETKEITNPYAMRLYESLCQYR YSFPPDYFHGLALNVCGFSRYT VQDVGGSIILGSGGQWLSSHSS SRQCP
29801	60169	A	29984	2	660	
29802	60170	A	29985	179	283	MGQGRNPQTRRTYGCQFRMV K*HGIEMKCEELIL
29803	60171	A	29986	1	643	
29804	60172	A	29987	2	1073	
29805	60173	A	29988	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYNV VFALAGSPEDADDTSIYMFYQK CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRK\PDGSGIVSLK/ID WIIKRSQLPQSAFYQPFMGLRR ESFYFRWERRTLGPLKSFSVKR GTEAGKFRLAALLVRL
29806	60174	A	29989	1	1692	
29807	60175	A	29990	1	1788	
29808	60176	A	29991	1	960	
29809	60177	A	29992	1	1385	

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29810	60178	A	29993	1	936	MWLVTTELESTDTEHFYHHSK CYWPRAHLGECILSIEAACQAA GGEAGNGGSAVTKATLGSRQG AQHWKALARTIRQEKEIKGIQI GKQEVKLLPFADDMIIYLENST DSSKKLSELCDNLKTCHTSHGS VMAETAVINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAH\SPFQRALYS CTICNP*ILIPFSF\IGLQNRFTQF R\LSETKEITNP\YAL\RLYQSLC
29811	60179	A	29994	1	1641	
29812	60180	A	29995	1	1551	
29813	60181	B	29996	90	1515	
29814	60182	A	29997	452	1523	
29815	60183	B	29998	9	2021	
29816	60184	A	29999	1	960	
29817	60185	A	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA SSSNCAPRGISPQELTVDLQTKC DNLKTCHTSHGSVMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESF\PWFIKR AHSP\SRGL\YSVHINPYLNSLFY GVQNRFTQFRLNFVQKSRLVD LALKGLRVLLVEGNDPQGTAS MYHGWVPDLHIHAEDTLLPFY LGEKDDVTYAIKPTCWPGLDIIP SCLALHRIETELMGKFDE

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29819	60187	A	30002	1	1756	MPASGNENDLNMPSGTIEIFVR CYVEVERIMDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLES GHQAPCMKSNNALIVILGTVTL DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWIYPLCDN LKTCHTSHGSVMAETAVINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAM/RIPL H*LFR*TLRQTKPDNSAGKCVK I**HTQNQRSGRSQNDF*RRPVL LASLLGATIDYAIMATTPVLWI YPLCDNLKTCHTSHGSVMAET AVINHKKRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYLI PFFIGLQNRFTQFRLSETKEITNP YAMQSPYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN
29820	60188	A	30003	1	1653	
29821	60189	A	30004	1	1128	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDRNRERHTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSVMAETAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYK\SL CQYRAFVNGGGEEKARGKPIL CRYGVGM

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29822	60190	A	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA QRKKKYPPWEKLQGSVRGETP VINHKERK\NSPRIVQSNDFPEA AYSLSRDQKRMLYLFVAQIRKS DGTLQEHDGICEIHVAKYAEIF GLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPW FIKRAHSPSRGLYSVHINPYLIPF FIGLQNRFTQFRLSETKEITNPY AMRLYESLCQYRKPDGSGIVSL KIDWIIERYQLPQSYQRMPDFR RRFLQVCVNEINSRTPMRLSYIE KKKGRQTTHIVFSFRDITSMGFF LESPTQGLASPE
29823	60191	A	30006	233	1538	
29824	60192	A	30007	1	2331	
29825	60193	A	30008	1	1857	MPLRFSSSSRIPYYVNLLHKAA TGFERIDYNFETHSSLEIATDAL TISDHHPCESAAINAETRPSTVL EELARAIRQEKEIKGIQIGKEEV KLSLFADDMIMYLENPKDSSRK LLEWIKESNKVSGYKTHVHKS VALLYTNSDQVENQIRTQPFYN SCENKIKYLAIYLTKESKDLYK RNYKTLLKEITDDTNKWKHIPC SWIVKVAGVESWIHHTQVEVW TPPEETAGSTAHGSQDQPDQPR YTCEPLEDLHLLFQKETSHTIKA STTDPEEKPLPPYKRYCDNLKT CHTSHGSVMAETAVINHKKRK NSPRIVQSNDLTEAAYSLSRDL KRMLYLFVDHIRKSDGTLQ\EH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLI\PFFIGLQ\NRF TQFRLSETKIPVIIQEAGLSQSEK QAADGIQGVAHPAFQVCDGCG SSLQHFFLLMLVDFQLPPLLNL RVLIMATLFTIACYVELRGYML HAFQLVSLAMSHLHLAHNQDT HPAISDVLWVCALSHSLEFHRA SDVRADLSNAYSEEVRKFGFLL WGLDCASLHRSDFITSSETKYH
29826	60194	A	30009	1	944	
29827	60195	A	30010	1912	1915	
29828	60196	A	30011	1503	1961	

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29829	60197	A	30012	1	6552	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQIRLGDP GSSRLSMEHGLRSIPAWTLDKFI EDYLLPDTTFGADVKSAVNVV CDFLKERCF
29830	60198	A	30013	1	2679	MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFG\LTSAEASKDIRQALK SFAGKEVVFYRPEEDAGDEKG YESFPWFIKRAHSPSRGLYSVHI NPYLIPFFIGLQNRFTQFRLSET KEITNPYAMRLYESLCQYRKPD GSGIVSLKIDWIIERYQLPKVPS PEARKITRRWRI\VKQRI*LGFLL RLSEMPRKQGDYRTRIWKFED GLSNVLVIQLNKLIICVMCLVR DCDVLKTYFHR
29831	60199	A	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGL\YSGHINPY\LIPFFIG LQNRFTHF\RFMEQKKSPSNRFT QVRLSETKEITNPYAMRLYESL CQYRKPDGSSIVSLKIDWIIERY QLPQSYQRMPDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THIVFSFRDITSMTTG

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29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK SESDIHLAEHHKQVLYDGKLAS SIAFTYNAKATDAQLCLESSPK ENASIFVHSPHALMLQILTEQV CTQVVHKPHPEPDSTVKIQNPS EQMAVLYCIVLVGGEFDLEMN FIIQDAESITCMTELLEHCDVTC QAEIWSMFTAILRKSVRNLQTS TEVGLIEQCDNLKTCHTSHGSV MAETAVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLQNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGL SIVSL\KIDWIIERYQLPQSYQR MP\DFRRRFLQDVQNETHGNT
29833	60201	A	30016	1514	6335	
29834	60202	A	30017	2033	4226	
29835	60203	B	30018	1	5670	
29836	60204	A	30019	1968	3130	
29837	60205	A	30020	34	431	
29838	60206	A	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	A	30023	3	1771	
29841	60209	B	30024	1	2299	
29842	60210	A	30025	2	488	
29843	60211	A	30026	1	127	
29844	60212	A	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	1	836	
29847	60215	A	30030	297	936	RTSSSLMRSSSSLLRICSGVSPRS IPRWFTSVSLPSSFIR\RITTFRYT PGHVAPASRRSCYKYRR*PMRL YTMIQSLS/VGSRPSGLRAFSSD CSPLPRTCSLSRRRVLMITTSRS *SLTYGVDPSVRPVLAAASEYF SRR\YAGFQNPHNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSSICTSTGGNTTL PPSSPPDC
29848	60216	A	30031	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW
29849	60217	A	30032	2	501	
29850	60218	A	30033	1419	1640	IFCASLSLGLYAGIEARILTKGY TRK*IQQ*APSDQKRDFLVPHG ADSAMAKHGGSHRAVLPQGC DPHMESLI

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29851	60219	A	30034	1	1593	
29852	60220	A	30035	107	195	
29853	60221	A	30036	1480	1605	TILRITFQFCRSNRRRQRQ*NRF STSQRRCYFLLNGEDVTLP
29854	60222	A	30037	1	373	MPSYFTSRIAAVHVSALREEQA HHESKHHESFIAQRMFRMFYQ ARNLLHAGQENLFSGLTALTAE FTVGEEATRGKTTGKRGPSPDG RILRTTKTRNPRGYMQGRYLES QRDVEATDKPFEFFMNRFRLLE AAPRVEFIAYTGLCEDVIRPQL DEAIAQGYLTECADYWQITEH GKLFLNSLLELFLADGYHMWR MIGAGAHLAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPLGIEQ LPALKAFDTVFSMGVLYHRRSP LEHLWQLKDQLVNEGELVLET LVIDGDENTVLVPGDRYAQMR NVYFIPSALALKNWLKKCGFV DIRIADVSVTTTEEQRRTEWMV TESLADFLDPHDPGKTVEGYPA PKRAVSDCAQAVKMTNMISYQ GLVRTFLSTSPNNWLVFMQNG QEVVIDSGKSVS*RSVCFGCFIK HGICSMRDKKISFLV*RRLLLNS LSAKKLHGAKQRAKGDLPRMG AFCVPPKRVIRVVICKEGIWKA SVMSKPQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCPSA PRSRRQRRRSGPLPEPAPRVS*Q IFPSQYWRYRQSTENQKQRLDP RGQIVNVPARRIIRQKRKCCKV AGSA
29856	60224	A	30039	1	1090	
29857	60225	A	30040	1	1384	
29858	60226	A	30041	1	1377	
29859	60227	A	30042	2268	2684	RCRRCKRRLLRRFRRSLLSLAG SPENHARFYCRNSLPDEWFFRH HPRST*PPRSREIRRCHCG*RQC SSDGRKITSVHRGRNADGRELT HQAVRLLAYLSDRFARHHRHL RNAHRRGPDRIPKERHFPATKL RHTPAV
29860	60228	A	30043	1130	1310	RLDKQNRRQGKRQRNNGVFHQ QPQRR*RTDVIQMPHSHHRHA QRRDHQQLGQHHAGRNFE
29861	60229	A	30044	395	689	VAASVSSSMSCAPVLMTVVTR CTLLILSQFMRRKAIKK/LSGSL LPASEVKVLKRDGDYSE/VQQ* APSDQKRDFLVPHGADSAMAK HGGSHRAVLPQGW

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29862	60230	A	30045	1	2142	
29863	60231	A	30046	1	2463	
29864	60232	A	30047	1	1066	
29865	60233	B	30048	790	820	
29866	60234	A	30049	3	126	
29867	60235	A	30050	1853	2257	
29868	60236	A	30051	90	411	
29869	60237	A	30052	1375	3174	
29870	60238	A	30053	5	206	
29871	60239	A	30054	1	1986	
29872	60240	A	30055	339	596	PPYKRRKRRRESVSDGMRNTG KTRRTR*IINLLGRS*NRNFVSV PSGQNYP*ISLDHGRENYGGYS TIQNRLLRLPLSRSGCILQ
29873	60241	A	30056	634	924	
29874	60242	A	30057	42	665	KYGV\NPGPYGGTT\RKLYEKK LLKLREQGTESRSSTPLPTISSSA ENTRQNGSSDSDRYSDNEEDSK IELKLEKREPLKGRAKTPVTLK QRRVEHNQSYSQAGITETEWTS GSSKGGPLQALTRESTRGSRRT PRKRVETSEHFRIDGPVISESTPI AETIMASSNESLVVNRVTGNFK HASPILPITEFSDIPRRAPKKPLT RAEVG
29875	60243	A	30058	1822	4791	
29876	60244	A	30059	310	1275	
29877	60245	A	30060	52	390	
29878	60246	A	30061	250	1530	
29879	60247	A	30062	1	1641	
29880	60248	A	30063	1009	1140	
29881	60249	A	30064	913	1218	
29882	60250	A	30065	900	999	
29883	60251	A	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	A	30068	1	2229	
29886	60254	A	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSRCFWWKTAWAQKMN LLPMARLTTTIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALSLLTVTT QATGRLRARQRKTATPRTIRPG ESTSSSPRSSGSLSAPACSVPWM

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29888	60256	A	30071	498	1155	KQPSAVSGTGAAGEANLHAVR TAEQTAVVYRHRQRVR\YLLR YGILDWSPTYLKEVKHFALDKS SWAYFLYEYAGIPGTLLCGWM SDKVFRGNRGATGVFFMTLVTI ATIVYWMNPAGNPTVDMICMI VIGFLIYGPVMLIGLHALELAPK KAAGTAAGFTGLFGYLGGSVA ASAIVGYTVDFFGWDVGFMLS HELWESEFTKLKYEYNNSCPAS VSGWL
29889	60257	A	30072	670	1100	NCRKTSPKRRFSFDDPKSDRAK DFLAKILH*SLWRAYPIARHLTL YRFAPRICYILALPLSQRSTQQG ATMALPILLDCDPGHDDAIAIV LALASPELDVKAITSSAGNQTP EKTLRNVLRMLTLLNRTDIPVA GGRGKTVNA
29890	60258	B	30073	861	935	
29891	60259	A	30074	1	2510	
29892	60260	A	30075	3	119	NALRKSASSCSGRNRYPGS*PS RPDCQRSCSHKHAGYG
29893	60261	A	30076	3	227	GGEGRASCSADTGWLPSDPPGC AAGALGGGGWAVAGAAAGGP CA*SAGGIGVHAPKAQHPATFS GPAEGVIPPQ
29894	60262	A	30077	1	2277	
29895	60263	A	30078	1	2187	
29896	60264	A	30079	1	3666	
29897	60265	A	30080	1	699	
29898	60266	A	30081	513	1019	TGGVCCWCARYVDALVVFAD QLFVAEVLASAHSPSRLYAHAH GDTPQRLRLNGRQALSP*FCCN HRAALQRHQPVRPLPARQSRQ MRRCNLLYQKASAQRSQRDSS *RSLFFRSVDADGG*R*SHGYA FRHGRFQCHRPHGLPGTGPPRH ADSAFSRRLIYPACRWRL
29899	60267	A	30082	389	462	
29900	60268	A	30083	1	278	MGVNDAVLEMHGLGNDFMVV DAGFDQLLVVEPPYDLELDFHY RMFNADGS/DSGAVRQRCALLC PFCASERTDQ*A*YPRQHRQRA DGSDRHR
29901	60269	A	30084	1240	4914	
29902	60270	A	30085	1	1308	
29903	60271	A	30086	30	164	VTWW*RAPTAGLMQC*YCRNR RARLRLTYGHAPAHRRNGPDV PS

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29904	60272	A	30087	3	264	TLRPANRF*HIPDAAGVIPVGY AL*RGTSVSAVHRW/CSTVFGV NWATLATKLMVAGIRRSGAAS RISRASPPSFSVPACSVGRKKVI
29905	60273	A	30088	1	3639	
29906	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLLV FADCLAWTCRHDKLDDISDVA KITGLTSKAIRFYEEKGLVTPPM RSENGYRTYTQQHLNELTLLRQ ARQVGFNLEESGELVNLFNDPQ RHSADVKRRTLEKVAEIERHIE ELQSMRDQLLALANACPGDDS ADCPIIENLSGCCHHRAGKYVG LIRRVKRRIRHRCWPIKTLSQRA VSEFQRLIQPNHQYQSYTRQCA PETDNHADNSYNAGLFIVNSLY TAEGVMDKHSLWQRYVPLMR HEALRLQVRLPASVELDDLLQA GGIGLLNAVERYDALQGTAFTT YAVQRIR\GAMLD
29907	60275	A	30090	1	699	
29908	60276	A	30091	430	660	HQTHFIVEHRRIMQRTARQNIG RHYQIQLSAVQRIRGAMLDELR SRDWVPRS\RRNAREVAQAIGQ MSLPMLQVALS
29909	60277	B	30092	1	1575	
29910	60278	A	30093	1	289	MISANRPIINLDLDLLRTFVAVA DLNTFAAAAAAVCRTQSAVSQ QMQRLEQ\PLGKNCSLVTVATN C*LNMAFNFLVTPGKSCVLMM RSCIQPNSD
29911	60279	A	30094	1	1095	
29912	60280	A	30095	1037	1297	LILRCPWSYSRCIRILIAPSSS*Q TEAKPFASRASRTSDDCQWANI SSVMPVKPNSTTPSILRRFSTPK CSATNCGEN*LSIMIGS
29913	60281	A	30096	905	2042	
29914	60282	A	30097	87	760	
29915	60283	A	30098	1	2793	
29916	60284	A	30099	308	485	KSLNAICYRNTRTSMACY*PA* VRWPKHSAGLMTISPVLHVISP RHWRLECATRVGRLG
29917	60285	A	30100	1	2784	
29918	60286	A	30101	453	1975	
29919	60287	A	30102	3	470	
29920	60288	A	30103	1447	1773	QFAFTEHHQTQEHHHQRSYDC PQRDPRHIDAQVSDQRPCPDSG LREPLHCAQPDSGG*ADNSADH IRRNGGDGAFQRKRNRTLTDPH KRQEHGGLTLRIKLSVEQAFAG
29921	60289	A	30104	1	449	

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29922	60290	A	30105	188	1508	
29923	60291	A	30106	171	410	
29924	60292	A	30107	3080	3232	
29925	60293	A	30108	1	1272	
29926	60294	A	30109	438	617	
29927	60295	A	30110	259	392	
29928	60296	A	30111	905	1545	RLTTPSLSVCWRPAAKRPILPRS LKQLKKIASRKVTP*/SLGNAW NNLEKQRAYLSMMAQKRVDG LLVMCSEYPEPLLAMLEEYRHI PMVVMDWGEAKADFTDAVID NAFEGGYMAGRYLIERGHREIG VIPGPLERNTGAGPPCRFYEGD GRSDDQVDGDIQFFFSTNTITGR GHFRTMVDGICPCKDGNLRFN RILEHREPFYPQIPATFAYA
29929	60297	A	30112	3	466	AIVKFKRNVHQDGGYCSVQIQ QCRFALIFKDFCRMRHNGLIRR TISQQSVGRIRCVSIASGRVYYC FFALEGKKPSSSISAAPTQMAVS ARLKVAKCQSPT*KSIISTTKPC HRRSNRLPSAPPIISATRVHRQM RYSTSSGAAALLSITVTPS
29930	60298	A	30113	1	1562	
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLLTS LLTSVV*IDAIDGIRFSFLSWAS GKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRR RREREKTSERTPAPV*VKITTRK LYPAEERTGRIFEA
29933	60301	A	30116	1	3095	MDKFLNTYTLPRLNREEVESLN RPVTASGLEVIINSLPIKKSPGPD GFTAAFYQRYKEDAGEREGEG GNQQVAVRGKRKTTERKKKLG EDVKVKESKNSGAYEVKQHRF FRSLDWNSLLRQKAEFIPQLESE DDTSYFDTRSEKYHHMETEEE DDTNDEDFNVEIRQFSSCSHRFS KAAEVSTRLLSTRVTEIEGWLI VQRNQKLLQSNLKQRSGEPLIL DDDSHVPPELRAGYRLLKNAG CLPPELEQRREAIQ
29934	60302	A	30117	1	2583	
29935	60303	A	30118	1	3141	

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29936	60304	A	30119	1	1037	MRVVILGSGVVGVASAWYLNQ AGHEVTVIDREPGAALETSAAN AGQISPGYAAPWAAPGVPLKAI KWMFQRHAPLAVRLDGTQFQL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRAPDTLNTMPIFKA CTPDNRRAVWRHRAQTSPESR LLDMTAAWIEIANHHLQRFTTR LQQLGIKTNNLRHSGKTNAVIV YMIQSISLVDEMSCHLVLTTGG TGPARRDVTPDATLAVADREM PGFGEQMRQISLHFVPTAILSRQ VGVIRKQALILNLPGQPKSIKET LEGVKDA/EGVPYCIQLLEGPY VETAPEVVAAFRPKSARRDVSE
29937	60305	A	30120	96	711	
29938	60306	C	30121	128	628	
29939	60307	A	30122	1024	1128	
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHVF ATTCNRALSIWYLMN
29941	60309	C	30124	202	321	
29942	60310	C	30125	150	491	
29943	60311	A	30126	1163	1257	
29944	60312	A	30127	929	1023	
29945	60313	A	30128	3	765	TARAWLLLGPVWPCVSERWSK KPSPRGGRDPSDRDPAAFAARS TVPPRISAYERPVPWPGEWNDP RGPGRRASAVVSPREGNWGVL RDPRLQARKPRMVRSRQMCNT NMSVPTDGAVTTSQIPASEQET LVRQESEDYSQP*LLVALFIAA KKM*KSLKGKKPKTKKRVWN LVCPLMPLNLV*FVKVDLKMV ALSMAKQDILWPALH/DAKKL KKRNKPCPVCRQ/HNSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	A	30129	2	430	
29947	60315	A	30130	3	1088	
29948	60316	A	30131	303	529	GTGQCANTKMSVPTDGA\VTTS QIPS/SPEQETRVR\PKPLL\LKLL KSVG\AQKDTYYYGKRFLFNLG QYIYGLNDYY
29949	60317	A	30132	3	619	
29950	60318	A	30133	123	385	

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29951	60319	A	30134	66	413	HQSEQMYQSSESCLLGTTAKA RGHQLRTASACHFPSTPPFWSL TLESQREGRFKQPTLISCF/CLF MSVPVVSAPPFSSSSSSSSSSSS SRPWFPDQEAR*LTSPVERPCR GLRPA
29952	60320	A	30135	257	465	VPTSPASLESKQSCPHVLCPVW EVEGHSV*TGKPDRPPRRKLLT LLLPVPWVPGQLAIKQEGQEPK KRH
29953	60321	A	30136	1564	1857	
29954	60322	A	30137	33	265	
29955	60323	A	30138	114	560	
29956	60324	B	30139	70	555	
29957	60325	A	30140	650	1045	
29958	60326	A	30141	374	575	
29959	60327	A	30142	1	1095	
29960	60328	A	30143	1	981	
29961	60329	A	30144	28	698	TACRIRHGHAGRLCCSPCLLVIP LKSSQHI\LRVLNPPNLDGRRKI A\FAHHCPFKGVG\RRYA\HVVL RKAD\IDLTKEGGENSLEDEVE RVITH/ILQNPRQYK\IP\DWFLN KTRRM*KDGTYSPGP*PIGLGQ QAPVKDLGAD*KKIRAH*/RGL RHFLGAFRVRGQAHQEPLGRR GRHPSGVSKEEIRSVGPCLVNKI VYIPKKKKKKKKVDAAANLVV VVVVGGR
29962	60330	A	30145	107	340	
29963	60331	A	30146	428	934	
29964	60332	A	30147	1	1533	
29965	60333	B	30148	1	2652	
29966	60334	A	30149	205	450	
29967	60335	A	30150	1	879	
29968	60336	A	30151	139	1029	
29969	60337	A	30152	237	422	WFETPAQYTNRSPESGTHYRRA RSRARWHGCMECVCRRRKSPR ANKPRRLPPVR*RCPPRA
29970	60338	A	30153	1	1134	
29971	60339	A	30154	136	411	
29972	60340	A	30155	1	3345	
29973	60341	A	30156	194	475	TPATVRRGWRPAVRVFRWWK PLTVPPRRKGPLSRGTGCRPVPL TTPSTGTVMRAGICAVKMLIVQ KSPCMPPC*HRQWTMTGLWQA PAAIRPV
29974	60342	A	30157	1	2988	
29975	60343	C	30158	1	3939	
29976	60344	A	30159	308	749	
29977	60345	A	30160	1	1338	

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29978	60346	A	30161	1	4342	MTRDNPVIPRFIHRREVVFIGQE NGGIQNARFIAALFFQHGVNLC QRVGGLLKGIGVEVFRYTSVVE RVVVDYYIRPAGFSIDTNDRGS VTDDFAPDGQLAKAIPGFKPRE PQRQMAVAVTQAIEKGQPLVV EAGTGTGKTYAYLAPALRAKK KVIISTGSKALQDQLYSRDLPTV SKALKYTGNVALLKGRSNYLC LERLEQQALAGGDLPVQILSDV ILLRSWSNQTVDGDISTCVSVA EDSQAWPLVTSTND
29979	60347	A	30162	1	1023	
29980	60348	A	30163	1	679	MFRVTWSSGRTGLGKRLFRTP YDNDDTGPYAFNKTHPKDNYT CTVLFIDDMSASGQSLDKAQD NYRQAMKKLSSGRGNVLAQAE AFRGLGVEIKREINPDLAEQAIR LQDCVFDTQETMTTTFTGTVSS ANSGNYYTIFNTDTGAAFNNVS LAIGNYVVLAFSAS/VGA/DMK MVNSTITASGSKRSTTVLRQGL SQRWLLSAGARNLLQHYSFRE TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	A	30165	1	1353	

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29983	60351	A	30166	1	1661	MRGEVLLAGVPRHVAEREIATL AGSFSLHEQNIHNLPRDQGPGN TVSLEVESENITERFFVVGEKRV SAEVVAAQLVKEVKRYLASTA AVGEYLADQLVLPMALAGAGE FTVAHPSCHLLTNIAVVERFLP VRFSLIETDGVTRQLLGVSYRIL AMGHAEFLIQIADMRNDGGWR DFQFSGNLVMDEPNRSAQTYIK LVKSRLGTTKRYNHKDDCPRC RWIAAMIDNPPRIRKPTKSASV WHATATSASPERQMSTTVIMS ARFISCWVMTPFCMPRSGPMRF VHLPCRFRDAFNTGVGKLDQL GPSMSTRIRQRFTTLCPMTLSSS STEFENVSDCRPSRARSCLRFRL CRSIRCVYRLADYVQRSLQAGF IQRPAIRHPYHHVKGAFTEYVR NNRLPETVIRVLQPALARFSPDI APLFSPFPLHDDDVTARLYAPS LMPKLRLIGLTLLALSATAVSH AEETRYVSDELNTWVRSGPGD HYRLVGTVNAGEEVTLLQTDA NTNYAQVKDSSGRTAWI/HVET T*H*AKPALPCARSGKSGQNPD R*THQYR
29984	60352	A	30167	254	496	RASRLKTCGDGCCSLSAVVSVG ASPFASRVKSSRRWV*S*VGPSS WPPGMSL*TAEIRRSRRIPVVSS GSLTASFANVVR
29985	60353	A	30168	1	984	
29986	60354	A	30169	1	429	
29987	60355	A	30170	1	523	
29988	60356	A	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	671	
29992	60360	C	30175	1	2649	
29993	60361	A	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	A	30178	3	108	

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29996	60364	A	30179	404	1347	DVTILARAVLQALLKILYH/KCE FNDEMLTEGVIREKMGFNPQTL REVLQACQQQGCVANNLDLDV VMIIIDGAFSGIVQNWLMNMA GYDLYKQAPALVDNRTGMER ASNGGPWQVQSLPARSYRQLD SYYGEAMAIGERALVALLDFSG PSPSGDWRYQTHHTFPPTGWR RQATLVKMRACIEAVKAVGEE LCPALGLTIPVGKDSMSMKTR WQEGNEEREMTSPLSLVISAFA RVEDVRHTITPQLSTEDNALLLI DLGKGNNALGATALAQVYRQL GDKPADVRDVAQLKGFYDAIQ ALVAQRKLLAYHDRLI
29997	60365	A	30180	494	1433	
29998	60366	A	30181	1092	1347	
29999	60367	A	30182	315	600	STPIEKTVSKAFSAGSCSILTVT NARASARSACIISITAAVSGSCA PTP*EVSSAFARSLICRSIRKPGL KLRSITIGALASKTVLPASPPRIA
30000	60368	A	30183	535	661	
30001	60369	A	30184	1	1491	
30002	60370	A	30185	1400	1852	
30003	60371	A	30186	199	534	
30004	60372	A	30187	2	539	
30005	60373	A	30188	1	690	
30006	60374	A	30189	127	939	
30007	60375	A	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLCL TDERTRR\NNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERS DEIPEAAKEIMREMGINPETWE Y
30009	60377	A	30192	242	709	NYMHYHADRCITRCHGNACTV NYAGLRSVPTSTVWTGLNLLT KRIKYLMAEWSGE/YISGPCVEP GKKSDQSKKITVSIPLKVLKILT DERTRRQVNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERT AE\IPEAAKREHA*HGGLTPET WEY
30010	60378	A	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263	514	PAHFSVAHSHLWQNINPLSSVQ CRQNHQAIPCRIFELLNVMRH/ VTRDSSSGLGCSWRLTASVNAR RFVDPVQILVMAMSGRRSR
30013	60381	A	30196	1	1995	
30014	60382	A	30197	141	229	

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30015	60383	A	30198	1	702	
30016	60384	A	30199	36	144	DGLLLMDERNISPLLQKRMPT* QAV*VWWWKDYGV
30017	60385	A	30200	462	646	QWVPIARPNMPACHVQRRTSSL ERRQPVMLMVMLRILWYIYCSI HVLG*WICRLYYKTLLK
30018	60386	A	30201	107	1200	
30019	60387	A	30202	366	500	
30020	60388	A	30203	1	1193	LADCSRYNGLEMTLSCCAGAS T\DAVGGIERGGLKSPEASEGEI APRLLLDGEPLALSGDKWRISP WLLVTDDTATITAFLQMIQEGK AITLRDGDQTISLSGLKAALLFI DAQQKRVGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPTPL SLEERNDLLDYGNWRMNGLRC SLDPLRREVNVTALTDDKALM MISSQIFNGHMVHIIKDLVFTDH APDKGISFGSDTGMDRPARGD HRLLVMHHDMTRFLRLPHHVE NAGVIIHIEIEINFHPALVGVTRH GVPLVTRSQLRQPHTRLAGFQY IRDQIFVNRATVTGEEIAYAELF TNFPANGNRFSYRHNAANNNS VNVAVNHGVLIGDKYLFNQKFI AQPLGIQRFCVRTVDALSYVHI
30021	60389	A	30204	3	1057	
30022	60390	A	30205	1	955	
30023	60391	A	30206	1281	1370	
30024	60392	B	30207	1	2199	
30025	60393	A	30208	1	589	MLKKREQTVFTHEKSVFQGLD RGNRELGPPKTFGVKGAQKGN LQIFSEDKNFGPGGSGEIWGHR GPKWDIPRGKRETLGKPHFFW KPSQEFGRKGLGSFGPWERVSG NKNSGKRIYPWGPVDGINCRW REPRNVDVAEYRRDCGSRFRSL RHFYRSLFSLHRPASTRHQKAQ SSAVT\VLQTNAQHGRRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRTCCAPLSSVWRCR PPRSSPWPASWRSVPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCLWTSSLAPASRP CPS*\LQPPGQQRWGEPIGAIAV PL

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30027	60395	A	30210	61	641	RHKHRRRIPGRWDQIRPAPNR WQTGFQWFALPVTGVRLISGY TELLPRL/PAQKNLPYTIHPAWR FVAHQGRESALECRYVPLPVRH *RNCRWREPRNVDVAEYRRDC GSRFRSLRHFYRSLFSLHRPAST RHPGAQTGAVTGFADECPARK AAALAKASVNKVVFHSTNATV CHRPDRSRRASGSFRRYWRQE
30028	60396	A	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLANSKNKRR WRKNIKLR*SSLLK*TESPLPMA ILVLTSLTAI
30030	60398	A	30213	451	834	IWTGKKVDSARALIARGWGLH VILRRTDDWMDGRRSRHTDDT DVLLRIHHVIGELPTYGYRRVW ASSQTGRT**FKVQNRYFPPVLS DFEHLQEPYEYFGKLR*PWLPA TGEFHAEIYRSVDFCKHPV
30031	60399	A	30214	1180	2547	
30032	60400	A	30215	341	505	
30033	60401	A	30216	293	4221	KPFSPCCRKGRWLFRNHSSARR PTVLYYRRSTMR*NSW*PNLRR QRGNPANRS/RQSMLELSGVKD GELIPAKLFNHLVTWLQARQTL SQQNTPRPGGGEIPPWCSSVLA ESERKKRGRKKQRGIDSPDVGA LLLVRATFYIWQQPPVNKIALGI EYAASKYYGWQRQNEVRSVQ EKLEKALSQVANEPITVFCAGR TDAGVHGTGQVVHFETTALRK DAAWTLGVNANLPGDIAVRW VKTVPDDFHARFSATAR
30034	60402	A	30217	1	1362	
30035	60403	A	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWRR*SP QYARHTRKRTSAGCSA
30037	60405	A	30220	1160	2385	
30038	60406	A	30221	290	373	
30039	60407	A	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	A	30224	1	469	
30042	60410	A	30225	241	615	
30043	60411	A	30226	1	1428	

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30044	60412	A	30227	862	1453	SFLLVSPSQACHHYYAP/KIFDL/SGYTSTTEQMWGTVIVGLTNVLATFIAIGLVDRLGFLAMPAGMGVLGTMMHIGIHSPSAQYFAIAMLLMFIVGFAMSAGPLIWVLCSEIQPLKGRDFGITCSTATNWIANMIVGATFLTMLNTLGNANTFWVYAALNVLFILLTLWLVPETKHVSLEHI/ERNLMKGRKLREIGAHD
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCCPPVSVHFFFHSRLCRDALNEAFHPSGFQVVKCCDIARIHRNRYGDLLFAIGVVHIANVNAIHRNATFHQRQEIGGCFTNQQDFLSIGGAMNVVDNFLQRPETYGDPFCQYHFHQVLLYRIFGNLIVGYQHQICPRKSDPLNADLTVNQAFINPA*NNIWHSVFLFVLLIGLHRLCGMRQDVLNMVDNEFPWRWLQLAGANFHVLQRQILADQRQRNW
30047	60415	A	30230	2553	3845	
30048	60416	A	30231	1	656	
30049	60417	A	30232	3	228	
30050	60418	A	30233	185	206	ATVDPPFITEPGDILAGGFA*PLSWFAGFALEHHNLPWATGDLHSLRA
30051	60419	A	30234	12	155	
30052	60420	A	30235	698	2684	
30053	60421	A	30236	1	2004	
30054	60422	A	30237	1	811	
30055	60423	B	30238	1	7521	
30056	60424	B	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPWNRKPVLSVIP*KWKLKGPVALKTAYPAKRLPLPITSFSLPGVA
30058	60426	A	30241	1	2067	
30059	60427	B	30242	1	2787	
30060	60428	A	30243	101	947	
30061	60429	A	30244	1	1917	
30062	60430	A	30245	239	469	KRVSISSRRRFSAQKASASALARWWRSAVNIYVFAI*TTAQRV*QLRMTNCVRTTITACHSR*RITLSLSPVKPAS
30063	60431	A	30246	1	4348	
30064	60432	A	30247	1141	2244	
30065	60433	A	30248	503	649	

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30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRLFIGAERFQHIAGSGHYR VV*NANAGSKIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNPFNFEIFQRLVDDDP HCTIGIMFANVDHGTTENRIRK LCFNLTNTGTQRKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	A	30250	1	526	
30068	60436	A	30251	442	684	
30069	60437	A	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPLPLPTENVP AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDRPRLAIRDATIGISG FCSLA
30071	60439	A	30254	62	298	
30072	60440	A	30255	904	1530	
30073	60441	A	30256	701	1329	HRLSMCRGRCSRWWSARTNVI SMLVFALSFASWRIVSPRTM/D ALTFAAESALPGSPTHISTDHQG QFVFVGSYNAGNVSVTRLEDG LTMLHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTPPPEA CTTNKQPAQPQRDKPQRGNQQ RLASVIFQCQQHDHEHKERHTY PAHQLAERHLVDRLLM
30074	60442	A	30257	8	382	
30075	60443	B	30258	1	2655	
30076	60444	A	30259	67	231	
30077	60445	A	30260	1109	1531	TFLHSIPAAKTQGPPPRNTLVDT PQHL*HQQRRTRQPQLALSLRT *VFLNRILRGALFAPKACLKPD LVISPRGPPQGLGVTRVQVSAH TNPRTTHRNTPHYTRNTQTRPE STPRRDTTTPQQRHTPPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDRSDSPISQSKMKIIA SITTIRMEP*AIATPYSPSSTRLR M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSPISQSKMKIIASITTIRMEP *AIATPYSPSSTRLRM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	A	30263	3026	3217	LPQCKWDPYGVTISPQVSIRSR ANPSCTSPFFV*SATKGLLYQQ TRIPALDIPPSSNRRNSHG

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30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPHYGRWPQ HDFPPFKKLRPQSVTSRIQPGSD VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSLRKTVVAHVFGE RSLFTGP*RERFATQIEVGKLFA AAVDMVLWLSGKAQPDTVVV KVVVL
30082	60450	A	30265	3174	4135	
30083	60451	A	30266	1	2771	
30084	60452	A	30267	1	1281	
30085	60453	A	30268	10	233	LRIQASDPEINSRRESGIHLPYTT DKAPSPLTVDGAK*EVSRSSI/R QNSQVQHPPDAAKYPSGCHKS FRGFRRA
30086	60454	A	30269	300	564	SANSTLKRTQVNRRPLTVKLSA RKLPMLKVNTRNSLVVVVSMV MLLSTCTRWSRVQTRKATSSST TLKVV*SLANTSRPLIKVSRNS
30087	60455	A	30270	5259	8003	
30088	60456	A	30271	1	819	
30089	60457	A	30272	1173	1369	
30090	60458	A	30273	1	4767	
30091	60459	A	30274	905	1162	FSSVVMCSSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSCRSS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	A	30275	1164	1582	
30093	60461	A	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGVS RLYAANQHRTCQ
30095	60463	B	30278	1	954	
30096	60464	A	30279	108	530	SIRQTHVQIVRRSCLAIRHQVPS TAIRVGIVKGNFAS*AGAQPSK TLR*HRCTTRALTSGVLAVRLS AGCNFPELVHRRLTLWRAGRT YPPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLTP PFPAGQRC
30097	60465	A	30280	1	1389	
30098	60466	A	30281	1	380	
30099	60467	A	30282	1	3255	
30100	60468	A	30283	569	2547	
30101	60469	A	30284	1	585	
30102	60470	A	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGSLG PSSGPKTAGAPSSRPPSPSARRP RTTETRWTLLRSKDYWLITRKV GLGNLQDGGRAGSLS

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30103	60471	A	30286	737	1088	NMLMNVCNLPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRCLPIIVGR RKSGGSKIRANVCSLPIFPSGI\G R*TTGESKRLCRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAEST\SPLAMVGD GINDAPAMKAAAIGIAMGSGT DVALETADAALTHNHLRGLVQ MIELARATHANIRQNITIALGLK GIFLVTTLLGMTGLWLAVLAD TGATVL
30106	60474	A	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPF IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFIVGTSGLFNHAENIDEAW RVMTAQILAAKSEQWGQQVY AIVQNTDQAQAVMPYGPKCLY VLAQNDALQRTENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTNASLAGIALNSMDLSP GGRVAVKESNQRWCSDGFEFC CDNGERLRVTFALDCCDREAL HWAVTTGGFNSETVQDVMLG AVETPLRQRSSVVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQSRHRPAPALRYPQLQ MPHWRRSICTSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIKSASLS*FK*LLKPAINAG*Q AS*WRASASKPCSASPDCAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	A	30294	1246	1300	
30112	60480	C	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCGVD
30114	60482	B	30297	1	3081	
30115	60483	A	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVATKLRR *RVFPAPCCG

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30116	60484	A	30299	3	421	QRRATGDLRLPTR*TARRGGRC DS*SSRRWHRAFTGACREISRQ QNRRHRQRPAGGVALVGSE*T SGILAGQRHYRVYRAGYRRSPP AGYAPD*SD*RPVDGRHECGRR PVWRRENVPATGGQIGARHET GGGLPRTVY
30117	60485	A	30300	1	3202	
30118	60486	A	30301	317	554	
30119	60487	A	30302	474	599	TTSVQRTFLPDTY*APTPVLLPA RKATAARKLHRFSGRQDR
30120	60488	A	30303	212	569	TSLKVVTPALRSMPSVPINNLS KVKCSKAFSASCP*NEADFLRN VPPGIRIVCSLSSSDSALTICRLL VITVMLLKRESRGTICKTVLPAS RMIESPSWIKLTAASAISSFLWV LMSVL
30121	60489	A	30304	1	160	WSKMSRAVRPSDWESWTQTRE VVRQTVRCRPDPPSAAVCLTAS SPANCGIPIG**MLAEILA*RAV RPSDWESWTQTREVVRQTVRC RPDPPSAAVCLTASSPANCGIPI G
30122	60490	A	30305	1	975	
30123	60491	A	30306	1	762	
30124	60492	A	30307	1	733	
30125	60493	A	30308	493	948	LGAIFLAGALFAAAWLADFRL GLGARLYRYGADWFCADGGM SAEELKFISENGAVVDMDHKKP GSAAASGPKLHYIKQLLSNRM MLGVFFGQYFINTITWFFLTWF PIYIGNVVSDNR*YVAQITFITW IKTYGRCPSFQRDGDGFVNRCL

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30126	60494	A	30309	153	2031	RRNYQRQQKKRGSEGAGRPDR RSRISAAYSPRSEFNNAAVTEH Y*NRF*T/LVPRSR/HANADTVT REAVNQVIALLDSGALRVAEKI DGLPTNQMQASRRAKEEEVHL TGQPSRVQSPPRRCEEKQYMVL MIVSGRSGSGKSVALRALEDM GFYCVDNLPVVLLPDLARTLA DREISAAVSIDVRNMPESPEIFE QAMSNLPDAFSPQLLFLDADRN TLIRRYSDTRRLHPLSSKNLSLE SAIDKESDLLEPLHGFPDYDTV GFSCKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKTR RSLLVTLVRIFCVRVIFAYDIRD GIHVRIIQINSKSGKVGSKHNSG YSAAKFGGVGLTQSLALDLAE YGITVHSLMLGNLLKSPMFQSL LPQYATKLGIKPDQVEQYYIDK VPFKRGCDYQDVLNMLLFYAS PKAVVLAPDSRSMSPAVSGRFK PRVVVAIALDDQQRIVDTLFMK GLTVFARPQKIPAITGRHSGATL QKQGKCSVEELAQYFDTTGTT MRKDLVILEHAGTVIRTSGGVV PDSPPHTRRDPRRFSMAFPWFD NIRSAEFHHVTTLLAEIPRQQND IHRPAHAAAAPKVETRSGDETN RRWNRPAQHLFA
30127	60495	A	30310	720	872	EKVPVSIGPGGMQELPMQSPDR RSAGKPGPASRAGR*TGGGAFS TKRDYR
30128	60496	A	30311	1967	2452	SRRCSASINQRPRPGHEKMVSV RIAPASNVPTCRPITVTTGSIALR SAWTIITRMRVSPLARAVRM*S SPSTSSIEERVIRTMTASGIVPST MAGKIIWATASIKLPSSPQMAV SISIKPVNGLESSRNTISLTRPET GVRFQCTETSMISIMPHQKIGIE
30129	60497	A	30312	1912	3960	
30130	60498	A	30313	2	250	LIRKVST*SVLMKAFLRIA*KDC ERLGLKCFWSGSEKGCPLVNT NAFGGHCEHHQWVSSVSRVRV SQSAGGCPLFNILLNTV
30131	60499	A	30314	1	300	SVFSH*AKKIWKGVSQRALGQ NSRGSGSGCQASWTIRFPVGFH TDGTRLRRNPGMQAFLGPVAR FLALEARSLDCAFSSSLLFKRKL SGRWGRASRGTKL

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30132	60500	A	30315	1	468	MTEKVKQQPAPVTASDEIDIGR LVGTVIEARWWVIGITTVFALC AVVYTFFATPIYSADALVQIEQ NSGNSLVQDIGSALANKPPASD AEIQLIRSRLVLGKTVDDLDLDI AVSKNTFPIFGAGWDRLMGRQ NETRRGFSARGTGQMLKKEGV TLMVEAIHASPGSEFTVTKYST LGMINQLHNSLTVTENGKDAG VLSLTYTGEDRYTNHAGVVNT MIIIAATHNLVFENNSCEYAHP MGNAPAGLTEYQNVFYKHDRI QGHYVWEWRDHGIQAQDDHG NVWYKFGGDYGDYPNNYNFC LDGLIYSDQTPGPGLKEYKQVI APVKIHARDLTRGELKVENKL WFTTLDDYTLHAEVRAEGETL ATQQIKLRDVAPNSEAPLQITLP QLDAREAFLNITVTKDSRTRYS EAGHPIATYQFPLKENTAQPVP FAPNNARPLTLEDDRLSCTVRG YNFAITFSKMSGKPTSWQVNGE SLLTREPKINFFKPMIDNHKQEY EGLWQPNHLQIMQEHLRDFAV EQSDGEVLIISRTVKPRGPARCP DSSVGTTYCTENNPPFDNGLLN AQLLQQAKPFVDERQSK*FGCH SPSYSCLWLSIIGLKKLIFGSRVS SDSPFTCQDVGLPLIFEKVIAKL
30133	60501	A	30316	1	524	
30134	60502	A	30317	1669	4421	
30135	60503	A	30318	2	349	SMAKCPLRKNQGPVRSCGAWS GCLWLPSPSGTPWRSSLWILLL F/SQISQLLSLLHQGQFQPKPNH RGNKYLAKPGGSRSAIPDTDGP SARAGGQTDPEQEEGPLDPEED LSVKQLL
30136	60504	B	30319	217	368	
30137	60505	A	30320	1	951	
30138	60506	C	30321	1	3729	
30139	60507	A	30323	1	2437	

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30140	60508	A	30324	1005	1815	PDLHCQKKHPTLCSGYWPTFRT PVHYAAFS**/HALGHLAFS/EA SLHSHRGTQALTTQKKSPAKSP TAATTETRVMRKISHGTRDPPG FASL\MQ*MHYGKLCAFQSELL FQSLQRSHWTQSWWLCWPHW RLCWTQNWWQCWPHWTLCW TQSWWLCWPHWRSCWTQRW WLCWPHWTLCWTQSWWLCW SHWRSCWTQSWWLCWPHWRL CWTQSWWLCWPHWRSCWTQS WWLCWPHWRLCWSQSWWLC WPHWRLYWTQSWWLCWPHW RVCWTQN
30141	60509	A	30325	2436	3678	KMPPWPPGSPGPLGCSAWAEA PPAHCPDVLLHLHPACPHIQAP CGTGAPGTGLAAAADSEPLGSS APPAGRPCPQAAAACGLAPPLP RGWCPPPTSSWMGRRLQSLSA HPTSPAPLLAAPTAVCSCSRCSA PRSRCVARPAARTGLPTPAPAS SPAPATSPAPAESPAATASHPV AEASPAPGAPPPRPAASPSPAAS PAPPAASPVLTASPPLPAASPAL AASPVHTASPPVHVASPPVHTA SPPVHTASPPVHVASPPVHVAS PPVSCSGDSTSDCFPPQPGAVFP HSL/VSFLRWLVSSCSCSTLDGP AGGCGARGSAVWFLSLNKLLP/ MLLYQMYLMLLLLLRCANQ*I DVFSELTDYCGA*IQGYC*FLV LAIPR*VVTTRSGCVRATAIDFL FPVSSCWNARALPLPICF
30142	60510	A	30326	929	2910	
30143	60511	A	30327	1	1488	
30144	60512	A	30328	203	701	
30145	60513	A	30329	493	924	SDPGFRHGKARITDPRGQPGRR LQGGSSEGNGSDMKAARKVSG NKHSTSSHQHAVWCPGVPS*SG KAWAADQRFVPRILGKGRGHV DAA*LSWKCRNHLSSVSLNGE NQRFVGDARYRTRLQRGSANL FKRQRCGTLHQNLELL
30146	60514	A	30330	1	2193	
30147	60515	A	30331	1	2990	
30148	60516	A	30332	2512	2560	FALRYRQPVRHRW*FHLVQRH GRFSRASGATWPASAAAFAWP LLVCAPLSAASAAPLARL
30149	60517	A	30333	1	2820	
30150	60518	C	30334	194	418	
30151	60519	A	30335	25	458	

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30152	60520	A	30336	860	1209	IPGNCRDSSGVGIKERETNAGS QHMH/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPENPVYEKKPK KEVKKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	A	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	A	30339	1723	1845	
30156	60524	A	30340	6	983	RRWACRSLSSSGRRSLFRRMGF VKVVKNKAYFKRYQVKFRRRR EGKTDYYARKRLVIQDKNKYN TPKYRMIV\RVTNRDIICQIAYA RIEGDMIVCATYAH\ELPKYGV KVGLTNYAAAYCTGLLLARRF L\NRFG\MDKIYEGQV\ELTGDE YNVESIDGQPGAFTCYLDAGLA RTTTGNKVFGALKGAVDGGLS YPLTVPKRFPWF/DDS*KPRNLI AEVHRKPHPWAQNVARLHAPT LMEED\EDA\YKKQFVRQYVKN SVT\PDMM\EEMY\KKAHAAIRE ESSSMEKKAQGKKFKKKRWNR P\KMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	B	30341	1	2043	
30158	60526	A	30342	390	1180	
30159	60527	A	30343	2	649	
30160	60528	A	30344	1	1929	
30161	60529	A	30345	1	773	
30162	60530	A	30346	3	484	NSSCRDPGY/CPIIVSLNSS*GSL LQDMPGPSKVISEILATRGAVNI TTVAYKSAVILSFTTASAVSLSS RNVIGPLFASQPSFTIHFSLFSHN GSAPLNAPDMANCFGLTALTSS LDERLFSRNSAGSCCGIRNCFIS TLPPNTSTLTSVNSKGSSSVHG
30163	60531	B	30347	1	2775	
30164	60532	A	30348	1	1386	
30165	60533	A	30349	439	555	
30166	60534	A	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITRCRTK/ EQRYALSQAKSIADELMTGCTN FAFSGKPGTGKNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMRSVGMLTNLNY EAMKTLLGERIMDRMTMNGG RW
30168	60536	A	30352	1	786	
30169	60537	A	30353	1	288	
30170	60538	A	30354	711	953	

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30171	60539	C	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	A	30357	1	420	
30174	60542	A	30358	1115	1561	
30175	60543	B	30359	501	555	
30176	60544	A	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	A	30361	386	1647	
30178	60546	A	30362	1	1179	
30179	60547	A	30363	1	1215	
30180	60548	A	30364	1282	1657	
30181	60549	A	30365	388	804	
30182	60550	A	30366	1328	1978	
30183	60551	A	30367	455	1000	
30184	60552	A	30368	291	303	RVRRMMYTVTLYSFSTNKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSLQTVSLL LLSSFALDPSSTMLTTEESVE
30185	60553	A	30369	284	433	RVRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	A	30370	290	425	RVRRMMYTVTLSSFSANKNTYI *E*E*GLGWRHHIFLG*IQHFNR
30187	60555	A	30371	842	905	
30188	60556	A	30372	784	3453	
30189	60557	A	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSPSGSLGP RGGRGGCILRPSRGGRGRHGPT KAGPWSPESRGR*DWKARGPP APSRGSPSRARARRGGSGGGPA DEPGLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	A	30375	1	340	
30192	60560	A	30376	2	3336	
30193	60561	A	30377	22	419	
30194	60562	A	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECWSLF*SH MHVLLPRNRKEKLIEIFRTQTY DVNAYKASAHRNSGPG
30196	60564	C	30380	169	415	
30197	60565	A	30381	3	1324	
30198	60566	A	30382	2	3455	
30199	60567	A	30383	85	2695	
30200	60568	A	30384	69	303	
30201	60569	A	30385	1	951	
30202	60570	A	30386	1	4749	
30203	60571	A	30387	176	1553	

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30204	60572	A	30388	1	425	MDQIISLFGRPDHVAYDIRSLRN KANPDDTFEAQLFYGDLKAIVK TSHLVKIDYPKFIVHGKKGSFIK YGIDQQETSLKANIMPGEPGFA ADDSVGVLEYVNDEGVTVREE MKPEMGDYG/PRL*CVVSNHHP RCAKLRQGI
30205	60573	A	30389	3	1890	PSQPLLWFAGRPRGRDTGCPRC KQNSTCIAAVKMEGPLSVFGDR STGETIRSQNDKESFNEQKTCRI *RKRLV*LYEVAEHEIVMAAAS IANIVKSSLGPVGLDKML\VDDI GDVTITNDGATILKLLEVEHPA AKVLCELADLQDKEVGDGTTS VVIIAAELLKNADELVKQEIHPT SVISGY\RLA\CKEAVR\YINENP NLLTQDELGRDCLINAAKTSMS S\QIIGINGDFFANMVVDAVLAI KYTDIRGQPRYPVNSVNILKAH GRSQMESML\ISGYALNCVVGS QGMPKRIVNAKIACLDFSLQKT KMKLGVQVVITDPEKLDQIRQR ESDITKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVRR VLKRDLKRIAKASGATILST\LA\ NLEGEETFEAAMLGQA\EEVVQ ERICDDELILIKSTKA\RTSASIIS RVPIDSMCDEMERSL\HDALC\V VK\RVLESK\SVVPR\GGAVEAA LSIY\LENYA\TSMGSREQLAIAR VCKITLWLFPNTLSS*CLPRDST DLVLQNLRAF\HNEAQV\NPER\ KNLKWIGLDLSNGTPRDNKQA GVFEPTIVKVRGLNFATEAAIT\I LRIDDLIKLHPESKDDKH/G/GS YEDAVHSGALND
30206	60574	B	30390	1	975	
30207	60575	B	30391	1	2577	
30208	60576	B	30392	1	3126	
30209	60577	B	30393	1	1134	
30210	60578	B	30394	1	2082	
30211	60579	B	30395	1	915	
30212	60580	B	30396	1	2658	
30213	60581	B	30397	1	2412	
30214	60582	B	30398	1	2454	
30215	60583	B	30399	89	2533	
30216	60584	B	30400	1	4083	
30217	60585	B	30401	1	1725	
30218	60586	C	30402	127	345	
30219	60587	A	30403	1	597	

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30220	60588	A	30404	3	3386	MPATASAGVPATVSEKQEFYQ LLKNLINPSCMVRRQAEEIYENI PGLCKTTFLLDAVRNRRAGYE VRQMAAALLRRLLSSGFEEVYP NLPADVQRDVKIELILAVKLET HASMRKKLCDIFAVLA\RNLID EDGTNHWPEGLKFLIDSIYSTN VALWEVALHVFWHFPGIFGTQ ERHDLDIIKRLLDQCIQDQDHP AIKTLSARAAAAFVLANENNIA LFKDFADLLPGILQAVNDSCYQ DDDSVLESLVEIADT
30221	60589	A	30405	1	1695	
30222	60590	A	30406	1126	1355	
30223	60591	A	30407	1	1610	MGSRCLNPPPPAHSDTTGKDSF GNIRGAETGQGASACSVTSARV TCGAGSEPHSHRNPGISAQVGL APSYGAARGRRRPLALQQSPQE RRHVGWNSTRGLLPASLPGTAS SQSASATASAALPLKVTGPLAR NPTPPWTAAAALATRGQRPEK GLFPGPAPFSLGKRKRGRGRTW ERRRRVSIETSTCFRPGCERLGA AAGANLSQLASSQRPLRERWV LYTIIMAAAGAPDGMEEPGMD TEAETVATEAPARPVNCLEAEA AAGAAAEDSGAARGSLQPAPA QPPGDPAAQASVSNGEDAGGG AGRELVDLKIIWNKTKHDVKFP LDSTGSELKQKIHSITGLPPAMQ KVMYKGLVPEDKTLREIKVTS GAKIMVVGSTINDVLAVNTPK DAAQQDAKAEENKKEPLCRQK QHRKVLDKGKPEDVMPSVKGA QERLPTVPLSGMYNKSGGKVR LTFKLEQDQLWIGTKERTEKLP MGSIK\NVV\SDPI\EGHEDYHN DGRFQLAPTEA\SYYWVYWVP TQYVDAIK\DTVLGKWQYF
30224	60592	A	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP SAAGRRAMKKKLVVLCLLAVV LVLVIVGLCLW/LPSASKEPDN HVYTRATVAADAKQCSEIGRK\ AEVINAREVAPSVAFASMFNSS EQSQKAL
30225	60593	A	30409	562	2376	

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30226	60594	A	30410	604	2475	RQREVTRSPPERSGLRVLQLFPP NPPVFRGQHPRQGLGPPSAAGR RAMKKKLVVLGLLAVVLVLVI VGLCLWLPSASKEPDNHVYTR AAVAADAKQCSKIGRDALRDG GSAVDAAIAALLCVGLMNAHS MGIGGGLFLTIYNSTTRKAEVIN AREVAPRLAFATMFNSSEQSQK GGLSVAVPGEIEGYELAHQRHG RLPWARLFQPSIQLARQGFPVG KGLAAALENKRTVIEQQPVLCE VFCRDRKVLREGERLTLPQLAD TYETLAIEGAQAFYNGSLTAQI VKDIQAAGGIVTAEDLNNYRA ELIEHPLNISLGDAVLYMPSAPL SGPVLALILNILKGYNFSRESVE SPEQKGLTYHRIVEAFRFAYAK RTLLGDPKFVDVTEASSGVSA\ VVRNMTSEFFAAQLRAQISDDT THPISYYKPEFYTPDDGGTAHL SVVAEDGSAVSATSTINLYFGS KVRSPVSGILFNNEMDDFSSPSI TNEFGVPPSPANFIQPGKQPLSS MCPTIMVGQDGQVRMVVGAA GGTQITTATALAIIYNLWFGYD VKRAVEEPRLHNQLLPNVTTVE RNIDQAVTAALETRHHHTQIAS TFIAVVQAIVRTAGGWAAASDS RKGGEPAGY
30227	60595	A	30411	63	342	GRTLVPHGGLPHHYLVQCEWL PGTS*AEFPVVHLPAFVARARG ADRQHHGPFLPLCHLHPARPRR EDLHRKSPGEPNPIEHHRSSGPG CRRI
30228	60596	A	30412	1	910	MLFRPALGSRQVVRNMTSEFF AAQLRAQISDDTTHPISYYKPEF YTPVDGGTAHLSVVAEDGSAV STTSTINLYFGSKVRSPVSEILFN DEMDDFSSPNITNEFGVPPSPAN FIQPGMGWR\KQPLSSMCPTIM VGQDGQVRMVVGAAGGTQITT ATALICVTAFLPGRAHPAQPPS HADHTPMPQAIIYNLWFGYDV KRAVEEPRLHNQLLPNVTTVER NIDQAVTAALETRHHHTQIAST FIAVVQAIVHTAGGWAAASDS RKGGAYRILSALQEDKADKQS RDKILTRTRKGTLGDWLPM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30229	60597	A	30413	110	868	DLCPLPTLPPHLLRPALGSRQV VRNMTSEFFSAQLRAQISDDTT HPISYYKPEFYMPDDGGTAHLS VVAEDGSAVSATSTINLYFGSK VRSPVSGILLNNEMDDFSSTSIT NE\LGVPPSPANFIQPGKQPLSS MCPTIMVGQDGQVRMVVGAA GGTQITMATALAIIYQPSWFGY DVKRAVEEPRLHNQL\LPNVTT VERNIDQAVTAAL\ETRHHHTQ IASTFIAVVQAIVRTAGGWAAA SDSRKGGEPAGY
30230	60598	A	30414	1	1626	
30231	60599	A	30415	171	2097	PSGEREGCLIRESLKKILWLQAS AECEGDPGYFLSYFHQILLSFV ANTPRQGLGPPSAAGRRAMKK KLVVLGLLAVVLELVIVGLCL WLPSASKEPDNHVYTRAAVAA DAN\LCSKIGRDALRDGGSAVD AAIAALLCVGLMNAHSMGIGG GLFLTIYNSTTRK\AEVINAREV APRLAFATMFNSSEQSQKGGLS VAVPGEIRG\YELAHQRHGRLP WARLFQPSIQLARQGFPVGKGL AAALENKRTVIEQQPVLCEVFC RDRKVLREGERLTLPQLADTYE TLAIEGAQAFYNGSLTAQIVKDI QAAGGIVTAEDLNNYRAELIEH PLNISLGDAVLYMPSAPLSGPV LAL\ILNILKGYNFSRESVESPEQ KGLTYHRI\VEVFRFAYAKRTL LGDPKFVDVTEASSGVSA\VVR NMTSEFFAAQLRAQISDDTTHPI SYYKPEFYTPDDGGTAHLSVV AEDGSAVSATS\TINLYFGSKVR SPVSG\ILFNNEMGDLSSPSI\TN EFGAPPSPANFIQPGKQPLLSMC LTIMVGQDGQVRMVVGAAGG TQITTDTALAIIYN\LCFGYDVK RAVEEPRLHNKLLPNVTTVERN IDQAVTAALETRHHHTQIASTFI AVVQAIVRTAGGWAAASDSRK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30232	60600	A	30416	645	2571	GRPRLFPQLFPPNPPVFRGQHPR QGLGPPSAAGRRAMKKKLVVL GLLAVVLVLVIVGLCLWLPSAS KEPDNHVYT\RAAVAADAKQC SEIGRVLVGGPAYLLLLGKAEV INAREVAPRLAFASMFNSSEQS QKGGLSVAVPGEIRGYELAHQ RHGRLPWARLFQPSIQLARQGF PVGKGLAAVLENKRTVIEQQPV LWYVCGKVLREGERLTLPRLA DTYEMLAIEGAQAFYNGSLMA QIVKDIQAAGGIVTAEDLNNYR AELIEHPLNISLGDAVLYMPSA RLSGPVLALILNILKGYNFSRES VETPEQKGLTYHRIVEAFRFAY AKRTLLGDPKFVDVTENSIAGL LCARMDSPALGSRQVVRNMTS EFFAAQLRSQISDHTTHPISYYK PEFYTPDDGGTAHLSVVAEDGS AVSATSTINLYFGSKVCSPVSGI LFNNEMDDFSS\PAFTNEFGAPP SPANFIQPGKQPLLSMCLTIMV GQDGQVRMVVGAAGGTQITTD TALPPSHADHTPMPQAIIYNLW FGYDVKRAVEEPRLHNKLLPN VTTVERNIDQAVTAALETRHH HTQIASTFIAVVQAIVRTAGGW AAALDSRKVPTPGAGFWEGLV EVGWWEAVITAQHLDITRGTG
30233	60601	A	30417	5	439	
30234	60602	A	30418	1	423	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30235	60603	A	30419	97	2012	WADEETWLCLPHLPVFSPTAHL PLLSSTPFSSLLPFISTPHPRGFA LPLPPSARLYLELRKLPATLPWS SVTDTGSYLSGRRERGGEGEGP GRRVRVADHGFALPRTGPQGS EEELANMQGL\VERLERAVSRL ESL\SAESHRPPGN\CGEVNGVI A\GVAPSRGKPLHKLMDSMVA EF\LKNSRILSGDVETLAEIVHS AFQAQRAFLLMASQYQQPHEN DV\AALLKP\ISEKI\KEIQTFQRE /RTRGSNMFNHLSAVSE*IPCPL DGIAVSPKPG\PY\VKEMND\AA TFYT\NRVLKD*KQSDLRHVDW VKSYLNIWSELQAYIKEHHTTG LTWE/SKTGPV\ASTVS\AFSVLS SGAWGFPPPPPPLPPPG\PPSTFS EEWKGKKEESSPSR\SALFAQL N/QGEKAITKGLRHVT\DDQKT YKNPSLRAQGGQTQSPTKSHTP SPTSPKSYPSQKHAPVLELEGK KWRVEYQEDRIDLVISETELKQ VAYIFKCEKSTIQIKGKVNSIIID NCKKLGLVFDNVVGIVEVINSQ DIQIQVMG\RVPTISI\NKTEGCH IYLSEDALDCEI\VSAKSIWKWN ILYPPQGWVD\YREFPHFP\EQF KTS/AWDGS\KLITEP\AEIMALT SLRDRTPSPESPSIKTNKKAAVK
30236	60604	B	30420	1	499	
30237	60605	B	30421	390	851	
30238	60606	B	30422	136	603	
30239	60607	B	30423	1	2190	
30240	60608	A	30424	82	242	
30241	60609	A	30425	1	330	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30242	60610	A	30426	215	1984	LLLVVTMSNNGLDIQDKPPAPP MRNTSTMIGAGSKDAGTLNHG SKPLPPNPEEKKKKDRFYRSILP GDKTNKKKEKERPEISLPSDFE HTIHVGFDAVTGEFTGMPEQW ARLLQTSNITKSEQKKNPQAVL DVLEFYNSKKTSNSQKYMSFTS GDKSAHGYIAAHPSSTKTASEP PLAPPVSEEEDEEEEEEEDENEP PPVIAPRPEHTKSIYTRSVVESIA SPAVPNKEVTPPSAENANSSTL YRNTDRQRKKSKMTDEEILEKL RSIVSVGDPKKKYTRFEKIGQG P\SGTVYTAMDVATGQEVAIKQ MNLQQQPKKELIINEILVMREN KNPNIVNYLDSYLVGDELWVV MEYLAGGSLTDVVTETCMDEG QIAAVCRECLQALEFLHSNQVI HRDIKSD\NILLGMDGSVKLTDF GFCAQITPEQSKLSTHG*GTPY W\M\APEVVDTERAYGPK/VLDI W\SLGIMAIEMIEGEPPYLNENP LRALYLIATNGTPELQNPEKL\S AIFR\DFL\NRCLEMDVEKRGFS/ SKELLQHQFLKIGQAPSPSLTPH *LLQPKEATKEQSPKTHTHPQP HCAQAFCEINAHFRNSNS
30243	60611	A	30427	2	337	
30244	60612	A	30428	1	1644	
30245	60613	A	30429	1	330	
30246	60614	A	30430	169	440	
30247	60615	A	30431	1	1689	
30248	60616	A	30432	17	283	GHAWQLASIWLLCLLWPAVPL NCLSSYGWTLWWRIALVGA*R SLAPSRGSWSTQARPLKQRRTK WCGKSWCLSGTSEPLSHWPRL RSW
30249	60617	A	30433	16	346	RTDTYHLEDSKEQSGNRAGSG GWL*SCAE/GRRVALKSWPGRT GMSGTRRVTASSRGTSWYCGG SAGRSSTPPTGRACSPGSFSSPE PQPPGPSAAGSSVSGQLGPCGG
30250	60618	A	30434	1	1772	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30251	60619	A	30436	1	2607	MLTMSVTLSPLRSQDLDPMAT DASPMAINMTPTVEQGEGEEA MKDMDSDQQYEKPPPLHTGAD WKIVLHLPEIETWLRMTSERVR DLTYSVQQDSDSKHVDVHLVQ LKDICEDISDHVEQIHALLETEF SLKLLSYSVNVIVDIHAVQLLW HQLRVSVLVLRERILQGLQDAN GNYTRQTDILQAFSEETKEGRL DSLTEVDDSGQLTIKCSQNYLS LDCGITAFELSDYSPSEDLLSGL GDMTSSQVKTKPFDSWSYSEM EKEFPELIRSVGLLTVAADSIST NGSEAVTEEVSQVSLSVDDKG GCEEDNASAVEEQPGLTLGVSS SSGEALTNAAQPSSETVQQESS SSSHHDAKNQQPVPCENATPKR TIRDCFNYNEDSPTQPTLPKRGL FLKEETFKNDLKGNGGKRQMV DLKPEMSRSTPSLVDPPDRSKL CLVLQSSYPNSPSAASQSYECL HKVGNGNLENTVKFHIKEISSS LGRLNDCYKEKSRLKKPHKTSE EVPPCRTPKRGTGSGKQAKNT KSSAVPNGELSYTSKAIEGPQT NSASTSSLEPCNQRSWNAKLQL QSETSSSPAFTQSSESSVGSDNI MSPVPLLSKHKSKKGQASSPSH VTRNGEVVEAWYGSDEYLALP SHLKQTEVLALKLENLTKLLPQ KPRGETIQNIDDWELSEMNSDS EIYPTYHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	
30253	60621	B	30438	1	702	
30254	60622	B	30439	1	936	
30255	60623	B	30440	1	1494	
30256	60624	B	30441	1	921	
30257	60625	B	30442	1	3342	
30258	60626	B	30443	1	1072	
30259	60627	B	30444	1	3711	
30260	60628	B	30445	15	674	
30261	60629	B	30446	1	2127	
30262	60630	B	30447	1	3132	
30263	60631	B	30448	103	438	
30264	60632	B	30449	1	3042	
30265	60633	B	30450	1	1425	
30266	60634	B	30451	84	1954	
30267	60635	B	30452	1	1419	
30268	60636	B	30453	130	1615	
30269	60637	B	30454	1	1794	
30270	60638	B	30455	1	3255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30271	60639	B	30456	1	945	
30272	60640	B	30457	1	7437	
30273	60641	B	30458	1	1122	
30274	60642	B	30459	317	1630	
30275	60643	B	30460	1	1716	
30276	60644	B	30461	46	915	
30277	60645	B	30462	1	624	
30278	60646	B	30463	244	2988	
30279	60647	B	30464	1	804	
30280	60648	B	30465	1	1455	
30281	60649	B	30466	1	732	
30282	60650	B	30467	340	777	
30283	60651	B	30468	1	714	
30284	60652	B	30469	166	1337	
30285	60653	B	30470	72	617	
30286	60654	B	30471	1	1002	
30287	60655	B	30472	1	4173	
30288	60656	B	30473	1	4488	
30289	60657	B	30474	1	3822	
30290	60658	B	30475	1	1866	
30291	60659	B	30476	1	1002	
30292	60660	B	30477	1	1407	
30293	60661	B	30478	99	1046	
30294	60662	B	30479	122	1113	
30295	60663	B	30480	302	4145	
30296	60664	B	30481	1	669	
30297	60665	B	30482	1	933	
30298	60666	B	30483	1	2136	
30299	60667	B	30484	1	4017	
30300	60668	B	30485	1	1335	
30301	60669	B	30486	1	1095	
30302	60670	B	30487	1	2895	
30303	60671	B	30488	1	1215	
30304	60672	B	30489	1	2001	
30305	60673	B	30490	1	1281	
30306	60674	B	30491	1	780	
30307	60675	B	30492	1	858	
30308	60676	B	30493	1	699	
30309	60677	B	30494	1	1624	
30310	60678	B	30495	1	2958	
30311	60679	B	30496	30	658	
30312	60680	B	30497	1	1755	
30313	60681	B	30498	1	631	
30314	60682	B	30499	1	1528	
30315	60683	B	30500	1	1056	
30316	60684	B	30501	1	2305	
30317	60685	B	30502	1	723	
30318	60686	B	30503	1	2691	
30319	60687	B	30504	1	2322	
30320	60688	B	30505	401	2677	
30321	60689	B	30506	1	1218	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30322	60690	B	30507	1	906	
30323	60691	B	30508	1	2865	
30324	60692	B	30509	45	820	
30325	60693	B	30510	1	783	
30326	60694	C	30511	18	410	
30327	60695	B	30512	1	840	
30328	60696	B	30513	1	945	
30329	60697	B	30514	1	2108	
30330	60698	B	30515	1	2457	
30331	60699	B	30516	1	1156	
30332	60700	B	30517	43	4677	
30333	60701	B	30518	80	964	
30334	60702	B	30519	1	4521	
30335	60703	B	30520	1	2460	
30336	60704	B	30521	1	1854	
30337	60705	B	30522	1	1367	
30338	60706	B	30523	273	419	
30339	60707	B	30524	1	1786	
30340	60708	B	30525	1169	1443	
30341	60709	B	30526	1	486	
30342	60710	B	30527	13	1260	
30343	60711	B	30528	270	723	
30344	60712	B	30529	1	834	
30345	60713	B	30530	1	1632	
30346	60714	B	30531	1	4831	
30347	60715	B	30532	184	1593	
30348	60716	B	30533	1	615	
30349	60717	B	30534	1	3513	
30350	60718	B	30535	113	1666	
30351	60719	B	30536	101	2667	
30352	60720	B	30537	1	1692	
30353	60721	B	30538	51	142	
30354	60722	B	30539	1	3198	
30355	60723	B	30540	251	1207	
30356	60724	B	30541	1	1491	
30357	60725	B	30542	1	4024	
30358	60726	B	30543	1	3316	
30359	60727	B	30544	1	1342	
30360	60728	B	30545	91	810	
30361	60729	B	30546	17	489	
30362	60730	A	30547	1	504	MGGSNRSAEAWKLANGINIIVA TSGRLLDHMQNTPGFMYKNLQ CLVIDEADRILDVGFEEELKQII KLLLTHRQTMLFSATQTQKVE DLARISLKKEP/LYVGDDDDNA NETVFG\TLLCTDVAARGLDITE VDCIVQYDPPDDPKEYIHSVGR TARGLNGRENWVFFAT
30363	60731	A	30548	1	2676	
30364	60732	B	30549	1	1071	
30365	60733	A	30550	1	348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30366	60734	A	30551	1	711	MAEIQHKTIRPLLEGRDLLAAV KTGSGKTLAVLIPAIELVVKLKF MPRNGTGVLILSPTRQLAMQTF GVLKELMTHHVHTYGLIIGGSN RSAEAQKLANGINIIVVTPGRLL DHTQNTPGFMYKNLQVEDLAR ISPKKEPLYVGVDEDKANATVD GLEQGHFVCPSEKRYLLLFTFL KKNQKKKLMVFFSACMSVKYP YGLLKYIDL/PVLAIHGKQKQN KHTTTFF*YCNADSGTLL
30367	60735	A	30552	661	987	VTFYSSEHSNPCHKNLRKARRK DTKRIILKW*HTLV*GRDI*N*NI IITRNTRYSLLCPWATKKLKAC FISQK*KRDVIERNSAQCLQPKS IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	KFQGASNLTLSETQNGDVSEET MGSRKVKKSKQKPMNVGLSET QNGGMSQEAVGNIKVTKSPQK STVLTNGEAAMQSSNSESKGK MKKKRKMVNDAEPDTKKAKT ENKGKSEEESAETTKETENNVE KPDNDEDESEVPSLPLGLTGAF EDTSFASLCNLVNENTLKAIKE MGFTNMTEIQHKSIRPLLEGRD LLAAAKTGSGKTLAFLIPAVELI \VKLRFMPRNGTGVLILSP\TRE LAMQTFGVLKELMTHHVHTYG LIMGGSNRSAEAQKLGNGINIIV ATPGRLLDHMQNTPGFMYKNL QCLVIDEADRILDVGFEEELKQI IKLLPTRRQTMLFSATQTRKVE DLARISLKKEPLYVGVDDDKA NATVDGLEQGYV\VCPSEKRFL LLFTFLKKNRKKKLMVFFSSCM SVKYHYELLNYIDLPVLAIHGK QKQNKRTT\TFFQFCNADSG\TL LCT\DV\AARGLDIPEVDWIVQY DPPDDPKEYI\HRVG*EQPEGLN GEEGHALASFLRPRKDLGFFFR LL*KHSKGFPLSGIWTFSW/SLK ISDIQFSAWRNWIGKVITFLHKS A\QEAYKSYITEPMDSPFL*NRS FN\VNNLNLASGLLCQFGFK\VP PFVDLNVNSNEGKQKKRGGGG GFGLPRKTQEKLEKS\KIF*TH* ARKSSGQAGQFSH

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

21 The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/08631

A. CLASSIFICATION OF SUBJECT MATTER
IPC(7) : C12N 15/00, 15/12
US CL : 536/23.1, 23.5; 435/6, 320.1, 325
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.1, 23.5; 435/6, 320.1, 325

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
NONE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- A	Database Genbank, Accession No. AL135937, 15 March 2001 (15.03.2001), particularly nucleotides 29925 through 30325.	1-8 --- 9, 19
X --- A	Database Genbank, Accession No. AA004350, HILLIER et al., Generation and analyhsis of 280,000 Human Expressed Sequence Tags. Genome Res. 07 May 1997 (07.05.1997), Vol. 6, No. 9, pages 807-828,	1-8 --- 9, 19

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
23 October 2001 (23.10.2001)

Date of mailing of the international search report
02 JAN 2002

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Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/08631

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I-III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct invention.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be searched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.